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# **BIGSdb Documentation**

***Release 1.34.0***

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*Gene-by-gene population annotation and analysis*

BIGSdb is software designed to store and analyse sequence data for bacterial isolates. Any number of sequences can be linked to isolate records - these can be small contigs assembled from dideoxy sequencing through to whole genomes (complete or multiple contigs generated from parallel sequencing technologies such as Illumina or Oxford Nanopore).

BIGSdb extends the principle of MLST to genomic data, where large numbers of loci can be defined, with alleles assigned by reference to sequence definition databases (which can also be set up with BIGSdb). Loci can also be grouped into schemes so that types can be defined by combinations of allelic profiles, a concept analagous to MLST.

The software has been released under the GNU General Public Licence version 3. The latest version of this documentation can be found at <https://bigsdb.readthedocs.org/>.



## CONCEPTS AND TERMS

### 1.1 BIGSdb

BIGSdb is the software platform - not a specific database. There are many instances of BIGSdb databases, so referring to 'the BIGSdb' is meaningless.

### 1.2 Loci

Loci are regions of the genome that are identified by similarity to a known sequence. They can be defined by DNA or peptide sequence. They are often complete coding sequences (genes), but may represent gene fragments (such as used in MLST), antigenic peptide loops, or indeed any sequence feature.

In versions of BIGSdb prior to 1.8.0, an isolate record could only have one live *allele* designation for a locus (inactive/pending designations could be stored within the database but were unavailable for querying or analysis purposes). Since biology is rarely so clean, and some genomes may contain more than one copy of a gene, later versions of the software allow multiple allele designations for a locus, all of which can be queried and analysed.

Paralogous loci can be difficult to differentiate by sequence similarity alone. Because of this, loci can be further defined by context, where in silico PCR or hybridization reactions can be performed to *filter the genome* to specific regions based on sequence external to the locus.

### 1.3 Alleles

Alleles are instances of loci. Every unique sequence, either DNA or peptide depending on the locus, is defined as a new allele and these are defined in a sequence definition database, where they are given an allele identifier. These identifiers are usually integers, but can be text strings. Allele identifiers in text format can be constrained by length and formatting.

When a specific allele of a locus is identified within the sequence data of an isolate record, the allele designation, i.e. identifier, is associated with the isolate record. This efficiently stores the sequence variation found within an isolate. Two isolates with the same allele designation for a locus have identical sequences at that locus. Once the sequence variation within a genome has been reduced to a series of allele designations, genomes can be efficiently compared by identifying which loci vary between them.

It is important to note that allele identifiers are usually arbitrary and are allocated sequentially in the order of discovery. Alleles with adjacent identifiers may vary by a single nucleotide or by many.

## 1.4 Schemes

Schemes are collections of loci that may be associated with additional field values. At their simplest they just group loci together. Example uses of simple schemes include:

- Antibiotic resistance genes
- Genes involved in specific biochemical pathways
- Antigens
- Vaccine components
- Whole genome MLST (wgMLST)

When schemes are associated with additional fields, one of these fields must be the primary key, i.e. its value uniquely defines a particular combination of alleles at its member loci. The pre-eminent example of this is MLST - where a sequence type (ST) is the primary key that uniquely defines combinations of alleles that make up the MLST profiles. Additional fields can also then be included. The values for these need not be unique. In the MLST example, a field for clonal complex can be included, and the same value for this can be set for multiple STs.

## 1.5 Profiles

Profiles are instances of *schemes*. A profile consists of a set of *allele identifiers* for the *loci* that comprise the scheme. If the scheme has a primary key field, e.g. sequence type (ST) in MLST schemes, then the unique combination of alleles in a complete profile can be defined by the value of this field.

## 1.6 Classification groups

Classification groups are a way to cluster scheme profiles using a specified threshold of pairwise allelic mismatches. Currently, single-linkage clustering is supported whereby each member of a group must have no more than the specified number of allelic differences with at least one other member of the group.

## 1.7 Sequence tags

Sequence tags record locus position within an isolate record's sequence bin. The process of creating these tags, is known as *tag-scanning*. A sequence tag consists of:

- sequence bin id - this identifies a particular contig
- locus name
- start position
- end position
- flag to indicate if sequence is reversed
- flag to indicate if sequence is complete and does not continue off the end of the contig

## 1.8 Sets

Sets provide a means to take a large database with multiple loci and/or schemes and present a subset of these as though it was a complete database. The loci and schemes chosen to belong to a set can be renamed when used with this set. The rationale for this is that in a database with disparate isolates and a large number of loci, the naming of these loci may have to be long to specify a species name. For example, you may have a database that contains multiple MLST schemes for different species, but since these schemes may use different fragments of the same genes they may have to be named something like ‘*Streptococcus pneumoniae*\_MLST\_aroE’ to uniquely specify them. If we define a set for ‘*Streptococcus pneumoniae*’ we can then choose to only include *S. pneumoniae* loci and therefore shorten their names, e.g. to ‘aroE’.



## BIGSDB DEPENDENCIES

### 2.1 Required packages

BIGSdb requires a number of software components to be installed:

#### 2.1.1 Linux packages

- Apache2 web server with mod\_perl2
- PostgreSQL database 9.5+
- Perl 5.10+
- BioPerl
- BLAST+
- EMBOSS
  - infoalign - use to extract alignment stats in Genome Comparator.
  - sixpack - used to translate sequences in multiple reading frames.
  - stretcher - used for sequence alignment in allele query.
- Ipcress - part of exonerate package - used to simulate PCR reactions which can be used to filter the genome to predicted amplification products.
- Xvfb - X virtual framebuffer - needed to support SplitsTree in command line mode as used in Genome Comparator.

#### 2.1.2 Perl modules

These are included with most Linux distributions.

- `Archive::Zip` - Used to upload to iTOL.
- `Bio::Biblio` - This used to be part of BioPerl but will need to be installed separately if using BioPerl 1.6.920 or later.
- `CGI` (version 4.04+) - Common Gateway Interface requests and responses (used to be a core module but recently removed).
- `Config::Tiny` - Configuration file handling.
- `Crypt::Eksblowfish::Bcrypt` - Used for password hashing.

- `Data::Random`
- `Data::UUID` - Globally unique identifier handling for preference storage.
- `DBD::Pg` - PostgreSQL database driver for DBI.
- `DBI` - Database independent interface - module used to interact with databases.
- `Email::MIME` - Used to format E-mail messages.
- `Email::Sender` - Used to send E-mail messages by submission system.
- `Email::Valid` - Used to validate E-mails sent by job manager.
- `Excel::Writer::XLSX` - Used to export data in Excel format.
- `Exception::Class` - Exception handling.
- `File::Map`
- `File::Type` - Used to determine what type of file has been uploaded.
- `IO::String`
- `JSON` - Used to manipulate JSON data.
- `List::MoreUtils` (version 0.28+).
- `Log::Dispatch::File` - Object for logging to file.
- `Log::Log4perl` - Configurable status and error logging.
- `LWP::UserAgent` - Used to upload via API
- `Net::Oauth` - Required for REST authentication (this needs to be installed even if you are not using REST).
- `Parallel::ForkManager` - Required for multi-threading tools and plugins.
- `PDL` - Required for LINcode calculations.
- `Time::Duration` - Used by Job Viewer to display elapsed time in rounded units.
- `TOML` - Used to define dashboard layouts.
- `Try::Tiny`
- `XML::Parser::PerlSAX` - part of libxml-perl - Used to parse XML configuration files.

### 2.1.3 Optional packages

Installing these packages will enable extra functionality, but they are not required by the core BIGSdb package.

- `ImageMagick` - mogrify used by some plugins.
- `MAFFT 6.8+` - sequence alignment used by some plugins.
- `Muscle` - sequence alignment used by some plugins.
- `Splitstree4` - used by `GenomeComparator` plugin.

## INSTALLATION AND CONFIGURATION OF BIGSDB

### 3.1 Software installation

BIGSdb consists of two main Perl scripts, `bigsdb.pl` and `bigscurate.pl`, that run the query and curator's interfaces respectively. These need to be located somewhere within the web cgi-bin directories. In addition, there are a large number of library files, used by both these scripts, that are installed by default in `/usr/local/lib/BIGSdb`. Plugin scripts are stored within a 'Plugins' sub-directory of this library directory.

All databases on a system can use the same instance of the scripts, or alternatively any database can specify a particular path for each script, enabling these script directories to be protected by apache htaccess directives.

- *Software requirements*
- Download from [SourceForge.net](#) or [GitHub](#).

1. Unpack the distribution package in a temporary directory:

```
gunzip bigsdb_1.x.x.tar.gz
tar xvf bigsdb_1.x.x.tar
```

2. Copy the `bigsdb.pl` and `bigscurate.pl` scripts to a subdirectory of your web server's cgi-bin directory. Make sure these are readable and executable by the web server daemon.
3. Copy the contents of the lib directory to `/usr/local/lib/BIGSdb/`. Make sure you include the Plugins and Offline directories which are subdirectories of the main lib directory.
4. Copy the javascript directory to the root directory of your website, i.e. accessible from [http://your\\_website/javascript/](http://your_website/javascript/).
5. Copy the css directory to root directory of your website, i.e. accessible from [http://your\\_website/css/](http://your_website/css/).
6. Copy the webfonts directory to the root directory of your website, i.e. accessible from [http://your\\_website/webfonts/](http://your_website/webfonts/).
7. Copy the images directory to the root directory of your website, i.e. accessible from [http://your\\_website/images/](http://your_website/images/).
8. Copy the contents of the conf directory to `/etc/bigsdb/`. Check the paths of helper applications and database names in the `bigsdb.conf` file and modify for your system.
9. Create a PostgreSQL database user called apache - this should not have any special privileges. First you will need to log in as the postgres user:

```
sudo su postgres
```

Then use the `createuser` command to do this, e.g.

```
createuser apache
```

From the psql command line, set the apache user password:

```
psql
ALTER ROLE apache WITH PASSWORD 'remote';
```

10. Create PostgreSQL databases called bigsdb\_auth, bigsdb\_prefs and bigsdb\_refs using the scripts in the sql directory. Create the database using the createdb command and set up the tables using the psql command.

```
createdb bigsdb_auth
psql -f auth.sql bigsdb_auth
createdb bigsdb_prefs
psql -f prefs.sql bigsdb_prefs
createdb bigsdb_refs
psql -f refs.sql bigsdb_refs
```

11. Create a writable temporary directory in the root of the web site called tmp, i.e. accessible from [http://your\\_website/tmp](http://your_website/tmp).
12. Create a log file, bigsdb.log, in /var/log owned by the web server daemon, e.g.

```
touch /var/log/bigsdb.log
chown www-data /var/log/bigsdb.log
```

(substitute www-data for the web daemon user).

## 3.2 Configuring PostgreSQL

PostgreSQL can be configured in many ways and how you do this will depend on your site requirements.

The following security settings will allow the appropriate users ‘apache’ and ‘bigsdb’ to access databases without allowing all logged in users full access. Only the UNIX users ‘postgres’ and ‘webmaster’ can log in to the databases as the Postgres user ‘postgres’.

You will need to edit the pg\_hba.conf and pg\_ident.conf files. These are found somewhere like /etc/postgresql/9.1/main/

### 3.2.1 pg\_hba.conf

```
# Database administrative login by UNIX sockets
local  all          postgres          ident map=mymap

# TYPE  DATABASE  USER          CIDR-ADDRESS  METHOD

# "local" is for Unix domain socket connections only
local  all          all            ident map=mymap
# IPv4 local connections:
host   all          all            127.0.0.1/32  md5
# IPv6 local connections:
host   all          all            ::1/128       md5
```

### 3.2.2 pg\_ident.conf

#	MAPNAME	SYSTEM-USERNAME	PG-USERNAME
	mymap	postgres	postgres
	mymap	webmaster	postgres
	mymap	www-data	apache
	mymap	bigsdb	bigsdb
	mymap	bigsdb	apache

You may also need to change some settings in the postgresql.conf file. As an example, a configuration for a machine with 16GB RAM, allowing connections from a separate web server may have the following configuration changes made:

```
listen_addresses = '*'
max_connections = 200
shared_buffers = 1024Mb
work_mem = 8Mb
effective_cache_size = 8192Mb
stats_temp_directory = '/dev/shm'
```

Setting stats\_temp\_directory to /dev/shm makes use of a ramdisk usually available on Debian or Ubuntu systems for frequently updated working files. This reduces a lot of unnecessary disk access.

See [Tuning Your PostgreSQL Server](#) for more details.

Restart PostgreSQL after any changes, e.g.

```
/etc/init.d/postgresql restart
```

## 3.3 Setting global connection parameters

Global database connection parameters can be entered in /etc/bigsdb/db.conf. This allows you to set default values for the host, port, user and password. Default values are as follows:

- dbhost: localhost
- dbport: 5432
- dbuser: apache
- dbpassword: remote

These can all be over-ridden in individual *database configuration config.xml files* using the terms host, port, user, and password.

## 3.4 Site-specific configuration

Site-specific configuration files are located in /etc/bigsdb by default.

- `bigsdb.conf` - main configuration file
- `logging.conf` - error logging settings. See log4perl project website for advanced configuration details.

Breadcrumb navigation links can be configured with a file called `breadcrumbs.conf`, placed either in the database configuration directory, the root directory of the website, or in `/etc/bigsdb/conf`. The file describes links that are higher in the hierarchy than the database index page. The file consists of lines that contain link text separated by a pipe symbol (`|`) followed by a URL for that link, e.g.

```
Home | /  
Organisms | /databases/
```

Global announcements can be made in a banner that appears on each database contents page. This is useful for service announcements such as for planned maintenance. Place a HTML file called `announcement.html` in `/etc/bigsdb` including the text that you wish to appear.

## 3.5 Setting up the offline job manager

To run plugins that require a long time to complete their analyses, an offline job manager has been developed. The plugin will save the parameters of a job to a job database and then provide a link to the job status page. An offline script, run frequently from CRON, will then process the job queue and update status and outputs via the job status page.

1. Create a 'bigsdb' UNIX user, e.g.:

```
sudo useradd -s /bin/sh bigsdb
```

2. As the postgres user, create a 'bigsdb' user and create a `bigsdb_jobs` database using the `jobs.sql` SQL file, e.g.:

```
createuser bigsdb [no need for special privileges]  
createdb bigsdb_jobs  
psql -f jobs.sql bigsdb_jobs
```

From the psql command line, set the bigsdb user password::

```
psql  
ALTER ROLE bigsdb WITH PASSWORD 'bigsdb';
```

3. Set up the jobs parameters in the `/etc/bigsdb/bigsdb.conf` file, e.g.:

```
jobs_db=bigsdb_jobs  
max_load=8
```

The jobs script will not process a job if the server's load average (over the last minute) is higher than the `max_load` parameter. This should be set higher than the number of processor cores or you may find that jobs never run on a busy server. Setting it to double the number of cores is probably a good starting point.

4. Copy the `job_logging.conf` file to the `/etc/bigsdb` directory.
5. Set the script to run frequently (preferably every minute) from CRON.

Copy `bigsjobs.pl` to `/usr/local/bin`

You should install `xvfb`, which is a virtual X server that may be required for third party applications called from plugins. This is required, for example, for calling `splitstree4` from the Genome Comparator plugin.

Add the following to `/etc/crontab`:

```
* * * * * bigsdb xvfb-run -a /usr/local/bin/bigsjobs.pl
```

(set to run every minute from the ‘bigsdb’ user account).

If you’d like to run this more frequently, e.g. every 30 seconds, multiple entries can be added to CRON with an appropriate sleep prior to running, e.g.:

```
* * * * * bigsdb xvfb-run -a /usr/local/bin/bigsjobs.pl
* * * * * bigsdb sleep 30;xvfb-run -a /usr/local/bin/bigsjobs.pl
```

6. Create a log file, `bigsdb_jobs.log`, in `/var/log` owned by ‘bigsdb’, e.g.:

```
sudo touch /var/log/bigsdb_jobs.log
sudo chown bigsdb /var/log/bigsdb_jobs.log
```

## 3.6 Setting up the submission system

The submission system allows users to submit new data to the database for curation. Submissions are placed in a queue for a curator to upload. All communication between submitters and curators can occur via the submission system.

1. Create a writable submissions directory in the root of the web site called `submissions`, i.e. accessible from [http://your\\_website/submissions](http://your_website/submissions). This is used for file uploads. The directory should be writable by the Apache web daemon (user ‘www-data’ on Debian/Ubuntu systems). If you are running the *RESTful interface* the directory should also be writable by the bigsdb user. To ensure this, make the directory group-writable and add the bigsdb user to the apache group (‘www-data’ on Debian/Ubuntu systems). If you will be allowing submissions via the RESTful interface, you should also add the apache user (‘www-data’ on Debian/Ubuntu systems) to the bigsdb group, e.g.

```
sudo usermod -a -G www-data bigsdb
sudo usermod -a -G bigsdb www-data
```

The actual directory can be outside of the web root and made accessible using a symlink provided your Apache configuration allows this, e.g. the default location is `/var/submissions` symlinked to `/var/www/submissions` (assuming your web site is located in `/var/www`), e.g.

```
sudo touch /var/submissions
sudo chown www-data:www-data /var/submissions
sudo chmod 775 /var/submissions
sudo ln -s /var/submissions /var/www
```

2. Set the `submission_dir` location in `bigsdb.conf`.
3. Set the `smtp_server` in `bigsdb.conf` to the IP or DNS name of your organisation’s SMTP relay. Depending on how your E-mail system is configured, you may be able to use the localhost address (127.0.0.1).
4. Make sure the `curate_script` and `query_script` values are set in `bigsdb.conf`. These point to the web-accessible location of the web scripts and are required to allow curators to be directed between the web interfaces as needed.
5. Set `submissions="yes"` in the system tag of the *database config.xml file* of each database for which submissions should be enabled.

### 3.7 Setting up a site-wide user database

A site-wide user database allows users to register themselves for accounts and associate these with specific databases. It means that a single set of log-in credentials can be used across databases, rather than each database maintaining its own.

Users can access/update their account details by calling the `bigsdbs.pl` script without any additional attributes, e.g. <http://website/cgi-bin/bigsdbs.pl>.

Site admins can access administration features by calling the `bigscurate.pl` script without any additional attributes.

1. Create a user database, e.g. `pubmlst_bigsdb_users`:

```
createdb pubmlst_bigsdb_users
psql -f users.sql pubmlst_bigsdb_users
```

Set up `sync_user_dbase_users.pl` to run every hour as a CRON JOB, e.g. in `/etc/crontab`, add the following to run this at 5 minutes past each hour

```
05 * * * * bigsdb /usr/local/bin/sync_user_dbase_users.pl --user_database_
pubmlst_bigsdb_users
```

Add the user database details to each database that you want to allow to use it.

You need to *add the users database details* to each client database that will use it.

2. If you want to allow users to register themselves you need to modify `bigsdbs.conf`.

You can define multiple user databases (as a comma-separated list) but usually you would have just one. Define this using the `site_user_dbs` attribute. Use a short domain (site) name separated by a pipe (|) and the name of the database, e.g. add the following to `/etc/bigsdbs.conf`:

```
site_user_dbs=PubMLST|pubmlst_bigsdb_users
```

Make sure default database connection parameters are set in `/etc/bigsdbs/db.conf`.

3. Set up site admin user in new user database. This has to be done manually - other users will either be able to register themselves or be created by curators from other databases.:

```
psql pubmlst_bigsdb_users
INSERT INTO USERS (user_name,surname,first_name,email,affiliation,
date_entered,datestamp,status) VALUES ('kjolley','Jolley','Keith',
'keith.jolley@zoo.ox.ac.uk','University of Oxford, UK','now','now',
'validated');
```

Set the password for this user using the `add_user.pl` script (change XXXXXXXXX to the password value):

```
add_user.pl -a -d pubmlst_bigsdb_users -n kjolley -p XXXXXXXX
```

Add specific permissions that this admin user can have by directly adding the following terms to the permissions table:

- `set_site_user_passwords`:
  - Allow admin to set user passwords.
- `import_dbase_configs`:
  - Allow admin to define which database configurations are made available for registration.

- merge\_users
  - Allow admin to merge user accounts.
- modify\_users
  - Allow admin to edit user details.

e.g.

```
psql pubmlst_bigsdb_users
INSERT INTO permissions (user_name,permission,curator,datestamp) VALUES
('kjolley','import_dbase_configs','kjolley','now');
```

- Specific *permissions can be set for curators* in individual databases:
  - import\_site\_users
    - This allows the curator to import site users in to the database.
  - modify\_site\_users
    - You may not wish to do this! - It allows the curator of any database with this permission to change the details of a user that may be used on other databases on the site.
- HTML header files can be defined for use when bigsdb.pl or bigscurate.pl are called without a database configuration, such as when a user is registering or modifying their user details. These files, site\_header.html, site\_footer.html, site\_curate\_header.html and site\_curate\_footer.html should be placed in the root directory of the web site.

## 3.8 Periodically delete temporary files

There are two temporary directories (one public, one private) which may accumulate temporary files over time. Some of these are deleted automatically when no longer required but some cannot be cleaned automatically since they are used to display results after clicking a link or to pass the database query between pages of results.

The easiest way to clean the temp directories is to run a cleaning script periodically, e.g. create a root-executable script in /etc/cron.hourly containing the following::

```
#!/bin/sh
#Remove temp BIGSdb files from secure tmp folder older than 1 week.
find /var/tmp/ -name '*BIGSdb_*' -type f -mmin +10080 -exec rm -f {} \; 2>/dev/null

#Remove .jnlp files from web tree older than 1 day
find /var/www/tmp/ -name '*.jnlp' -type f -mmin +1440 -exec rm -f {} \; 2>/dev/null

#Remove other tmp files from web tree older than 1 week
find /var/www/tmp/ -type f -mmin +10080 -exec rm -f {} \; 2>/dev/null
```

## 3.9 Prevent preference database getting too large

The preferences database stores user preferences for BIGSdb databases running on the site. Every user will have a globally unique identifier (guid) stored in this database along with a timestamp indicating the last access time. On public databases that do not require logging in, this guid is stored as a cookie on the user's computer. Databases that require logging in use a combination of database and username as the identifier. Over time, the preferences database can get quite large since every unique user will result in an entry in the database. Since many of these entries represent casual users, or even web indexing bots, they can be periodically cleaned out based on their last access time. A weekly CRON job can be set up to remove any entries older than a defined period. For example, the following line entered in `/etc/crontab` will remove the preferences for any user that has not accessed any database in the past 6 months (the script will run at 6pm every Sunday).

```
#Prevent prefs database getting too large
00 18 * * 0 postgres psql -c "DELETE FROM guid WHERE last_accessed < NOW() -
↳INTERVAL '6 months'" bigsdb_prefs
```

## 3.10 Log file rotation

Set the log file to auto rotate by adding a file called 'bigsdb' with the following contents to `/etc/logrotate.d`:

```
/var/log/bigsdb.log {
    weekly
    rotate 4
    compress
    copytruncate
    missingok
    notifempty
    create 640 root adm
}

/var/log/bigsdb_jobs.log {
    weekly
    rotate 4
    compress
    copytruncate
    missingok
    notifempty
    create 640 root adm
}
```

## 3.11 Upgrading BIGSdb

Major version changes, e.g. 1.7 -> 1.8, indicate that there has been a change to the underlying database structure for one or more of the database types. Scripts to upgrade the database are provided in `sql/upgrade` and are named by the database type and version number. For example, to upgrade an isolate database (`bigsdb_isolates`) from version 1.7 to 1.8, log in as the `postgres` user and type:

```
psql -f isolatedb_v1.8.sql bigsdb_isolates
```

Upgrades are sequential, so to upgrade from a version earlier than the last major version you would need to upgrade to the intermediate version first, e.g. to go from 1.6 -> 1.8, requires upgrading to 1.7 first.

Minor version changes, e.g. 1.8.0 -> 1.8.1, have no modifications to the database structures. There will be changes to the Perl library modules and possibly to the contents of the Javascript directory, images directory and CSS files.

## 3.12 Running the BIGSdb RESTful interface

BIGSdb has an Application Programming Interface (API) that allows third-party applications to access the data within the databases. The script that runs this is called `bigrest.pl`. This is a `Dancer2` application that can be run using a wide range of options, e.g. as a stand-alone script, using Perl webserver with `plackup`, or from `apache`. Full documentation for [deploying Dancer2 applications](#) can be found online.

The script requires a new database that describes the resources to make available. This is specified in the `bigbdb.conf` file as the value of the `'rest_db'` attribute. By default, the database is named `bigbdb_rest`.

A SQL file to create this database can be found in the `sql` directory of the download archive. It is called `rest.sql`. To create the database, as the `postgres` user, navigate to the `sql` directory and type

```
createdb bigbdb_rest
psql -f rest.sql bigbdb_rest
```

This database will need to be populated using `psql` or any tool that can be used to edit PostgreSQL databases. The database contains three tables that together describe and group the databases resources that will be made available through the API. The tables are:

- **resources**
  - **this contains two fields (both compulsory):**
    - \* **dbase\_config** - the name of the database configuration used with the database. This is the same as the name of the directory that contains the `config.xml` file in the `/etc/bigbdb/dbases` directory.
    - \* **description** - short description of the database.
- **groups (used to group related resources together)**
  - **this contains two fields (compulsory fields shown in bold):**
    - \* **name** - short name of group. This is usually a single word and is also the key that links resources to groups.
    - \* **description** - short description of group.
    - \* `long_description` - fuller description of group.
- **group\_resources (used to add resources to groups)**
  - **this contains two fields (both compulsory)**
    - \* **group\_name** - name of group. This must already exist in the `groups` table.
    - \* **dbase\_config** - the name of database resource. This must already exist in the `resources` table.

For example, to describe the PubMLST resources for *Neisseria*, connect to the `bigbdb_rest` database using `psql`,

```
psql bigbdb_rest
```

Then enter the following SQL commands. First add the database resources:

```
INSERT INTO resources (dbase_config,description) VALUES
('pubmlst_neisseria_seqdef','Neisseria sequence/profile definitions');
INSERT INTO resources (dbase_config,description) VALUES
('pubmlst_neisseria_isolates','Neisseria isolates');
```

Then create a 'neisseria' group that will contain these resources:

```
INSERT INTO groups (name,description) VALUES
('neisseria','Neisseria spp.');
```

Finally, add the database resources to the group:

```
INSERT INTO group_resources (group_name,dbase_config) VALUES
('neisseria','pubmlst_neisseria_seqdef');
INSERT INTO group_resources (group_name,dbase_config) VALUES
('neisseria','pubmlst_neisseria_isolates');
```

The REST API will need to run on its own network port. By default this is port 3000. To run as a stand-alone script, from the script directory, as the bigsdb user, simply type:

```
./bigsrest.pl
```

This will start the API on port 3000. You will be able to check that this is running using a web browser by navigating to <http://localhost:3000> on the local machine, or using the server IP address from a remote machine. You may need to modify your server firewall rules to allow connection to this port.

Running as a stand-alone script is useful for testing, but you can achieve much better performance using a Perl webserver with plackup. There are various options to choose. PubMLST uses [Starman](#).

To run the API using Starman, type the following as the bigsdb user:

```
plackup -a /var/rest/bigsrest.pl -s Starman -E deployment
```

where the value of -a refers to the location of the bigsrest.pl script. Starman defaults to using port 5000.

Different Linux distributions use different means to control services/daemons. To start the REST interface on system boot on systems using upstart, create a file called bigsdb-rest.conf in /etc/init. The contents of this file should be something like (modify file paths as appropriate):

```
description "Start BIGSdb REST interface"
version "1.0"
author "Keith Jolley"

start on runlevel [12345]

## tell upstart we're creating a daemon
expect fork

script

exec su -s /bin/sh -c 'exec "$0" "$@"' bigsdb -- /usr/local/bin/plackup -a /var/rest/
↪bigsrest.pl -s Starman -E deployment

end script
```

The service will then start automatically on boot or can be manually started by calling:

```
sudo service bigsdb-rest start
```

For systems using systemd, create a file in /etc/systemd/system called bigsdb-rest.service with the following contents (again, modify file paths as appropriate):

```
[Unit]
Description=BIGSdb REST interface
After=network.target

[Service]
User=bigsdb
ExecStart=/usr/bin/plackup -a /var/rest/bigsrest.pl -s Starman -E deployment
Restart=always

[Install]
WantedBy=multi-user.target
```

To start the service automatically on boot you need to enable it:

```
sudo systemctl enable bigsdb-rest.service
```

It can also be manually started by calling:

```
sudo systemctl start bigsdb-rest.service
```

### 3.12.1 Proxying the API to use a standard web port

Usually you will want your API to be available on the standard web port 80. To do this you will need to set up a virtual host using a different domain name from your web site to proxy the API port. For example, PubMLST has a separate domain '<http://rest.pubmlst.org>' for its API. This is set up as a virtual host directive in apache with the following configuration file:

```
<VirtualHost *>
  ServerName rest.pubmlst.org
  DocumentRoot /var/rest
  ServerAdmin keith.jolley@zoo.ox.ac.uk
  <Directory /var/rest>
    AllowOverride None
    Require all granted
  </Directory>

  ProxyPass / http://rest.pubmlst.org:5000/
  ProxyPassReverse / http://rest.pubmlst.org:5000/

  <Proxy *>
    Order allow,deny
    Allow from all
  </Proxy>

  ErrorLog /var/log/apache2/rest.pubmlst.org-error.log
  CustomLog /var/log/apache2/rest.pubmlst.org-access.log common
```

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```
</VirtualHost>
```

You should also set 'rest\_behind\_proxy=1' in bigsdb.conf.

## DATABASE SETUP

There are two types of BIGSdb database:

- sequence definition databases, containing
  - allele sequences and their identifiers
  - scheme data, e.g. MLST profile definitions
- isolate databases, containing
  - isolate provenance metadata
  - genome sequences
  - allele designations for loci defined in sequence definition databases.

These two databases are independent but linked. A single isolate database can communicate with multiple sequence definition databases and vice versa. Different access restrictions can be placed on different databases.

Databases are described in XML files telling BIGSdb everything it needs to know about them. Isolate databases can have any fields defined for the isolate table, allowing customisation of metadata - these fields are described in the XML file (config.xml) and must match the fields defined in the database itself.

### 4.1 Creating databases

There are templates available for the sequence definition and isolate databases. These are SQL scripts found in the sql directory.

To create a database, you will need to log in as the postgres user and use these templates. For example to create a new sequence definition database called bigsdb\_test\_seqdef, navigate to the sql directory and log in as the postgres user, e.g.

```
sudo su postgres
```

then

```
createdb bigsdb_test_seqdef  
psql -f seqdef.sql bigsdb_test_seqdef
```

Create an isolate database the same way:

```
createdb bigsdb_test_isolates  
psql -f isolatedb.sql bigsdb_test_isolates
```

The standard fields in the isolate table are limited to essential fields required by the system. To add new fields, you need to log in to the database and alter this table. For example, to add fields for country and year, first log in to the newly created isolate database as the postgres user:

```
psql bigsdb_test_isolates
```

and alter the isolate table:

```
ALTER TABLE isolates ADD country text;  
ALTER TABLE isolates ADD year int;
```

Remember that any fields added to the table need to be described in the config.xml file for this database.

The xml directory of the software archive contains example XML files for sequence definition and isolate databases (rename these to config.xml). The isolates\_config.xml file contains the minimum required isolate table fields and matches the isolate table that will be generated using the isolatedb.sql SQL script.

## 4.2 Database-specific configuration

Each BIGSdb database on a system has its own configuration directory, by default in /etc/bigsdb/dbases. The database has a short configuration name used to specify it in a web query and this matches the name of the configuration sub-directory, e.g. [http://pubmlst.org/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst\\_neisseria\\_isolates](http://pubmlst.org/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst_neisseria_isolates) is the URL of the front page of the PubMLST Neisseria isolate database whose configuration settings are stored in /etc/bigsdb/dbases/pubmlst\_neisseria\_isolates. This database sub-directory contains a number of optional files:

- **config.xml** - the database configuration file. Fields defined here correspond to fields in the isolate table of the database.
- **banner.html** - optional file containing text that will appear as a banner within the database index pages. HTML markup can be used within this text.
- **header.html** - HTML markup that is inserted at the top of all pages. This can be used to set up site-specific menubars and logos.
- **footer.html** - HTML markup that is inserted at the bottom of all pages.
- **curate\_header.html** - HTML markup that is inserted at the top of all curator's interface pages.
- **curate\_footer.html** - HTML markup that is inserted at the bottom of all curator's interface pages.
- **profile\_submit.html** - HTML markup for text that is inserted in to the submission interface prior to profile submission finalization. This can be used to add specific instructions such as the requirement to make an isolate submission.
- **allele\_submit.html** - HTML markup for text that is inserted in to the submission interface prior to allele submission finalization. This can be used to add specific instructions such as the requirement to attach Sanger trace files.
- **isolate\_submit.html** - HTML markup for text that is inserted in to the submission interface prior to isolate submission finalization. This can be used to add specific instructions such as the request to also make a new profile submission if the isolate has a new profile.
- **profile\_curate.html** - HTML markup for text that is inserted on submission curation page if profile submissions are pending. This can be used to add specific information to curators.
- **allele\_curate.html** - HTML markup for text that is inserted on submission curation page if allele submissions are pending. This can be used to add specific information to curators.

- `isolate_curate.html` - HTML markup for text that is inserted on submission curation page if isolate submissions are pending. This can be used to add specific information to curators.
- `registration_success.txt` - Text file containing message content to be used in an automated E-mail when granting access to a user who has requested access to the database using the site-wide account system (where auto-registration is not enabled).
- `registration.html` - HTML markup for text that will appear on the login page for the current database. This appears right before the “Log in” button.

The header and footer files can alternatively be placed in the root directory of the web site, or in `/etc/bigsdb`, for site-wide use. If files exist in multiple locations, they are used in the following order of preference: database config directory > web root directory > `/etc/bigsdb`.

There are four additional files, `site_header.html`, `site_footer.html`, `curate_site_header.html` and `curate_site_footer.html` which are used when either `bigsdb.pl` or `bigscurate.pl` are called without a database configuration. These should be placed in the root directory of the web site or in `/etc/bigsdb`.

You can also add HTML meta attributes (such as a favicon) by including a file called `meta.html` in the database configuration directory. For example to set a favicon this file can contain something like the following:

```
<link rel="shortcut icon" href="/favicon.ico" type="image/ico" />
```

These attributes will appear in the `<head>` section of the HTML page.

## 4.3 XML configuration attributes used in config.xml

The following lists describes the attributes used in the `config.xml` file that is used to describe databases.

### 4.3.1 Isolate database XML attributes

Please note that database structure described by the field elements must match the physical structure of the database isolate table. Required attributes are in **bold**:

```
<db>
```

Top level element. Contains child elements: `system` and `field`:

```
<system>
```

Any value set here can be overridden in a *`system.overrides` file*.

- **authentication**
  - Method of authentication: either ‘builtin’ or ‘apache’. See *[user authentication](#)*.
- **db**
  - Name of database on system.
- **dbtype**
  - Type of database: either ‘isolates’ or ‘sequences’.
- **description**
  - Description of database used throughout interface (see also ‘formatted\_description’).
- **align\_limit**

- Overrides the sequence export record alignment limit in the Sequence Export plugin. Default: ‘200’.
- all\_plugins
  - Enable all appropriate plugins for database: either ‘yes’ or ‘no’, default ‘no’.
- annotation
  - Semi-colon separated list of accession numbers with descriptions (separated by a |), eg. ‘AL157959|Z2491;AM421808|FAM18;NC\_002946|FA 1090;NC\_011035|NCCP11945;NC\_014752|020-06’. Currently used only by Genome Comparator plugin.
- BLAST
  - Enable Blast plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to ‘yes’. If the all\_plugins attribute is set to ‘yes’, the Blast plugin can be disabled by setting this attribute to ‘no’.
- BURST
  - Enable BURST plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to ‘yes’. If the all\_plugins attribute is set to ‘yes’, the BURST plugin can be disabled by setting this attribute to ‘no’.
- cache\_schemes
  - Enable automatic refreshing of scheme field caches when batch adding new isolates: either ‘yes’ or ‘no’, default ‘no’.
  - See *[scheme caching](#)*.
- CodonUsage
  - Enable Codon Usage plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to ‘yes’. If the all\_plugins attribute is set to ‘yes’, the Codon Usage plugin can be disabled by setting this attribute to ‘no’.
- codon\_usage\_limit
  - Overrides the record limit for the Codon Usage plugin. Default: ‘500’.
- contig\_analysis\_limit
  - Overrides the isolate number limit for the Contig Export plugin. Default: ‘1000’.
- ContigExport
  - Enable contig export plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to ‘yes’. If the all\_plugins attribute is set to ‘yes’, the contig export plugin can be disabled by setting this attribute to ‘no’.
- curate\_config
  - The database configuration that should be used for curation if different from the current configuration. This is used when the submission system is being used so that curation links in the ‘Manage submissions’ pages for curators load the correct database configuration.
- curate\_link
  - URL to curator’s interface, which can be relative or absolute. This will be used to create a link in the public interface dropdown menu.
- curate\_path\_includes
  - Partial path of the bigscurate.pl script used to curate the database. See user authentication.
- curate\_script

- Relative web path to curation script. Default 'bigscurate.pl' (version 1.11+).
- This is only needed if automated submissions are enabled. If bigscurate.pl is in a different directory from bigsdb.pl, you need to include the whole web path, e.g. /cgi-bin/private/bigsdb/bigscurate.pl.
- curators\_only
  - Set to 'yes' to prevent ordinary authenticated users having access to database configuration. This is only effective if read\_access is set to 'authenticated\_users'. This may be useful if you have different configurations for curation and querying with some data hidden in the configuration used by standard users. Default 'no'.
- daily\_pending\_submissions
  - Overrides the daily limit on pending submissions that a user can submit via the web submission system. Default: '15'.
- daily\_rest\_submissions\_limit
  - Overrides the limit on number of submissions that can be made to the database via the RESTful interface. This is useful to prevent flooding of the submission system by aberrant scripts. Default: '100'.
- default\_access
  - The default access to the database configuration, either 'allow' or 'deny'. If 'allow', then specific users can be denied access by creating a file called 'users.deny' containing usernames (one per line) in the configuration directory. If 'deny' then specific users can be allowed by creating a file called 'users.allow' containing usernames (one per line) in the configuration directory. See [default access](#).
- default\_private\_records
  - The default number of private isolate records that a user can upload. The user account must have a status of either 'submitter', 'curator', or 'admin'. This value is used to set the private\_quota field when creating a new user record (which can be overridden for individual users). Changing it will not affect the quotas of existing users. Default: '0'.
- default\_seqdef\_config
  - Isolate databases only: Name of the default seqdef database configuration used with this database. Used to automatically fill in details when adding new loci.
- default\_seqdef\_dbase
  - Isolate databases only: Name of the default seqdef database used with this database. Used to automatically fill in details when adding new loci.
- default\_seqdef\_script
  - Isolate databases only: URL of BIGSdb script running the seqdef database (default: '/cgi-bin/bigsdb/bigsdb.pl').
- delete\_retire\_only
  - Set to 'yes' to retire the id of any isolate that is deleted. This prevents re-use of ids. This setting will override the global setting in bigsdb.conf.
- disable\_updates
  - Set to 'yes' to prevent updates. This is useful when moving databases or temporarily running on a backup server.
- disable\_update\_message
  - Message shown when updates are disabled.
- eav\_fields

- Name to call sparsely-populated fields. Default: ‘secondary metadata’.
- eav\_field\_icon
  - Icon class from FontAwesome to use on isolate info page for sparsely- populated fields. Default ‘fas fa-microscope’.
- eav\_groups
  - Comma-separated list of category names that sparsely-populated fields can be grouped in to. If this value is set, a category drop-down list will appear when adding or updating sparsely-populated fields. You can add an icon to appear by following the name with a pipe symbol (|) and an icon class from the FontAwesome library, e.g. ‘Vaccine reactivity|fas fa-syringe,Risk factors|fas fa-smoking’.
- export\_limit
  - Overrides the default allowed number of data points (isolates x columns) to export. Default: ‘25000000’.
- fast\_scan
  - Sets whether fast mode scanning is enabled via the web interface. This will scan all loci together, using exemplar sequences. In cases where multiple loci are being scanned this should be significantly faster than the standard locus-by-locus scan, but it will take longer for the first results to appear. *Allele exemplars* should be defined if you enable this option. Set to ‘yes’ to enable. Default: ‘no’.
- field\_groups
  - Comma-separated list of category names that standard isolate fields can be grouped in to in the isolate information page. You can add an icon to appear by following the name with a pipe symbol (|) and an icon class from the FontAwesome library, e.g. ‘Antimicrobial resistance|fas fa-capsules’.
- fieldgroup1 - fieldgroup10
  - Allows multiple fields to be queried as a group. Value should be the name of the group followed by a colon (:) followed by a comma-separated list of fields to group, e.g. identifiers:id,strain,other\_name.
- formatted\_description
  - Markdown formatted description of database. If set, this will be used throughout the HTML interface wherever formatting can be applied (main body of text) and overrides the value set in ‘db\_description’. Currently only supports *\*italics\** and **\*\*bold\*\***.
- genepresence\_record\_limit
  - Overrides the record number limit (isolates x loci) for the Gene Presence plugin. Default: 500000 (this can also be set globally in bigsdb.conf).
- genepresence\_taxa\_limit
  - Overrides the isolate limit for the Gene Presence plugin. Default: 10000 (this can also be set globally in bigsdb.conf).
- GenomeComparator
  - Enable Genome Comparator plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to ‘yes’. If the all\_plugins attribute is set to ‘yes’, the Genome Comparator plugin can be disabled by setting this attribute to ‘no’.
- genome\_comparator\_limit
  - Overrides the isolate number limit for the Genome Comparator plugin. Default: 1000 (this can also be set globally in bigsdb.conf).
- genome\_comparator\_max\_ref\_loci
  - Overrides the limit on number of loci allowed in a reference genome. Default: 10000.

- `genome_comparator_threads`
  - The number of threads to use for data gathering (BLAST, database queries) to populate data structure for Genome Comparator analysis. You should not set this to less than 2 as this will prevent job cancelling due to the way isolates are queued. Default: '2'.
- `genome_submissions`
  - Enable genome submissions (automated submission system): either 'yes' or 'no', default 'yes'.
  - To enable, you will also need to set `submissions="yes"`. By default, genome submissions are enabled.
- `hide_unused_schemes`
  - Sets whether a scheme is shown in a main results table if none of the isolates on that page have any data for the specific scheme: either 'yes' or 'no', default 'no'.
- `host`
  - Host name/IP address of machine hosting isolate database, default 'localhost'.
- `itol_record_limit`
  - Overrides the maximum number of records that can be included in an ITOL job. Default: 2000 (this can also be set globally in `bigssdb.conf`).
- `itol_seq_limit`
  - Overrides the maximum number of sequences (records x loci) that can be included in an ITOL job. Default: 100,000 (this can also be set globally in `bigssdb.conf`).
- `job_priority`
  - Integer with default job priority for offline jobs (default:5).
- `job_quota`
  - Integer with number of offline jobs that can be queued or currently running for this database.
- `labelfield`
  - Field that is used to describe record in isolate info page, default 'isolate'.
- `locus_aliases`
  - Display locus aliases and use them in dropdown lists by default: must be either 'yes' or 'no', default 'no'. This option can be overridden by a user preference.
- `locus_superscript_prefix`
  - Superscript the first letter of a locus name if it is immediately following by an underscore, e.g. `f_abcZ` would be displayed as `fabcZ` within the interface: must be either 'yes' or 'no', default 'no'. This can be used to designate gene fragments (or any other meaning you like).
- `maindisplay_aliases`
  - Default setting for whether isolates aliases are displayed in main results tables: either 'yes' or 'no', default 'no'. This setting can be overridden by individual user preferences.
- `Microreact`
  - Enable Microreact plugin: either 'yes' or 'no'. If no value is set then the plugin will not be available unless the `all_plugins` attribute is set to 'yes'. If the `all_plugins` attribute is set to 'yes', the Microreact plugin can be disabled by setting this attribute to 'no'. Note that for the plugin to be active, a country field containing a defined list of allowed values and an integer year field must be defined in the isolates table. The plugin also requires `microreact_token` to be provided in `bigssdb.conf`.

- `microreact_country_field`
  - Overrides the field in which country is stored. Default: 'country'
- `microreact_record_limit`
  - Overrides the maximum number of records that can be included in a Microreact job. Default: 2000 (this can also be set globally in `bigssdb.conf`).
- `microreact_seq_limit`
  - Overrides the maximum number of sequences (records x loci) that can be included in an Microreact job. Default: 100,000 (this can also be set globally in `bigssdb.conf`).
- `microreact_year_field`
  - Overrides the field in which year is stored. Default: 'year'
- `min_genome_size`
  - Size in bp that is the minimum size of the sequence bin considered to represent a whole genome. This is used in the REST interface to differentiate records with genomes. You can also pass a 'genomes=1' attribute to the an isolate query form and this will populate the appropriate search to return genome records.
- `new_version`
  - Set to 'no' to prevent copying field value when creating a new version of the isolate record.
- `noshow`
  - Comma-separated list of fields not to use in breakdown statistic plugins.
- `no_publication_filter`
  - Isolate databases only: Switches off display of publication filter in isolate query form by default: either 'yes' or 'no', default 'no'.
- `only_sets`
  - Don't allow option to view the 'whole database' - only list sets that have been defined: either 'yes' or 'no', default 'no'.
- `password`
  - Password for access to isolates database, default 'remote'.
- `pcr_limit`
  - Overrides the isolate number limit for the in silico PCR plugin. Default: '10000'.
- `PhyloViz`
  - Enable third party PhyloViz plugin: either 'yes' or 'no'. If no value is set then the plugin will not be available unless the `all_plugins` attribute is set to 'yes'. If the `all_plugins` attribute is set to 'yes', the PhyloViz plugin can be disabled by setting this attribute to 'no'.
- `port`
  - Port number that the isolate host is listening on, default '5432'.
- `privacy`
  - Displays E-mail address for sender in isolate information page if set to 'no'. Default 'yes'.
- `public_login`
  - Optionally allow users to log in to a public database - this is useful as any jobs will be associated with the user and their preferences will also be linked to the account. Set to 'no' to disable. Default 'yes'.

- `query_script`
  - Relative web path to bigsdb script. Default 'bigsdb.pl' (version 1.11+).
  - This is only needed if automated submissions are enabled. If bigsdb.pl is in a different directory from bigscurate.pl, you need to include the whole web path, e.g. /cgi-bin/bigsdb/bigsdb.pl.
- `read_access`
  - Describes who can view data: either 'public' for everybody or 'authenticated\_users' for anybody who has been able to log in. Default 'public'.
- `related_databases`
  - Semi-colon separated list of links to related BIGSdb databases on the system. This should be in the form of database configuration name followed by a '|' and the description, e.g. 'pubmlst\_neisseria\_seqdef|Typing'. This is used to populate the menu items.
- `remote_contigs`
  - Optionally allow the use of remote contigs. These are stored in a remote BIGSdb database, accessible via the RESTful API. Set to 'yes' to enable.
- `rest_kiosk`
  - If 'kiosk' attribute is set, then the REST interface will be disabled for the configuration unless a value is set here. The only supported value currently is 'sequenceQuery' which will enable API routes for querying sequences.
- `rMLSTSpecies`
  - Enable rMLST Species identifier plugin: either 'yes' or 'no'. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to 'yes'. If the all\_plugins attribute is set to 'yes', the plugin can be disabled by setting this attribute to 'no'. Note that for the plugin to be active, a country field containing a defined list of allowed values and an integer year field must be defined in the isolates table.
- `script_path_includes`
  - Partial path of the bigsdb.pl script used to access the database. See [user authentication](#).
- `SeqbinBreakdown`
  - Enable Sequence bin breakdown plugin: either 'yes' or 'no'. If no value is set then the plugin will not be available unless the all\_plugins attribute is set to 'yes'. If the all\_plugins attribute is set to 'yes', the plugin can be disabled by setting this attribute to 'no'. Note that for the plugin to be active, a country field containing a defined list of allowed values and an integer year field must be defined in the isolates table.
- `seq_export_limit`
  - Overrides the sequence export limit (records x loci) in the Sequence Export plugin. Default: '1000000'.
- `sets`
  - Use [sets](#): either 'yes' or 'no', default 'no'.
- `set_id`
  - Force the use of a specific set when accessing database via this XML configuration: Value is the name of the set.
- `start_codons`
  - Semi-colon separated list of start codons to allow. Note that this list will replace the built-in defaults of ATG, GTG, and TTG, and is used for all functions that require recognising complete coding sequences, such as automated allele definition.

- `start_id`
  - Defines the minimum record id to be used when uploading new isolate records. This can be useful when it is anticipated that two databases may be merged and it would be easier to do so if the id numbers in the two databases were different. Default: '1'.
- `submissions`
  - Enable automated submission system: either 'yes' or 'no', default 'no' (version 1.11+).
  - The `curate_script` and `query_script` paths should also be set, either in the `bigsdbs.conf` file (for site-wide configuration) or within the system attribute of `config.xml`.
- `submissions_deleted_days`
  - Overrides the default number of days before closed submissions are deleted from the system. Default: '90'.
- `TagStatus`
  - Enable Tag status plugin: either 'yes' or 'no'. If no value is set then the plugin will not be available unless the `all_plugins` attribute is set to 'yes'. If the `all_plugins` attribute is set to 'yes', the plugin can be disabled by setting this attribute to 'no'. Note that for the plugin to be active, a country field containing a defined list of allowed values and an integer year field must be defined in the isolates table.
- `tblastx_tagging`
  - Sets whether tagging can be performed using TBLASTX: either 'yes' or 'no', default 'no'.
- `total_pending_submissions`
  - Overrides the total limit on pending submissions that a user can submit via the web submission system. Default: '20'.
- `user`
  - Username for access to isolates database, default 'apache'.
- `user_job_quota`
  - Integer with number of offline jobs that can be queued or currently running for this database by any specific user - this parameter is only effective if users have to log in.
- `user_projects`
  - Sets whether authenticated users can create their own projects in order to group isolates: either 'yes' or 'no', default 'no'.
- `view`
  - Database view containing isolate data, default 'isolates'.
- `views`
  - Comma-separated list of views of the isolate table defined in the database. This is used to set a view for a set, or to restrict loci or schemes to a subset of isolate data.
- `warn_max_contigs`
  - Set a threshold for the number of contigs in a submitted genome assembly to trigger a warning in the submission interface. This value overrides the value set in `bigsdbs.conf`.
- `warn_max_total_length`
  - Set an upper threshold for the total size of a submitted genome assembly to trigger a warning in the submission interface.
- `warn_min_n50`

- Set a threshold for the minimum N50 value in a submitted genome assembly to trigger a warning in the submission interface. This value overrides the value set in bigsdb.conf.
- warn\_min\_total\_length
  - Set a lower threshold for the total size of a submitted genome assembly to trigger a warning in the submission interface.
- webroot
  - URL of web root, which can be relative or absolute. This is used to provide a hyperlinked item in the dropdown menu. Default '/'.
- webroot\_label
  - Label text for the breadcrumb link defined by the webroot value. This can be formatted using Markdown. Currently only supports *italics* and **bold**.

```
<field>
```

Element content: Field name + optional list <optlist> of allowed values, e.g.:

```
<field type="text" required="no" length="40" maindisplay="no"
  web="http://somewebsite.com/cgi-bin/script.pl?id=[?]" optlist="yes">epidemiology
<optlist>
  <option>carrier</option>
  <option>healthy contact</option>
  <option>sporadic case</option>
  <option>endemic</option>
  <option>epidemic</option>
  <option>pandemic</option>
</optlist>
</field>
```

- type
  - Data type: int, text, float, bool, or date.
- allow\_submissions
  - Show in submission template and allow data to be submitted even if field is set as 'curate\_only'. This has no effect on fields that do not have the 'curate\_only' attribute as these fields are included in submissions by default. This attribute will be overridden if the field has the 'no\_submissions' attribute set.
- comments
  - Comments about the field. These will be displayed in the field description plugin and as tooltips within the curation interface.
- curate\_only
  - Set to 'yes' to hide field unless logged-in user is a curator or admin. Set the 'allow\_submissions' attribute to still include the field in the submission template so that it can be included in submissions of new records by standard users.
- default
  - Default value. This will be entered automatically in the web form but can be overridden.
- dropdown

- Select if you want this field to have its own dropdown filter box on the query page. If the field has an option list it will use the values in it, otherwise all values defined in the database will be included: ‘yes’ or ‘no’, default ‘no’. This setting can be overridden by individual user preferences.
- group
  - Fields can be grouped in the isolate information page by specifying the group attribute. The group name must be defined in the field\_groups system attribute, otherwise the field will not be shown at all. If undefined, the field will be in the default provenance/primary metadata group.
- length
  - Length of field, default 12.
- log\_delete
  - Sets if the field value will be recorded in the log table if the isolate is deleted. Set to ‘yes’ or ‘no’, default is ‘no’. The id and isolate name are always recorded if deletion is logged.
- maindisplay
  - Sets if field is displayed in the main table after a database search, ‘yes’ or ‘no’, default ‘yes’. This setting can be overridden by individual user preferences.
- max
  - Maximum value for integer and date types. Special values such as CURRENT\_YEAR and CURRENT\_DATE can be used.
- min
  - Minimum value for integer and date types.
- multiple
  - Sets if field allows multiple values to be set for it, ‘yes’ or ‘no’, default ‘no’. If set to ‘yes’, then the underlying field in the database must be an ARRAY type, e.g. text[].
- no\_curate
  - Setting this will hide the field in the curator interface and prevent it from being manually modified. This is useful for fields that are populated by automated scripts or database triggers. Can be ‘yes’ or ‘no’, default ‘no’.
- no\_submissions
  - Setting this will hide the field in the submission template. The field is still available if it is added back to the template manually.
- optlist
  - Sets if this field has a list of allowed values, default ‘no’. Surround each option with an <option> tag.
- prefixes
  - Sets the name of a field that this field should be used as a prefix for. That field must be defined. An example of where this would be useful is for defining AMR fields, where one field is a modifier (>,<=) for a MIC value field. A field with this attribute defined will not be shown as a separate field within the isolate record, but will be displayed as a prefix to the value of the set field. The prefix field will also not be labelled in the curation interface isolate add/update form, but will appear immediately before and inline with the prefixed field.
- regex
  - Regular expression used to constrain field values, e.g. regex="^[A-Z].\*\$" forces the first letter of the value to be capitalized.

- **required**
  - Sets if data is required for this field, ‘yes’, ‘no’, or ‘expected’, default ‘yes’. If set to ‘expected’, the value cannot be left empty when batch adding an isolate record or using the submission system, but a null value can be explicitly set using the value ‘null’. The use of this is to encourage submitters to include a value for this field if it is available, while still allowing empty values if it is not.
- **separator**
  - Optional string to place between field prefix value and field value if the prefixes attribute is defined.
- **suffix**
  - Optional string that is displayed after value in isolate information page and curation interface. Useful for adding units for numerical values.
- **userfield**
  - Select if you want this field to have its own dropdown filter box of users (populated from the users table): ‘yes’ or ‘no’, default ‘no’.
- **web**
  - URL that will be used to hyperlink field values. If [?] is included in the URL, this will be substituted for the actual field value.

### Special values

The following special variables can be used in place of an actual value:

- **CURRENT\_DATE**: current date in yyyy-mm-dd format
- **CURRENT\_YEAR**: the 4 digit value of the current year

### 4.3.2 Sequence definition database XML attributes

Required attributes are in **bold**.

```
<db>
```

Top level element. Contains child element: **system**.

```
<system>
```

Any value set here can be overridden in a *system.overrides file*.

- **authentication**
  - Method of authentication: either ‘builtin’ or ‘apache’. See *user authentication*.
- **db**
  - Name of database on system.
- **dbtype**
  - Type of database: either ‘isolates’ or ‘sequences’.
- **description**
  - Description of database used throughout interface.
- **align\_limit**

- Overrides the sequence export record alignment limit in the Sequence Export plugin. Default: ‘200’.
- `allele_comments`
  - Enable comments on allele sequences: either ‘yes’ or ‘no’, default ‘no’.
  - This is not enabled by default to discourage the practice of adding isolate information to allele definitions (this sort of information belongs in an isolate database).
- `allele_flags`
  - Enable flags to be set for alleles: either ‘yes’ or ‘no’, default ‘no’.
- `BURST`
  - Enable BURST plugin: either ‘yes’ or ‘no’. If no value is set then the plugin will not be available unless the `all_plugins` attribute is set to ‘yes’. If the `all_plugins` attribute is set to ‘yes’, the BURST plugin can be disabled by setting this attribute to ‘no’.
- `curate_config`
  - The database configuration that should be used for curation if different from the current configuration. This is used when the submission system is being used so that curation links in the ‘Manage submissions’ pages for curators load the correct database configuration.
- `curate_path_includes`
  - Partial path of the `bigscurate.pl` script used to curate the database. See [user authentication](#).
- `curate_script`
  - Relative web path to curation script. Default ‘bigscurate.pl’ (version 1.11+).
  - This is only needed if automated submissions are enabled. If `bigscurate.pl` is in a different directory from `bigsdbs.pl`, you need to include the whole web path, e.g. `/cgi-bin/private/bigsdbs/bigscurate.pl`.
- `curators_only`
  - Set to ‘yes’ to prevent ordinary authenticated users having access to database configuration. This is only effective if `read_access` is set to ‘authenticated\_users’. This may be useful if you have different configurations for curation and querying with some data hidden in the configuration used by standard users. Default ‘no’.
- `daily_pending_submissions`
  - Overrides the daily limit on pending submissions that a user can submit via the web submission system. Default: ‘15’.
- `daily_rest_submissions_limit`
  - Overrides the limit on number of submissions that can be made to the database via the RESTful interface. This is useful to prevent flooding of the submission system by aberrant scripts. Default: ‘100’.
- `delete_retire_only`
  - Set to ‘yes’ to retire the id of any allele or profile that is deleted. This prevents re-use of ids. This setting will override the global setting in `bigsdbs.conf`.
- `diploid`
  - Allow IUPAC 2-nucleotide ambiguity codes in allele definitions for use with diploid typing schemes: either ‘yes’ or ‘no’, default ‘no’.
- `disable_seq_downloads`
  - Prevent users or curators from downloading all alleles for a locus (admins always can). ‘yes’ or ‘no’, default ‘no’.

- `exemplars`
  - Use exemplar sequences in the BLAST caches used for the sequence query pages. This is useful on larger databases as it speeds up the query significantly. *Exemplar alleles* **MUST** be defined otherwise sequence queries will fail. ‘yes’ or ‘no’, default ‘no’.
- `formatted_description`
  - Markdown formatted description of database. If set, this will be used throughout the HTML interface wherever formatting can be applied (main body of text) and overrides the value set in ‘db\_description’. Currently only supports *\*italics\** and **\*\*bold\*\***.
- `genome_submissions`
  - Enable link to genome submissions (automated submission system): either ‘yes’ or ‘no’, default ‘yes’.
  - To enable, you will also need to set `isolate_submissions=“yes”`.
- `isolate_database`
  - The config name of the isolate database. This is used to provide a link to isolate submissions. You also need to set `isolate_submissions=“yes”`.
- `isolate_submissions`
  - Set to yes to provide a link to isolate submissions. The `isolate_database` attribute also needs to be set. Default: ‘no’.
- `job_priority`
  - Integer with default job priority for offline jobs (default:5).
- `job_quota`
  - Integer with number of offline jobs that can be queued or currently running for this database.
- `kiosk`
  - Set to a page name to restrict configuration to always start on this page, rather than an index page. This facilitates running in a cut-down *kiosk mode* that doesn’t allow access to all features. *Currently only ‘sequenceQuery’ is supported.*
- `kiosk_allowed_pages`
  - Comma-separated list of pages that the configuration is allowed to show, apart from the page set in the ‘kiosk’ attribute. Example for a sequence query configuration would be ‘sequenceTranslate’ to allow access to the translated sequence page following a query.
- `kiosk_help`
  - URL to context-sensitive help page.
- `kiosk_locus`
  - Restrict sequence query to a specific locus or scheme. Use either the locus primary name or ‘SCHEME\_X’ where X is the scheme number.
- `kiosk_no_genbank`
  - Set to “yes” to hide the Genbank accession form element in kiosk mode.
- `kiosk_no_upload`
  - Set to “yes” to hide the sequence file upload in kiosk mode.
- `kiosk_simple`
  - Remove most explanatory text from kiosk page.

- `kiosk_text`
  - Alternative text to show on kiosk page.
- `kiosk_title`
  - Title text to use when running in kiosk mode.
- `profile_submissions`
  - Enable profile submissions (automated submission system): either ‘yes’ or ‘no’, default ‘no’ (version 1.11+).
  - To enable, you will also need to set `submissions=’yes’`. By default, profile submissions are disabled since generally new profiles should be accompanied by representative isolate data, and the profile can be extracted from that.
- `public_login`
  - Optionally allow users to log in to a public database - this is useful as any jobs will be associated with the user and their preferences will also be linked to the account. Set to ‘no’ to disable. Default ‘yes’.
- `query_script`
  - Relative web path to bigsdb script. Default ‘bigsdb.pl’ (version 1.11+).
  - This is only needed if automated submissions are enabled. If bigsdb.pl is in a different directory from bigscurate.pl, you need to include the whole web path, e.g. `/cgi-bin/bigsdb/bigsdb.pl`.
- `read_access`
  - Describes who can view data: either ‘public’ for everybody, or ‘authenticated\_users’ for anybody who has been able to log in. Default ‘public’.
- `related_databases`
  - Semi-colon separated list of links to related BIGSdb databases on the system. This should be in the form of database configuration name followed by a ‘|’ and the description, e.g. ‘pubmlst\_neisseria\_isolates|Isolates’. This is used to populate the menu items.
- `script_path_includes`
  - Partial path of the bigsdb.pl script used to access the database. See [user authentication](#).
- `seq_export_limit`
  - Overrides the sequence export limit (records x loci) in the Sequence Export plugin. Default: ‘1000000’.
- `sets`
  - Use [sets](#): either ‘yes’ or ‘no’, default ‘no’.
- `set_id`
  - Force the use of a specific set when accessing database via this XML configuration: Value is the name of the set.
- `start_codons`
  - Semi-colon separated list of start codons to allow. Note that this list will replace the built-in defaults of ATG, GTG, and TTG, and is used for all functions that require recognising complete coding sequences.
- `submissions`
  - Enable automated submission system: either ‘yes’ or ‘no’, default ‘no’ (version 1.11+).
  - The `curate_script` and `query_script` paths should also be set, either in the bigsdb.conf file (for site-wide configuration) or within the system attribute of config.xml.

- `submissions_deleted_days`
  - Overrides the default number of days before closed submissions are deleted from the system. Default: '90'.
- `total_pending_submissions`
  - Overrides the total limit on pending submissions that a user can submit via the web submission system. Default: '20'.
- `user_job_quota`
  - Integer with number of offline jobs that can be queued or currently running for this database by any specific user - this parameter is only effective if users have to log in.
- `webroot`
  - URL of web root, which can be relative or absolute. This is used to provide a hyperlinked item in the dropdown menu. Default '/'.
- `webroot_label`
  - Label text for the breadcrumb link defined by the webroot value. This can be formatted using Markdown. Currently only supports *italics* and **bold**.

## 4.4 Over-riding global defaults set in bigsdb.conf

Certain values set in bigsdb.conf can be over-ridden by corresponding values set in a database-specific config.xml file. These can be set within the system tag like other attributes:

- `query_script`
  - Relative web path to bigsdb script.
- `curate_script`
  - Relative web path to curation script.
- `prefs_db`
  - The name of the preferences database.
- `auth_db`
  - The name of the authentication database.
- `tmp_dir`
  - Path to the web-accessible temporary directory.
- `secure_tmp_dir`
  - Path to the web-inaccessible (secure) temporary directory.
- `ref_db`
  - The name of the references database.

## 4.5 Over-riding values set in config.xml

Any attribute used in the system tag of the database config.xml file can be over-ridden using a file called **system.overrides**, placed in the same directory as config.xml. This is very useful as it allows you to set up multiple configs for a database, with the config.xml files symlinked so that any changes to one will be seen in each database configuration. An example of why you may wish to do this would be if you create separate public and private views of the isolate table that filters on some attribute. The system.overrides file uses key value pairs separated by = with the values quoted, e.g.

```
view="private"
read_access="authenticated_users"
description="Private view of database"
```

It is also possible to override the required, maindisplay or curate\_only attributes of a particular field using a file called **field.overrides**. The field.overrides file uses the format 'field:attribute="value"' on each line, e.g.

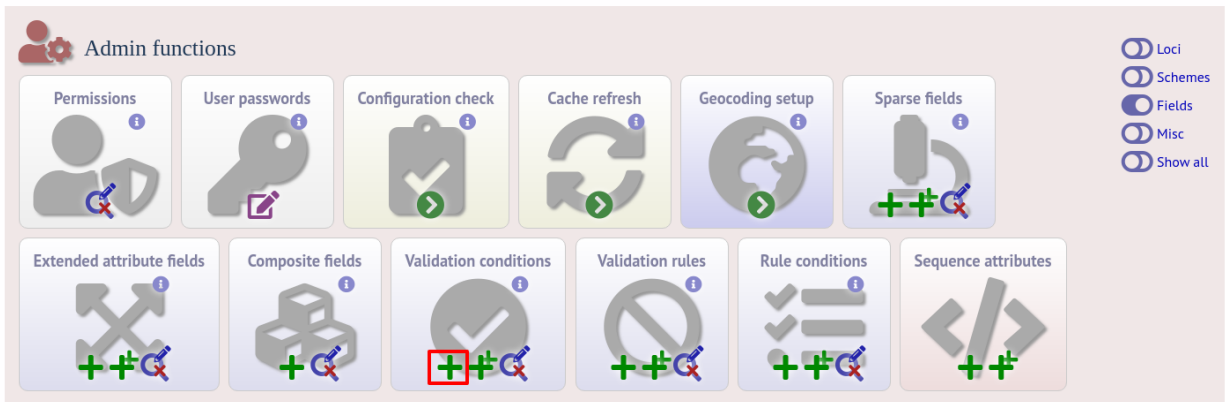
```
date_received:required="yes"
```

## 4.6 Setting field validation rules

Sometimes it may be necessary to restrict the allowed values in one isolate field depending on the values submitted for another field. It is possible to do this using field validation rules. These combine one or more conditions which all have to match for validation to fail and an isolate record upload to be rejected.

An example of this may be if you have an age\_year and an age\_month field but you only want age\_month to be populated if the subject is less than one year old. You can do this as follows.

As an admin, on the curator interface, click the 'Field' toggle to show the validation table links. Then click 'Add' on the 'Validation conditions' setting:



Add the following conditions separately:

- age\_year > 0
- age\_month NOT null

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new validation condition

Add new validation condition

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 1

field: age\_yr

operator: >

value: 0

curator: Keith Jolley (keith)

timestamp: 2020-07-18

Action

RESET SUBMIT

Now add a new 'Validation rule', by clicking 'Add' on the 'Validation rules' setting:

Admin functions

Permissions User passwords Configuration check Cache refresh Geocoding setup Sparse fields

Extended attribute fields Composite fields Validation conditions Validation rules Rule conditions Sequence attributes

Validation rules

Locis Schemes Fields Misc Show all

Here you just enter the message that will be returned when the validation fails:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new validation rule

Add new validation rule

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 1

message: age\_mth should only be set when age\_yr < 1

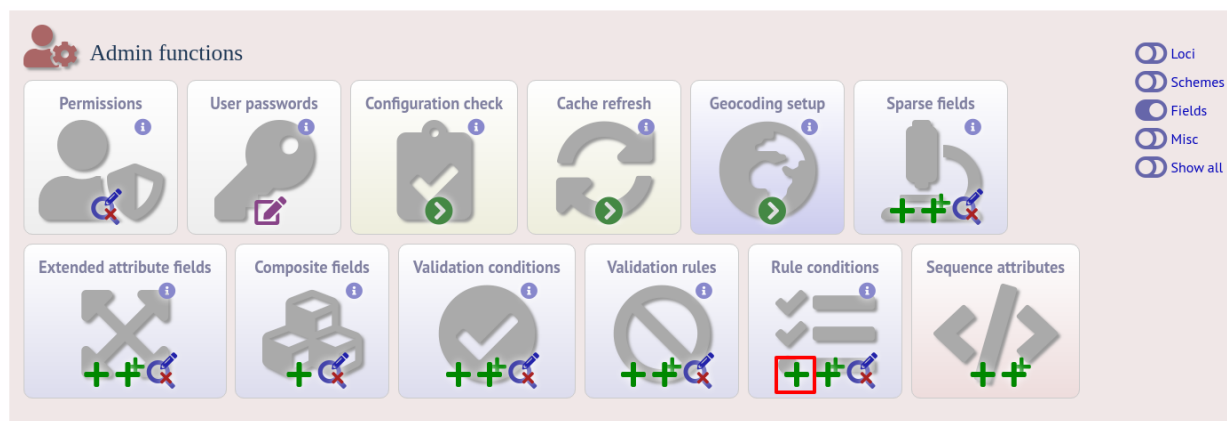
curator: Keith Jolley (keith)

timestamp: 2020-07-18

Action

RESET SUBMIT

Finally add the conditions to the rule by clicking 'Add' on the 'Rule conditions' setting:



Select the rule message and the condition from the dropdown boxes:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new rule condition

## Add new rule condition

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
rule id: 1) age_mth should only be set when age_yr < 1. condition id: 1) age_yr > 0 curator: Keith Jolley (keith) timestamp: 2020-07-18	RESET SUBMIT

Make sure you do this for each of the conditions that have to match.

Validation checks are performed when adding or updating an isolate record, or when a user submits via the automated submission interface. Currently these checks are not enforced when doing a batch update.

### 4.6.1 Special condition values

Use the value **null** to indicate that the field is empty, e.g.

- age\_month NOT null

Use a field name in square brackets to compare the value in that field, e.g. suppose you have two date fields, 'date\_sampled' and 'date\_received', and you want to ensure that 'date\_received' is not before 'date\_sampled'. You can do this with the following condition:

- date\_received < [date\_sampled]

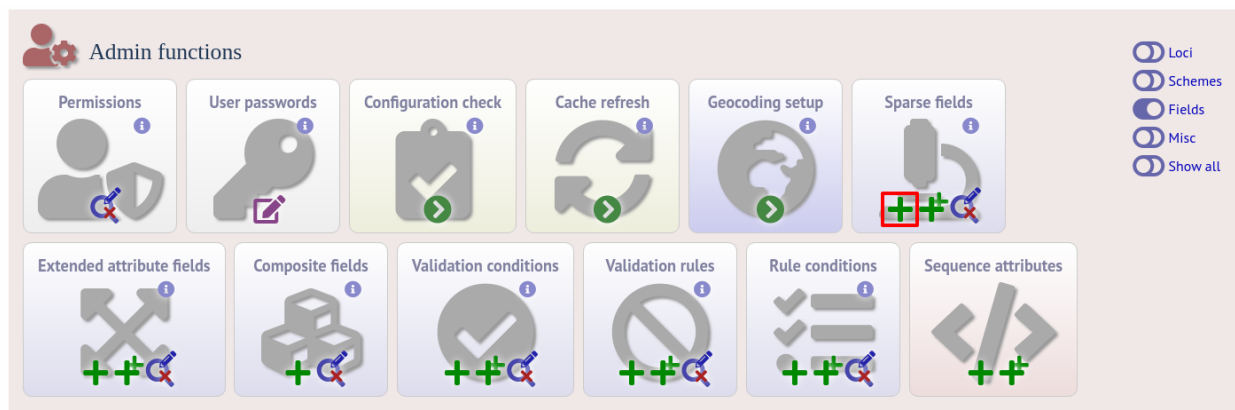
The two fields have to be of the same data type in order to be compared (you cannot compare a text field to an integer field for example).

## 4.7 Sparsely-populated fields

Commonly used isolate fields should be described in the config.xml file and included as columns within the isolates table. Sometimes, however, you may have a need to record information that is only likely to be found in a minority of records. This can be done more efficiently with the use of sparsely-populated fields. These are stored differently in the database (using an [entity-attribute-value \[EAV\] model](#)) but can still be searched and exported in a similar way to normal fields. There is no limit to the number of such fields that can be defined.

The default name for these fields is ‘secondary metadata’ and this is how they will be grouped in the interface. You can change this by setting the ‘eav\_fields’ attribute in the *system tag of config.xml*. It is also possible to group these fields in to categories - these can be defined with a comma-separated list in the ‘eav\_groups’ attribute in the *system tag of config.xml*.

You will need to be an admin to define sparsely-populated fields. Make sure that the ‘Fields’ toggle is selected on the curators’ page. Click the add (+) button on the ‘Sparse fields’ function.



Fill in the form and click ‘Submit’.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new sparse field

Add new sparse field

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

field: cigarettes\_smoked\_per\_day

value format: text

no curate: ☐ true ☒ false

no submissions: ☐ true ☒ false

curator: Keith Jolley (keith)

timestamp: 2020-07-18

category: Risk factors

description:

length:

option list: none;1-5;6-10;11-20;21+

value regex:

conditional formatting:

html link text:

html message:

min value:

max value:

field order:

Action

RESET

SUBMIT

Field options are:

- **field**
  - name of field
- **value\_format**
  - date type - either integer, float, text, date or boolean.
- **no\_curate**
  - Set to true to prevent user updates of fieldThis setting could be used if the value is calculated by an external script rather than entered by a curator.
- **no\_submissions**
  - Set to true to prevent the field being listed in the submissions template.
- **description**
  - Tooltip text that will appear on curator forms.
- **length**
  - Restrict allowed length of value.
- **option\_list**
  - Semi-colon separated list of allowed values.
- **value\_regex**

- Regular expression that can constrain allowed values.
- conditional\_formatting
  - Semi-colon separated list of values - each consisting of the value, followed by a pipe character (|) and HTML to display instead of the value. If you need to include a semi-colon within the HTML, use two semi-colons (;;) otherwise it will be treated as the list separator.
- html\_link\_text
  - This defines the text that will appear on an information link that will trigger a slide-in message (if defined in the next field). Default is 'info'.
- html\_message
  - This message will slide-in on the isolate information page when the field value is populated and the information link is clicked. Full HTML formatting is supported.
- min\_value
  - Valid for number fields only.
- max\_value
  - Valid for number fields only.
- field\_order
  - Integer indicating the order that fields should be displayed. If this is not set they will appear alphabetically.

## 4.8 Kiosk mode

Kiosk mode allows you to run a cut-down interface that offers a single main functionality. Currently, only a sequence query page is supported. The interface is locked down so that only specified functionality is supported and data cannot be exported.

See the *kiosk\_\* attributes* in config.xml.

As an example, the following settings are used for the rMLST 'Identify species' tool at <https://pubmlst.org/rmlst/>. The database usually requires a user to log in, but this tool offers a restricted functionality without logging in.

```
kiosk="sequenceQuery"
kiosk_allowed_pages="sequenceTranslate"
kiosk_title="Identify species"
kiosk_locus="SCHEME_1"
kiosk_simple="yes"
kiosk_no_upload="no"
kiosk_no_genbank="no"
rest_kiosk="sequenceQuery"
```

When you go to this [example kiosk page](#) you see only the sequence query page and trying to access any other functionality is prevented.

The rest\_kiosk attribute enables queries to also be performed using the *RESTful API* which will be similarly locked down.

## 4.9 User authentication

You can choose whether to allow Apache to handle your authentication or use built-in authentication.

### 4.9.1 Apache authentication

Using apache to provide your authentication allows a flexible range of methods and back-ends (see the [Apache authentication HowTo](#) for a start, or any number of tutorials on the web).

At its simplest, use a .htaccess file in the directory containing the bigscurate.pl (and bigsdb.pl for restriction of read-access) script or by equivalent protection of the directory in the main Apache server configuration. It is important to note however that, by default, any BIGSdb database can be accessed by any instance of the BIGSdb script (including one which may not be protected by a .htaccess file, allowing public access). To ensure that only a particular instance (protected by a specific htaccess directive) can access the database, the following attributes can be set in the system tag of the database XML description file:

- script\_path\_includes: the BIGSdb script path must contain the value set.
- curate\_path\_includes: the BIGSdb curation script path must contain the value set.

For public databases, the 'script\_path\_includes' attribute need not be set.

To use apache authentication you need to set the authentication attribute in the system tag of the database XML configuration to 'apache'.

### 4.9.2 Built-in authentication

BIGSdb has its own built-in authentication, using a separate database to store password and session hashes. The advantages of using this over many forms of apache authentication are:

- Users are able to update their own passwords.
- Passwords are not transmitted over the Internet in plain text.

When a user logs in, the server provides a random one-time session variable and the user is prompted to enter their username and password. The password is encrypted within the browser using a Javascript one-way hash algorithm, and this is combined with the session variable and hashed again. This hash is passed to the server. The server compares this hash with its own calculated hash of the stored encrypted password and session variable that it originally sent to the browser. Implementation is based on [perl-md5-login](#). Stored passwords are salted and hashed using bcrypt.

To use built-in authentication you need to set the authentication attribute in the system tag of the database XML configuration to 'builtin'.

## 4.10 Setting up the admin user

The first admin user needs to be manually added to the users table of the database. Connect to the database using `psql` and add the following (changing details to suit the user):

```
INSERT INTO users (id, user_name, surname, first_name, email, affiliation, status, date_
→entered,
timestamp, curator) VALUES (1, 'keith', 'Jolley', 'Keith', 'keith.jolley@zoo.ox.ac.uk',
'University of Oxford, UK', 'admin', 'now', 'now', 1);
```

If you are using built-in authentication, set the password for this user using the `add_user.pl` script. This hashes the password and stores this within the authentication database. Other users can be added by the admin user from the curation interface accessible from [http://your\\_website/cgi-bin/private/bigscurate.pl?db=test\\_db](http://your_website/cgi-bin/private/bigscurate.pl?db=test_db) (or wherever you have located your bigscurate.pl script).

## 4.11 Retrieving PubMed citations from NCBI

Publications listed in PubMed can be associated with individual isolate records, profiles, loci and sequences. Full citations for these are stored within a local reference database, enabling these to be displayed within isolate records and searching by publication and author. This local database is populated by a script that looks in BIGSdb databases for PubMed records not locally stored and then requests the full citation record from the PubMed database.

The script is called `retrieve_pubmed_records.pl` and can be found in the `scripts/maintenance` directory.

Simply run the script either as the 'postgres' user or an account that is allowed to connect as the postgres user.

This should be run periodically from a CRON job, e.g. every hour.

## 4.12 Configuring access to remote contigs

It is possible for isolate records to have contigs in an external BIGSdb database. These must be accessible via the *RESTful API*. The advantage of this is that it enables multiple isolate databases to use the same genome assemblies without having to duplicate the storage of those assemblies. If access to the external database requires authenticated access, OAuth settings can be set to enable contig retrieval.

To enable remote contigs, set the `remote_contigs` attribute in the `<system>` tag of `config.xml`, i.e.

```
remote_contigs = "yes"
```

### 4.12.1 Setting up authentication

A client key for the BIGSdb remote contig manager needs to be generated. This can be done using the `create_client_credentials.pl` script, e.g.

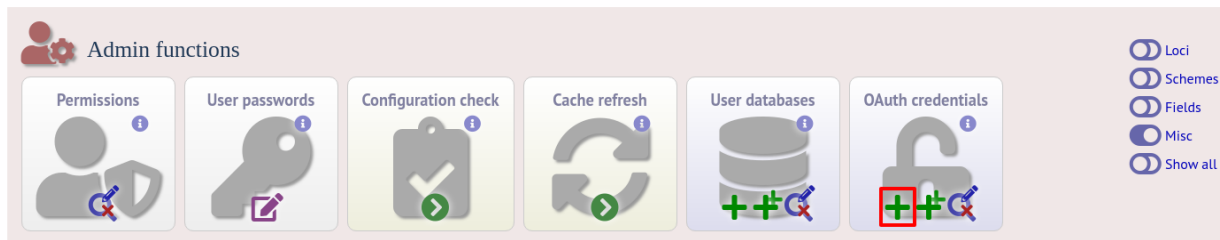
```
create_client_credentials.pl --a 'BIGSdb remote contig manager' --insert
```

This will generate a client id (key) and a client secret and add them to the authentication database.

You will then need to obtain an access token and access secret using the client key and secret with the `get_oauth_access_token.pl` script. You will need to enter the API database URI (e.g. [http://rest.pubmlst.org/db/pubmlst\\_rmlst\\_isolates](http://rest.pubmlst.org/db/pubmlst_rmlst_isolates)) and the web database URL (e.g. [https://pubmlst.org/bigsdb?db=pubmlst\\_rmlst\\_isolates](https://pubmlst.org/bigsdb?db=pubmlst_rmlst_isolates)). You

will then be prompted to follow a link and log in to the database with your user credentials. A verification code will be generated. You need to enter this in to the script when prompted. An access token and secret will be returned to you.

From the curators' page, click the oauth credentials add link in the administrator settings. This function is normally hidden, so you may need to click the 'Misc' toggle to display it.



Populate the OAuth\_credentials table with the client key/secret and access token/secret. You should also enter the root REST URI for the database (e.g. [http://rest.pubmlst.org/db/pubmlst\\_rmlst\\_isolates](http://rest.pubmlst.org/db/pubmlst_rmlst_isolates)).

## 4.12.2 Processing remote contigs

When remote contigs are first linked to a record, the sequences are downloaded in bulk (without their metadata). This allows the sequence lengths to be recorded as this is needed for various queries and outputs. The curator is then given an option to process the contigs, which involves downloading each contig individually to record metadata including the original designation and the sequence platform used. This may take a while so it may be preferable to perform this task offline. This can be done using the `process_remote_contigs.pl` script found in the `scripts/automation` directory. Options for using this script are shown below:

```
remote_contigs.pl --help
NAME
    process_remote_contigs.pl
    Download, check length and create checksum contigs stored as URIs

SYNOPSIS
    process_remote_contigs.pl --database NAME [options]

OPTIONS
    --database NAME
```

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```

Database configuration name.

--exclude_isolates LIST
    Comma-separated list of isolate ids to ignore.

--exclude_projects LIST
    Comma-separated list of projects whose isolates will be excluded.

--help
    This help page.

--isolates LIST
    Comma-separated list of isolate ids to scan (ignored if -p used).

--isolate_list_file FILE
    File containing list of isolate ids (ignored if -i or -p used).

--min ID
    Minimum isolate id.

--max ID
    Maximum isolate id.

--projects LIST
    Comma-separated list of project isolates to scan.

--quiet
    Only display errors.

.. _setup_dashboard:

```

## 4.13 Setting up front-end dashboards

Dashboards can be used as an alternative front-end to isolate databases. In order to enable dashboards for a particular database, they have to be enabled either globally or specifically for the database configuration. If enabled, users will have the option to toggle between the dashboard and the standard index page.

To enable globally and use the dashboard by default, set the following in bigsdb.conf:

```

enable_dashboard=1
default_dashboard_view=1

```

Each of these values can be overridden for a particular database by setting the same attribute in the database config.xml file, with either 'yes' or 'no', i.e. dashboards can be enabled globally but disabled for a particular database configuration, or disabled globally but enabled for a particular database configuration.

### 4.13.1 Defining a default dashboard

A default global dashboard can be set up by placing a dashboard.toml file in /etc/bigsdb. This can be overridden for individual database configurations by adding a TOML file (dashboard.toml), in the same format, to the database configuration directory. An example of the format can be seen below.

```
#Configuration for default front-end dashboard for isolate databases. This
#defines the visual elements that will be included. If field-specific elements
#are defined and that field does not exist in a particular database then it
#will be ignored.

#The default configuration can be overridden for a particular database by
#including a dashboard.toml file, using the same format, in the database
#configuration directory.

#Width can be 1, 2, 3, or 4.
#Height can be 1, 2, or 3.

#Field names have prefixes indicating the field type:
#f_ are standard provenance/primary fields
#e_ are extended attributes with the main field and the attribute separated
# by ||, e.g. e_country||continent.

elements = [
  { #Isolate count.
    display      = 'record_count',
    name         = 'Isolate count',
    width        = 2,
    background_colour = '#79cafb',
    main_text_colour = '#404040',
    watermark     = 'fas fa-bacteria',
    change_duration = 'month',
    url_text      = 'Browse isolates',
    hide_mobile   = 0
  },
  { #Genome count (will only display if there are genomes in the database).
    display      = 'record_count',
    name         = 'Genome count',
    genomes      = 1,
    width        = 2,
    background_colour = '#7ecc66',
    main_text_colour = '#404040',
    watermark     = 'fas fa-dna',
    change_duration = 'month',
    url_text      = 'Browse genomes',
    post_data     = { genomes = 1 },
    hide_mobile   = 0
  },
  {
    display      = 'field',
    name         = 'Country',
    field        = 'f_country',
    breakdown_display = 'map',
  }
]
```

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```

    width          = 3,
    height         = 2,
    hide_mobile    = 1
  },
  {
    #Top 5 list of continents (Geocoding should be set up with default country
    #list linked to continent - see 'Geocoding setup' on admin curator page.
    display        = 'field',
    name           = 'Continent',
    field          = 'e_country||continent',
    breakdown_display = 'top',
    top_values     = 5,
    width          = 2,
    hide_mobile    = 1
  },
  {
    name           = 'Sequence size',
    display        = 'seqbin_size',
    genomes        = 1,
    hide_mobile    = 1,
    width          = 2,
    height         = 1
  },
  {
    #Doughnut chart of species.
    display        = 'field',
    name           = 'Species',
    field          = 'f_species',
    breakdown_display = 'doughnut',
    height         = 2,
    width          = 2,
    hide_mobile    = 1
  },
  {
    #Treemap of disease.
    display        = 'field',
    name           = 'Disease',
    field          = 'f_disease',
    breakdown_display = 'treemap',
    height         = 2,
    width          = 2,
    hide_mobile    = 1
  },
  {
    #Bar chart of submission years.
    display        = 'field',
    name           = 'Year',
    field          = 'f_year',
    breakdown_display = 'bar',
    width          = 3,
    bar_colour_type = 'continuous',
    chart_colour   = '#126716',
    hide_mobile    = 1
  },

```

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```
{
  #Cumulative chart of submissions by date.
  display      = 'field',
  name         = 'Date entered',
  field        = 'f_date_entered',
  width        = 2,
  breakdown_display = 'cumulative',
  hide_mobile  = 1
}
]
```

## Attributes

The allowed attributes are listed below.

- background\_colour
  - RGB hex code for the background colour, e.g. '#79cafb'. This is used only for 'big number' fields, e.g. isolate count.
- bar\_colour\_type
  - categorical - use contrasting colours for bars.
  - continuous - use the same colour for all bars (set colour use 'chart\_colour' attribute).
- breakdown\_display - type of visualisation. Allowed values are:
  - bar
    - \* bar chart - particularly useful for continuous data such as year.
  - cumulative
    - \* cumulative line chart - used for date\_entered or datestamp fields.
  - doughnut
    - \* doughnut chart
  - pie
    - \* pie chart
  - top
    - \* top values list. You can choose the number of values to display by also setting the top\_values attributes to either 3, 5, or 10.
  - treemap
    - \* treemap chart
  - word
    - \* word cloud. This can only be used for fields that have a defined list of allowed values.
  - map
    - \* global map. This can only be used for 'country' fields with a defined list allowed values or 'continent' fields which are an extended attribute of country.
- change\_duration

- Show the rate of change, e.g. the number of new records in past month. Used for ‘big number’ fields, e.g. isolate count or specific value count. Allowed values are ‘week’, ‘month’, or ‘year’.
- chart\_colour
  - RGB hex code for bar or cumulative line charts, e.g. ‘#126716’.
- display
  - Element type. Allowed values are:
    - \* field - This is used for most elements.
    - \* record\_count - Used for isolate count fields.
    - \* seqbin\_size - Used to display a histogram of genome sizes.
- field
  - The name of the field to display. Different types of field have different prefixes as follows:
    - \* Primary isolate field - prefix with ‘f\_’, e.g. ‘f\_country’.
    - \* *Secondary metadata fields* - prefix with ‘eav\_’.
    - \* *Extended attributes* - prefix with ‘e\_’, followed by the primary field name, followed by ‘||’ and then the extended attribute name, e.g. for continent linked to country you would use ‘e\_country||continent’.
    - \* Scheme fields - e.g. clonal complex - prefix with ‘s\_’ followed by the scheme id number, then ‘\_’, followed by the scheme field name, e.g. for a field called ‘clonal\_complex’ defined for scheme 1, you would use ‘s\_1\_clonal\_complex’.
- gauge\_background\_colour
  - RGB hex code, e.g. ‘#79cafb#’, for the background colour on a gauge chart.
- gauge\_foreground\_colour
  - RGB hex code, e.g. ‘#79cafb#’, for the foreground colour on a gauge chart.
- header\_background\_colour
  - RGB hex code, e.g. ‘#79cafb#’, for the header background for a top values list.
- header\_text\_colour
  - RGB hex code, e.g. ‘#79cafb#’, for the header text colour for a top values list.
- height
  - Height of element - either 1, 2, or 3.
- hide\_mobile
  - Set to 1 to hide element on small mobile devices (width <= 480 pixels).
- main\_text\_colour
  - RGB hex code, e.g. ‘#79cafb#’, for the colour of the text used in big number elements.
- name
  - The name used for the title of the element.
- palette
  - ColorBrewer palette used for map displays. Allowed values are:
    - \* blue

- \* green
- \* purple
- \* orange
- \* red
- \* blue/green
- \* blue/purple
- \* green/blue
- \* orange/red
- \* purple/blue
- \* purple/blue/green
- \* purple/red
- \* red/purple
- \* yellow/green
- \* yellow/green/blue
- \* yellow/orange/brown
- \* yellow/orange/red
- post\_data
  - Used to pass data attributes for linked queries. Currently only ‘genomes’ is used to specify that isolates should be filtered to those with genome assemblies, e.g. ‘{genomes = 1}’.
- specific\_value\_display
  - Type of display to use for specific values. Allowed values are:
    - \* gauge - gauge chart
    - \* number - big number value
- specific\_values
  - list of field values to include in count shown in gauge chart or big number display, e.g. ‘[‘Neisseria meningitidis’]’.
- url\_text
  - link text to display when hovering over link leading to data query. Only available for isolate count or specific value charts.
- visualisation\_type
  - Either ‘breakdown’ (default) or ‘specific values’. You need to then set the visualisation using either the breakdown\_display or specific\_value\_display attribute.
- watermark
  - FontAwesome icon class used for background watermark on big number charts, e.g. ‘fas fa-bacteria’. See <https://fontawesome.com/icons?m=free>.
- width
  - Width of element - either 1, 2, 3, or 4.

## ADMINISTRATOR'S GUIDE

Please note that links displayed within the curation interface will vary depending on database contents and the permissions of the curator.

### 5.1 Types of user

There are four types of user in BIGSdb:

- User - can view data but never modify it. Users should be created for every submitter of data so that records can be tracked, even if they do not actually use the database.
- Submitter (isolate databases only) - can add and modify their own isolate data and data submitted by anybody else that is in the same *user group* as them but not anyone else's. A limited range of *Individual permissions* can be set for each submitter, so their roles can be controlled. A submitter with no specific permissions set has no more power than a standard user.
- Curator - can modify data but does not have full control of the database. *Individual permissions* can be set for each curator, so their roles can be controlled. A curator with no specific permissions set has no more power than a standard user.
- Admin - has full control of the database, including setting permissions for curators and setting user passwords if built-in authentication is in use.

### 5.2 User groups

User groups allow submitter accounts to be grouped such that the submitter can edit isolates where the sender is either themselves or any member of a user group to which they belong.

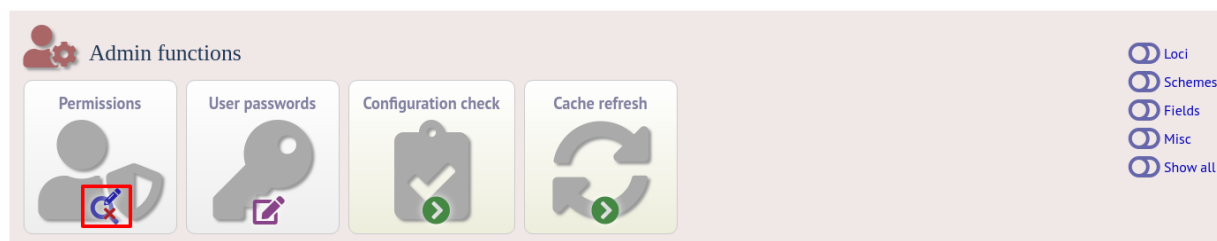
### 5.3 Curator permissions

Individual permissions can be set for each curator:

- `disable_access` - if set to true, this user is completely barred from access.
- `query_users` - allowed to query and view users registered to the database. This is automatically allowed if permission is set to modify users.
- `modify_users` - allowed to add or modify user records. They can change the status of users, but can not revoke admin privileges from an account. They can also not raise the status of a user to admin level.
- `modify_usergroups` - allowed to add or modify user groups and add users to these groups.

- `set_user_passwords` - allowed to modify other users' passwords (if built-in authentication is in use).
- `modify_loci` - allowed to add or modify loci.
- `modify_locus_descriptions` - allowed to modify the description text and external hyperlinks used. Even with this setting, only loci for which a user is explicitly set as a curator can be modified.
- `modify_schemes` - allowed to add or modify schemes.
- `modify_sequences` - allowed to add sequences to the sequence bin (for isolate databases) or new allele definitions (for sequence definition databases).
- `modify_isolates` - allowed to add or modify isolate records.
- `modify_projects` - allowed to create projects, modify their descriptions and add or remove isolate records to these.
- `modify_composites` - allowed to add or modify composite fields (fields made up of other fields, including scheme fields defined in external databases). Composite fields involve defining regular expressions that are evaluated by Perl - this can be dangerous so this permission should be granted with discretion.
- `modify_field_attributes` - allow user to create or modify secondary field attributes (lookup tables) for isolate record fields.
- `modify_value_attributes` - allow user to add or modify secondary field values for isolate record fields.
- `modify_probes` - allow user to define PCR or hybridization reactions to filter tag scanning.
- `tag_sequences` - allowed to tag sequences with locus information.
- `designate_alleles` - allowed to manually designate allele numbers for isolate records.
- `modify_profiles` - allowed to add or modify scheme profiles (only used in a sequence definitions database).
- `import_site_users` - allowed to import site users in to the database.
- `modify_site_users` - allowed to modify site user details (you may not want to this! The user account can be used by multiple databases on the site and any changes to user details will be seen throughout the site).

Permissions can be set by clicking the Update/delete button in the Permissions box in the admin functions area of the curator's interface:



Choose one or more curators from the list (hold down Ctrl to select multiple values). click 'Select'.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Set curator permissions

Set curator permissions

Select curator(s) Action

de Korne, Joana (jokorne)  
 Debech, Nadia (ndebech)  
 Deghmane, Ala-Eddin (deghmane)  
 Demczuk, Walter (wdemczuk)  
 Desmet, Stefanie (sdsmet6)  
 Diallo, Kanny (kdiallo)  
 Dillon, Jo-Anne (jdillon)  
 Exley, Rachel (rexley)

SELECT

All None

Click the appropriate checkboxes to modify permissions. There are also 'All/None' buttons to facilitate quicker selection of options. Click 'Update'.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Set curator permissions

Set curator permissions

Select curator(s) Action

Cehovin, Ana (acehovin)  
 Chan, Hannah (hchan)  
 Chen, Mingliang (cmibright)  
 Choi, Eunhwa (eunchoi)  
 Christodoulides, Myron (mchristodoul)  
 Clark, Stephen (SClark)  
 Claus, Heike (hclaus)  
 Clemence, Marianne (mclemence)

SELECT

All None

Check the boxes for the required permissions. Users with a status of 'submitter' have a restricted list of allowed permissions that can be selected. Attributes with a red background add restrictions.

Update permissions Action

Permission	Curator		All/None
	Clemence, Marianne	Diallo, Kanny	
query users	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify users	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify isolates	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
modify projects	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
modify sequences	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
tag sequences	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
designate alleles	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
modify usergroups	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
set user passwords	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify loci	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
modify schemes	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
modify composites	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify field attributes	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify value attributes	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify sparse fields	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify probes	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify experiments	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
delete all	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
import site users	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify site users	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
only private	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
disable access	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
All/None	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

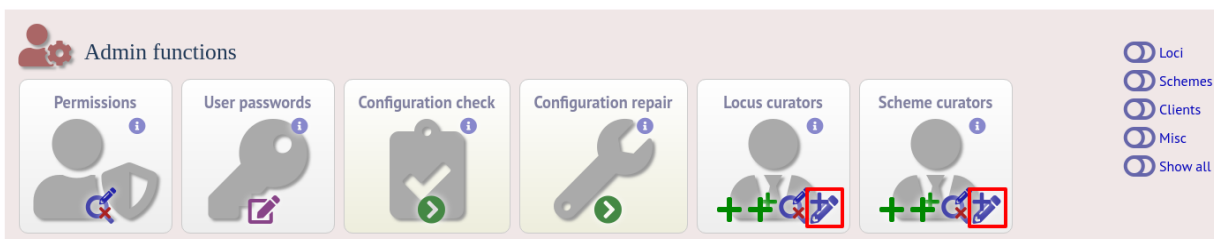
UPDATE

The 'disable access' option provides a quick way to disable access to a curator. This will not be selected by the 'All/None' buttons.

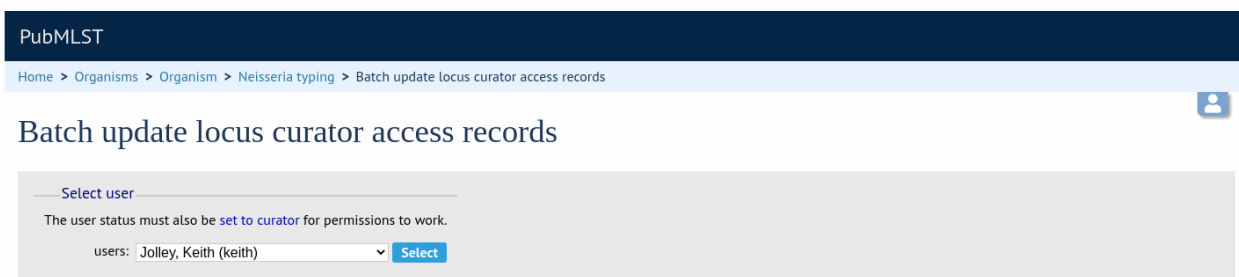
## 5.4 Locus and scheme permissions (sequence definition database)

To be allowed to define alleles or scheme profiles, curators must be granted specific permission for each locus and scheme by adding their user id number to the ‘locus curator’ and ‘scheme curator’ lists.

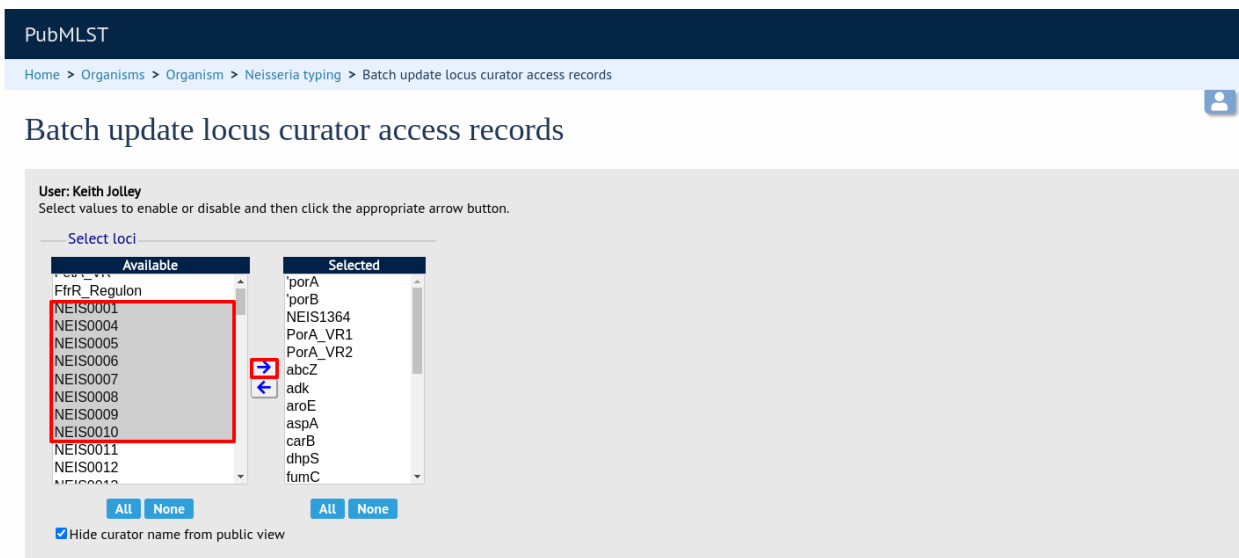
The easiest way to modify these lists is to use the batch update link next to ‘locus curator control list’ and ‘scheme curator control list’:



Select the curator from the list:



Then select loci/schemes that the user is allowed to curate in the left hand ‘Available’ list, and click the right button to move these to the ‘Selected’ list:



If you uncheck the ‘Hide curator name from public view’ checkbox, the curator name and E-mail address will appear alongside loci in the download table on the website.

## 5.5 Controlling access

### 5.5.1 Restricting particular configurations to specific user accounts

Suppose you only wanted specific users to access a database configuration.

In the config.xml, add the following directive:

```
default_access="deny"
```

This tells BIGSdb to deny access to anybody unless their account name appears within a file called users.allow within the config directory. The users.allow file should contain one username per line. You can also use a usergroups.allow file. This file should contain the names of user groups, the members of which are allowed access. The file should contain one user group name per line.

Alternatively, you can deny access to specific users, while allowing every other authenticated user. In config.xml, add the following directive:

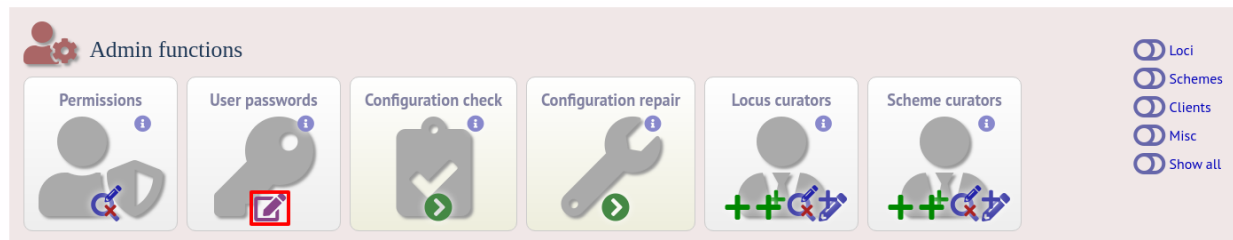
```
default_access="allow"
```

This tells BIGSdb to allow access to anybody unless their account name appears within a file called users.deny within the config directory. The users.deny file should contain one username per line.

## 5.6 Setting user passwords

*Please note that these instructions only apply if using the built-in BIGSdb authentication system.*

If you are an administrator or a curator with specific permission to change other users' passwords, you should see a 'User passwords' box in the admin section of the curator's index page. Click the 'Set passwords' link.



Select the appropriate user from the drop-down list box and enter the new password twice where prompted.

PubMLST

Home > Organisms > Organism > Neisseria typing > Change password

Set user password

Passwords must be at least 8 characters long.

Passwords	Action
User: Jolley, Keith (keith) ▼	SET PASSWORD
New password: ●●●●●●	
Retype password: ●●●●●●	

Click 'Set password' and the password will be updated.

## 5.7 Setting the first user password

To set the first administrator's password for a new database, use the `add_user.pl` script found in the `scripts/maintenance` directory:

```
add_user.pl [-a] -d <dbase> -n <username> -p <password>
```

The first user account needs to be added to the database *manually*.

## 5.8 Enabling plugins

Some plugins can be enabled/disabled for specific databases. If you look in the `get_attributes` function of the specific plugin file and see a value for `system_flag`, this value can be used in the `system` tag of the database configuration XML file to enable the plugin.

For example, the `get_attributes` function of the BURST plugin looks like:

```
sub get_attributes {
    my %att = (
        name          => 'BURST',
        author        => 'Keith Jolley',
        affiliation    => 'University of Oxford, UK',
        email         => 'keith.jolley@zoo.ox.ac.uk',
        description    => 'Perform BURST cluster analysis on query results query_
↪results',
        category      => 'Cluster',
        buttontext     => 'BURST',
        menutext       => 'BURST',
        module         => 'BURST',
        version        => '1.0.0',
        dbtype         => 'isolates,sequences',
        section        => 'postquery',
        order          => 10,
        system_flag    => 'BURST',
        input          => 'query',
        requires        => 'mogrify',
        min            => 2,
        max            => 1000
    );
    return \%att;
}
```

The `'system_flag'` attribute is set to `'BURST'`, so this plugin can be enabled for a database by adding:

```
BURST="yes"
```

to the `system` tag of the database XML file. If the `system_flag` value is not defined then the plugin is always enabled if it is installed on the system. If the `system_flag` value is set to `'no'` then the plugin will be disabled even if the `all_plugins` attribute is set to `'yes'`.

## 5.9 Temporarily disabling database updates

There may be instances where it is necessary to temporarily disable database updates. This may be during periods of server or database maintenance, for instance when running on a backup database server.

Updates can be disabled on a global or database-specific level.

### 5.9.1 Global

In the `/etc/bigsdb/bigsdb.conf` file, add the following line:

```
disable_updates=yes
```

An optional message can also be displayed by adding a `disable_update_message` value, e.g.

```
disable_update_message=The server is currently undergoing maintenance.
```

### 5.9.2 Database-specific

The same attributes described above for use in the `bigsdb.conf` file can also be used within the system tag of the database `config.xml` file, e.g.

```
<system
  db="bigsdb_neisseria"
  dbtype="isolates"
  ...
  disable_updates="yes"
  disable_update_message="The server is currently undergoing maintenance."
```

## 5.10 Host mapping

During periods of server maintenance, it may be necessary to map a database host to an alternative server. This would allow a backup database server to be used while the primary database server is unavailable. In this scenario, you would probably also want to *disable updates*.

Host mapping can be achieved by editing the `/etc/bigsdb/host_mapping.conf` file. Each host mapping is placed on a single line, with the current server followed by any amount of whitespace and then the new mapped host, e.g.

<i>#Existing_host</i>	<i>Mapped_host</i>
server1	server2
localhost	server2

[Lines beginning with a hash are comments and are ignored.]

This configuration would use `server2` instead of `server 1` or `localhost` wherever they are defined in the database configuration (either host attribute in the database `config.xml` file, or within the loci or schemes tables).

## 5.11 Improving performance

### 5.11.1 Use mod\_perl

The single biggest improvement to speed can be obtained by running BIGSdb under mod\_perl. There's very little point trying anything else until you have mod\_perl set up and running - this can improve start-up performance a hundred-fold since the script isn't compiled on each page access but persists in memory.

### 5.11.2 Cache scheme definitions within an isolate database

If you have a large number of allelic profiles defined for a scheme, you can cache these definitions within an isolate database to speed up querying of isolates by scheme criteria (e.g. by ST for a MLST scheme).

To do this use the update\_scheme\_caches.pl script found in the scripts/maintenance directory, e.g. to cache all schemes in the pubmlst\_bigsdb\_neisseria\_isolates database

```
update_scheme_caches.pl --database pubmlst_bigsdb_neisseria_isolates
```

This script creates indexed tables within the isolate database called temp\_scheme\_X and temp\_isolates\_scheme\_fields\_1 (where X is the scheme\_id). If these table aren't present, they are created as temporary tables every time a query is performed that requires a join against scheme definition data. This requires importing all profile definitions from the definitions database and determining scheme field values for all isolates. This may sound like it would be slow but caching only has a noticeable effect once you have >5000 profiles.

You are able to update the cache for a single scheme, or a list of schemes, and choose the method of update. For large schemes, such as cgMLST, a full refresh may take a long time, so you may wish to only perform this infrequently (perhaps once a week) with more regular 'daily' or 'daily\_replace' updates. A full list of options available are shown by typing

```
update_scheme_caches.pl --help
```

#### NAME

update\_scheme\_caches.pl - Update scheme field caches

#### SYNOPSIS

update\_scheme\_caches.pl --database NAME [options]

#### OPTIONS

--database NAME

Database configuration name.

--help

This help page.

--method METHOD

Update method - the following values are allowed:

full: Completely recreate caches

incremental: Only add values **for** records **not in** cache.

daily: Only add values **for** records **not in** cache updated today.

daily\_replace: Refresh values only **for** records updated today.

--quiet

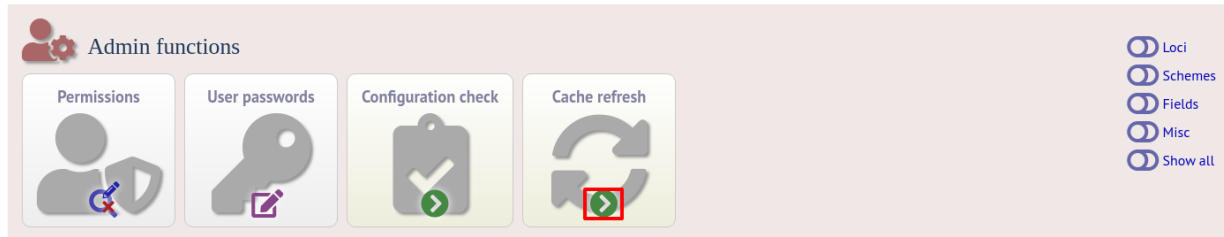
(continues on next page)

(continued from previous page)

```
Don't output progress messages.
```

```
--schemes SCHEMES
    Comma-separated list of scheme ids to use.
    If left empty, all schemes will be updated.
```

Note that you will need to run this script periodically as a CRON job to refresh the cache. Admins can also refresh the caches manually from a link on the curators' page. This link is only present if the caches have been previously generated.



You can also set `cache_schemes="yes"` in the system tag of `config.xml` to enable automatic refreshing of the caches (using the 'daily' method) when batch adding new isolates (you should still periodically run the `update_scheme_caches.pl` script via CRON to ensure any changes in the sequence definition database are picked up).

If queries are taking longer than 5 seconds to perform and a cache is not in place, you will see a warning message in `bigsd.log` suggesting that the caches be set up. Unless you see this warning regularly, you probably don't need to do this.

### 5.11.3 Use a ramdisk for the secure temporary directory

If you are running BIGSdb on a large server with lots of RAM, you could use some of this as a ramdisk for temporary files. Debian/Ubuntu systems make available up to half the system RAM as a ramdisk mounted under `/run/shm` (or `/dev/shm`) by default. Set the `secure_tmp_dir` to this RAM disk and you should see significant improvement in operations requiring the writing of lots of temporary files, e.g. tag scanning and the Genome Comparator plugin. This is only likely to be appropriate if you have very large amounts of RAM available. As an example, the server hosting the PubMLST databases is a dedicated machine with 1TB RAM with temporary files rarely using more than 50GB space.

## 5.12 Dataset partitioning

### 5.12.1 Sets

Sets provide a means to partition the database in to manageable units that can appear as smaller databases to an end user. Sets can include constrained groups of isolates, loci, and schemes from the complete database.

**See also:**

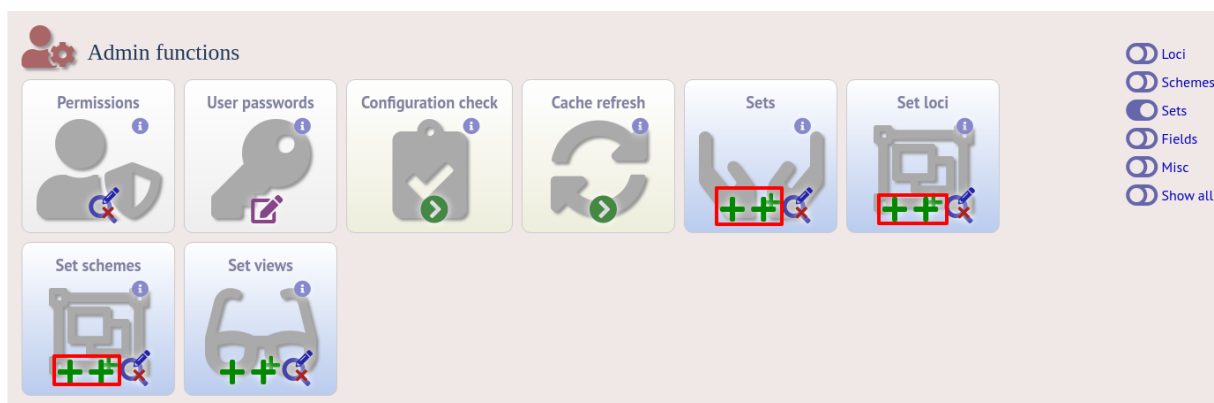
*Sets (concept)*

## 5.12.2 Configuration of sets

First sets need to be enabled in the XML configuration file (config.xml) of the database. Add the following attribute to the system tag:

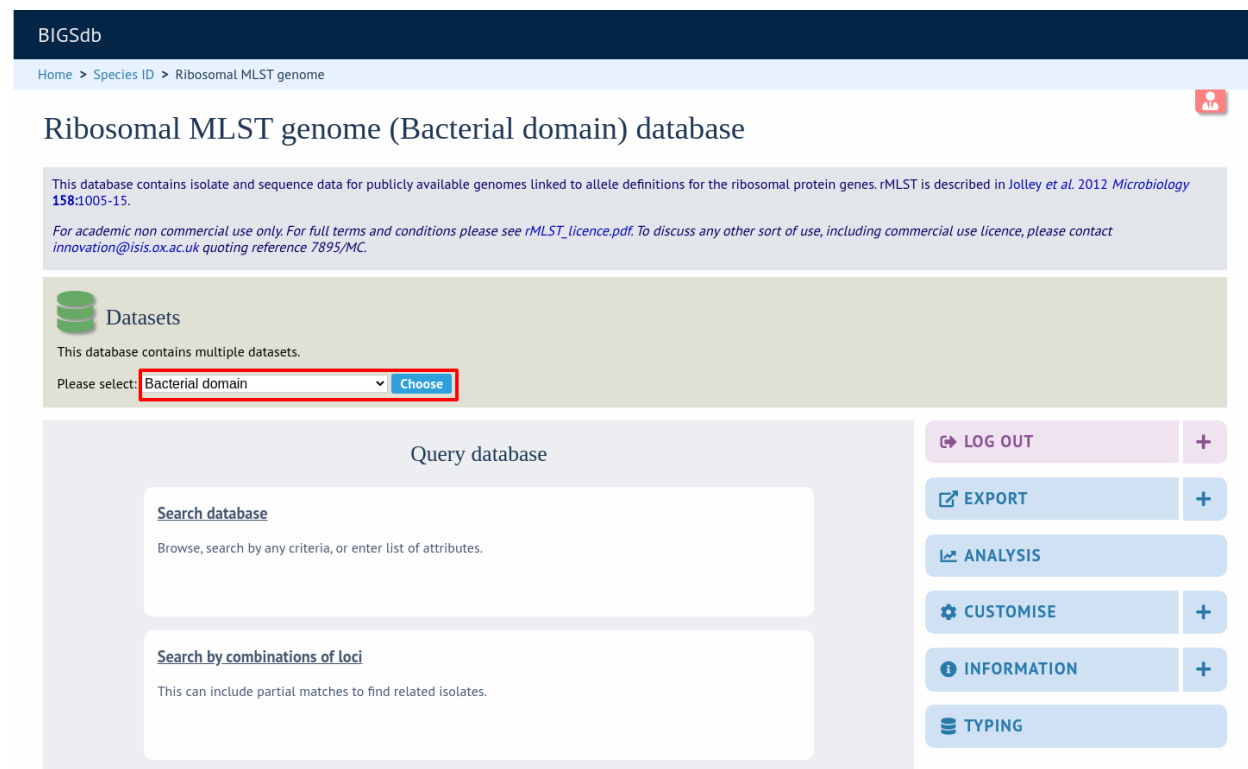
```
sets="yes"
```

With this attribute, the curation interface now has options to add sets, and then add loci or schemes to these sets. These functions are normally hidden, so you may need to click the ‘Sets’ toggle to display it.



The name of a locus or scheme to use within a set can be defined in the set\_name field when adding loci or schemes to a set. Common names can also be set for loci - equivalent to the common name used within the loci table.

Now when a user goes to the contents page of the database they will be presented with a dropdown menu of datasets and can choose either the ‘whole database’ or a specific set. This selection is remembered between sessions.



Alternatively, a specific set can be selected within the XML config file so that only a specific set is available when

accessed via that configuration. In that case, the user would be unaware that the database contains anything other than the loci and schemes available within the set.

To specify this, add the following attribute to the system tag:

```
set_id="1"
```

where the value is the name of the set.

**Note:** If the `set_id` attribute is set, database configuration settings in the curator's interface are disabled. This is because when the configuration is constrained to a set, only loci and schemes already added to the set are visible, so functionality to edit schemes/loci would become very confusing. To modify these settings, you either need to access the interface from a different configuration, i.e. an alternative `config.xml` with the `set_id` attribute not set, or temporarily remove the `set_id` directive from the current `config.xml` while making configuration changes.

### 5.12.3 Set views

Finally the isolate record table can be partitioned using database views and these views associated with a set. Create views using something like the following:

```
CREATE VIEW spneumoniae AS SELECT * FROM isolates WHERE species = 'Streptococcus_
↪pneumoniae';
GRANT SELECT ON spneumoniae TO apache;
```

Add the available views to the XML file as a comma separated list in the system tag 'views' attribute:

```
<system
  ....
  sets="yes"
  views="spneumoniae,saureus"
>
</system>
```

Set the view to the set by using the 'Add set view' link on the curator's page.

### 5.12.4 Using only defined sets

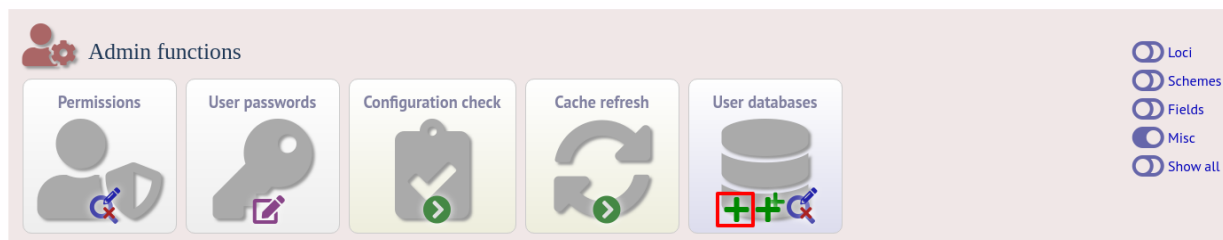
The `only_sets` attribute can be set to 'yes' to disable the option for 'Whole database' so that only sets can be viewed, e.g.

```
<system
  ....
  sets="yes"
  only_sets="yes"
>
</system>
```

## 5.13 Setting a site-wide users database

On large sites you may wish to employ a site-wide users database so that user details are kept in a single location and the user can log in to any database using the same credentials.

Once a *site-wide user database has been set up*, this can be defined within each client database as follows. From the curators' contents page, click the add (+) user databases link. This function is normally hidden, so you may need to click the 'Misc' toggle to display it.



Enter the user database details. You only need to enter the full database connection details if these are different from those set in db.conf. Press submit.

PubMLST

Home > Organisms > Organism > Neisseria Isolates > Add new user database

**Add new user database**

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
<p>id: 1</p> <p>name: PubMLST <small>! Site/domain name</small></p> <p>dbase name: pubmlst_bigsdb_users <small>! Name of the database holding user data</small></p> <p>curator: Keith Jolley (keith)</p> <p>datestamp: 2020-07-19</p> <p>list order: <input type="text"/></p> <p>auto registration: <input type="radio"/> true <input type="radio"/> false <small>Allow user to register themselves for database</small></p> <p>dbase host: <input type="text"/> <small>! IP address of database host</small></p> <p>dbase port: <input type="text"/> <small>! Network port accepting database connections</small></p> <p>dbase user: <input type="text"/></p> <p>dbase password: <input type="password"/></p>	<p>RESET SUBMIT</p>

Curators will need *specific permissions* set to be able to modify details in, or import users from a site-wide users database.

## 5.14 Adding new loci

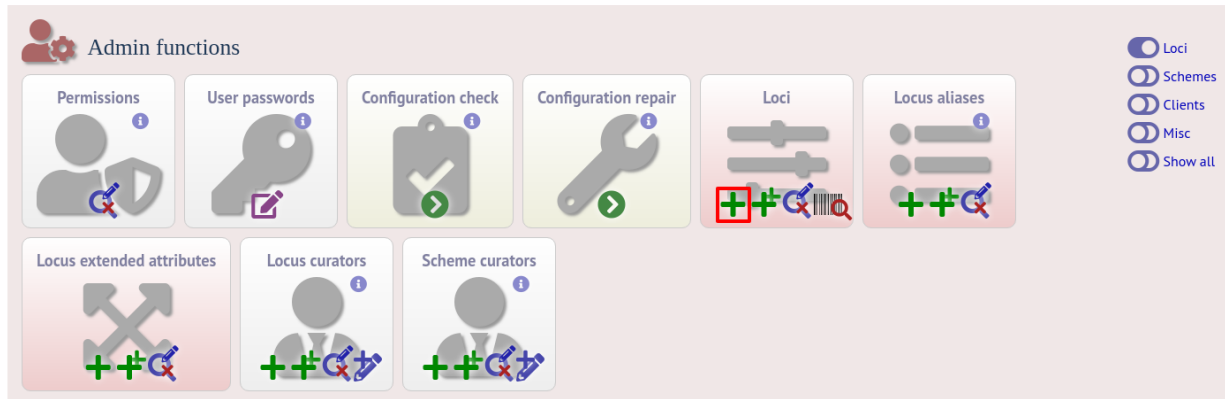
See also:

*Loci (concept)*

### 5.14.1 Sequence definition databases

#### Single locus

Click the add (+) loci link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Loci' toggle to display it.



Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

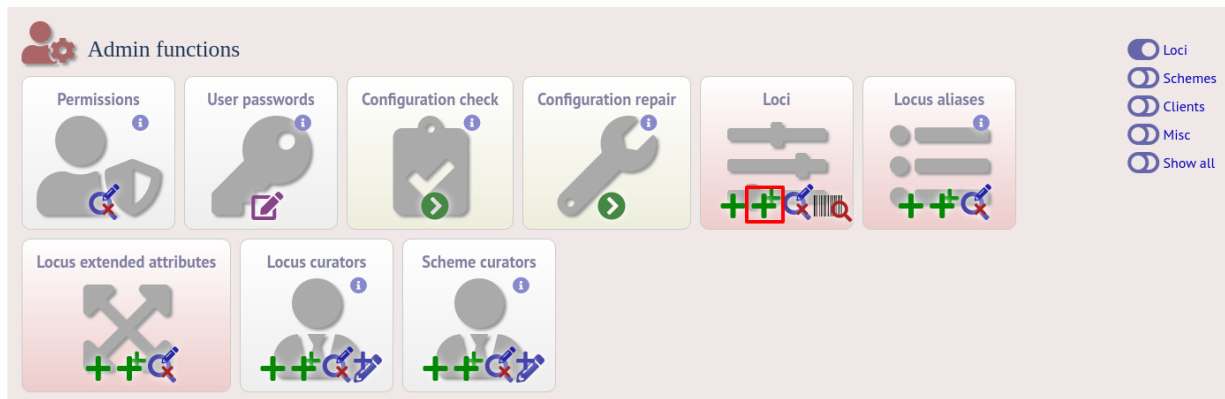
- id - The name of the locus.
  - Allowed: any value starting with a letter, number or underscore.
- data\_type - Describes whether the locus is defined by nucleotide or peptide sequence.
  - Allowed: DNA/peptide.
- allele\_id\_format - The format for allele identifiers.
  - Allowed: integer/text.
- length\_varies - Sets whether alleles can vary in length.
  - Allowed: true/false.
- coding\_sequence - Sets whether the locus codes for a protein.
  - Allowed: true/false.
- formatted\_name - Name with HTML formatting (optional).
  - This allows you to add formatting such as bold, italic, underline and superscripting to locus names as they appear in the web interface.
  - Allowed: valid HTML.
- common\_name - The common name for the locus (optional).
  - Allowed: any value.
- formatted\_common\_name - Common name with HTML formatting (optional).

- Allowed: valid HTML.
- `allele_id_regex` - [Regular expression](#) to enforce allele id naming (optional).
  - `^`: the beginning of the string
  - `$`: the end of the string
  - `d`: digit
  - `D`: non-digit
  - `s`: white space character
  - `S`: non white space character
  - `w`: alpha-numeric plus `'_'`
  - `.`: any character
  - `*`: 0 or more of previous character
  - `+`: 1 or more of previous character
  - e.g. `^Fd-d+$` states that an allele name must begin with a `F` followed by a single digit, then a dash, then one or more digits, e.g. `F1-12`
- `length` - Standard length of locus (required if `length_varies` is set to false).
  - Allowed: any integer.
- `min_length` - Minimum length of locus (optional).
  - Allowed: any integer.
- `max_length` - Maximum length of locus (optional).
  - Allowed: any integer (larger than the minimum length).
- `complete_cds` - Whether locus represents a complete coding sequence (optional)
- `start_codons` - Semi-colon separated list of alternative start codons to allow
  - Note that these are in addition to the built-in defaults of `ATG`, `GTG`, `TTG`.
- `orf` - Open reading frame of locus (optional).
  - 1-3 are the forward reading frame, 4-6 are the reverse reading frames.
  - Allowed: 1-6.
- `genome_position` - The start position of the locus on a reference genome (optional).
  - Allowed: any integer.
- `match_longest` - Specifies whether in a sequence query to only return the longest match (optional).
  - This is useful for some loci that can have some sequences shorter than others, e.g. peptide loci defining antigenic loops. This can lead to instances of one sequence being longer than another but otherwise being identical. In these cases, usually the longer sequence is the one that should be matched.
  - Allowed: `true/false`.
- `full_name` - Full name of the locus (optional).
  - Allowed: any value.
- `product` - Name of gene product (optional).
  - Allowed: Any value.

- description - Description of the locus (optional).
  - Allowed: any value.
- aliases - Alternative names for the locus (optional).
  - Enter each alias on a separate line in the text box.
  - Allowed: any value.
- pubmed\_ids - PubMed ids of publications describing the locus (optional).
  - Enter each PubMed id on a separate line in the text box.
  - Allowed: any integer.
- links - Hyperlinks pointing to additional resources to display in the locus description (optional).
  - Enter each link on a separate line in the format with the URL first, followed by a | then the description (URL|description).

### Batch adding

Click the batch add (++) loci link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Loci' toggle to display it.



Click the link to download a header line for an Excel spreadsheet:

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Batch add locus records](#)

Batch insert loci

Instructions

This page allows you to upload locus data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

Templates

Check the [description of database fields](#) for help with filling in the template.

Upload

Paste in tab-delimited text (Include a field header line).

RESET

SUBMIT

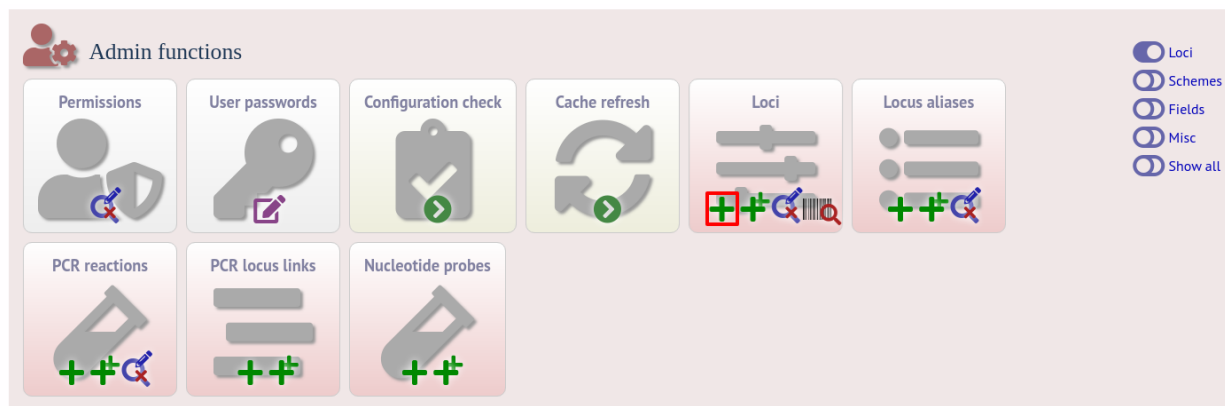
Fill in the spreadsheet using the fields described for *adding single loci*.

Fill in the spreadsheet fields using the table above as a guide, then paste the completed table into the web form and press ‘Submit query’.

## 5.14.2 Isolate databases

### Single locus

Click the add (+) loci link on the curator’s interface contents page. This function is normally hidden, so you may need to click the ‘Loci’ toggle to display it.



Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

## Add new locus

Please fill in the fields below - required fields are marked with an exclamation mark (!).

[Record](#)

id!:

data type!: DNA

allele id format!: integer

length varies!: ☐ true ☒ false

coding sequence!: ☒ true ☐ false

isolate display!: allele only

main display!: ☐ true ☒ false

query field!: ☒ true ☐ false

analysis!: ☒ true ☐ false

curator!: Keith Jolley (keith)

date entered!: 2020-07-19

datestamp!: 2020-07-19

formatted name:

common name:

formatted common name:

locus type:

allele id regex:

length:

complete cds: ☐ true ☐ false

orf:

genome position:

match longest: ☐ true ☐ false

reference sequence:

pcr filter: ☐ true ☐ false Do NOT set to true unless you define PCR reactions linked to this locus.

probe filter: ☐ true ☐ false Do NOT set to true unless you define probe sequences linked to this locus.

introns: ☐ true ☐ false Set to true if locus can contain introns.

dbase name: pubmlst\_bigsdb\_neisseria\_seqdef  Name of the database holding allele sequences

dbase host:  IP address of database host

dbase port:  Network port accepting database connections

dbase user:

dbase password:

dbase id: PUT\_LOCUS\_NAME\_HERE  Name of locus in seqdef database

description url: 

/cgi-bin/bigsdb/bigsdb.pl?  
db=pubmlst\_neisseria\_seqdef&page=LocusInfo&locus=PUT\_LOCUS\_NAME\_HERE

url: 

/cgi-bin/bigsdb/bigsdb.pl?  
db=pubmlst\_neisseria\_seqdef&page=alleleInfo&locus=PUT\_LOCUS\_NAME\_HERE&allele  
id=[?]

submission template: ☐ true ☒ false Include column in isolate submission template for this locus

view:

aliases:

[Action](#)

[RESET](#) [SUBMIT](#)

[Show tools](#)

- id - The name of the locus
  - Allowed: any value starting with a letter or underscore.
- data\_type - Describes whether the locus is defined by nucleotide or peptide sequence.
  - Allowed: DNA/peptide.
- allele\_id\_format - The format for allele identifiers.
  - Allowed: integer/text.
- length\_varies - Sets whether alleles can vary in length.
  - Allowed: true/false.
- coding\_sequence - Sets whether the locus codes for a protein.

- Allowed: true/false.
- isolate\_display - Sets how alleles for this locus are displayed in a detailed isolate record - this can be overridden by user preference.
  - Allowed: allele only/sequence/hide.
- main\_display - Sets whether or not alleles for this locus are displayed in a main results table by default - this can be overridden by user preference.
  - Allowed: true/false.
- query\_field - Sets whether or not alleles for this locus can be used in queries by default - this can be overridden by user preference.
  - Allowed: true/false.
- analysis - Sets whether or not alleles for this locus can be used in analysis functions by default - this can be overridden by user preference.
  - Allowed: true/false.
- formatted\_name - Name with HTML formatting (optional).
  - This allows you to add formatting such as bold, italic, underline and superscripting to locus names as they appear in the web interface.
  - Allowed: valid HTML.
- common\_name - The common name for the locus (optional).
  - Allowed: any value.
- formatted\_common\_name - Common name with HTML formatting (optional).
  - Allowed: valid HTML.
- allele\_id\_regex - [Regular expression](#) to enforce allele id naming.
  - ^: the beginning of the string
  - \$: the end of the string
  - d: digit
  - D: non-digit
  - s: white space character
  - S: non white space character
  - w: alpha-numeric plus ‘\_’
  - .: any character
  - \*: 0 or more of previous character
  - +: 1 or more of previous character
  - e.g. ^Fd-d+\$ states that an allele name must begin with a F followed by a single digit, then a dash, then one or more digits, e.g. F1-12
- length - Standard length of locus (required if length\_varies is set to false).
  - Allowed: any integer.
- complete\_cds - Whether locus represents a complete coding sequence (optional)
- start\_codons - Semi-colon separated list of alternative start codons to allow

- Note that these are in addition to the built-in defaults of ATG, GTG, TTG.
- orf - Open reading frame of locus (optional). 1-3 are the forward reading frame, 4-6 are the reverse reading frames.
  - Allowed: 1-6.
- genome\_position - The start position of the locus on a reference genome.
  - Allowed: any integer.
- match\_longest - Only select the longest exact match when tagging/querying.
  - This is useful for some loci that can have some sequences shorter than others, e.g. peptide loci defining antigenic loops. This can lead to instances of one sequence being longer than another but otherwise being identical. In these cases, usually the longer sequence is the one that should be matched.
  - Allowed: true/false.
- reference\_sequence - Sequence used by the automated sequence comparison algorithms to identify sequences matching this locus. **This is only used if a sequence definition database has not been set up for this locus.**
- pcr\_filter - Set to true if this locus is further defined by genome filtering using in silico PCR.
  - Allowed: true/false.
- probe\_filter - Set to true if this locus is further defined by genome filtering using in silico hybridization.
  - Allowed: true/false.
- introns - Set to true if locus may contain introns. This setting will only be available if BLAT is configured in bigsdb.conf.
  - Allowed: true/false.
- dbase\_name - Name of database (system name).
  - Allowed: any text.
- dbase\_host - Resolved name of IP address of database host - leave blank if running on the same machine as the isolate database.
  - Allowed: network address, e.g. 129.67.26.52 or zoo-oban.zoo.ox.ac.uk
- dbase\_port - Network port on which the sequence definition database server is listening - leave blank unless using a non-standard port (5432).
  - Allowed: integer.
- dbase\_user - Name of user with permission to access the sequence definition database - depending on the database configuration you may be able to leave this blank.
  - Allowed: any text (no spaces).
- dbase\_password - Password of database user - again depending on the database configuration you may be able to leave this blank.
  - Allowed: any text (no spaces).
- dbase\_id - Name of locus in seqdef database. This is usually the same as the id field.
  - Allowed: any text (no spaces).
- description\_url - The URL used to hyperlink to locus information in the isolate information page. This can either be a relative (e.g. /cgi-bin/...) or an absolute (containing <http://>) URL.
  - Allowed: any valid URL.

- url - The URL used to hyperlink to information about the allele. This can either be a relative or absolute URL. If [?] (including the square brackets) is included then this will be substituted for the allele value in the resultant URL. To link to the appropriate allele info page on a corresponding seqdef database you would need something like /cgi-bin/bigsdb/bigsdb.pl?db=pubmlst\_neisseria\_seqdef&page=alleleInfo&locus=abcZ&allele\_id=[?].
  - Allowed: any valid URL.
- submission\_template - Sets whether or not a column for this locus is included in the Excel submission template.
  - Allowed: true/false (default: false)
- view - Restrict this locus to only isolates contained in the specified database view. This option will only appear if the views attribute is set in the system tag. The view needs to have been defined in the database as a subset of the isolate table (usually filtered by the value of one or more of its fields).

## Using existing locus definition as a template

When defining a new locus in the isolate database, it is possible to use an existing locus record as a template. To do this, click the ‘Show tools’ link in the top-right of the screen:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new locus

### Add new locus

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

id:!

data type: DNA

allele id format: integer

length varies: ☐ true ☒ false

coding sequence: ☒ true ☐ false

isolate display: allele only

main display: ☐ true ☒ false

query field: ☒ true ☐ false

analysis: ☒ true ☐ false

curator: Keith Jolley (keith)

date entered: 2020-07-19

datestamp: 2020-07-19

formatted name:

common name:

formatted common name:

locus type:

allele id regex:

length:

complete cds: ☐ true ☐ false

orf: ☐

genome position:

match longest: ☐ true ☐ false

reference sequence:

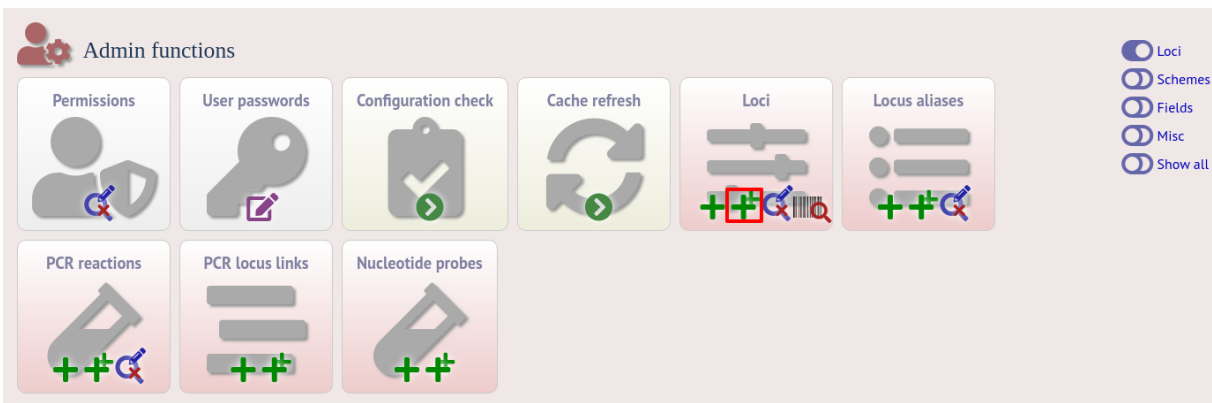
Show tools

This displays a drop-down box containing existing loci. Select the locus that you wish to use as a template, and click ‘Copy’.



## Batch adding

Click the batch add (++) loci link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Loci' toggle to display it.



Click the link to download an Excel template:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Batch add locus records



Batch insert loci

**Instructions**

This page allows you to upload locus data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- Enter aliases (alternative names) for your locus as a semi-colon (;) separated list.

**Templates**

Check the [description of database fields](#) for help with filling in the template.

**Upload**

Paste in tab-delimited text (include a field header line).

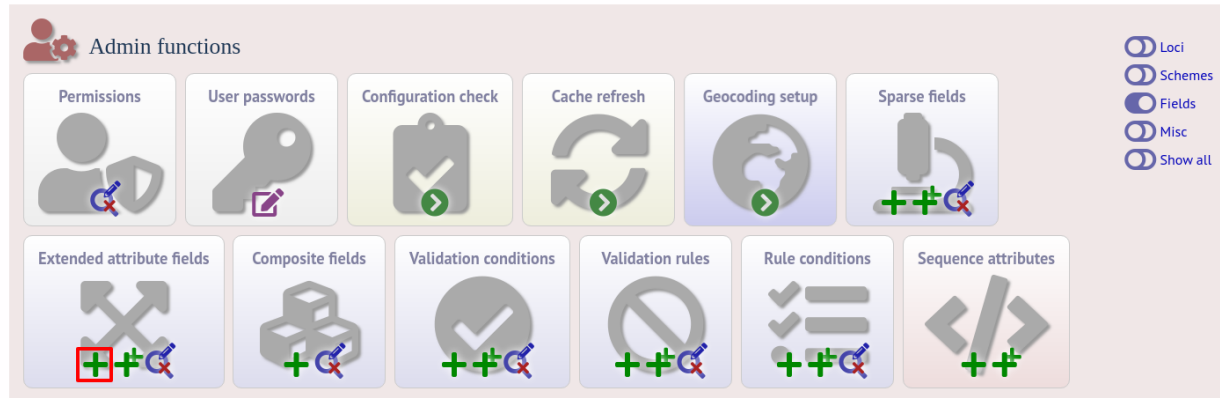
Action

Fill in the spreadsheet fields using the *table above as a guide*, then paste the completed table into the web form and press 'Submit query'.

## 5.15 Defining locus extended attributes

You may want to add additional metadata for the allele definitions of some loci. Since these are likely to be specific to each locus, they cannot be defined generically within the standard locus definition. We can, instead, define extended attributes. Examples of these include higher order grouping of antigen sequences, antibody reactivities, identification of important mutations, or cross-referencing of alternative nomenclatures.

To add extended attributes for a locus, click add (+) locus extended attributes in the sequence definition database curator's interface contents page. This function is normally hidden, so you may need to click the 'Fields' toggle to display it.



Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new isolate field extended attribute

### Add new isolate field extended attribute

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
isolate field!: <input type="text"/> attribute!: <input type="text"/> value format!: <input type="text"/> text curator!: Keith Jolley (keith) datestamp!: 2020-07-19 value regex: <input type="text"/> description: <input type="text"/> url: <input type="text"/> length: <input type="text"/> field order: <input type="text"/>	<input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

- locus - Select locus from dropdown box.
  - Allowed: existing locus name.
- field - Name of extended attributes.
  - Allowed: any value.
- value\_format - Data type of attribute.
  - Allowed: integer/text/boolean.

- required - Specifies whether the attribute value must be defined when adding a new sequence.
  - Allowed: true/false.
- value\_regex - [Regular expression](#) to enforce allele id naming (optional).
  - ^: the beginning of the string
  - \$: the end of the string
  - d: digit
  - D: non-digit
  - s: white space character
  - S: non white space character
  - w: alpha-numeric plus ‘\_’
  - .: any character
  - \*: 0 or more of previous character
  - +: 1 or more of previous character
- description - Description that will appear within the web form when adding new sequences (optional).
  - Allowed: any value.
- option\_list - Pipe (|) separated list of allowed values (optional).
- length - Maximum length of value (optional).
  - Allowed: any integer.
- field\_order - Integer that sets the position of the field within scheme values in any results (optional).
  - Allowed: any integer.

Once extended attributes have been defined, they will appear in the web form when adding new sequences for that locus. The values are searchable when using a [locus-specific sequence query](#), and they will appear within query results and allele information pages.

## 5.16 Defining schemes

Schemes are collections of loci that may be associated with particular fields - one of these fields can be a primary key, i.e. a field that uniquely defines a particular combination of alleles at the associated loci.

A specific example of a scheme is MLST - [see workflow for setting up a MLST scheme](#).

To set up a new scheme, you need to:

1. Add a new scheme description.
2. Define loci as ‘scheme members’.
3. Add ‘scheme fields’ associated with the scheme.

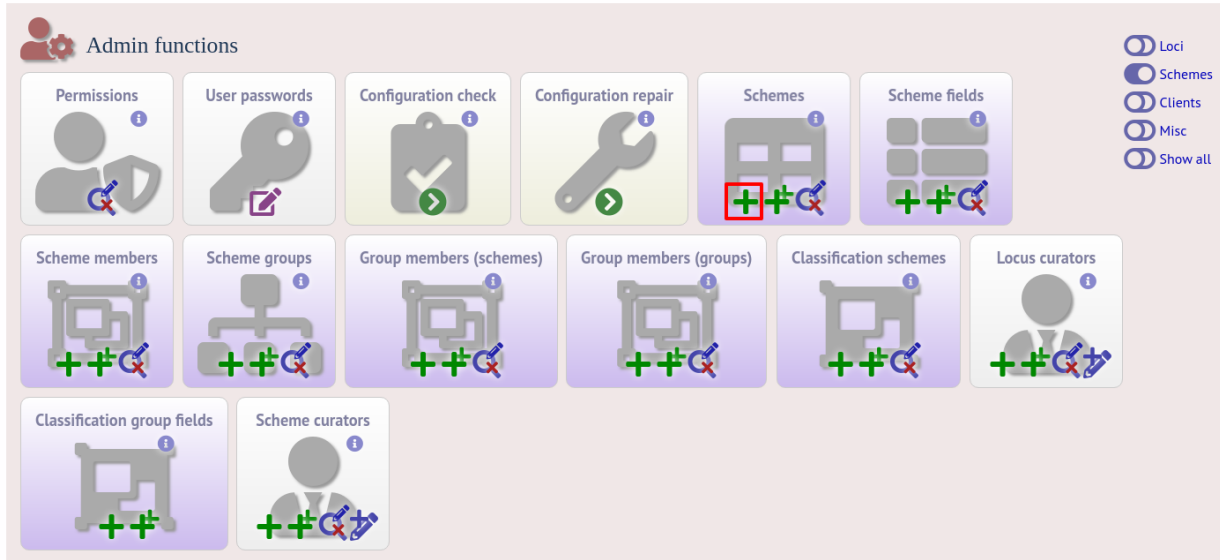
**See also:**

[Schemes \(concept\)](#)

### 5.16.1 Sequence definition databases

As with all configuration, tables can be populated using the batch interface (++) or one at a time (+). Details for the latter are described below:

Click the add (+) scheme link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Fill in the scheme description in the web form. The next available scheme id number will be filled in already.

The display\_order field accepts an integer that can be used to order the display of schemes in the interface - this can be left blank if you wish.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new scheme

Add new scheme

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 1

name: MLST

curator: Keith Jolley (keith)

timestamp: 2020-07-19

date entered: 2020-07-19

description:

display order:

allow missing loci: ☐ true ☐ false

max missing:

disable: ☐ true ☐ false

no submissions: ☐ true ☐ false

flags: experimental, in development, please cite, unpublished

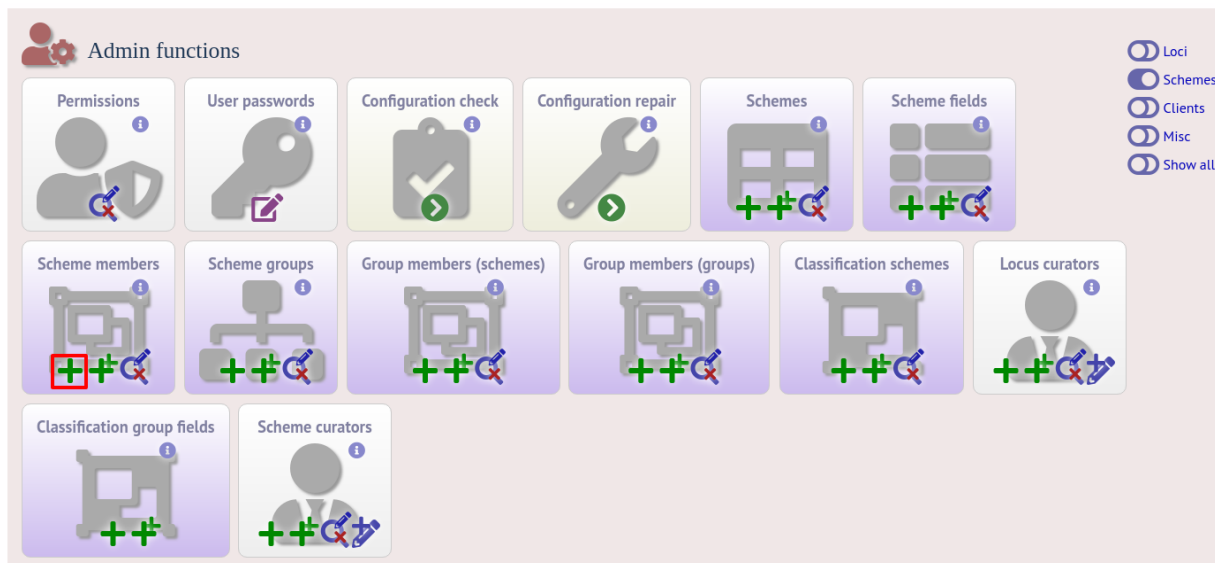
PubMed ids:

links: (Format: URL(description))

Action

RESET SUBMIT

To add loci to the scheme, click the add (+) scheme members link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Select the scheme name and a locus that you wish to add to the scheme from the appropriate drop-down boxes. *Loci need to have already been defined*. The field\_order field allows you to set the display order of the locus within a profile - if these are left blank that alphabetical ordering is used.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new scheme member

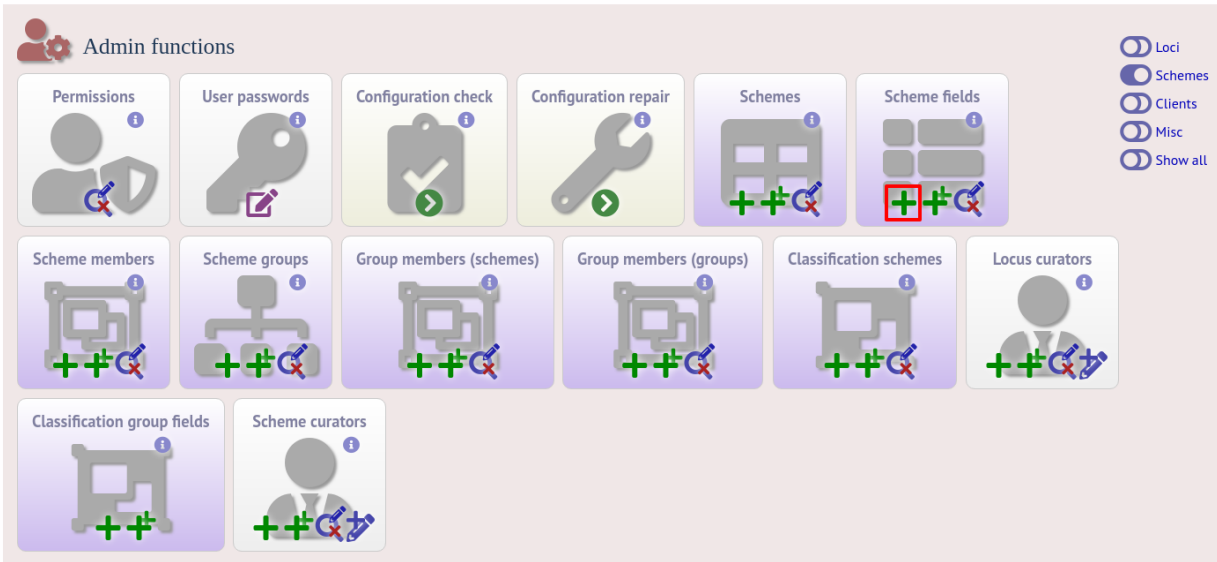
## Add new scheme member

Please be aware that any modifications to the structure of this scheme will result in the removal of all data from it. This is done to ensure data integrity. This does not affect allele designations, but any profiles will have to be reloaded.

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
scheme id: MLST locus: abcZ curator: Keith Jolley (keith) timestamp: 2020-07-19 field order: 1	<input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

To add scheme fields, click the add (+) scheme fields link on the curator's interface contents page.



Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new scheme field

## Add new scheme field

Please be aware that any modifications to the structure of this scheme will result in the removal of all data from it. This is done to ensure data integrity. This does not affect allele designations, but any profiles will have to be reloaded.

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
<p>scheme id: <input type="text"/></p> <p>field: <input type="text"/></p> <p>type: <input type="text"/></p> <p>primary key: <input type="radio"/> true <input checked="" type="radio"/> false</p> <p>dropdown: <input type="radio"/> true <input checked="" type="radio"/> false</p> <p>curator: Keith Jolley (keith)</p> <p>timestamp: 2020-07-19</p> <p>description: <input type="text"/></p> <p>field order: <input type="text"/></p> <p>index: <input type="radio"/> true <input checked="" type="radio"/> false</p> <p>value regex: <input type="text"/></p>	<p>RESET SUBMIT</p>

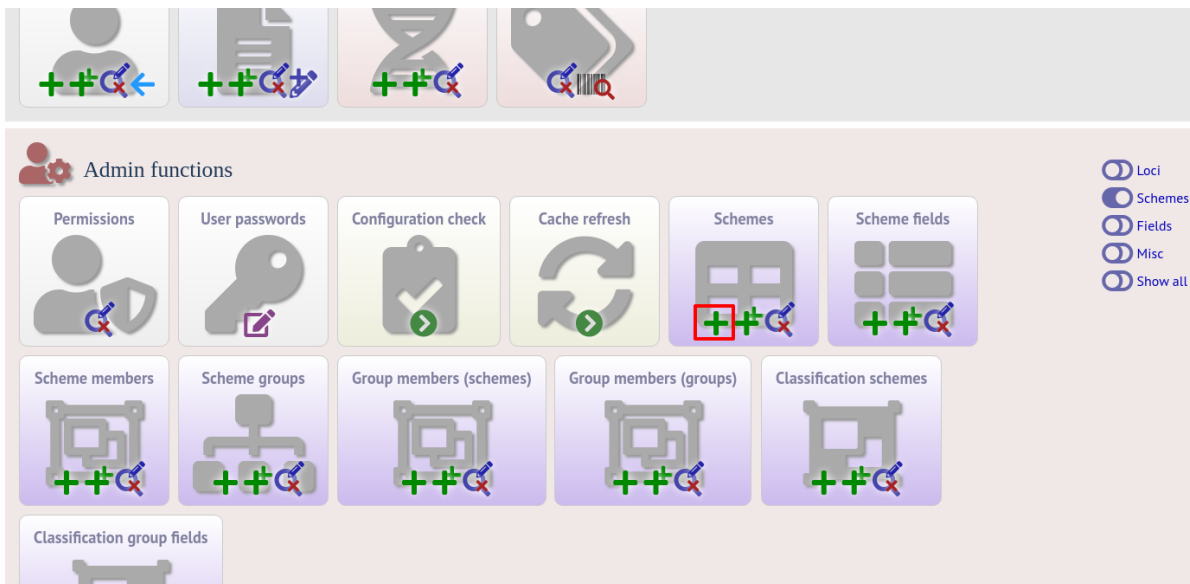
- `scheme_id` - Dropdown box of scheme names.
  - Allowed: selection from list.
- `field` - Field name.
  - Allowed: any value.
- `type` - Format for values.
  - Allowed: text/integer/date.
- `primary_key` - Set to true if field is the primary key. There can only be one primary key for a scheme.
  - Allowed: true/false.
- `dropdown` - Set to true if a dropdown box is displayed in the query interface, by default, for values of this field to be quickly selected. This option can be overridden by user preferences.

- Allowed: true/false.
- description - This field isn't currently used.
- field\_order - Integer that sets the position of the field within scheme values in any results.
  - Allowed: any integer.
- value\_regex - [Regular expression](#) to enforce field values.
  - ^: the beginning of the string
  - \$: the end of the string
  - d: digit
  - D: non-digit
  - s: white space character
  - S: non white space character
  - w: alpha-numeric plus ' \_ '
  - .: any character
  - \*: 0 or more of previous character
  - +: 1 or more of previous character

### 5.16.2 Isolate databases

As with all configuration, tables can be populated using the batch interface (++) or one at a time (+). Details for the latter are described below:

Click the add (+) scheme link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Fill in the scheme description in the web form. Required fields have an exclamation mark (!) next to them:



## Add new scheme

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record** **Action**

id: 122 **RESET** **SUBMIT**

name:  !

isolate display: ☒ true ☐ false !

main display: ☒ true ☐ false !

query field: ☒ true ☐ false !

query status: ☐ true ☒ false !

analysis: ☒ true ☐ false !

curator: Keith Jolley (keith)

timestamp: 2020-07-19

date entered: 2020-07-19

description:

dbase name:  !

dbase host:  !

dbase port:  !

dbase user:  !

dbase password:  !

dbase id:  !

view:  !

display order:  !

allow missing loci: ☐ true ☐ false ! This is only relevant to schemes with primary key fields, e.g. MLST.

flags: experimental  
in development  
please cite  
unpublished Use CTRL/SHIFT click to select or deselect values

PubMed ids:

links:   
(Format: URL|description)

- id - Index number of scheme - the next available number will be entered automatically.
  - Allowed: any positive integer.
- description - Short description - this is used in tables so make sure it's not too long.
  - Allowed: any text.
- isolate\_display - Sets whether or not fields for this scheme are displayed in a detailed isolate record - this can be overridden by user preference.
  - Allowed: allele only/sequence/hide.
- main\_display - Sets whether or not fields for this scheme are displayed in a main results table by default - this can be overridden by user preference.
  - Allowed: true/false.
- query\_field - Sets whether or not fields for this scheme can be used in queries by default - this can be overridden by user preference.
  - Allowed: true/false.
- query\_status - Sets whether a dropdown list box should be displayed in the query interface to filter results based on profile completion for this scheme - this can be overridden by user preference.
  - Allowed: true/false.

- analysis - Sets whether or not alleles for this locus can be used in analysis functions by default - this can be overridden by user preference.
  - Allowed: true/false.
- recommended - Sets whether the scheme will appear in a list of recommended schemes for use in some analysis plugins. Selecting this option makes the scheme easier to select when there are a lot of schemes defined. It should be used sparingly.
- quality\_metric - Sets whether the scheme can be used to help assess the quality of a genome assembly. For a well annotated genome it would be expected for all loci in the scheme to have an allele designated. The annotation status can be searched in an isolate query. This can be used in conjunction with the quality\_metric\_good and quality\_metric\_bad attributes that can be used to set the thresholds for what constitutes a good or bad annotation.
- dbase\_name - Name of seqdef database (system name) containing scheme profiles (optional).
  - Allowed: any text.
- dbase\_host - Resolved name of IP address of database host - leave blank if running on the same machine as the isolate database (optional).
  - Allowed: network address, e.g. 129.67.26.52 or zoo-oban.zoo.ox.ac.uk
- dbase\_port - Network port on which the sequence definition database server is listening - leave blank unless using a non-standard port, 5432 (optional).
  - Allowed: integer.
- dbase\_user - Name of user with permission to access the sequence definition database - depending on the database configuration you may be able to leave this blank (optional).
  - Allowed: any text (no spaces).
- dbase\_password - Password of database user - again depending on the database configuration you may be able to leave this blank (optional).
  - Allowed: any text (no spaces).
- dbase\_id - Id of scheme in the sequence definition database.
  - Allowed: any integer.
- quality\_metric\_good - threshold number of loci that must have allele designations for a genome annotation to be considered good for this scheme. If this isn't set then the number of loci in the scheme is used.
- quality\_metric\_bad - threshold number of loci that must have allele designations below which a genome annotation is to be considered bad for this scheme. If this isn't set then the value used for quality\_metric\_good is used (or the number of scheme loci if this also is not set).
- view - Restrict this scheme to only isolates contained in the specified database view. This option will only appear if the views attribute is set in the system tag. The view needs to have been defined in the database as a subset of the isolate table (usually filtered by the value of one or more of its fields).
- display\_order - Integer reflecting the display position for this scheme within the interface (optional).
  - Allowed: any integer.
- allow\_missing\_loci - Allow profile definitions to contain 'O' (locus missing) or 'N' (any allele).

## 5.17 Organizing schemes into hierarchical groups

Schemes can be organized into groups, and these groups can in turn be members of other groups. This facilitates hierarchical ordering of loci, but with the flexibility to allow loci and schemes to belong to multiple groups.

This hierarchical structuring can be seen in various places within BIGSdb, for example the [allele download](#) page.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Download alleles

Help

### Download allele sequences

Select loci by scheme | [Alphabetical list](#) | [All loci by scheme](#)

Click within the tree to display details of loci belonging to schemes or groups of schemes - clicking a group folder will display the loci for all schemes within the group and any subgroups. Click the nodes to expand/collapse.

- All loci
  - Strain typing
  - Capsule
  - Genetic Information Processing
  - Genomic islands
  - Lineage Schemes
  - Metabolism
  - N. gonorrhoeae AMR
  - Plasmids
  - Typing
    - MLST**
    - Finotyping antigens

#### MLST

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison, K. Jolley	2020-06-23
adk		DNA	841	Fixed: 465 bp	464	465		O. Harrison, K. Jolley	2020-07-14
aroE		DNA	1118	Fixed: 490 bp	489	493		O. Harrison, K. Jolley	2020-06-12
fumC		DNA	1184	Fixed: 465 bp	463	467		O. Harrison, K. Jolley	2020-06-12
gdh		DNA	1156	Fixed: 501 bp	501	513		O. Harrison, K. Jolley	2020-07-03
pdhC		DNA	1096	Fixed: 480 bp	480	503		O. Harrison, K. Jolley	2020-06-04
pgm		DNA	1172	Fixed: 450 bp	447	489		O. Harrison, K. Jolley	2020-06-12

Scheme groups can be added in both the sequence definition and isolate databases. To add a new group, click the add (+) scheme group link on the curator's contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.

Admin functions

Permissions

User passwords

Configuration check

Configuration repair

Schemes

Scheme fields

Scheme members

Scheme groups

Group members (schemes)

Group members (groups)

Classification schemes

Locus curators

Classification group fields

Scheme curators

☒ Loci  
☒ Schemes  
☐ Clients  
☐ Misc  
☐ Show all

Enter a short name for the group - this will appear within drop-down list boxes and the hierarchical tree, so it needs to be fairly short.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new scheme group

Add new scheme group

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 1

name:  !

curator: Keith Jolley (keith)

timestamp: 2020-07-19

description:

display order:

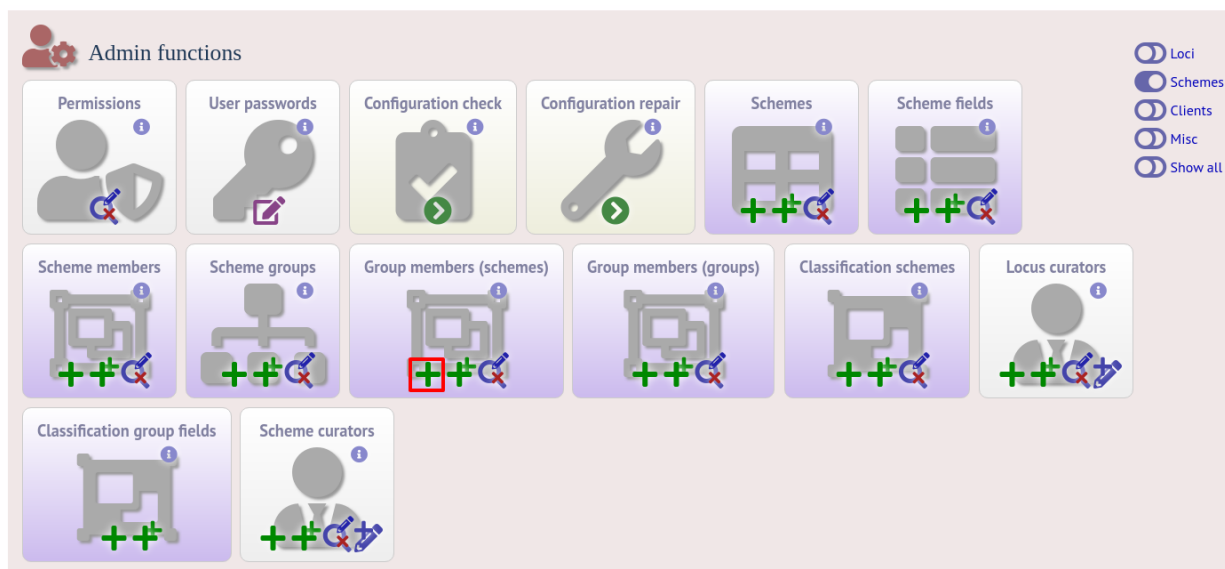
seq query: ☒ true ☐ false !

Action

RESET SUBMIT

If you are creating a scheme group in the sequence definition database, there is an additional field called 'seq\_query'. Set this to true to add the scheme group to the dropdown lists in the *sequence query* page. This enables all loci belonging to schemes within the group to be queried together.

Schemes can be added to groups by clicking the add (+) group members (scheme) link.



Select the scheme and the group to add it to, then click 'Submit'.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new scheme group scheme member

Add new scheme group scheme member

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
group id: Typing scheme id: MLST curator: Keith Jolley (keith) datestamp: 2020-07-19	RESET SUBMIT

Scheme groups can be added to other scheme groups in the same way by clicking the add (+) scheme group group members link.

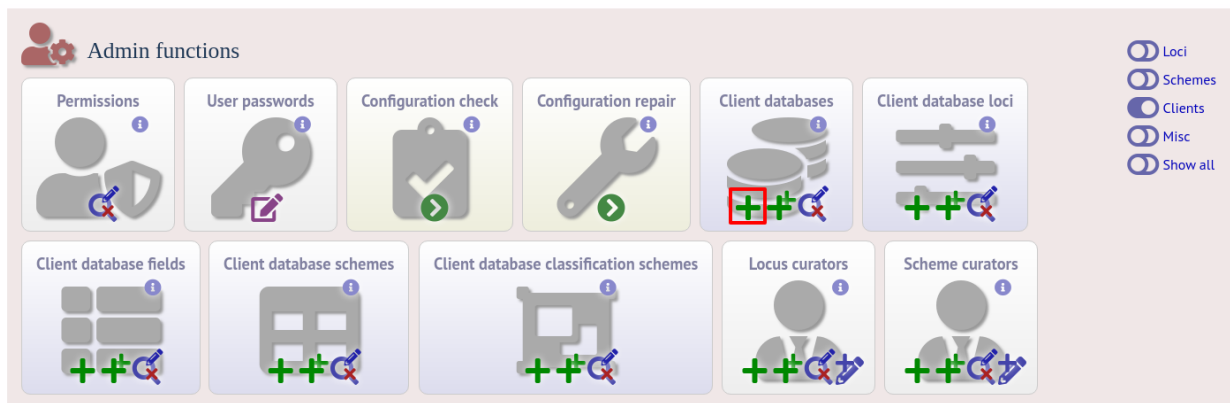
## 5.18 Setting up client databases

Sequence definition databases can have any number of isolate databases that connect as clients. Registering these databases allows the software to perform isolate data searches relevant to results returned by the sequence definition database, for example:

- Determine the number of isolates that a given allele is found in and link to these.
- Determine the number of isolates that a given scheme field, e.g. a sequence type, is found in and link to these.
- Retrieve specific attributes of isolates that have a given allele, e.g. species that have a particular 16S allele, or penicillin resistance given a particular penA allele.

Multiple client databases can be queried simultaneously.

To register a client isolate database for a sequence definition database, click the add (+) client database link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Clients' toggle to display it.



Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

PubMLST
Home > Organisms > Organism > Neisseria typing > Add new client database

Add new client database

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 1  
name: PubMLST isolates  
description: Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.  
dbase name: pubmlst\_bigsdb\_neisseria\_isolates Name of the database holding isolate data  
dbase config name: pubmlst\_neisseria\_isolates Name of the database configuration  
curator: Keith Jolley (keith)  
timestamp: 2020-07-19  
dbase host: IP address of database host  
dbase port: Network port accepting database connections  
dbase user:  
dbase password:  
dbase view: isolates View of isolates table to use  
url: /cgi-bin/bigsdb/bigsdb.pl Web URL to database script

Action

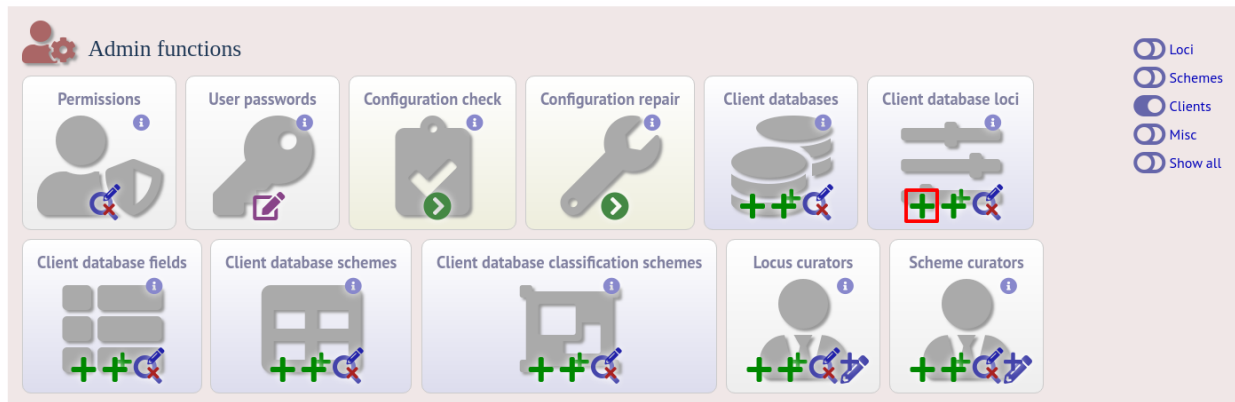
RESET SUBMIT

- id - Index number of client database. The next available number is entered automatically but can be overridden.
  - Allowed: any positive integer.
- name - Short description of database. This is used within the interface result tables so it is better to make it as short as possible.
  - Allowed: any text.
- description - Longer description of database.
  - Allowed: any text.
- dbase\_name - Name of database (system name).
  - Allowed: any text.
- dbase\_config\_name - Name of database configuration - this is the text string that appears after the db= part of script URLs.
  - Allowed: any text (no spaces)
- dbase\_host - Resolved name of IP address of database host (optional).
  - Allowed: Network address, e.g. 129.67.26.52 or zoo-oban.zoo.ox.ac.uk
  - Leave blank if running on the same machine as the seqdef database.
- dbase\_port - Network port on which the client database server is listening (optional).
  - Allowed: integer.
  - Leave blank unless using a non-standard port (5432).
- dbase\_user - Name of user with permission to access the client database.
  - Allowed: any text (no spaces).
  - Depending on the database configuration you may be able to leave this blank.
- dbase\_password - Password of database user

- Allowed: any text (no spaces).
- Depending on the database configuration you may be able to leave this blank.
- url - URL of client database bigsdb.pl script
  - Allowed: valid script path.
  - This can be relative (e.g. /cgi-bin/bigsdb/bigsdb.pl) if running on the same machine as the seqdef database or absolute (including <http://>) if on a different machine.

### 5.18.1 Look up isolates with given allele

To link a locus, click the add (+) client database loci link on the curator's interface contents page.



Link the locus to the appropriate client database using the dropdown list boxes. If the locus is named differently in the client database, fill this name in the locus\_alias.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new locus to client database definition

### Add new locus to client database definition

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

client dbase id: 1) PubMLST isolates

locus: abcZ

curator: Keith Jolley (keith)

timestamp: 2020-07-19

locus alias: name that this locus is referred by in client database (if different)

**Action**


RESET SUBMIT

Now when information on a given allele is shown following a query, the software will list the number of isolates with that allele and link to a search on the database to retrieve these.


BIGSdb

Home > Organisms > Organism > Neisseria typing > Allele information


Allele information - abcZ: 5

 Provenance/meta data

locus: [abcZ](#)  
 allele: 5  
 sequence: TTTGATACCG TTGCCGAAGG TTTGGGCGAA ATTCGCGATT TATTGCGCCG TTATCATCAT GTCAGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCTTTGT  
 TGAAGAGCT TAACGAATTG CAACTTGAAA TCGAAGCGAA GGACGGCTGG AAGCTGGATG CGGCAGTCAA GCAGACTTTG GGTGAATTG GTTTGCCAGA  
 AACGAAAAA ATCGCAACC TCTCCGCGG ACAGAAAAAG CGTGTGCCC TAGCGCAGGC TTGGGTGCAG AAGCCTGATG TATTGCTGCT GGACGAACCG  
 ACCAACCAAT TGGACATTGA CGCGATTATT TGGCTGGAAA ATCTGCTTAA AGCGTTTGAA GGCAGCCTGG TTGTGATTAC CCACGACCGC CGTTTTTTGG  
 ACAATATCGC CACGCGCATC GTCGAATCG ATC  
 length: 433  
 status: Sanger trace checked  
 date entered: 2001-02-07  
 datestamp: 2009-11-11  
 sender: Keith Jolley, University of Oxford, UK  
 curator: [Man-Suen Chan](#), University of Oxford

 Profiles containing this allele

MLST: [302 profiles](#)

 Isolate databases

**PubMLST isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [1578 isolates](#)

### 5.18.2 Look up isolates with a given scheme primary key

Setting this up is identical to setting up for alleles (see above) except you click on the add (+) client database schemes link and choose the scheme and client databases in the dropdown list boxes.

Now when information on a given scheme profile (e.g. MLST sequence type) is shown following a query, the software will list the number of isolates with that profile and link to a search on the database to retrieve these.


BIGSdb

Home > Organisms > Organism > Neisseria typing > Profile information

Profile information for ST-11 (MLST)

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
11	2	3	4	3	8	4	6	ST-11 complex

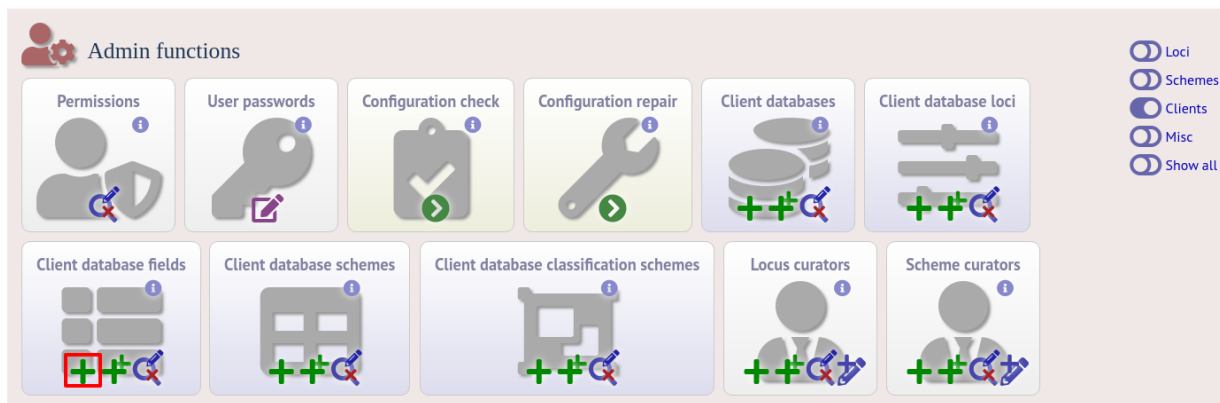
sender: Paula Kriz, Paula Kriz and Keith Jolley  
 curator: [Keith Jolley](#), University of Oxford, UK  
 date entered: 2001-02-07  
 datestamp: 2009-11-11

 Client database

**PubMLST isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [7313 isolates](#)

### 5.18.3 Look up specific isolate database fields linked to a given allele

To link an allele to an isolate field, click the add (+) ‘client database fields linked to loci’ link on the curator’s interface contents page.



Select the client database and locus from the dropdown lists and enter the isolate database field that you’d like to link. The ‘allele\_query’ field should be set to true.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new locus to client database isolate field definition

### Add new locus to client database isolate field definition

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
client dbase id: 1) PubMLST isolates locus: penA isolate field: penicillin_range curator: Keith Jolley (keith) timestamp: 2020-07-19 allele query: <input checked="" type="radio"/> true <input type="radio"/> false	set to true to display field values when an allele query is done. <input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

Now, in the allele record or following a sequence query that identifies an allele, all values for the chosen field from isolates with the corresponding allele are shown.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Allele information

Help

## Allele information - penA: 9

Provenance/meta data
 

locus: [penA](#)  
 allele: 9  
 sequence: GACGGCGTTT TGCTGCCGGT CAGCTTTGAA AACAGGCGG TTGCGCCGCA AGGCAACGCT ATATTTAAAG CATCGACCGC ACGTCAAGTG CGTGAGTTGA  
 TGGTTTCTGT AACGGAACCT GCGGTACGG GTACGGCGGG TGCGGTAGAT GGTTCGACG TCGCGCAAA AACCGGTACG GCGCGTAAGT TGGTTAACGG  
 TCGTTACGTC GATTACAAC ACCTTGCCAC TTTCATCGGT TTGCCCCGG CTAATAATCC GCGTGTGATT GTGGCGGTAA CCATTGACGA GCCGACTGCA  
 AACGGTTACT ACGGCGGCGT AGTGACAGT CCGGCTTCA AACAAAGTTAT GGGCGGTAGC CTGAACATCT TGGGCGTTTC TCCGACCAA CCTCTGACCA AT  
 length: 402  
 status: Sanger trace checked  
 date entered: 2006-09-04  
 datestamp: 2006-09-04  
 sender: Muhamed-Kheir Taha, National Reference Center for Meningococci, Institut Pasteur, France  
 curator: [Keith Jolley](#), University of Oxford, UK  
 mutation F504L: yes  
 mutation A510V: yes  
 mutation I515V: yes  
 mutation H541N: yes  
 mutation I566V: yes

Publication (1)
 

- Taha MK, Vázquez JA, Hong E, Bennett DE, Bertrand S, Bukovski S, Cafferkey MT, Carion F, Christensen JJ, Diggle M, Edwards G, Enriquez R, Fazio C, Frosch M, Heuberger S, Hoffmann S, Jolley KA, Kadubowski M, Kechrid A, Kesanopoulos K, Kriz P, Lamberts L, Levenet I, Musilek M, Paragi M, Saguer A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zarantonelli ML (2007). Target gene sequencing to characterize the penicillin G susceptibility of *Neisseria meningitidis*. *Antimicrob Agents Chemother* **51**:2784-92

Isolate databases
 

**PubMLST isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [979 isolates](#)

Linked data
 

penicillin\_range: >0.06 - 1 (intermediate) [n=143]; <=0.06 (susceptible) [n=1]; >1 (resistant) [n=1] [PubMLST isolates](#)

## 5.19 Workflow for setting up a MLST scheme

The workflow for setting up a MLST scheme is as follows (the example seqdef database is called seqdef\_db):

### Seqdef database

1. Create appropriate loci
2. Create new scheme 'MLST'
3. Add scheme\_field 'ST' with primary\_key=TRUE (add clonal\_complex if you want; set this with primary\_key=FALSE)
4. Add each locus as a scheme\_member
5. You'll then be able to add profiles

### Isolate database

1. Create the same loci with the following additional parameters (example locus 'atpD')
  - dbase\_name: seqdef\_db
  - dbase\_id: atpD
  - url: something like /cgi-bin/bigsdb/bigsdb.pl?db=seqdef\_db&page=alleleInfo&locus=atpD&allele\_id=[?]
2. Create scheme 'MLST' with:

- `dbase_name`: `seqdef_db`
  - `dbase_id`: 1 (or whatever the id of your `seqdef` scheme is)
3. Add `scheme_field ST` as before
  4. Add `loci` as `scheme_members`

## 5.20 Automated assignment of scheme profiles

It is not practical to define `cgMLST` profiles via the web interface. A script is provided in the `scripts/automation` directory of the BIGSdb package called `define_profiles.pl` that can be used to scan an isolate database and automatically define `cgMLST` profiles in the corresponding sequence definition database.

The script is run as follows:

```
define_profiles.pl --database <name> --scheme <scheme_id>
```

A full list of options can be found by typing:

```
define_profiles.pl --help
NAME
    define_profiles.pl - Define scheme profiles found in isolate database

SYNOPSIS
    define_profiles.pl --database NAME --scheme SCHEME_ID [options]

OPTIONS

--cache
    Update scheme field cache in isolate database.

--database NAME
    Database configuration name.

--help
    This help page.

--exclude_isolates LIST
    Comma-separated list of isolate ids to ignore.

--exclude_projects LIST
    Comma-separated list of projects whose isolates will be excluded.

--ignore_multiple_hits
    Set allele designation to 'N' if there are multiple designations set for
    a locus. The default is to use the lowest allele value in the profile
    definition.

--isolates LIST
    Comma-separated list of isolate ids to scan (ignored if -p used).

--isolate_list_file FILE
    File containing list of isolate ids (ignored if -i or -p used).
```

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```
--match_missing
    Treat missing loci as specific alleles rather than 'any'. This will
    allow profiles for every isolate that has <= threshold of missing alleles
    to be defined but may result in some isolates having >1 ST.

--max ID
    Maximum isolate id.

--min ID
    Minimum isolate id.

--min_size SIZE
    Minimum size of seqbin (bp) - limit search to isolates with at least this
    much sequence.

--missing NUMBER
    Set the number of loci that are allowed to be missing in the profile. If
    the remote scheme does not allow missing loci then this number will be set
    to 0. Default=0.

--projects LIST
    Comma-separated list of project isolates to scan.

--scheme SCHEME_ID
    Scheme id number.

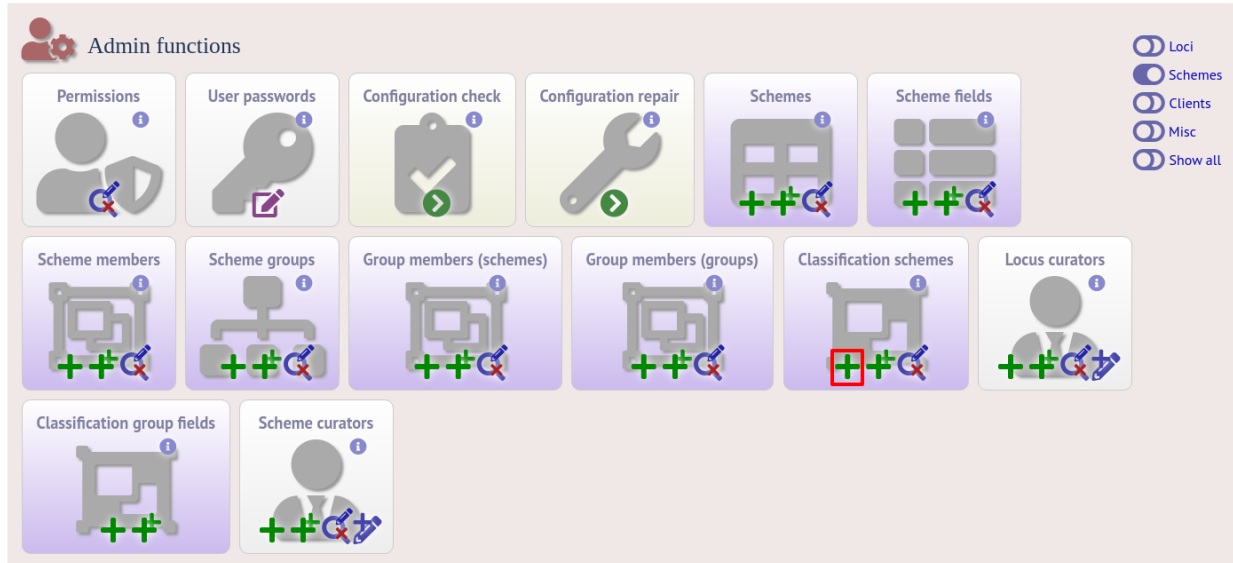
--view VIEW
    Limit isolates searched to specified view.
```

## 5.21 Scheme profile clustering - setting up classification schemes

Classification groups are a way to cluster scheme profiles using a specified threshold of pairwise allelic mismatches. Any number of different classification schemes can sit on top of a standard scheme (such as cgMLST), allowing different similarity thresholds to be pre-determined. Currently, single-linkage clustering is supported whereby each member of a group must have no more than the specified number of allelic differences with at least one other member of the group.

### 5.21.1 Defining classification scheme in sequence definition database

Once a scheme has been defined, add a classification scheme by clicking the add classification schemes (+) link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Select the underlying scheme and enter a name for the classification scheme, the number of mismatches allowed in order to include a scheme profile in a group, and a description. An example name for such a scheme could be 'Nm\_cgc\_25' indicating that this is a classification scheme for *Neisseria meningitidis* core genome cluster with a threshold of 25 mismatches.

You can additionally choose whether a relative threshold is used to calculate the number of mismatches to account for missing loci in pairwise comparisons. In this case, in order to be grouped, the number of matching alleles must exceed:

$$(\text{number of common loci} \times (\text{total loci} - \text{defined threshold})) / \text{total loci}$$

rather than

$$\text{total loci} - \text{defined threshold}$$

when an absolute threshold is used.

As this threshold has to be calculated for each pairwise comparison, clustering using relative thresholds is slower than using an absolute value, and probably makes little real world difference.

The status can be 'experimental' or 'stable'. The status of a scheme will be shown in the web interface to indicate that any groupings are subject to change and do not form part of the stable nomenclature.

Press 'Submit' to create the classification scheme.

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > Add new classification scheme

## Add new classification scheme

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 2

scheme id: N. gonorrhoeae cgMLST v1.0

name: Nm\_cgc\_25

inclusion threshold: 25

use relative threshold: ☐ true ☒ false

status: experimental

curator: Keith Jolley (keith)

timestamp: 2020-07-19

description: Single linkage clustering with each group member having fewer than 25 allelic mismatches to at least one other member of the group. Missing loci are ignored in comparisons.

display order:

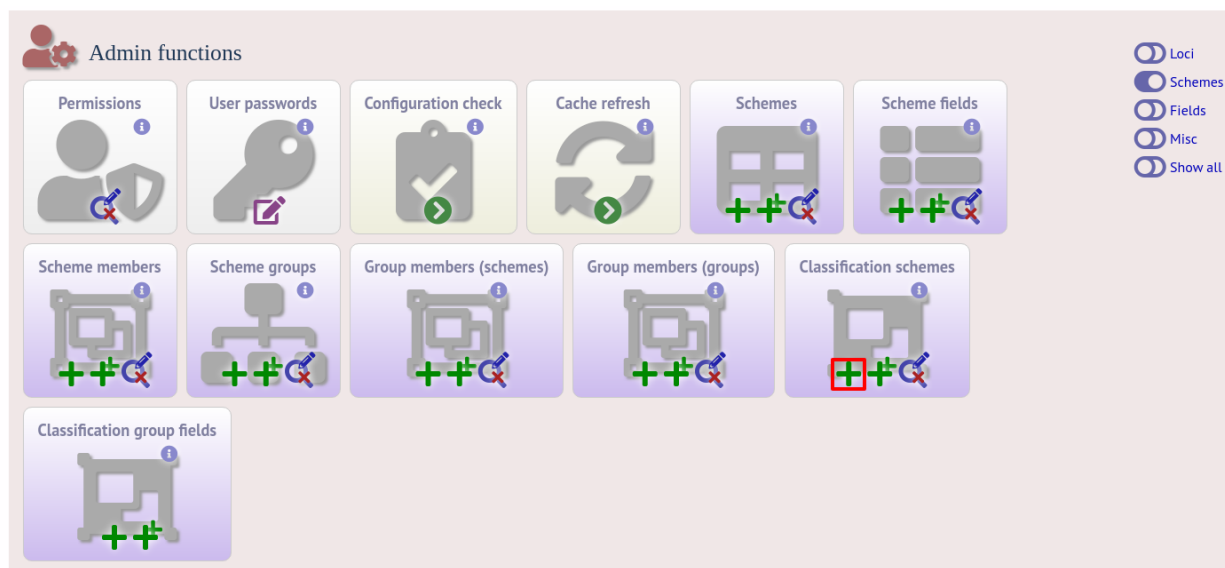
Action

RESET

SUBMIT

### 5.21.2 Defining classification scheme in isolate database

Duplicate the scheme definition from the sequence definition database. Click the add classification schemes (+) link on the curator's interface contents page. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Enter the same details used in the sequence definition database. If a different id number is used in the isolate and sequence definition databases, you can set the seqdef id in the seqdef\_cscheme\_id field (the default is to use the same id).

You can also define a display order - this is an integer field on which the ordering of classification schemes is sorted when displayed in the isolate information page.

PubMLST

Home > Organisms > Organism > Neisseria Isolates > Add new classification scheme

Add new classification scheme

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 2  
scheme id: N. meningitidis cgMLST v1.0  
name: Nm\_cgc\_25  
inclusion threshold: 25  
use relative threshold: ☐ true ☒ false  
status: experimental  
curator: Keith Jolley (keith)  
timestamp: 2020-07-19  
description: Single linkage clustering with each group member having fewer than 25 allelic mismatches to at least one other member of the group. Missing loci are ignored in comparisons.  
seqdef cscheme id: 2  
display order:

Action

RESET SUBMIT

It is a good idea to *check the configuration*.

### 5.21.3 Clustering

Clustering is performed using the `cluster.pl` script found in the `scripts/automation` directory of the BIGSdb package. It should be run by the `bigsdbs` user account (or any account with access to the databases).

Currently only single-linkage clustering is supported.

The script is run as follows from the command line:

```
cluster.pl --database <database configuration> --cscheme <classification scheme id>
```

A full list of options can be found by typing:

```
cluster.pl --help
NAME
    cluster.pl - Cluster cgMLST profiles using classification groups.

SYNOPSIS
    cluster.pl --database NAME --cscheme_id SCHEME_ID [options]

OPTIONS
    --cscheme CLASSIFICATION_SCHEME_ID
        Classification scheme id number.

    --database NAME
        Database configuration name.

    --help
        This help page.
```

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`--reset`Remove **all** groups **and** profiles currently defined **for** classification group.

**Note:** Note that for classification schemes to be accessible within the isolate database, *scheme cache tables* must be generated and kept up-to-date.

Where an isolate has been clustered in to a group with other isolates, this information is available in the *isolate information page*.

Publications (2)
 

- Feavers IM, Gray SJ, Urwin R, Russell JE, Bygraves JA, Kaczmarek EB, Maiden MC (1999). Multilocus sequence typing and antigen gene sequencing in the investigation of a meningococcal disease outbreak. *J Clin Microbiol* **37**:3883-7 [12 isolates](#)
- Jolley KA, Hill DM, Bratcher HB, Harrison OB, Feavers IM, Parkhill J, Maiden MC (2012). Resolution of a meningococcal disease outbreak from whole-genome sequence data with rapid Web-based analysis methods. *J Clin Microbiol* **50**:3046-53 [12 isolates](#)

Sequence bin
 

contigs: 259  
 total length: 2,135,447 bp  
 max length: 130,716 bp  
 mean length: 8,245 bp

N50 contig number: 18  
 N50 length (L50): 38,364  
 N90 contig number: 63  
 N90 length (L90): 8,066

N95 contig number: 79  
 N95 length (L95): 4,593  
 loci tagged: 2,205

[Show sequence bin](#)

Similar isolates (determined by classification schemes)
 

Experimental schemes are subject to change and are not a stable part of the nomenclature.

Classification scheme	Underlying scheme	Clustering method	Mismatch threshold	Status	Group
Nm_cgc_200	N. meningitidis cgMLST v1.0	Single-linkage	200	experimental	group: 17 (1007 isolates)
Nm_cgc_100	N. meningitidis cgMLST v1.0	Single-linkage	100	experimental	group: 38 (735 isolates)
Nm_cgc_50	N. meningitidis cgMLST v1.0	Single-linkage	50	experimental	group: 45 (4 isolates)
Nm_cgc_25	N. meningitidis cgMLST v1.0	Single-linkage	25	experimental	group: 45 (4 isolates)

Schemes and loci
 

All loci  
 Capsule  
 Genetic Information Processing

Navigate and select schemes within tree to display allele designations

Clicking the hyperlinks will take you to a table containing matching isolates, from where standard analyses can be performed.

BIGSdb

Home > Organisms > Organism > Neisseria isolates > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields Allele designations/scheme fields

id = Enter value... Nm\_cgc\_25 group = 45

Display/sort options Action

Order by: id ascending

Display: 25 records per page

RESET SEARCH

4 records returned. Click the hyperlinks for detailed information.

Your projects Bookmark query

Select project... Add these records 2020-07-19:1 Add bookmark

Isolate fields							MLST		Finetyping antigens			
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
662	2837	M97/252508	UK	1997	invasive (unspecified/other)	Neisseria meningitidis	C	50	ST-11 complex	5-1	10-4	F3-6
670	2840	M97/252535	UK	1997	invasive (unspecified/other)	Neisseria meningitidis	C	50	ST-11 complex	5-1	10-4	F3-6
671	2844	M97/252781	UK	1997	invasive (unspecified/other)	Neisseria meningitidis	C	50	ST-11 complex	5-1	10-4	F3-6
672	2847	M97/252943	UK	1997	invasive (unspecified/other)	Neisseria meningitidis	C	50	ST-11 complex	5-1	10-4	F3-6

Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree ITOL PhyloViz Microreact

## 5.22 Defining new loci based on annotated reference genome

An annotated reference genome can be used as the basis of defining loci. The ‘Database scan’ function will create an upload table suitable for pasting directly in to the batch locus add form of the *sequence definition* or *isolate* databases.

Click ‘Database scan’ within the ‘Loci’ group on the curator’s contents page. This function is normally hidden, so you may need to click the ‘Loci’ toggle to display it.

Admin functions

Permissions User passwords Configuration check Cache refresh Loci Locus aliases

PCR reactions PCR locus links Nucleotide probes

Loci Schemes Fields Misc Show all

Enter an EMBL or Genbank accession number for a complete annotated genome and press ‘Submit’.

PubMLST

Home > Organisms > Organism > *Neisseria* isolates > Scan EMBL/Genbank record

Scan EMBL/Genbank record for loci

This function allows you to scan an EMBL or Genbank (whole genome) file in order to create a batch upload file for setting up new loci.

Please enter accession number      Primary identifier      Action

Accession:       ☒ locus tag      ☐ gene name     

A table of loci will be generated provided a valid accession number is provided.

PubMLST

Home > Organisms > Organism > *Neisseria* isolates > Scan EMBL/Genbank record

Scan EMBL/Genbank record for loci

This function allows you to scan an EMBL or Genbank (whole genome) file in order to create a batch upload file for setting up new loci.

Please enter accession number      Primary identifier      Action

Accession:       ☒ locus tag      ☐ gene name     

Download table

  Suitable for batch upload of loci.

Download alleles

  Suitable for defining the first allele in the seqdef database.

Annotation information

accession: AM421808  
 version: 1  
 type: dna  
 length: 2194961  
 description: *Neisseria meningitidis* serogroup C FAM18 complete genome.  
 coding regions: 1975

Coding sequences

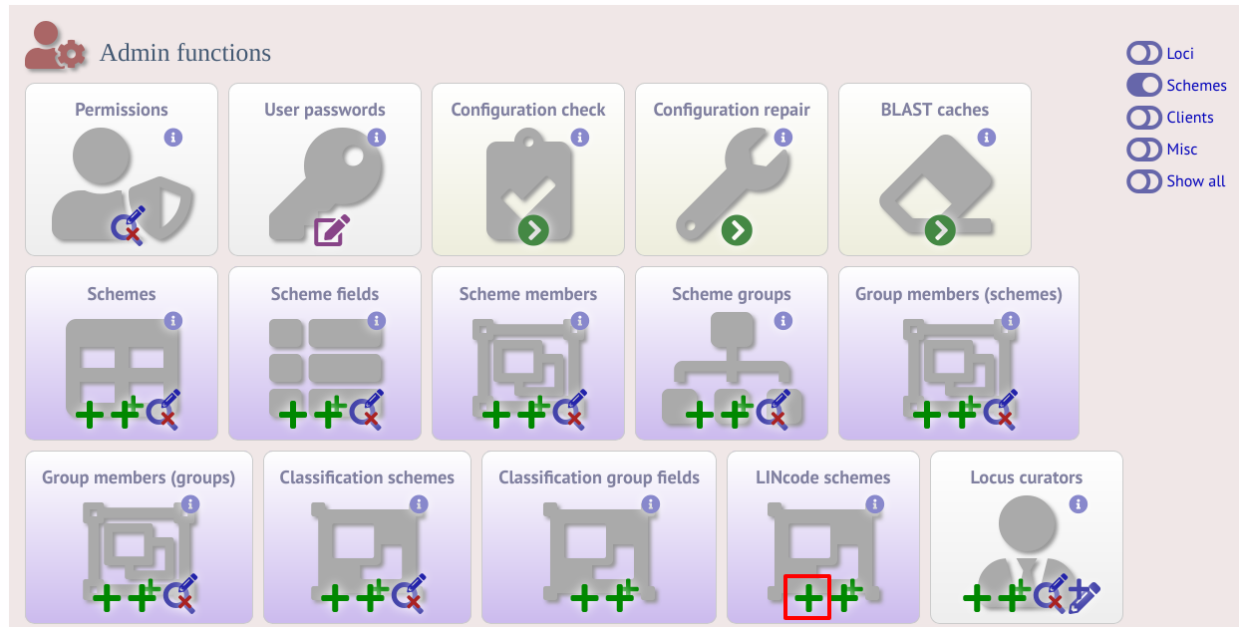
Locus	Aliases	Product	Length
NMC0001	lpxC; envA	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	924
NMC0002	pilS1	pilin (fragment)	291
NMC0003	pilS2	truncated pilin	366
NMC0004	fbp	peptidyl-prolyl cis-trans isomerase	330
NMC0005		putative membrane protein	219
NMC0006		putative glycerate dehydrogenase	954
NMC0007	metG	methionyl-tRNA synthetase	2058
NMC0008	glmS	glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	1839
NMC0009		putative lipoprotein	519
NMC0010	gna33	outer membrane lipoprotein Gna33 ⓘ	1326
NMC0011		putative integral membrane protein	840
NMC0012		putative lipoprotein	1167
NMC0013		possible membrane protein	1266

Tab-delimited text and Excel format files will be created to be used as the basis for upload files for the sequence definition and isolate databases. Batch sequence files, in text and Excel formats, are also created for defining the first allele once the locus has been set up in the sequence definition database.

## 5.23 Setting up LINcode definitions for cgMLST schemes

**Note:** The idea behind LINcodes is described in [Hennart et al. 2021 bioRxiv 2021.07.26.453808](#).

LINcode schemes can be defined by administrators by clicking the add LINcode scheme button within the ‘Schemes’ group on the curator index page of both the sequence definition and isolate databases. This function is normally hidden, so you may need to click the ‘Schemes’ toggle to display it. An indexed scheme, e.g. MLST or cgMLST whereby a field defines each unique combination of alleles, needs to be defined before the link will be enabled.



Select the indexed scheme from the dropdown list and enter your locus thresholds in descending order as a semi-colon separated list, e.g. 500;250;100;50;25;10;5;2;1;0. Also enter the number of missing alleles that are allowed within a profile for a LINcode to be assigned. Click ‘Submit’.

BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > Add new LINcode scheme

User interface

### Add new LINcode scheme

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

scheme id: N. meningitidis cgMLST v1.0

thresholds: 500;250;100;50;25;10;5;2;1;0

Semi-colon separated list of thresholds

max missing: 50

Number of loci that are allowed to be missing for a LINcode to be defined.

curator: Keith Jolley (keith)

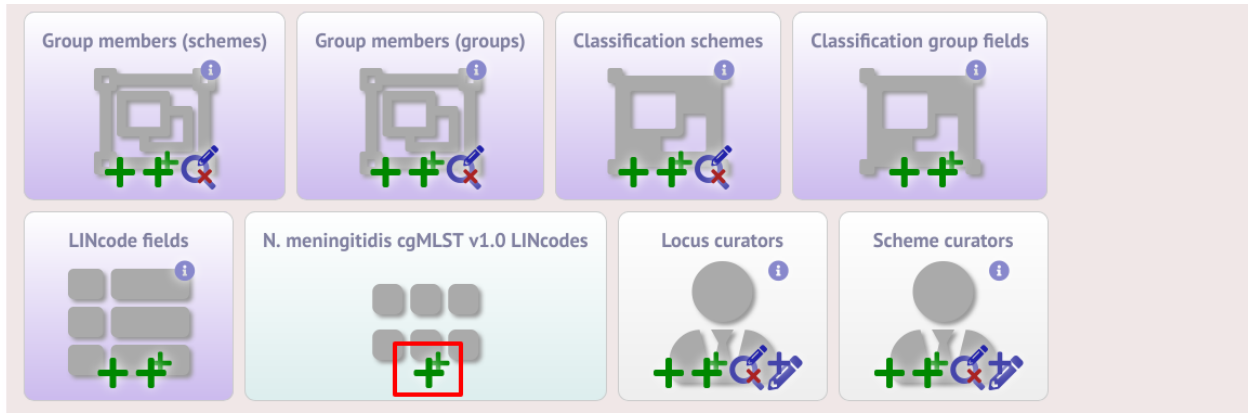
datestamp: 2022-03-07

Action

RESET

SUBMIT

If LINcodes have been previously defined, the existing assignments can be uploaded by clicking the batch add LINcodes button (sequence definition database). This allows you to copy and paste assignments from a spreadsheet template. The template consists of the index field (e.g. cgST), and separate columns for each threshold level.



LINcodes can then be assigned automatically using the `lincodes.pl` script found within the `scripts/maintenance` directory. A full list of arguments can be found by typing:

```
lincodes.pl --help
NAME
    lincodes.pl - Define LINcodes from cgMLST profiles.

SYNOPSIS
    lincodes.pl --database DB_CONFIG --scheme SCHEME_ID [options]

OPTIONS

--batch_size NUMBER
    Sets a maximum number of profiles to use to initiate assignment order.
    The order of assignment is optimally determined using Prim's algorithm,
    but can take a long time if there are thousands of profiles. Up to the
    number of profiles set here will be ordered and assigned first before
    further batches are ordered and assigned. The default value is 10,000
    but it is recommended that you allow ordering to be determined from all
    defined profiles if LINcodes have not been previously determined, i.e.
    set this value to greater than the number of assigned profiles.

--database DATABASE CONFIG
    Database configuration name. This must be a sequence definition database.

--missing NUMBER
    Set the maximum number of loci that are allowed to be missing in a profile
    for LINcodes to be assigned. If not set, the value defined in the LINcode
    schemes table will be used.

--mmap
    Write distance matrix to disk rather than memory. Use this if calculating a
    very large distance matrix on a machine with limited memory. This may run
    slower.

--quiet
    Only output errors.

--scheme SCHEME ID
    Scheme id number for which a LINcode scheme has been defined.
```

It is also possible to provide nomenclature for specific LINcode prefixes. These can be used to define lineages or sublineages. LINcode fields are first defined by clicking the add lincode field button.



Enter the name of the field you wish to define, e.g. 'lineage' and the data type for any values (either text or integer).

**BIGSdb**

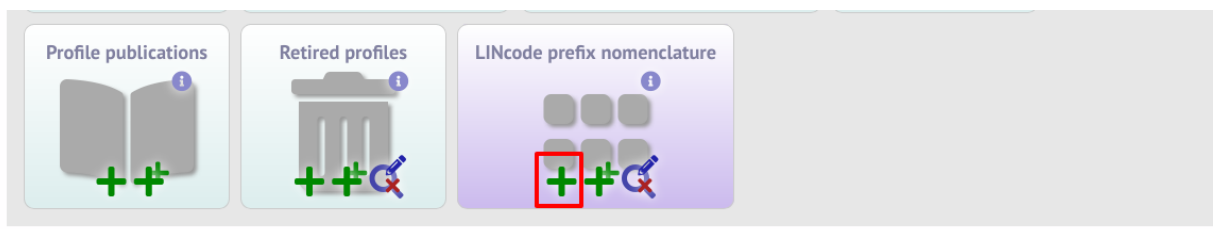
Home > Organisms > Organism > *Neisseria* typing > Add new LINcode field

**Add new LINcode field**

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
scheme id: N. meningitidis cgMLST v1.0 field: lineage type: text curator: Keith Jolley (keith) datestamp: 2022-03-08 display order:	RESET SUBMIT

A new menu item called 'LINcode prefix nomenclature' will appear in the curator part of the index page. It is hidden by default so you may need to click the 'Show all' button. Click the add button.



Enter a LINcode prefix (left-hand part of LINcode) and assign a name to it. Make sure you do the same in both the sequence definition and isolate database. You will then be able to search isolates based on these field values and they will appear in isolate records.

BIGSdb

Home > Organisms > Organism > *Neisseria* typing > Add new LINcode prefix nomenclature

User interface

## Add new LINcode prefix nomenclature

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
scheme id: N. meningitidis cgMLST v1.0 prefix: 1_0_0 field: lineage value: Lineage 3 curator: Keith Jolley (keith) timestamp: 2022-03-08	RESET SUBMIT

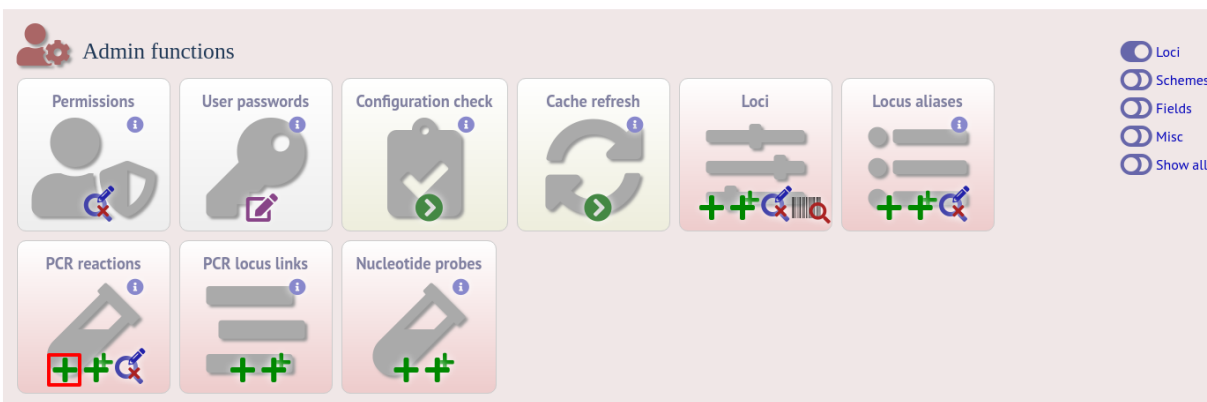
## 5.24 Genome filtering

Within a genome there may be multiple loci that share allele pools. If an allele sequence is tagged from a genome using only BLAST then there is no way to determine which locus has been identified. It is, however, possible to further define loci by their context, i.e. surrounding sequence.

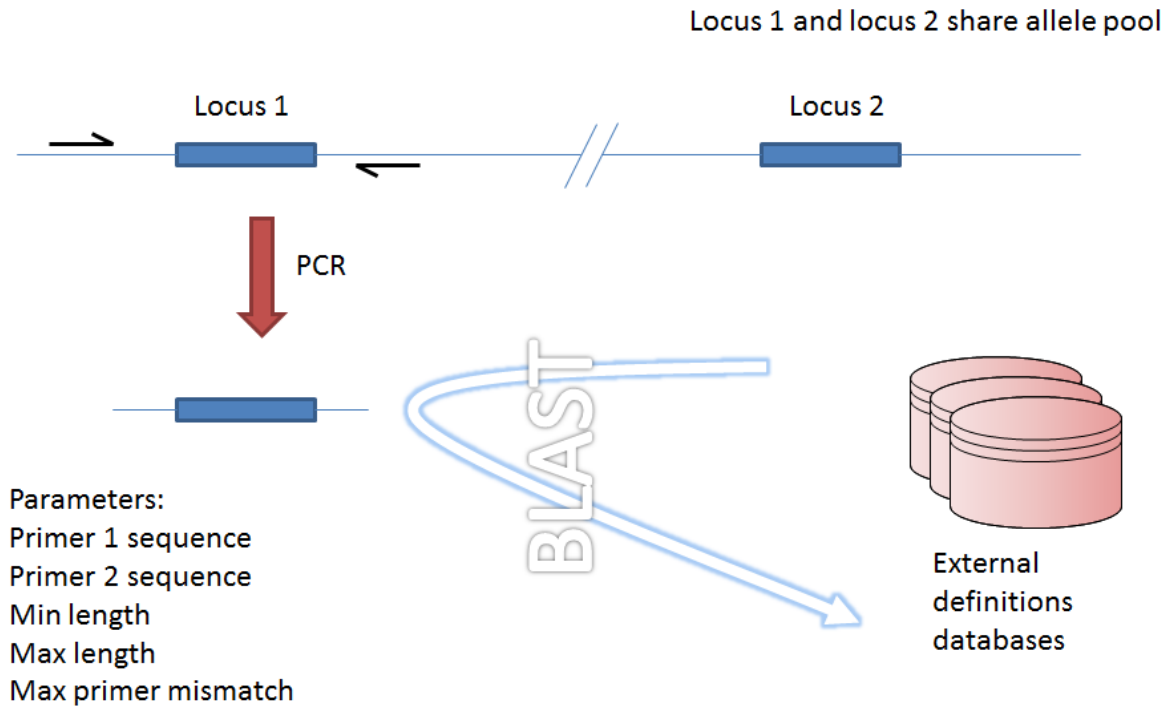
### 5.24.1 Filtering by *in silico* PCR

Provided a locus can be predicted to be specifically amplified by a PCR reaction, the genome can be filtered to only look at regions predicted to fall within amplification products of one or more PCR reactions. Since this is *in silico* we don't need to worry about problems such as sequence secondary structure and primers can be any length.

To define a PCR reaction that can be linked to a locus definition, click the add (+) PCR reaction link on the curator's main page. This function is normally hidden, so you may need to click the 'Loci' toggle to display it.



In the resulting web form you can enter values for your two primer sequences (which can be any length), the minimum and maximum lengths of reaction products you wish to consider and a value for the allowed number of mismatches per primer.

Fig. 1: Genome filtering by *in silico* PCR.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new PCR reaction

### Add new PCR reaction

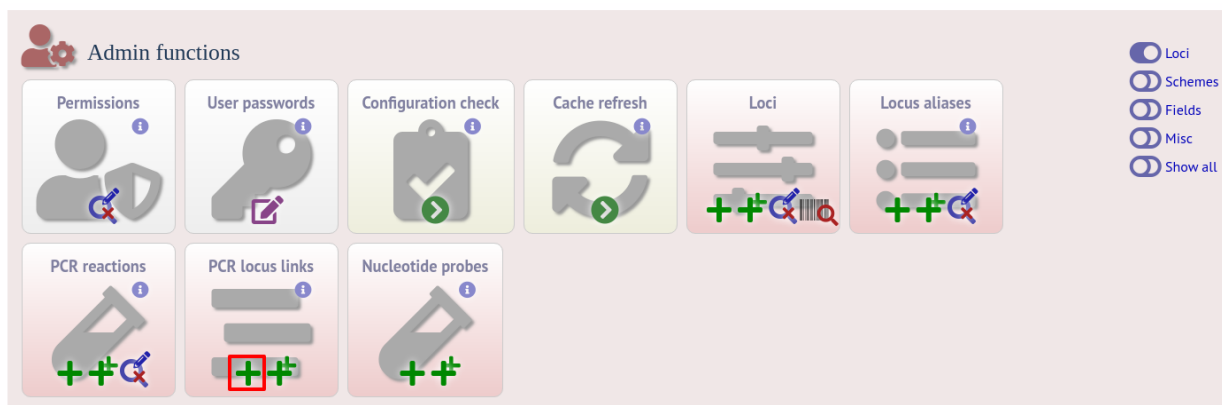
Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
<p>id: 2</p> <p>description:</p> <p>primer1:</p> <p>primer2:</p> <p>curator: Keith Jolley (keith)</p> <p>timestamp: 2020-07-19</p> <p>min length: Minimum length of product to return</p> <p>max length: Maximum length of product to return</p> <p>max primer mismatch: Maximum sequence mismatch per primer</p>	<p>RESET</p> <p>SUBMIT</p>

- id - PCR reaction identifier number.
  - Allowed: integer.
- description - Description of PCR reaction product.
  - Allowed: any text.
- primer1 - Primer 1 sequences
  - Allowed: nucleotide sequence (IUPAC ambiguous characters allowed).

- primer2 - Primer 2 sequence.
  - Allowed: nucleotide sequence (IUPAC ambiguous characters allowed).
- min\_length - Minimum length of predicted PCR product.
  - Allowed: integer.
- max\_length - Maximum length of predicted PCR product.
- max\_primer\_mismatch - Number of mismatches allowed in primer sequence.
  - Allowed: integer.
  - Do not set this too high or the simulation will run slowly.

Associating this with a particular locus is a two step process. First, create a locus link by clicking the add (+) PCR locus link on the curator's main page. This link will only appear once a PCR reaction has been defined.



Select the locus and PCR reaction name from the dropdown lists to create the link. You also need to edit the locus table and set the pcr\_filter field to 'true'.

Now when you next perform *tag scanning* there will be an option to use PCR filtering.

### 5.24.2 Filtering by *in silico* hybridization

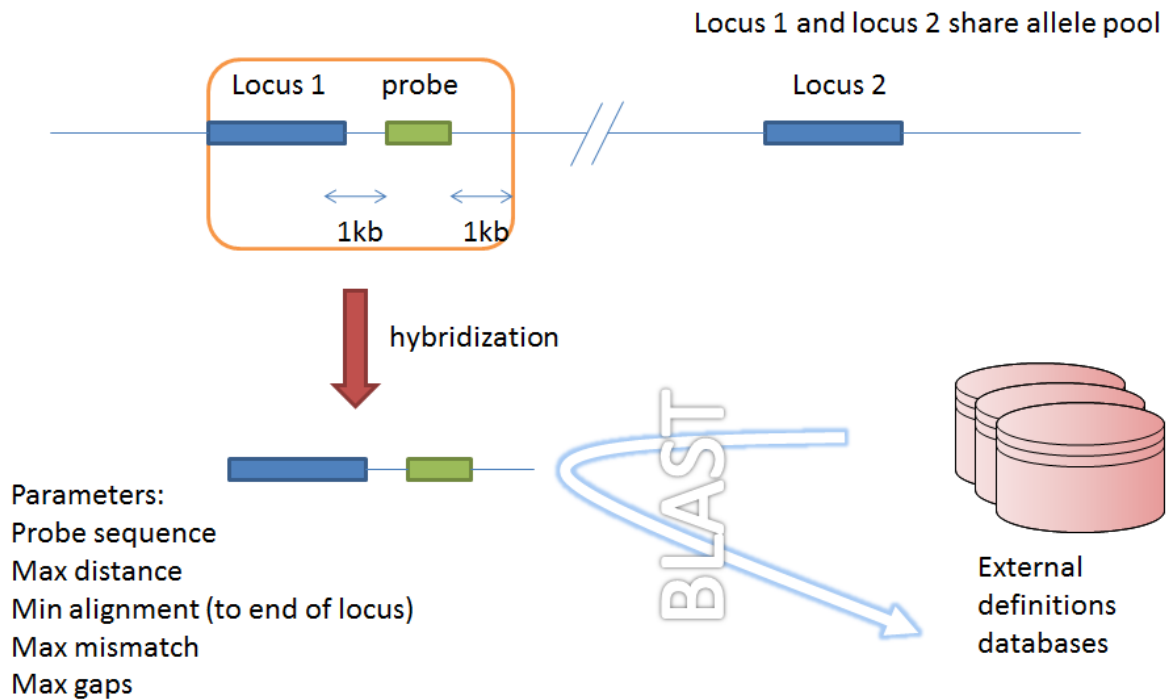
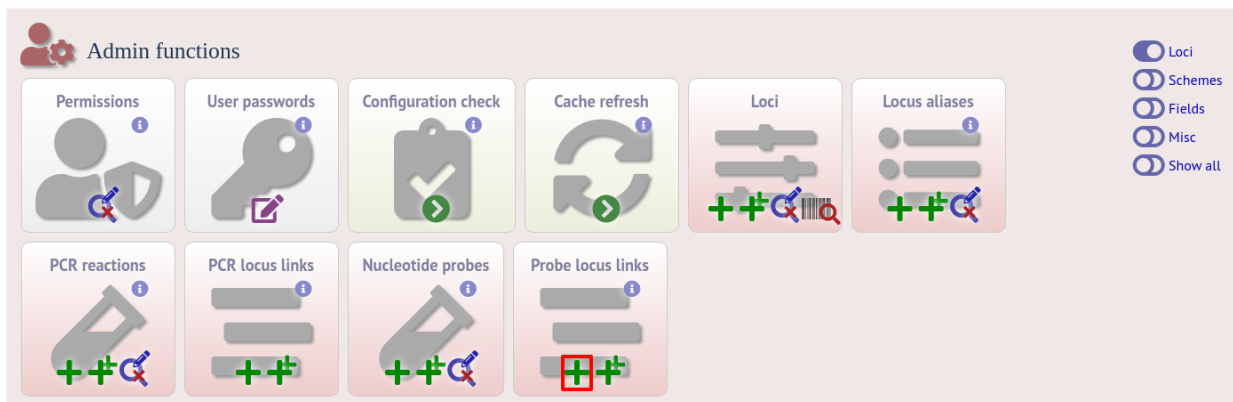
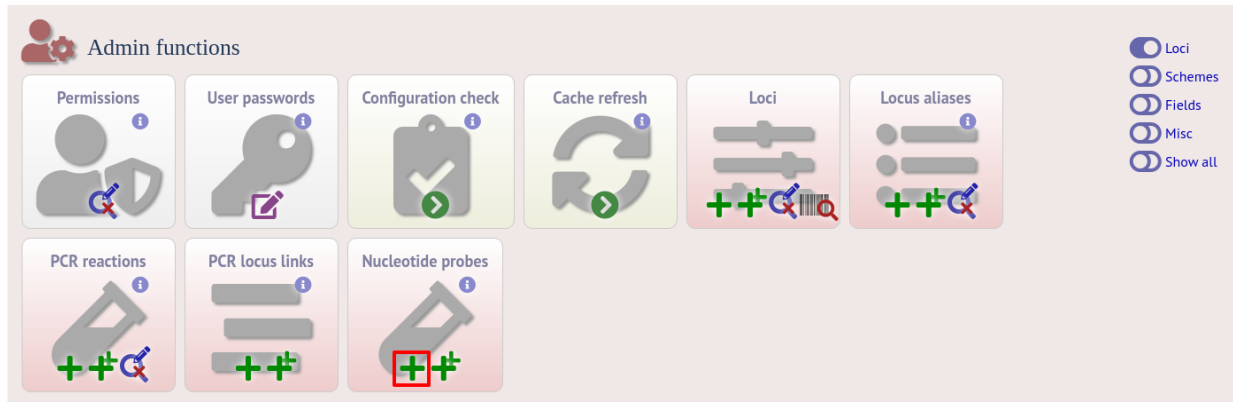
An alternative is to define a locus by proximity to a single probe sequence. This is especially useful if you have multiple contigs and the locus in question may be at the end of a contig so that it doesn't have upstream or downstream sequence available for PCR filtering.

The process is very similar to setting up PCR filtering, but this time click the nucleotide probe link on the curator's content page.

Enter the nucleotide sequence and a name for the probe. Next you need to link this to the locus in question. Click the add (+) probe locus links link on the curator's main page. This link will only appear once a probe has been defined.

Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

- probe\_id - Dropdown list of probe names.
  - Allowed: selection from list.
- locus - Dropdown list of loci.
  - Allowed: selection from list.
- max\_distance - Minimum distance of probe from end of locus.
  - Allowed: any positive integer.

Fig. 2: Filtering by *in silico* hybridization

- `min_alignment` - Minimum length of alignment allowed.
  - Allowed: any positive integer.
- `max_mismatch` - Maximum number of mismatches allowed in alignment.
  - Allowed: any positive integer.
- `max_gaps` - Maximum number of gaps allowed in alignment.
  - Allowed: any positive integer.

Finally edit the locus table and set the `probe_filter` field for the specified locus to ‘true’.

Now when you next perform *tag scanning* there will be an option to use probe hybridization filtering.

## 5.25 Setting locus genome positions

The genome position for a locus can be set directly by editing the locus record. To batch update multiple loci based on a tagged genome, however, a much easier way is possible. For this method to work, the reference genome must be represented by a single contig.

From the curator’s main page, you need to do a query to find the isolate that you will base your numbering on. Click ‘isolate query’ to take you to a standard query form.



Perform your search and click the hyperlinked id number of the record.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Query or update isolates

Query or update isolates

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

isolate = MC58

Display/sort options

Order by: id ascending

Display: 25 records per page

Action

RESET SEARCH

1 record returned.

Delete Tag scanning Projects Your projects


Delete ALL Scan Select project... Link Select project... Add these records

Bookmark query


2020-07-19:1 Add bookmark

Delete	Update	Sequence bin	New version	Isolate fields										MLST		Finotyping antigens		
				id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR		
				<a href="#">240</a>	MC58	BennettTree07; Z7176	UK	1983	Neisseria meningitidis		B	74	ST-32 complex	7	16-2	F1-5		

In the isolate record, click the ‘Show sequence bin’ button to bring up details of the isolate contigs.

 Publications (7)

- Bennett JS, Bentley SD, Vernikos GS, Quail MA, Cherevach I, White B, Parkhill J, Maiden MC (2010). Independent evolution of the core and accessory gene sets in the genus *Neisseria*: insights gained from the genome of *Neisseria lactamica* isolate 020-06. *BMC Genomics* **11**:652 | [78 isolates](#)
- Bennett JS, Jolley KA, Earle SG, Corton C, Bentley SD, Parkhill J, Maiden MC (2012). A genomic approach to bacterial taxonomy: an examination and proposed reclassification of species within the genus *Neisseria*. *Microbiology* **158**:1570-80 | [55 isolates](#)
- Bennett JS, Jolley KA, Maiden MC (2013). Genome sequence analyses show that *Neisseria oralis* is the same species as '*Neisseria mucosa* var. *heidelbergensis*'. *Int J Syst Evol Microbiol*

 Sequence bin

contigs: 1  
length: 2272360 bp  
loci tagged: 2,230

[Show sequence bin](#)

Click the 'Renumber' button:

Sequence	Sequencing method	Original designation	Length	Comments	Locus	Start	End	Direction	Annotation	Renumber
1	Sanger		2272360	whole genome	NEIS2139	7	498	←	EMBL GBK	Renumber
					NEIS2140	502	897	←		
					NEIS2141	918	2312	←		
					NEIS2142	2517	3161	←		
					NEIS2143	3158	3511	←		
					NEIS2144	3635	4117	→		
					NEIS2145	4311	4961	→		
					NEIS2146	4958	5875	→		
					NEIS2147	5936	6214	→		
					NEIS2148 (pgk)	6281	7492	←		
					NEIS2149	7573	8826	←		
					tRNA-lys	9197	9272	←		
					NEIS2150	9346	10317	←		
					NEIS2151	10350	10811	←		
					NEIS2152 (kdtA)	10840	12177	←		
					NEIS2153	12174	13622	←		
					NEIS2979	13848	13964	←		
					NEIS0001 (lpxC)	15221	16144	←		
					NEIS0210 (pilE)	17229	17741	←		
					NEISp0210	17232	17741	←		
					pilS	18127	23903	←		
					NEIS0004 (fbp)	23904	24233	←		
					NEIS0005	24311	24529	←		

A final confirmation screen is displayed with the option to remove existing numbering that doesn't appear within the reference genome. Click 'Renumber'.

PubMLST

Home > Organisms > Organism > *Neisseria* isolates > Renumber locus genome positions

## Renumber locus genome positions based on tagged sequences

You have selected to renumber the genome positions set in the locus table based on the tagged sequences in sequence id#1.

Option Action

☐ Remove positions for loci not tagged in this sequence RENUMBER

The following designations will be made:

Locus	Existing genome position	New genome position
NEIS2139		7
NEIS2140		502
NEIS2141		918
NEIS2142		2517
NEIS2143		3158
NEIS2144		3635
NEIS2145		4311
NEIS2146		4958
NEIS2147		5936
NEIS2148		6281
NEIS2149		7573
tRNA-lys		9197
NEIS2150		9346
NEIS2151		10350
NEIS2152		10840

## 5.26 Defining composite fields

Composite fields are virtual fields that don't themselves exist within the database but are made up of values retrieved from other fields or schemes and formatted in a particular way. They are used for display and analysis purposes only and can not be searched against.

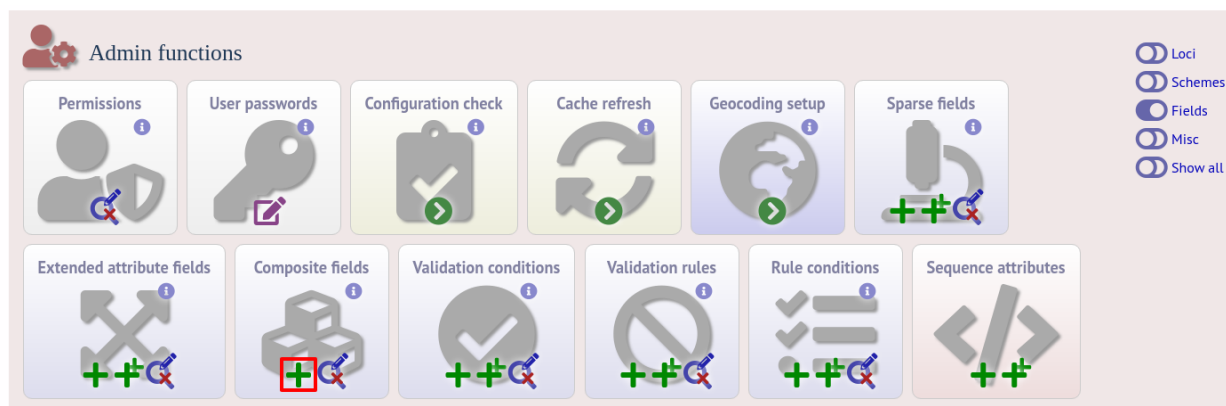
One example of a composite field is used in the Neisseria PubMLST database which has a strain designation composite field made up of serogroup, PorA VR1 and VR2, FetA VR, ST and clonal complex designations in the format:

```
[serogroup]: P1.[PorA_VR1],[PorA_VR2]: [FetA_VR]: ST-[ST] ([clonal_complex])
```

e.g. A: P1.5-2,10: F1-5: ST-4 (cc4)

Additionally, the clonal complex field in the above example is converted using a regular expression from 'ST-4 complex/subgroup IV' to 'cc4'.

Composite fields can be added to the database by clicking the add (+) composite fields link on the curator's main page. This function is normally hidden, so you may need to click the 'Fields' toggle to display it.



Initially you just enter a name for the composite field and after which field it should be positioned. You can also set whether or not it should be displayed by default in main results tables following a query - this is overrideable by user preferences.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new composite field

Add new composite field

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: strain\_designation

name of the field as it will appear in the web interface

position after: isolate

field present in the isolate table

main display: ☐ true ☒ false

Sets whether to display field in isolate query results table (can be overridden by user preference).

curator: Keith Jolley (keith)

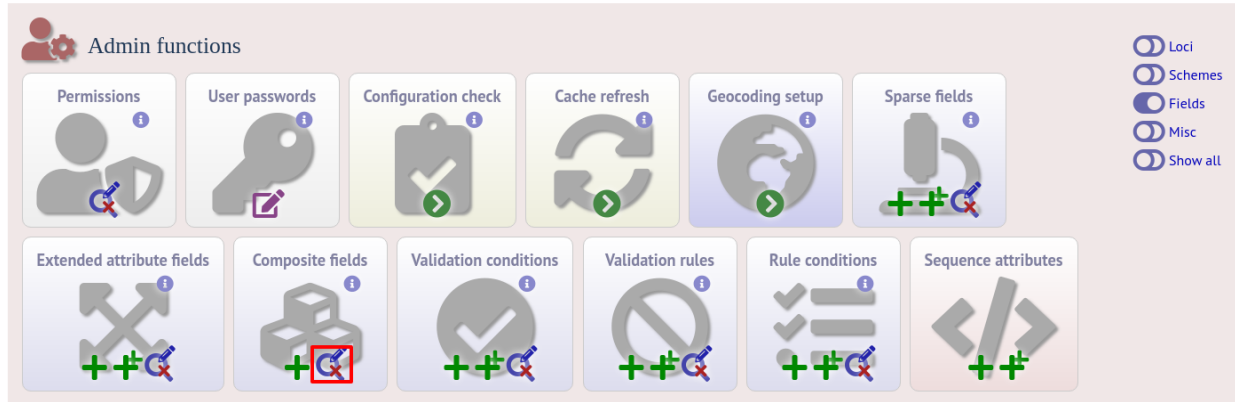
timestamp: 2020-07-19

Action

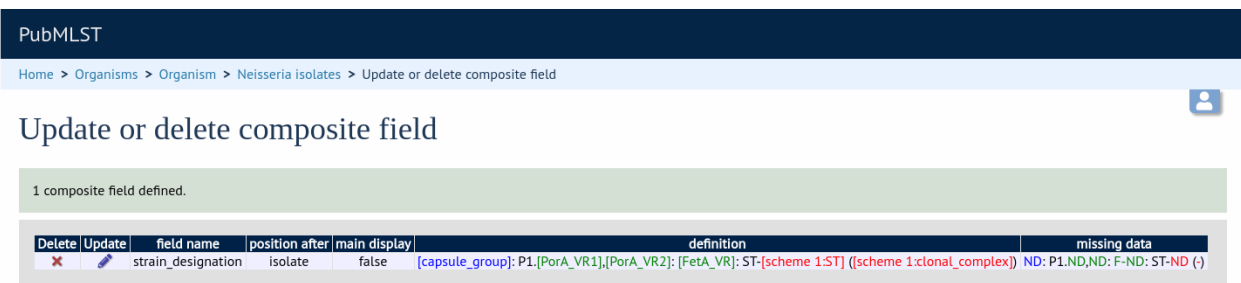
RESET

SUBMIT

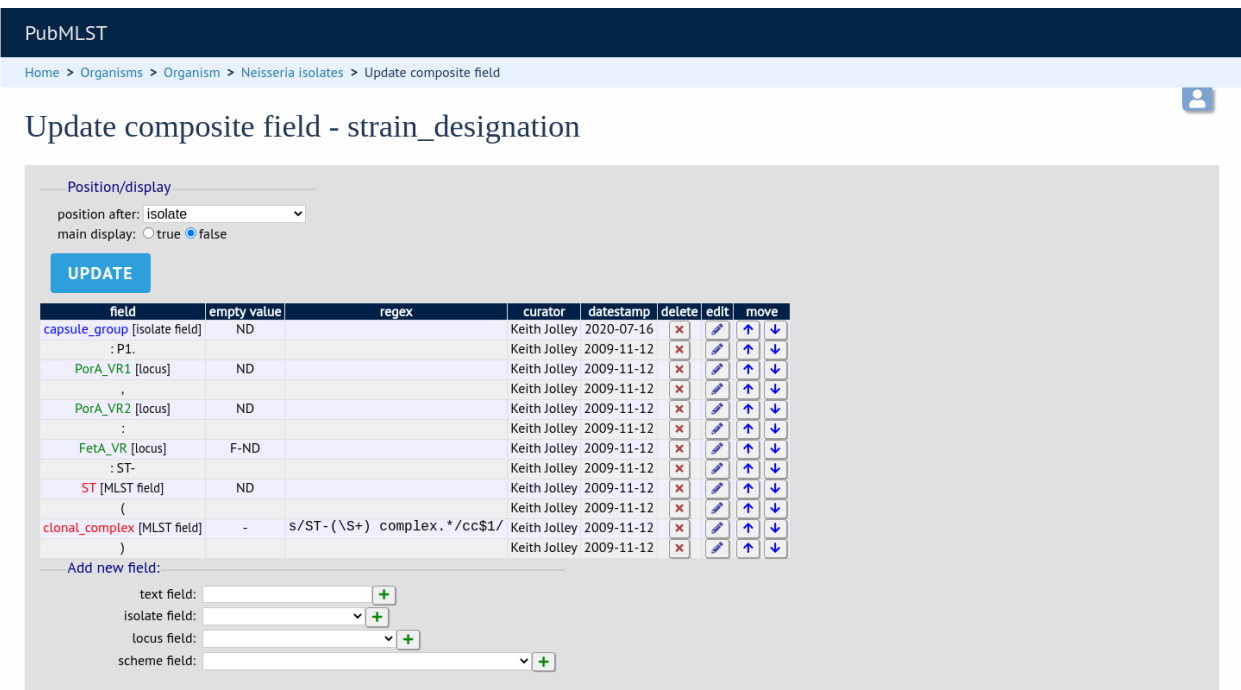
Once the field has been created it needs to be defined. This can be done from query composite field link on the main curator's page.



Select the composite field from the list and click ‘Update’.



From this page you can build up your composite field from snippets of text, isolate field, locus and scheme field values. Enter new values in the boxes at the bottom of the page.



Once a field has been added to the composite field, it can be edited by clicking the ‘edit’ button next to it to add a regular expression to modify its value by specific rules, e.g. in the clonal complex field above, the regular expression is set as:

```
s/ST-(\S+) complex.*/cc$1/
```

which extracts one or more non-space characters following the 'ST-' in a string that then contains the word 'complex', and appends this to 'cc' to produce the final string.

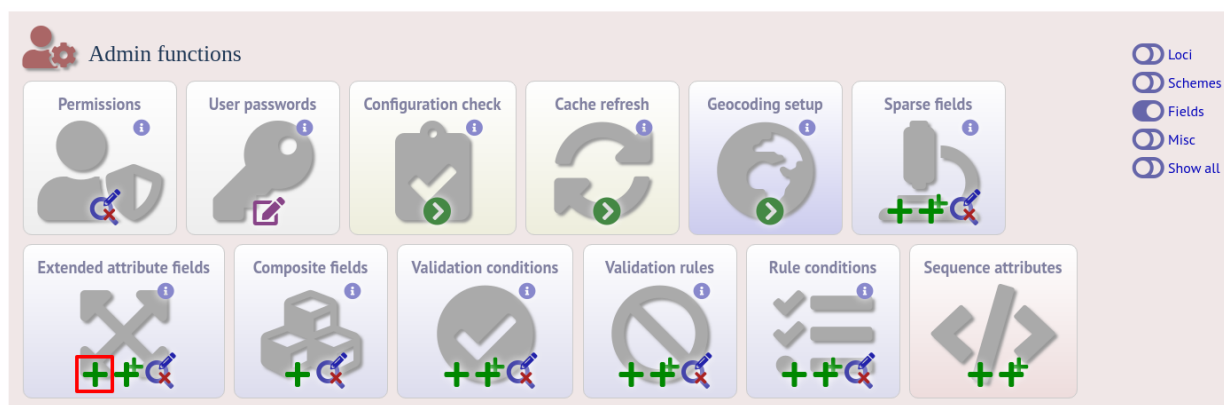
This will convert 'ST-4 complex/subgroup IV' to 'cc4'.

You can also define text to be used for when the field value is missing, e.g. 'ND'.

## 5.27 Extended provenance attributes (lookup tables)

Lookup tables can be associated with an isolate database field such that the database can be queried by extended attributes. An example of this is the relationship between continent and country - every country belongs to a continent but you wouldn't want to store the continent with each isolate record (not only could data be entered inconsistently but it's redundant). Instead, each record may have a country field and the continent is then determined from the lookup table, allowing, for example, a search of isolates limited to those from Europe.

To set up such an extended attribute, click the add (+) isolate field extended attributes link on the curator's main page. This function is normally hidden, so you may need to click the 'Fields' toggle to display it.

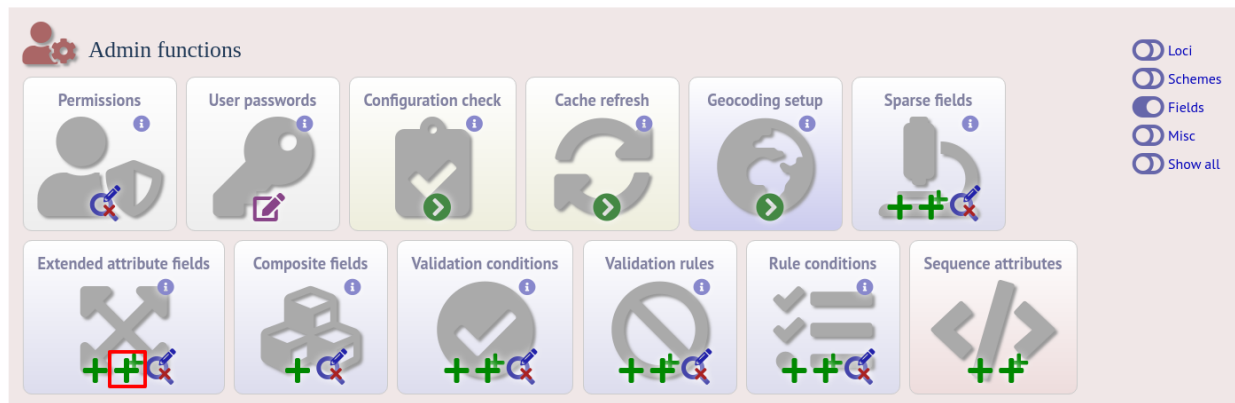


Fill in the web form with appropriate values. Required fields have an exclamation mark (!) next to them:

- isolate\_field - Dropdown list of isolate fields.
  - Allowed: selection from list.
- attribute - Name of extended attribute, e.g. continent.
  - Allowed: any text (no spaces).
- value\_format - Format for values.
  - Allowed: integer/float/text/date.
- value\_regex - [Regular expression](#) to enforce allele id naming.
  - ^: the beginning of the string
  - \$: the end of the string
  - d: digit
  - D: non-digit
  - s: white space character
  - S: non white space character

- w: alpha-numeric plus ‘\_’
- .: any character
- \*: 0 or more of previous character
- +: 1 or more of previous character
- e.g. ^Fd-d+\$ states that a value must begin with a F followed by a single digit, then a dash, then one or more digits, e.g. F1-12
- description - Long description - this isn’t currently used but may be in the future.
  - Allowed: any text.
- url - URL used to hyperlink values in the isolate information page. Instances of [?] within the URL will be substituted with the value.
  - Allowed: any valid URL (either relative or absolute).
- length - Maximum length of extended attribute value.
  - Allowed: any positive integer.
- field\_order - Integer that sets the order of the field following it’s parent isolate field.
  - Allowed: any integer.

The easiest way to populate the lookup table is to do a batch update copied from a spreadsheet. Click the batch add (++) isolate field extended attribute values link on the curator’s main page (this link will only appear once an extended attribute has been defined). This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Download the Excel template:

PubMLST

Home > Organisms > Organism > Neisseria isolates > Batch add isolate field extended attribute records

## Batch insert isolate field extended attributes

### Instructions

This page allows you to upload isolate field extended attribute data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

### Templates

Check the [description of database fields](#) for help with filling in the template.

### Upload

Paste in tab-delimited text (Include a field header line).

Action

RESET

SUBMIT

Fill in the columns with your values, e.g.

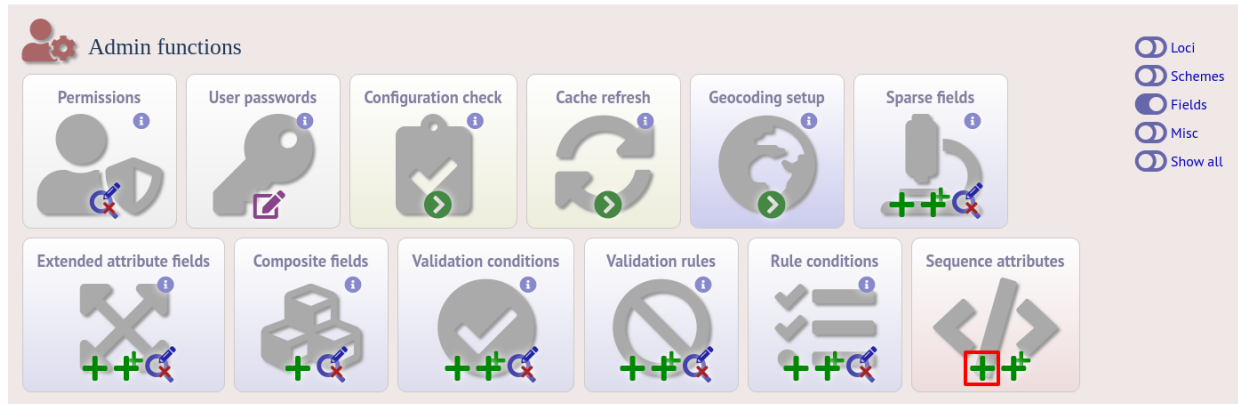
isolate_field	attribute	field_value	value
country	continent	Afghanistan	Asia
country	continent	Albania	Europe
country	continent	Algeria	Africa
country	continent	Andorra	Europe
country	continent	Angola	Africa

Paste from the spreadsheet in to the upload form and click ‘Submit’.

## 5.28 Sequence bin attributes

It is possible that you will want to store extended attributes for sequence bin contigs when you upload them. Examples may be read length, assembler version, etc. Since there are almost infinite possibilities for these fields, and they are likely to change over time, they are not hard-coded within the database. An administrator can, however, create their own attributes for a specific database and these will then be available in the web form when uploading new contig data. The attributes are also searchable.

To set up new attributes, click the add (+) ‘sequence attributes’ link on the isolate database curator’s index page. This function is normally hidden, so you may need to click the ‘Fields’ toggle to display it.



Enter the name of the attribute as the 'key', select the type of data (text, integer, float, date) and an optional short description. Click 'Submit'.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new sequence attribute

### Add new sequence attribute

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
key: <input type="text" value="read_length"/> type: <input type="text" value="integer"/> curator: Keith Jolley (keith) timestamp: 2020-07-19 description: <input type="text"/>	<input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

This new attribute will then be available when *uploading contig data*.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Add new sequences

Upload sequences

This page allows you to upload sequence data for a specified isolate record in FASTA format.

Please note that you can reach this page for a specific isolate by [querying isolates](#) and then clicking 'Upload' within the isolate table.

Please fill in the following fields - required fields are marked with an exclamation mark (!).

Paste in sequences in FASTA format:

Attributes

isolate id: ! Enter isolate id...

sender: ! Select sender...

method:

run id:

assembly id:

read length:

Options

☒ Don't insert sequences shorter than 100 bps.

☒ Don't insert sequences containing only homopolymers.

Link to experiment:

Alternatively upload FASTA file

or enter Genbank accession

Select FASTA file:

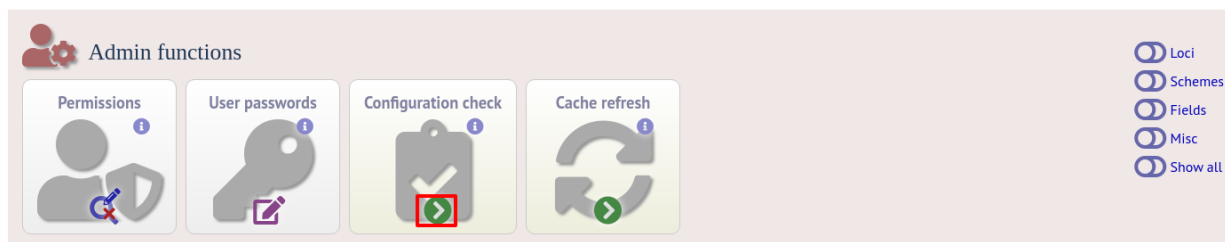
Choose file | No file chosen

Action

RESET SUBMIT

## 5.29 Checking external database configuration settings

Click the 'Configuration check' link on the curator's index page.



The software will check that required helper applications are installed and executable and, in isolate databases, test every locus and scheme external database to check for connectivity and that data can be retrieved. By default, only loci which have an issue will be displayed but you can click the 'show all loci' link to display them all.

## PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria isolates](#) > Configuration check - Neisseria isolates


## Configuration check - Neisseria isolates

## PostgreSQL

BIGSdb requires Pg 9.5 or higher. You are running version 10.12. ✓

## Helper applications

Program	Path	Installed	Executable
EMBOSS infoalign	/usr/bin/infoalign	✓	✓
EMBOSS sixpack	/usr/bin/sixpack	✓	✓
EMBOSS stretcher	/usr/bin/stretcher	✓	✓
GrapeTree	/usr/local/GrapeTree/grapetree.py	✓	✓
blastn	/usr/bin/blastn	✓	✓
blastp	/usr/bin/blastp	✓	✓
blastx	/usr/bin/blastx	✓	✓
blat	/usr/local/bin/blat	✓	✓
clustalw	/usr/bin/clustalw	✓	✓
ipccress	/usr/bin/ipccress	✓	✓
mafft	/usr/bin/mafft	✓	✓
makeblastdb	/usr/bin/makeblastdb	✓	✓
mogrify	/usr/bin/mogrify	✓	✓
muscle	/usr/bin/muscle	✓	✓
tblastx	/usr/bin/tblastx	✓	✓

Locus databases (only showing loci with potential problems - [show all loci](#))

Locus	Database	Host	Port	Id field value	Database accessible	Sequence query	Sequences assigned
NEIS0895 (parA)	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS0895	✓	✓	✗
NEIS0903 (opaD)	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS0903	✓	✓	✗
NEIS1454	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS1454	✓	✓	✗
NEIS1551 (opaC)	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS1551	✓	✓	✗
NEIS2013	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS2013	✓	✓	✗
NEIS2538	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	NEIS2538	✓	✓	✗

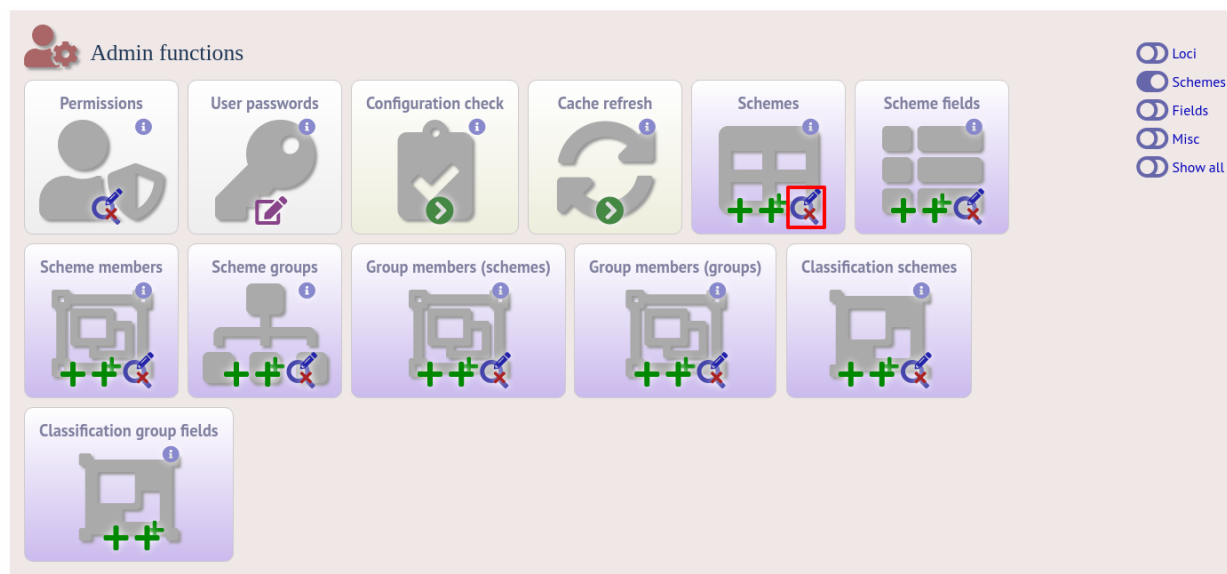
## Scheme databases

Scheme description	Database	Host	Port	Id	Database accessible	Profile query
MLST	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	1	✓	✓
Ribosomal MLST	bigsdb_multispecies_seqdef	zoo-aberlour	5432	1	✓	✓
rplF species	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	42	✓	✓
N. meningitidis cgMLST v1.0	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	47	✓	✓
Conjugative Plasmid	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	49	✓	✓
beta lactamase plasmid	pubmlst_bigsdb_neisseria_seqdef	zoo-aberlour	5432	52	✓	✓

Any problems will be highlighted with a red X.

## 5.30 Exporting table configurations

Sometimes it is useful to transfer configurations between different databases or to export a configuration for troubleshooting. Data from most of the tables can be exported in tab-delimited text format suitable for batch uploading. For example, to export scheme configuration data, click the query link (Update or delete) next to schemes in the curator's interface. This function is normally hidden, so you may need to click the 'Schemes' toggle to display it.



Expand the filters and select the required scheme in the dropdown box, then press submit.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Query scheme information

Query scheme information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

id = + ⓘ

**Display**

Order by: id ascending

Display: 25 records per page ⓘ

**Filter query by**

isolate display: ⓘ

main display: ⓘ

query field: ⓘ

query status: ⓘ

analysis: ⓘ

view: ⓘ

allow missing loci: ⓘ

curator: ⓘ

scheme: MLST ⓘ

**Action**

RESET SUBMIT

Click the button 'Export configuration/data'.

PubMLST

Home > Organisms > Organism > Neisseria isolates > Query scheme information

Query scheme information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

id =

**Display**

Order by:  ascending   
 Display: 25 records per page

**Filter query by**

isolate display:    
 main display:    
 query field:    
 query status:    
 analysis:    
 view:   
 allow missing loci:    
 curator:    
 scheme: MLST

**Action**

1 record returned.

Delete	Update	id	name	dbase name	dbase host	dbase port	dbase id	isolate display*	main display*	query field*	query status*	analysis*	view	display order	allow missing loci	curator	datestamp	date entered
<input checked="" type="checkbox"/>	<input type="checkbox"/>	1	MLST	pubmlst_bigsdb_neisseria_seqdef			1	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>		1	<input type="checkbox"/>	Keith Jolley	2019-07-26	2009-11-12

\* Default values are displayed for this field. These may be overridden by user preference.

The three tables that are used to define a scheme (schemes, scheme\_members and scheme\_fields) are displayed in a format suitable for copy and pasting.

```
schemes
-----
id description dbase_name dbase_host dbase_port dbase_user dbase_password dbase_
table isolate_display main_display query_field query_status analysis display_
order allow_missing_loci curator datestamp date_entered
1 MLST pubmlst_bigsdb_neisseria_seqdef mv_scheme_1 1 1 1 1 1 1 2
2012-03-22 2009-11-12

scheme_members
-----
scheme_id locus profile_name field_order curator datestamp
1 abcZ 1 2 2009-11-12
1 adk 2 2 2009-11-12
1 aroE 3 2 2009-11-12
1 fumC 4 2 2009-11-12
1 gdh 5 2 2009-11-12
1 pdhC 6 2 2009-11-12
1 pgm 7 2 2009-11-12

scheme_fields
-----
scheme_id field type primary_key description field_order url isolate_display main_
display query_field dropdown curator datestamp
1 ST integer 1 1 /cgi-bin/bigsdb/bigsdb.pl?page=profileInfo&db=pubmlst_neisseria_
seqdef&scheme_id=1&profile_id=[?] 1 1 1 0 2 2010-01-20
1 clonal_complex text 0 2 1 1 1 1 2 2009-11-16
```

## 5.31 Authorizing third-party client software to access authenticated resources

If you are running the *RESTful API*, you will need to specifically authorize client software to connect to authenticated resources. This involves creating a client key and a client secret that is used to sign requests coming from the application. The client key and secret should be provided to the application developer.

There is a script to do this in the scripts/maintenance directory of the download archive. The script is called `create_client_credentials` and should be run by the postgres user. A full list of options can be found by typing:

```
create_client_credentials.pl --help

NAME
    create_client_credentials.pl - Generate and populate
    authentication database with third party application (API client)
    credentials.

SYNOPSIS
    create_client_credentials.pl --application NAME [options]

OPTIONS
    -a, --application NAME
        Name of application.

    -d, --deny
        Set default permission to 'deny'. Permissions for access to specific
        database configurations will have to be set. If not included, the default
        permission will allow access to all resources by the client.

    -h, --help
        This help page.

    -i, --insert
        Add credentials to authentication database. This will fail if a matching
        application version already exists (use --update in this case to overwrite
        existing credentials).

    -u, --update
        Update existitng credentials in the authentication database.

    -v, --version VERSION
        Version of application (optional).
```

## 5.32 BLAST caches

Sequence definition databases cache any BLAST databases that they create in order to perform sequence queries. These caches can be found in subdirectories named with the database name in the temp directory defined by the `secure_tmp_dir` attribute in `bigsdbs.conf`, e.g. `/var/tmp/pubmlst_bigsdb_neisseria_seqdef`.

These BLAST databases will be marked stale if new alleles are added to the BIGSdb database for any locus covered by the cache. A cache marked stale will be recreated the next time a matching sequence query needs to use it. BLAST databases will also be marked stale if they are older than the `cache_days` setting in `bigsdbs.conf` (default = 7 days).

It is possible to also manually create and refresh these caches using the `update_blast_caches.pl` script found in the `scripts/maintenance` directory.

A full list of options can be found by typing:

```
update_blast_caches.pl --help

NAME
    update_cached_blast_dbs.pl - Refresh BLAST database caches

SYNOPSIS
    update_cached_blast_dbs.pl --database DB_CONFIG [options]

OPTIONS
--all_loci
    Refresh or create cache for all loci.

--database DATABASE CONFIG
    Database configuration name.

--delete_all
    Remove all cache files.

--delete_old
    Remove cache files older than the cache_days setting in bigsdbs.conf or
    that have been marked stale.

--delete_single_locus
    Remove caches containing only one locus. There can be many of these and
    they can clutter the cache directory. They are generally quick to recreate
    when needed.

--help
    This help page.

--quiet
    Only show errors.

--refresh
    Refresh existing caches.

--scheme SCHEME_ID
    Refresh or create cache for specified scheme.
```

## 5.33 Config-specific file downloads

You can make files available on a static website but restrict their access only to users who can authenticate for access to the current database configuration.

This can be done by adding a file called `download_files.conf` to the database configuration directory within `/etc/bigsdb/dbases`. This file consists of three columns in tab-delimited format:

- The full path of the file in the file system
- Label which will be used to hyperlink to the file
- A description of the file
- The file type (docx, html, gif, jpg, pdf, png, tar, tar, xlsx currently supported)

The files can be downloaded directly from a BIGSdb URL: `/cgi-bin/bigsdb.pl?db=CONFIG&page=downloadFiles&file=LABEL` (where `CONFIG` is the database config name and `LABEL` is the label used in the `download_files.conf` file. These URLs can be used as standard links within a web page.

You can also list all available files with the URL: `/cgi-bin/bigsdb.pl?db=CONFIG&page=downloadFiles`

Navigating to these links will prompt the user to log-in if they are not already (if the database config requires this).

## CURATOR'S GUIDE

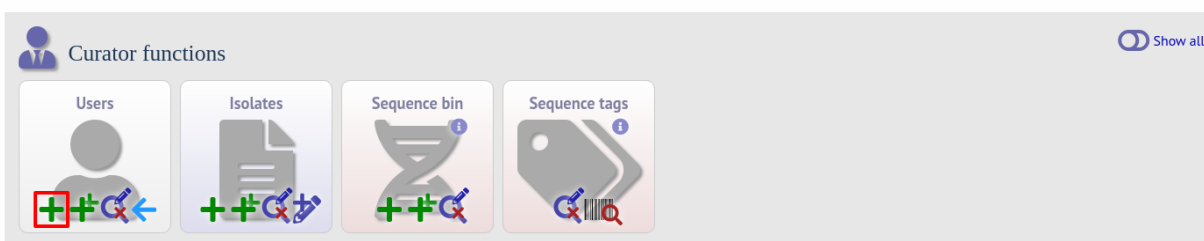
Please note that links displayed within the curation interface will vary depending on database contents and the permissions of the curator. Some infrequently used links are usually hidden by default. These can be enabled by clicking the 'Show all' toggle switch. The admin section has feature- specific toggles as well as a 'Show all' toggle.



### 6.1 Adding new sender details

All records within the databases are associated with a sender. Whenever somebody new submits data, they should be added to the users table so that their name appears in the dropdown lists on the data upload forms.

To add a user, click the add users (+) link on the curator's contents page.



Enter the user's details in to the form.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Add new user

Help

## Add new user

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

id: 548

user name: jbloggs

surname: Bloggs

first name: Joe

email: joe.bloggs@zoo.ox.ac.uk

affiliation: University of Oxford, UK

status: user

date entered: 2020-07-22

timestamp: 2020-07-22

curator: Keith Jolley (keith)

submission emails: ☐ true ☒ false <sup>?</sup> Receive new submission E-mails (curators only)

account request emails: ☐ true ☒ false <sup>?</sup> Receive new account request E-mails (curators only)

private quota: 0 User must be either a submitter, curator, or admin to upload private records

Action

RESET SUBMIT

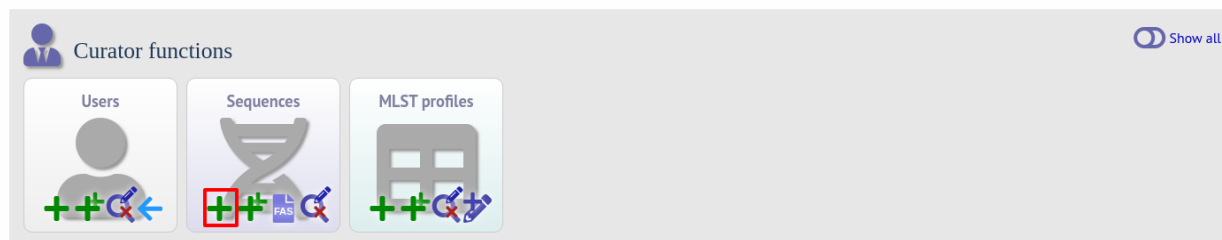
Normally the status should be set as 'user'. Only admins and curators with special permissions can create users with a status of curator or admin.

If the submission system is in operation there will be an option at the bottom called 'submission\_emails'. This is to enable users with a status of 'curator' or 'admin' to receive E-mails on receipt of new submissions. It is not relevant for users with a status of 'user' or 'submitter'.

## 6.2 Adding new allele sequence definitions

### 6.2.1 Single allele

To add a single new allele, click the sequences add (+) link on the curator's main page.



Select the locus from the dropdown list box. The next available allele id will be entered automatically (if the allele id format is set to integer). Paste the sequence in to form, set the status and select the sender name from the dropdown box. If the sender does not appear in the box, you will need to add them to the registered users.

The status reflects the level of curation that the curator has done personally - the curator should not rely on assurances from the submitter. The status can either be:

- Sanger trace checked
  - Sequence trace files have been assembled and inspected *by the curator*.
- WGS: manual extract (BIGSdb)
  - The sequence has been extracted manually from a BIGSdb database *by the curator*. There may be some manual intervention to identify the start and stop sites of the sequence.

- WGS: automated extract (BIGSdb)
  - The sequences have been generated by a BIGSdb tag scanning run and have had no manual inspection or intervention.
- WGS: visually checked
  - Short read data has been inspected visually using an alignment program *by the curator*.
- WGS: automatically checked
  - The sequences have been checked by an automated algorithm that assesses the quality of the data to ensure it meets specified criteria.
- unchecked
  - If none of the above match, then the sequence should be entered as unchecked.

You can also choose whether to designate the sequence as a type allele or not. Type alleles can be used to constrain the sequence search space when defining new alleles using the [web-based scanner](#) or [offline auto allele definer](#).

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Add new allele sequence](#)

[Help](#)

### Add new allele sequence

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

Action

locus:

allele id:

sequence:

status:

sender:

curator:

date entered:

date stamp:

type allele: ☐ true ☐ false New allele searches can be constrained to use just type alleles in comparisons

comments:

Flags:

PubMed ids:

ENA ids:

Genbank ids:

☐ Override sequence similarity check  
☐ Override sequence length check

Press submit. By default, the system will test whether your sequence is similar enough to existing alleles defined for that locus. The sequence will be rejected if it isn't considered similar enough. This test can be overridden by checking the 'Override sequence similarity check' checkbox at the bottom. It will also check that the sequence length is within the allowed range for that locus. These checks can also be overridden by checking the 'Override sequence length check' checkbox, allowing the addition of unusual length alleles.

See also:

[allele sequence flags](#)

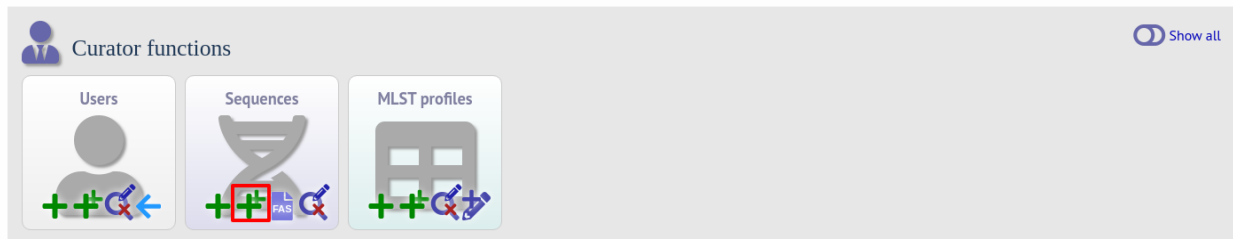
Sequences can also be associated with PubMed, ENA or Genbank id numbers by entering these as lists (one value per line) in the appropriate form box.

## 6.2.2 Batch adding multiple alleles

There are two methods of batch adding alleles. You can either upload a spreadsheet with all fields in tabular format, or you can upload a FASTA file provided all sequences are for the same locus and have the same status.

### Upload using a spreadsheet

Click the batch add (++) sequences link on the curator's main page.



Download a template Excel file from the following page.

## Batch insert sequences

## Instructions

This page allows you to upload allele sequence data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- If the locus uses integer allele ids you can leave the allele\_id field blank and the next available number will be used.
- The status defines how the sequence was curated. Allowed values are: 'Sanger trace checked', 'WGS: manual extract (BIGSdb)', 'WGS: automated extract (BIGSdb)', 'WGS: visually checked', 'WGS: automatically checked', 'unchecked'.
- Sequence flags can be added as a semi-colon (;) separated list.
- Please note, some loci have extended attributes which may be required. For affected loci please use the batch insert page specific to that locus:

Reload page specific for locus:

## Templates



## Upload

Please select the sender from the list below:

Select sender ... Value will be overridden if you include a sender field in your pasted data.

- ☒ Ignore existing or duplicate sequences
- ☐ Ignore sequences containing non-nucleotide characters
- ☐ Silently reject all sequences that are not complete reading frames - these must have a start and in-frame stop codon at the ends and no internal stop codons. Existing sequences are also ignored.
- ☐ Override sequence similarity check

Paste in tab-delimited text (Include a field header line).

Action



Fill in the spreadsheet. If the locus uses integer allele identifiers, the allele\_id can be left blank and the next available number will be used automatically.

The status can be either: 'Sanger trace checked', 'WGS: manual extract (BIGSdb)', 'WGS: automated extract (BIGSdb)', 'WGS: visually checked', 'WGS: automatically checked' or 'unchecked'. See full explanations for these in the [single allele upload](#) section.

The 'type\_allele' field is boolean (true/false) and specifies if the sequence should be considered as a type allele. These can be used to constrain the sequence search space when defining new alleles using the [web-based scanner](#) or [offline auto allele definer](#).

Paste the entire sheet in to the web form and select the sender from the dropdown box.

Additionally, there are a number of options available. Some of these will ignore sequences if they don't match certain criteria - this is useful when sequence data has been extracted from genomes automatically. Available options are:

- Ignore existing or duplicate sequences.
- Ignore sequences containing non-nucleotide characters.
- Silently reject all sequences that are not complete reading frames - these must have a start and in-frame stop codon at the ends and no internal stop codons. Existing sequences are also ignored.

- Override sequence similarity check.

## PubMLST

Home > Organisms > Organism > Neisseria typing > Batch add new allele sequence records



## Batch insert sequences

## Instructions

This page allows you to upload allele sequence data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- If the locus uses integer allele ids you can leave the allele\_id field blank and the next available number will be used.
- The status defines how the sequence was curated. Allowed values are: 'Sanger trace checked', 'WGS: manual extract (BIGSdb)', 'WGS: automated extract (BIGSdb)', 'WGS: visually checked', 'WGS: automatically checked', 'unchecked'.
- Sequence flags can be added as a semi-colon (;) separated list.
- Please note, some loci have extended attributes which may be required. For affected loci please use the batch insert page specific to that locus:

Reload page specific for locus: Select ... Reload

## Templates



## Upload

Please select the sender from the list below:

Jolley, Keith (keith) Value will be overridden if you include a sender field in your pasted data.

- ☒ Ignore existing or duplicate sequences
- ☐ Ignore sequences containing non-nucleotide characters
- ☐ Silently reject all sequences that are not complete reading frames - these must have a start and in-frame stop codon at the ends and no internal stop codons. Existing sequences are also ignored.
- ☐ Override sequence similarity check

Paste in tab-delimited text (Include a field header line).

Action

RESET

SUBMIT

```
locus allele_id status sequence
abcZ WGS: automated extract (BIGSdb)
TTTGATACCGTTGCCGAAGTTTGGGTAAAATTCGCGATTATTGCACCGTTACACCGCGTCGGTCATGAGTTGAAAAAC
GGTTCGGGTGAGGCTTTGTTGAAAGAACTCAACGAATTACAACCTGAAATCGAAGCGAAGGACGGCTGGAAGCTGGATGCG
GCAGTCAAGCAGACTTTGGGCAACTCGGTTTCCGGAAAAACGAAAAATCGGCAACCTTTCCGGCGGTGAGAAAAAGCGT
GTCGCTTGGCGCAGGCTTGGGTGAGAAGCCGACGATTGCTGCTGGACGAACCGACCAACATTGGATATTGACGCG
ATTATCTGGTTGAAAAACCTGCTCAAGGCGTTTGAAGGCAGCTTGGTCGTGATTACCCACGACCGCGTTTTTGGATAAT
ATCGCTACGCGGATTGTTGAACCTTGACC
abcZ WGS: automated extract (BIGSdb)
TTTGATACCGTTGCCGAAGTTTGGGTAAAATTCGCGATTATTGCACCGTTACACCGCGTCGGTCATGAGTTGAAAAAC
GGTTCGGGTGAGGCTTTGTTGAAAGAACTCAACGAATTACAACCTGAAATCGAAGCGAAGGACGGCTGGAAGCTGGATGCG
GCAGTCAAGCAGACTTTGGGCAACTCGGTTTCCGGAAAAACGAAAAATCGGCAACCTTTCCGGCGGTGAGAAAAAGCGT
GTCGCTTGGCGCAGGCTTGGGTGAGAAGCCGACGATTGCTGCTGGACGAACCGACCAACATTGGATATTGACGCG
ATTATCTGGTTGAAAAACCTGCTCAAGGCGTTTGAAGGCAGCTTGGTCGTGATTACCCACGACCGCGTTTTTGGATAAT
ATCGCTACGCGGATTGTTGAACCTTGACC
```

Press submit. You will be presented with a page indicating what data will be uploaded. This gives you a chance to back out of the upload. Click 'Import data'.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch add new allele sequence records

Help

## Batch insert sequences

**Import status**

Sender: Keith Jolley

No obvious problems identified so far.

Action

**IMPORT DATA**

**Data to be imported**

The following table shows your data. Any field with red text has a problem and needs to be checked. *Note: valid sequence flags are displayed with a red background not red text.*

locus	allele_id	sequence	status	type_allele	sender	curator	date_entered	timestamp	comments	flags
abcZ	1079	TTTGATACCGTTGCCGAAGG . . . GCGGATTGTTGAACCTTGACC	WGS: automated extract (BIGSdb)		2	2	2020-07-22	2020-07-22		
abcZ	1080	TTTGATACCGTTGCCGAAGG . . . GCGGATTGTTGAACCTTGACC	WGS: automated extract (BIGSdb)		2	2	2020-07-22	2020-07-22		

If there are any problems with the submission, these should be indicated at this stage, e.g.:

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch add new allele sequence records

Help

## Batch insert sequences

**Import status**

Primary key	Problem(s)
locus: abcZ; allele_id: 1079	Sequence contains non nucleotide (A C G T) characters.

**Data to be imported**

The following table shows your data. Any field with red text has a problem and needs to be checked. *Note: valid sequence flags are displayed with a red background not red text.*

locus	allele_id	sequence	status	type_allele	sender	curator	date_entered	timestamp	comments	flags
abcZ	1079	TTTGATACCGTTGCCGAAGG . . . GCGGATTGTTGAACCTTGACC	WGS: automated extract (BIGSdb)		2	2	2020-07-22	2020-07-22		
abcZ	1080	TTTGATACCGTTGCCGAAGG . . . GCGGATTGTTGAACCTTGACC	WGS: automated extract (BIGSdb)		2	2	2020-07-22	2020-07-22		

## Upload using a FASTA file

Uploading new alleles from a FASTA file is usually more straightforward than generating an Excel sheet.

Click 'FASTA' upload on the curator's contents page.

Curator functions

Show all

Users

Sequences

MLST profiles

FASTA

Select the locus, status and sender from the dropdown boxes and paste in the new sequences in FASTA format.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Batch insert sequences

This page allows you to upload allele sequence data in FASTA format. The identifiers in the FASTA file will be used unless you select the option to use the next available id (loci with integer ids only). Do not include the locus name in the identifier in the FASTA file.

Please note that you can not use this page to upload sequences for loci with extended attributes.

**Enter parameters**

locus:

status:

sender:

sequence (FASTA):

```
>isolate1
TTTGATACCGTTGCCGAAGGTTCCGGCGAAATTCGTGATTATTGCGCGTTATCATCAT
GTCAGCCATGAGTTGGAAATGGTTCGAGTGAGGCTTTGTTGAAAGAACTCAACGAATTG
CAACTTGAAATCGAAGCGAAGGACGGCTGGAACTGGATGCGGCAGTCAAGCAGACTTTG
GGGGAACTCGGTTTGCCGGAATGAAAAATCGGCAACCTTTCCGGCGGTGAGAAAAAG
CGCGTCGCTTGGCTCAGGCTTGGGTGCAAAAGCCGACGATTGCTGCTGGACGAGCCG
ACCAACCATTTGGATATCGACGCGATTATTGGCTGGAAATCTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCAGACCGCCGTTTTTGGACAATATGCCACGCGGATT
GTCGAATCGATC
>isolate2
```

☐ Reject all sequences that are not complete reading frames - these must have a start and in-frame stop codon at the ends and no internal stop codons. Existing sequences are also ignored.

☐ Override sequence similarity check

☒ Use next available id (only for loci with integer ids)

**Action**

For loci with integer ids, the next available id number will be used by default (and the identifier in the FASTA file will be ignored). Alternatively, you can indicate the allele identifier within the FASTA file (do not include the locus name in this identifier).

As with the spreadsheet upload, you can select options to ignore selected sequences if they don't match specific criteria. Click 'Check'.

The sequences will be checked. You will be presented with a page indicating what data will be uploaded. This gives you a chance to back out of the upload. Click 'Upload valid sequences'.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Batch insert sequences

Sequence check

Locus: abcZ

Original designation	Allele id	Status	Action
isolate1	1079	OK	<input type="button" value="UPLOAD VALID SEQUENCES"/>
isolate2	1080	OK	

Any invalid sequences will be indicated in this confirmation page and these will not be uploaded (you can still upload the others), e.g.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Help

## Batch insert sequences

Sequence check

Locus: abcZ

Original designation	Allele id	Status	Action
isolate1	1079	OK	UPLOAD VALID SEQUENCES
isolate2	1080	Sequence contains non nucleotide (A C G T) characters.	

## 6.3 Updating and deleting allele sequence definitions

**Note:** You cannot update the sequence of an allele definition. This is for reasons of data integrity since an allele may form part of a scheme profile and be referred to in multiple databases. If you really need to change a sequence, you will have to remove the allele definition and then re-add it. If the allele is a member of a scheme profile, you will also have to remove that profile first, then re-create it after deleting and re-adding the allele.

In order to update or delete an allele, first you must select it. Click the update/delete sequences link.

Curator functions

Show all

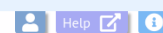
Users

Sequences

MLST profiles

Either search for specific attributes in the search form, or leave it blank and click 'Submit' to return all alleles. For a specific allele, select the locus in the filter (click the small arrow next to 'Filter query by' to expand the filter) and enter the allele number in the allele\_id field.

## PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Sequence attribute search](#)


## Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

allele id

=

4

+

i

**Display**

Order by:

locus

ascending

Display:

25

records per page

i

**Filter query by**

locus:

abcZ

i

status:

type allele:

sender:

i

curator:

i

allele flag:

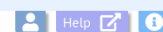
**Action**

RESET

SUBMIT

Click the appropriate link to either update the allele attributes or to delete it. If you have appropriate permissions, there may also be a link to 'Delete ALL'. This allows you to quickly delete all alleles returned from a search.

## PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Sequence attribute search](#)


## Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

allele id

=

1

+

i

**Display**

Order by:

locus

ascending

Display:

25

records per page

i

**Filter query by**

locus:

abcZ

i

status:

type allele:

sender:

i

curator:

i

allele flag:

**Action**

RESET

SUBMIT

1 record returned.

[Delete](#)
[Database configuration](#)
[Flags](#)

Delete ALL

Export configuration/data

Batch set

Delete	Update	locus	allele id	sequence	sequence length	status	type allele	sender	curator	date entered	timestamp	comments	flags
		abcZ	1	TTTGATACTGTTGCC ... TTGTCGAACTCGATC	433	Sanger trace checked	<input type="checkbox"/>	Keith Jolley	Keith Jolley	2001-02-07	2001-02-07		

If you choose to delete, you will be presented with a final confirmation screen. To go ahead, click 'Delete'. Deletion will not be possible if the allele is part of a scheme profile - if it is you will need to delete any profiles that it is a member of first. You can also choose to delete and retire the allele identifier. If you do this, the allele identifier will not be re-used. It is possible to set the configuration so that you only have the option to delete and retire.

## PubMLST

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Delete allele sequence



## Delete allele sequence

You have chosen to delete the following record. Select 'Delete and Retire' to prevent the identifier being reused.



locus: abcZ  
 allele id: 1  
 sequence: TTTGATACTG TTGCCGAAGG TTTGGGCGAA ATTGCGGATT TATTGCGCCG TTATCATCAT GTCAGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCCTTAT  
 TGAAGAGCT CAACGAATTG CAACTTGAGA TCGAAGCGAA GGACGGCTGG AAGTTGGATG CGCGGTGAA GCAGACTTTG GGCGAACCTG GTTTGCCGGA  
 AACGAAAA ATCGGCAACC TCTCCGGCGG TCAGAAAAAG CGCTCGCCT TGGCGCAGG TTGGGTGAG AAGCCGACG TATTGCTGCT CGATGAACCG  
 ACCAACCAT TGGACATCGA CGCGATTATT TGGTTGAAA ACCTGCTCAA AGCGTTGAA GGCAGCCTGG TTGTGATTAC CCACGACCGC CGTTTTTTGG  
 ACAATATCGC CACGCGGATT GTCGAACCTG ATC  
 status: Sanger trace checked  
 type allele: false  
 sender: Keith Jolley  
 curator: Keith Jolley  
 date entered: 2001-02-07  
 timestamp: 2001-02-07  
 comments:

Action

DELETE AND RETIRE

If instead you clicked 'Update', you will be able to modify attributes of the sequence, or link PubMed, ENA or Genbank records to it. You will not be able to modify the sequence itself.

**Note:** Adding flags and comments to an allele record requires that this feature is enabled in the [database configuration](#).

## PubMLST

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Update allele sequence



## Update allele sequence

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

Action

RESET

SUBMIT



locus: abcZ  
 allele id: 1  
 sequence: TTTGATACTG TTGCCGAAGG TTTGGGCGAA  
 ATTGCGGATT TATTGCGCCG TTATCATCAT  
 GTCAGCCATG AGTTGGAAAA TGGTTCGAGT  
 GAGGCCTTAT TGAAGAGCT CAACGAATTG  
 CAACTTGAGA TCGAAGCGAA GGACGGCTGG  
 AAGTTGGATG CGCGGTGAA GCAGACTTTG

status: Sanger trace checked

sender: Jolley, Keith (keith)

curator: Keith Jolley (keith)

date entered: 2001-02-07

timestamp: 2020-07-22

type allele: ☐ true ☐ false New allele searches can be constrained to use just type alleles in comparisons

comments:

Flags: alternative start codon  
 atypical  
 contains IS element  
 downstream fusion  
 frameshift

PubMed ids:



ENA ids:



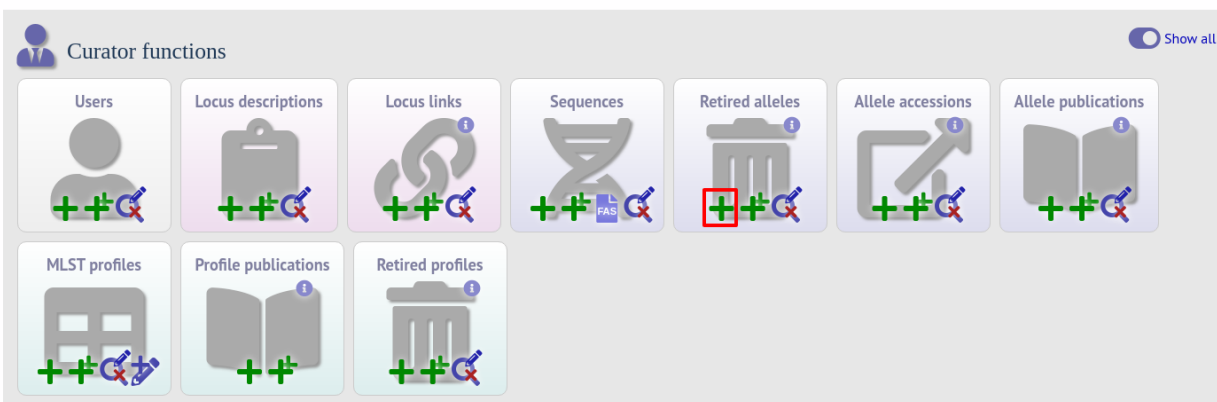
Genbank ids:

☐ Override sequence length check

## 6.4 Retiring allele identifiers

Sometimes there is a requirement to prevent the automated assignment of a particular allele identifier - an allele with that identifier may have been commonly used and has since been removed. Reassignment of the identifier to a new sequence may lead to confusion, so in this instance, it would be better to prevent this.

You can retire an allele identifier by clicking the ‘Add’ retired allele ids link on the sequence database curators’ page. This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Select the locus from the dropdown list box and enter the allele id. Click ‘Submit’.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new retired allele id

### Add new retired allele id

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
locus: NEIS0844 allele id: 67 curator: Keith Jolley (keith) timestamp: 2020-07-22	<input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

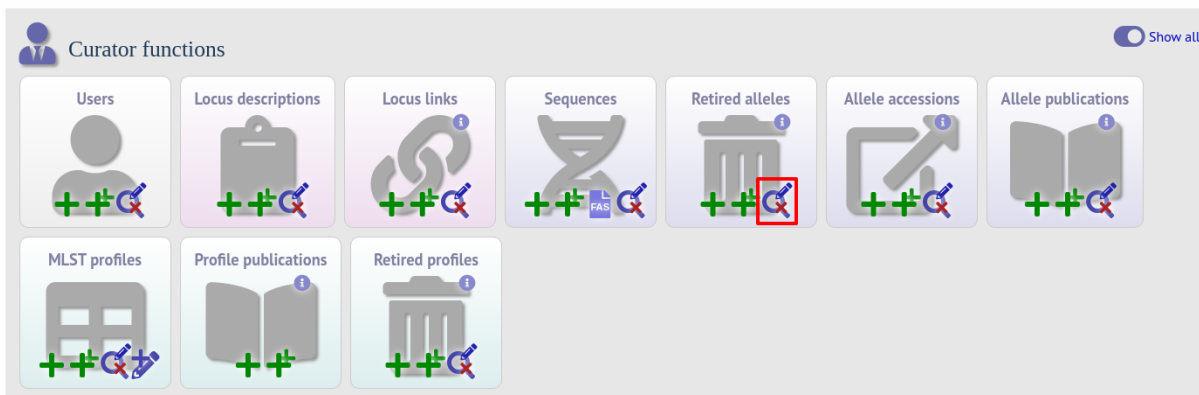
You cannot retire an allele that already exists, so you must delete it before retiring it. Once an identifier is retired, you will not be able to create a new allele with that name.

You can also retire an allele identifier when you *delete an allele*.

## 6.5 Un-retiring allele identifiers

If an allele identifier has been retired, it is possible to un-retire it so that it can be re-assigned. To do this, you need to remove the identifier from the retired\_alleles table.

First, find the allele identifier in the retired\_alleles table by clicking the ‘Update/delete’ retired alleles link on the sequence database curators’ page. This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Search by any criteria to find the allele identifier.

PubMLST

Home > Organisms > Organism > Neisseria typing > Query retired allele id information

### Query retired allele id information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**  
 timestamp = today

**Display**  
 Order by: locus ascending  
 Display: 25 records per page

**Filter query by**  
 locus: abcZ  
 curator:

**Action**  
 RESET SEARCH

1 record returned.

Delete

Delete ALL

Delete	Update	locus	allele id	curator	timestamp
		abcZ	1079	Keith Jolley	2020-08-05

Click the delete link on the identifier to be un-retired.

PubMLST

Home > Organisms > Organism > Neisseria typing > Query retired allele id information

### Query retired allele id information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**  
 timestamp = today

**Display**  
 Order by: locus ascending  
 Display: 25 records per page

**Filter query by**  
 locus: abcZ  
 curator:

**Action**  
 RESET SEARCH

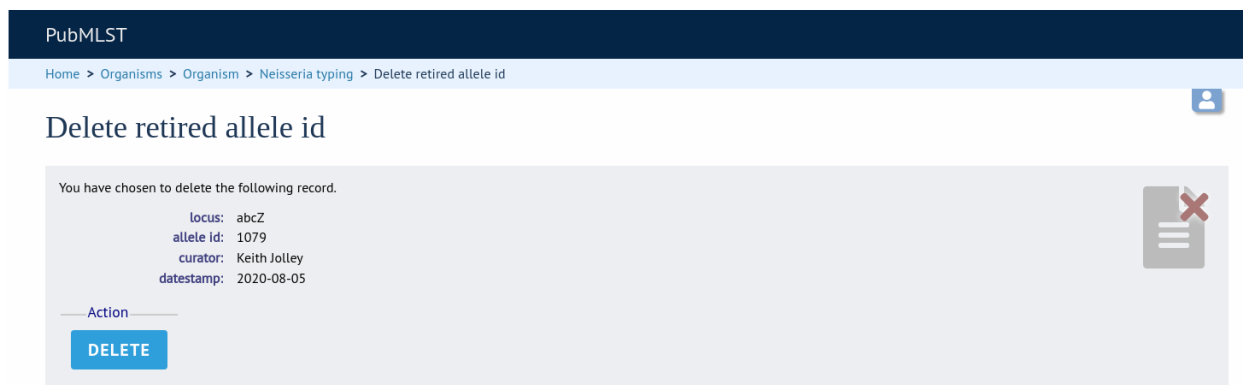
1 record returned.

Delete

Delete ALL

Delete	Update	locus	allele id	curator	timestamp
		abcZ	1079	Keith Jolley	2020-08-05

A confirmation page will be displayed. Click ‘Delete’ to remove the identifier from the retired alleles table.



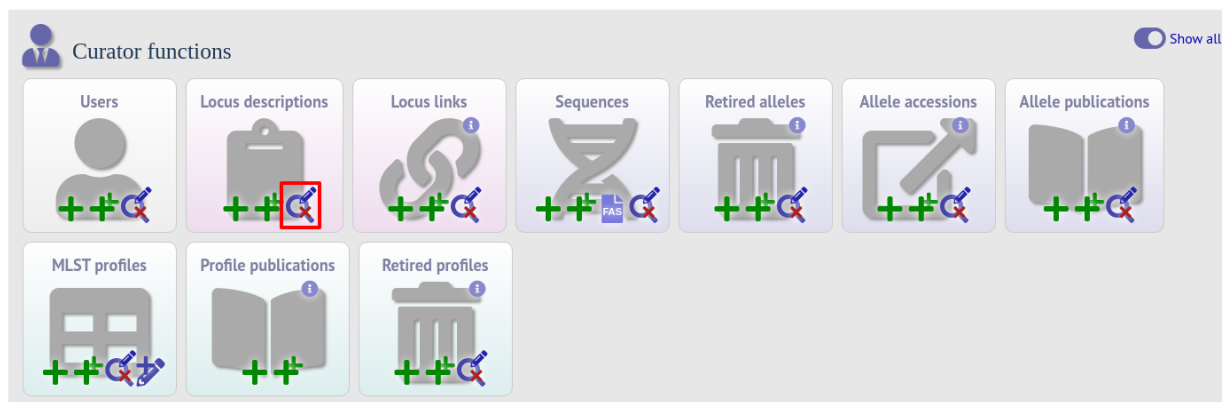
The identifier can now be re-assigned when adding a new allele.

## 6.6 Updating locus descriptions

Loci in the sequence definitions database can have a description associated with them. This may contain information about the gene product, the biochemical reaction it catalyzes, or publications providing more detailed information etc. This description is accessible from various pages within the interface such as an [allele information page](#) or from the [allele download page](#).

**Note:** In recent versions of BIGSdb, a blank description record is created when a new locus is defined. The following instructions assume that this is the case. It is possible for this record to be deleted or it may never have existed if the locus was created using an old version of BIGSdb. If the record does not exist, it can be added by clicking the Add (+) button in the ‘locus descriptions’ box. Fill in the fields in the same way as described below.

To edit a locus description, first you need to find it. Click the update/delete button in the ‘locus descriptions’ box on the sequence database curator’s page (depending on the permissions set for your user account not all the links shown here may be displayed). This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Either enter the name of the locus in the query box:

PubMLST

Home > Organisms > Organism > Neisseria typing > Query locus description information

Query locus description information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

locus = NEIS0620 + ⓘ

**Display**

Order by: locus ascending

Display: 25 records per page ⓘ

**Filter query by**

**Action**

RESET SUBMIT

or expand the filter list and select it from the dropdown box:

PubMLST

Home > Organisms > Organism > Neisseria typing > Query locus description information

Query locus description information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

locus = + ⓘ

**Display**

Order by: locus ascending

Display: 25 records per page ⓘ

**Filter query by**

locus: NEIS0620 (maeA) ⓘ

curator: ⓘ

common name: ⓘ

**Action**

RESET SUBMIT

Click 'Submit'.

If the locus description exists, click the 'Update' link (if it doesn't, see the note above).

PubMLST

Home > Organisms > Organism > Neisseria typing > Query locus description information

Query locus description information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

locus = + ⓘ

**Display**

Order by: locus ascending

Display: 25 records per page ⓘ

**Filter query by**

locus: NEIS0620 (maeA) ⓘ

curator: ⓘ

common name: ⓘ

**Action**

RESET SUBMIT

1 record returned.

— Delete — Database configuration —

Delete ALL Export configuration/data

Delete	Update	locus	full name	product	description	curator	timestamp
		NEIS0620	malate oxidoreductase (EC 1.1.1.38)	Final step in TCA cycle producing oxaloacetate.	Keith Jolley	2010-10-28	

Fill in the form as needed:

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Update locus description](#)

## Update locus description

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

Action

locus: **NEIS0620**  
curator: **Keith Jolley (keith)**  
datestamp: **2020-07-22**  
full name:   
product: **malate oxidoreductase (EC 1.1.1.38)**  
description: **Final step in TCA cycle producing oxaloacetate.**  
aliases:   
   
PubMed ids:    
links:   
(Format: URL|description)

- **full\_name**

The full name of the locus - often this can be left blank as it may be the same as the locus name. An example of where it is appropriately used is where the locus name is an abbreviation, e.g. PorA\_VR1 - here we could enter 'PorA variable region 1'. This should not be used for the 'common name' of the locus (which is defined within the locus record itself) or the gene product.

- **product**

The name of the protein product of a coding sequence locus.

- **description**

This can be as full a description as possible. It can include the specific part of the biochemical pathway the gene product catalyses or may provide background information, as appropriate.

- **aliases**

These are alternative names for the locus as perhaps found in different genome annotations. Don't duplicate the locus name or common name defined in the locus record. Enter each alias on a separate line.

- **Pubmed\_ids**

Enter the PubMed id of any paper that specifically describes the locus. Enter each id on a separate line. The software will retrieve the full citation from PubMed (this happens periodically so it may not be available for display immediately).

- **Links**

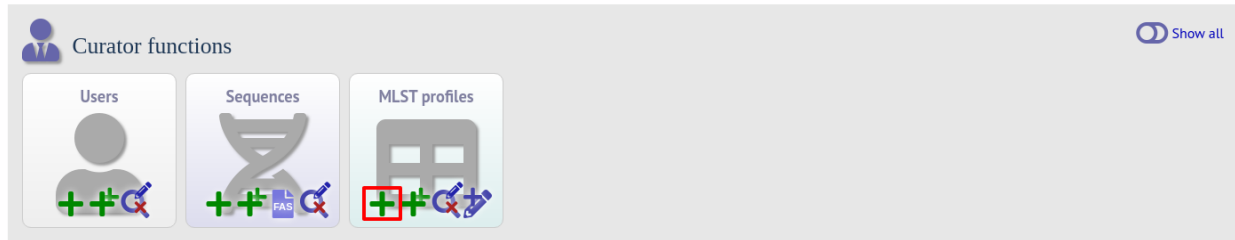
Enter links to additional web-based resources. Enter the URL first followed by a pipe symbol (|) and then the description.

Click 'Submit' when finished.

## 6.7 Adding new scheme profile definitions

Provided a scheme has been set up with at least one locus and a scheme field set as a primary key, there will be links on the curator's main page to add profiles for that scheme.

To add a single profile you can click the add (+) profiles link in the box named after the scheme name (e.g. MLST):



A form will be displayed with the next available primary key number already entered (provided integers are used for the primary key format). Enter the new profile, associated scheme fields, and the sender, then click 'Submit'. The new profile will be added provided the primary key or the profile has not previously been entered.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new profile

Add new MLST profile

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

ST: ! 15581

abcZ: ! 2

adk: ! 3

aroE: ! 4

fumC: ! 122

gdh: ! 8

pdhC: ! 4

pgm: ! 6

sender: ! Jolley, Keith (keith)

clonal\_complex:

curator: ! Keith Jolley (keith)

date\_entered: ! 2020-07-22

datestamp: ! 2020-07-22

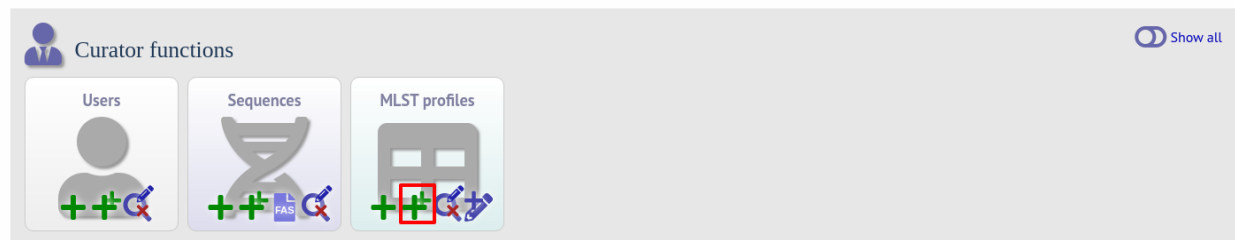
PubMed ids:

**Action**

RESET SUBMIT

More usually, profiles are added in a batch mode. It is often easier to do this even for a single profile since it allows copying and pasting data from a spreadsheet.

Click the batch add (++) profiles link next to the scheme name:



Click the 'Download submission template (xlsx format)' link to download an Excel submission template.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch add new MLST profiles - Neisseria typing

Help


## Batch insert MLST profiles

### Instructions

This page allows you to upload profiles as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- You can choose whether or not to include a ST field - if it is omitted, the next available ST will be used automatically. If however, you include it in the header line, then you must also provide it for each profile record.

### Templates



### Upload

Please paste in tab-delimited text (Include a field header line)

Parameters

Action

Sender: Select sender ...  
Value will be overridden if you include a sender field in your pasted data.

☐ Ignore previously defined profiles

☐ Ignore duplicate profiles

RESET

SUBMIT

Fill in the spreadsheet using the copied template, then copy and paste the whole spreadsheet in to the large form on the upload page. If the primary key has an integer format, you can exclude this column and the next available number will be used automatically. If the column is included, however, a value must be set. Select the sender from the dropdown list box and then click 'Submit'.

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Batch add new MLST profiles - Neisseria typing](#)

## Batch insert MLST profiles

### Instructions

This page allows you to upload profiles as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- You can choose whether or not to include a ST field - if it is omitted, the next available ST will be used automatically. If however, you include it in the header line, then you must also provide it for each profile record.

### Templates

### Upload

Please paste in tab-delimited text (Include a field header line)

abcZ

adk

aroE

fumC

gdh

pdhC

pgm

clonal\_complex

2

3

4

122

8

4

6

Parameters

Action

Sender: 

Jolley, Keith (keith)

Value will be overridden if you include a sender field in your pasted data.
☐ Ignore previously defined profiles
☐ Ignore duplicate profiles

RESET

SUBMIT

You will be given a final confirmation page stating what will be uploaded. If you wish to proceed with the submission, click 'Import data'.

PubMLST

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Batch add new MLST profiles - Neisseria typing](#)

## Batch insert MLST profiles

### Import status

Sender: Keith Jolley

No obvious problems identified so far.

Action

IMPORT DATA

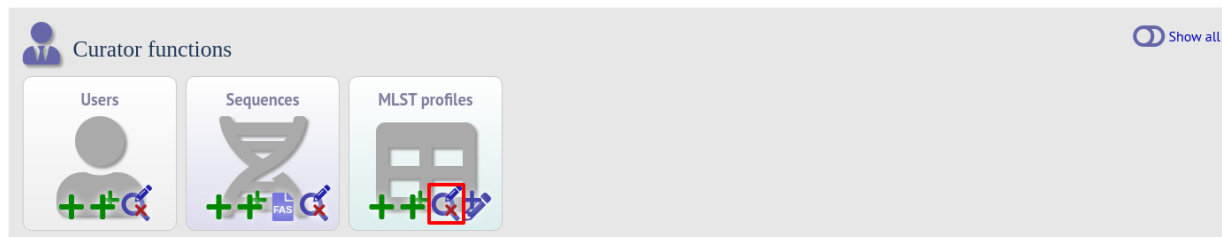
### Data to be imported

The following table shows your data. Any field coloured red has a problem and needs to be checked.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal_complex	sender	curator	date_entered	datestamp
15581	2	3	4	122	8	4	6		2	2	2020-07-22	2020-07-22

## 6.8 Updating and deleting scheme profile definitions

In order to update or delete a scheme profile, first you must select it. Click the update/delete profiles link in the scheme profiles box named after the scheme (e.g. MLST):



Search for your profile by entering search criteria (alternatively you can use the browse or list query functions).

PubMLST

Home > Organisms > Organism > Neisseria typing > Query or update profiles

Query or update profiles

Schemes

Please select the scheme you would like to query:

MLST

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Locus/scheme fields      Display/sort options      Action

ST      =      4563      +      i      Order by: ST      ascending      Display: 25 records per page     

1 record returned.

Delete	Update	ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
<input checked="" type="checkbox"/>	<input type="checkbox"/>	4563	2	7	6	13	9	18	8	ST-167 complex

Analysis tools

Export:

To delete the profile, click the 'Delete' link next to the profile. Alternatively, if your account has permission, you may be able to 'Delete ALL' records retrieved from the search.

For deletion of a single record, the full record will be displayed. Confirm deletion by clicking 'Delete'. You can also choose to delete and retire the profile identifier. If you do this, the profile identifier will not be re-used. The database configuration can be set so that you can only delete and retire.

PubMLST

Home > Organisms > Organism > Neisseria typing > Delete profile

Delete profile

You have chosen to delete the following record. Select 'Delete and Retire' to prevent the identifier being reused.

scheme id: 1) MLST  
 ST: 4563  
 abcZ: 2  
 adk: 7  
 aroE: 6  
 fumC: 13  
 gdh: 9  
 pdhC: 18  
 pgm: 8  
 clonal\_complex: ST-167 complex  
 sender: Ana-Belen Ibarz-Pavon  
 curator: Keith Jolley  
 date entered: 2005-03-03  
 datestamp: 2009-11-11

Action

To modify the profile, click the 'Update' link next to the profile following the query. A form will be displayed - make any changes and then click 'Update'.

PubMLST

Home > Organisms > Organism > Neisseria typing > Update profile

Update profile

Record

Update your record as required - required fields are marked with an exclamation mark (!):

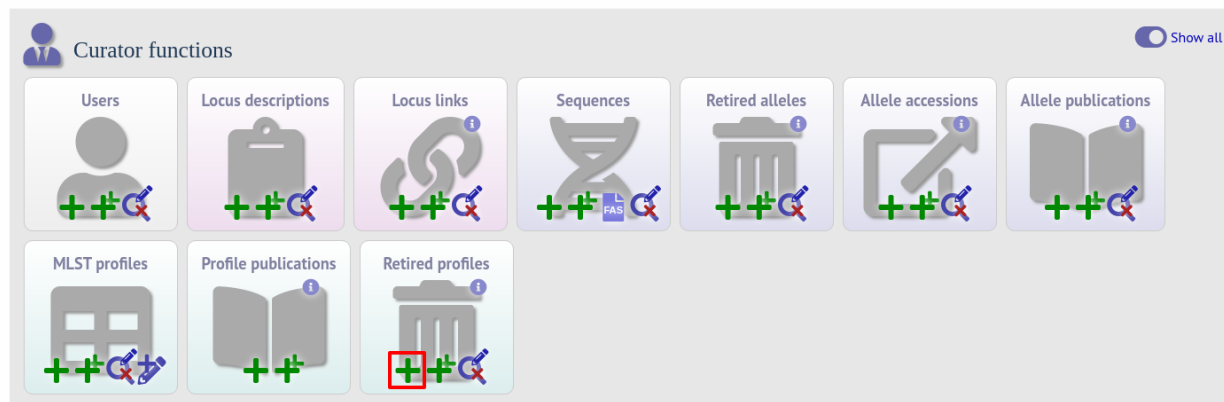
ST: ! 4563  
 abcZ: ! 2  
 adk: ! 7  
 aroE: ! 6  
 fumC: ! 13  
 gdh: ! 9  
 pdhC: ! 18  
 pgm: ! 8  
 clonal\_complex: ST-167 complex  
 sender: ! Ibarz-Pavon, Ana-Belen (aibarz)  
 curator: ! Keith Jolley (keith)  
 date\_entered: ! 2005-03-03  
 datestamp: ! 2020-07-22  
 PubMed ids:

Action

## 6.9 Retiring scheme profile identifiers

Sometimes there is a requirement to prevent the automated assignment of a particular profile identifier (e.g. ST) - a profile with that identifier may have been commonly used and has since been removed. Reassignment of the identifier to a new profile may lead to confusion, so in this instance, it would be better to prevent this.

You can retire a profile identifier by clicking the 'Add' link in the 'Retired profiles' box on the sequence database curators' page. This function is normally hidden, so you may need to click the 'Show all' toggle to display it.



Select the scheme from the dropdown list box and enter the profile id. Click 'Submit'.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new retired profile

### Add new retired profile

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
scheme id: MLST (id 1) profile id: 67232 curator: Keith Jolley (keith) datestamp: 2020-07-22	RESET SUBMIT

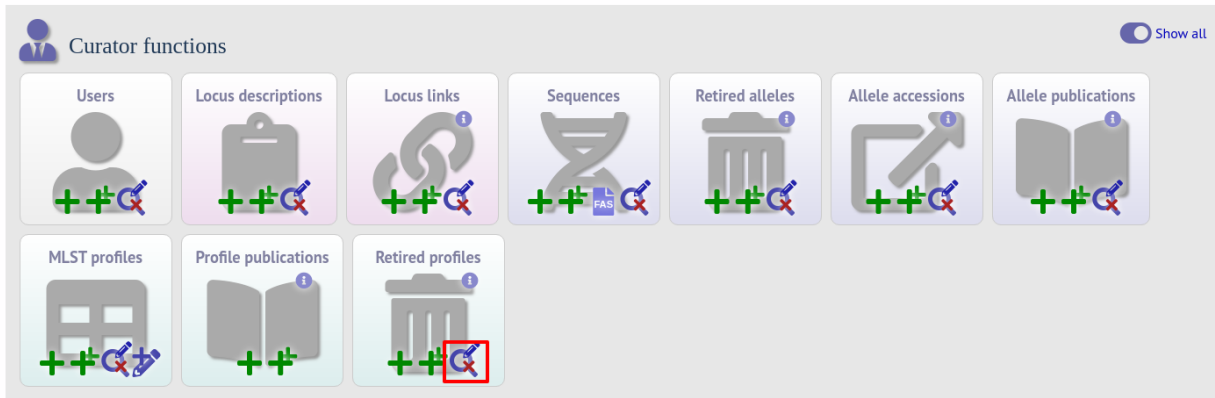
You cannot retire a profile identifier that already exists, so you must delete it before retiring it. Once an identifier is retired, you will not be able to create a new profile with that name.

You can also retire a profile definition when you *delete a profile*.

## 6.10 Un-retiring scheme profile identifiers

If a profile identifier, e.g. ST, has been retired, it is possible to un-retire it so that it can be re-assigned. To do this, you need to remove the identifier from the retired\_profiles table.

First, find the profile identifier in the retired\_profiles table by clicking the 'Update/delete' retired profiles link on the sequence database curators' page. This function is normally hidden, so you may need to click the 'Show all' toggle to display it.



Search by any criteria to find the profile identifier.

PubMLST

Home > Organisms > Organism > Neisseria typing > Query retired profile information

### Query retired profile information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**  
 timestamp = today + ⓘ

**Display**  
 Order by: scheme id ascending  
 Display: 25 records per page ⓘ

**Filter query by**  
 scheme: MLST ⓘ  
 curator: ⓘ

**Action**  
 RESET SEARCH

1 record returned.

Delete  
 Delete ALL

Delete	Update	scheme id	profile id	curator	timestamp
		MLST (id 1)	15581	Keith Jolley	2020-08-05

Click the delete link on the identifier to be un-retired.

PubMLST

Home > Organisms > Organism > Neisseria typing > Query retired profile information

### Query retired profile information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**  
 timestamp = today + ⓘ

**Display**  
 Order by: scheme id ascending  
 Display: 25 records per page ⓘ

**Filter query by**  
 scheme: MLST ⓘ  
 curator: ⓘ

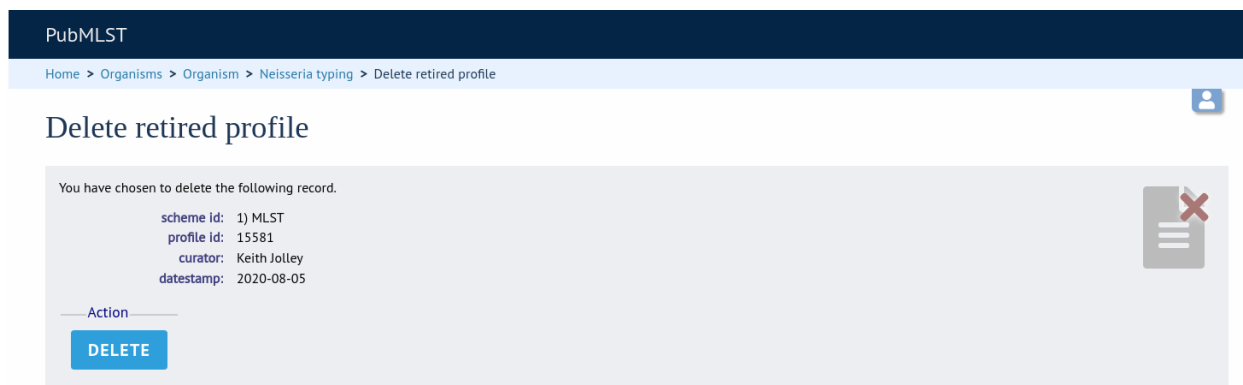
**Action**  
 RESET SEARCH

1 record returned.

Delete  
 Delete ALL

Delete	Update	scheme id	profile id	curator	timestamp
		MLST (id 1)	15581	Keith Jolley	2020-08-05

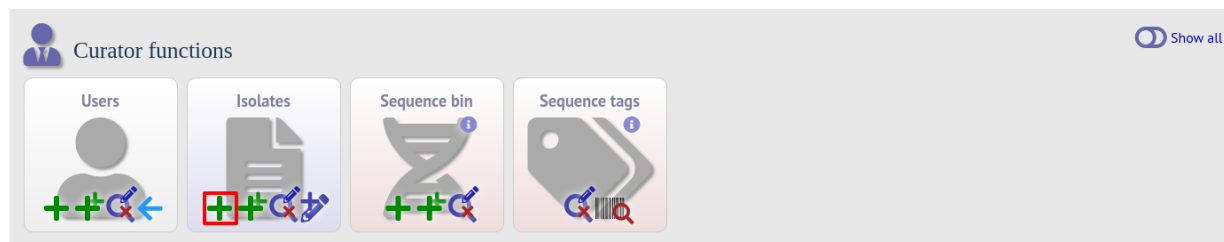
A confirmation page will be displayed. Click ‘Delete’ to remove the identifier from the retired profiles table.



The identifier can now be re-assigned when adding a new profile.

## 6.11 Adding isolate records

To add a single record, click the add (+) isolates link on the curator’s index page.



The next available id will be filled in automatically but you are free to change this. Fill in the individual fields. Required fields are listed first and are marked with an exclamation mark (!). Some fields may have drop-down list boxes of allowed values. You can also enter allele designations for any loci that have been defined.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Add new isolate

[Help](#) [Add](#) [Info](#)

## Add new isolate

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Primary metadata**

id: 81776 [?](#)

isolate: J323\_2 [?](#) [?](#)

country: UK [?](#)

species: *Neisseria meningitidis* [?](#)

sender: Jolley, Keith (keith) [?](#)

curator: Keith Jolley (keith) [?](#)

date entered: 2020-07-23 [?](#)

datestamp: 2020-07-23 [?](#)

region:  [?](#)

Supports multiple values - enter each one on separate line

year: 2014 [?](#)

date sampled: dd/mm/yyyy ☐ [?](#)

date received: dd/mm/yyyy ☐ [?](#)

non culture: ☐ true ☐ false [?](#)

epidemiological year:  [?](#)

age yr:  [?](#)

age range:  [?](#)

age mth:  [?](#)

sex:  [?](#)

Press submit when finished.

More usually, isolate records are added in batch mode, even when only a single record is added, since the submission can be prepared in a spreadsheet and copied and pasted.

Select batch add (++) isolates link on the curator's index page.



Download a submission template in Excel format from the link.

PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Batch add isolate records](#)

## Batch insert isolates

### Instructions

This page allows you to upload isolate data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- Optionally enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- Optionally enter references for your isolates as a semi-colon (;) separated list of PubMed ids (non-integer ids will be ignored).
- You can also upload allele fields along with the other isolate data - simply create a new column with the locus name (see the 'allowed\_loci' tab in the Excel template for locus names). These will be added with a confirmed status and method set as 'manual'.
- You can choose whether or not to include an id number field - if it is omitted, the next available id will be used automatically.

### Templates

Check the [description of database fields](#) for help with filling in the template.

### Upload

Please select the sender from the list below:

Select sender ...

Value will be overridden if you include a sender field in your pasted data.

Paste in tab-delimited text (Include a field header line).

Action

RESET

SUBMIT

Prepare your data in the spreadsheet - the column headings must match the database fields. In databases with large numbers of loci, there won't be columns for each of these. You can, however, manually add locus columns.

Pick a sender from the drop-down list box and paste the data from your spreadsheet in to the web form. The next available isolate id number will be used automatically (this can be overridden if you manually add an id column).

## PubMLST

Home &gt; Organisms &gt; Neisseria spp. &gt; Neisseria isolates &gt; Batch add isolate records



## Batch insert isolates

## Instructions

This page allows you to upload isolate data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- Optionally enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- Optionally enter references for your isolates as a semi-colon (;) separated list of PubMed ids (non-integer ids will be ignored).
- You can also upload allele fields along with the other isolate data - simply create a new column with the locus name (see the 'allowed\_loci' tab in the Excel template for locus names). These will be added with a confirmed status and method set as 'manual'.
- You can choose whether or not to include an id number field - if it is omitted, the next available id will be used automatically.

## Templates



Check the [description of database fields](#) for help with filling in the template.

## Upload

Please select the sender from the list below:

Jolley, Keith (keith)

Value will be overridden if you include a sender field in your pasted data.

Paste in tab-delimited text (Include a field header line).

Action

RESET

SUBMIT

```
isolate aliases references country region year date_sampled
date_received non culture epidemiological year age_yr age_range
age_mth sex disease source epidemiology species serogroup genogroup
MLEE designation serotype sero subtype ET no penicillin
penicillin range amoxicillin sulphonamide ceftriaxone
ceftriaxone range chloramphenicol chloramphenicol range cefotaxime
cefotaxime range rifampicin rifampicin range ciprofloxacin
ciprofloxacin range tetracycline cefixime azithromycin
spectinomycin pending assembly assembly status bioproject accession
biosample accession ENA_run accession private project comments
abcZ adk aroE fumC gdh pdhC pgm PorA VR1 PorA VR2
FetA VR gyrA penA rpoB NG-MAST porB NG-MAST tbpB
J323_2 UK 2014
meningitis CSF Neisseria meningitidis B
```

Press submit. Data are checked for consistency and if there are no problems you can then confirm the submission.

## PubMLST

Home &gt; Organisms &gt; Neisseria spp. &gt; Neisseria isolates &gt; Batch add isolate records



## Batch insert isolates

## Import status

Sender: Keith Jolley

No obvious problems identified so far.

Action

IMPORT DATA

## Data to be imported

The following table shows your data. Any field with red text has a problem and needs to be checked.

id	isolate	aliases	references	country	region	year	date_sampled	date_received	non culture	epidemiological	year	age_yr	age_range	age_mth	sex	disease	source	epidemiology	speci
81776	J323_2			UK		2014										meningitis	CSF		Neisse mening

Any problems with the data will be listed and highlighted within the table. Fix the data and resubmit if this happens.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Batch add isolate records

Batch insert isolates

Import status

Primary key	Problem(s)
id: 81776	species value is not on the list of allowed values for this field.

Data to be imported

The following table shows your data. Any field with red text has a problem and needs to be checked.

year	date_sampled	date_received	non_culture	epidemiological_year	age_yr	age_range	age_mth	sex	disease	source	epidemiology	species	serogroup	genogroup	genogroup_notes	MLE
2014									meningitis	CSF		<i>Neisseria meningitidis</i>	B			

## 6.12 Updating and deleting single isolate records

First you need to locate the isolate record. You can either browse or use a search or list query.

Curator functions

Users Isolates Sequence bin Sequence tags

Isolates

Sequence bin

Sequence tags

The query interface is the same as the *public query interface*. Following a query, a results table of isolates will be displayed. There will be delete and update links for each record.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Query or update isolates

Query or update isolates

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

Combine with: AND

country = USA

year = 2009

Display/sort options

Order by: id

Display: 25 records per page

Action

RESET SEARCH

154 records returned (1 - 25 displayed).

Delete Tag scanning Projects Bookmark query

Delete ALL Scan Select project... Link 2020-07-23:1 Add bookmark

Delete	Update	Sequence bin	New version	id	isolate	aliases	country	year	disease	species	capsule group	ST	MLST	clonal complex	Finotyping antigens	PorA_VR1	PorA_VR2	FetA_VR
				12674	M18700		USA	2009	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	7301	ST-32 complex		+	+	+	
				12675	M18701		USA	2009	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	7302	ST-32 complex		+	+	+	
				12676	M18725		USA	2009	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	7303	ST-1572 complex		+	+	+	
				13090	M19024	PA09015	USA	2009	meningitis	<i>Neisseria meningitidis</i>	B	7575			+	+	+	

Clicking the 'Delete' link takes you to a page displaying the full isolate record.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Delete isolate

Delete isolate

You have chosen to delete the following record. Select 'Delete and Retire' to prevent the isolate id being reused.

Provenance/primary metadata

id: 12676

isolate: M18725

strain designation: B: P1.ND,ND: F-ND: ST-7303 (cc1572)

country: USA

continent: North America

region: WI

year: 2009

disease: invasive (unspecified/other)

source: CSF

species: *Neisseria meningitidis*

serogroup: B

capsule group: B

sender: Xin Zhao, Novartis (formerly at US CDC)

curator: Julia Bennett, University of Oxford, UK (E-mail: julia.bennett@zoo.ox.ac.uk)

date entered: 2009-03-24

datestamp: 2009-03-24

Action

DELETE DELETE AND RETIRE

Pressing 'Delete' from this record page confirms the deletion. You can also choose to delete and retire the isolate. If you do this, the isolate id number will not be re-used. It is possible to set the configuration so that you only have the option to delete and retire.

Clicking the 'Update' link for an isolate takes you to an update form. Make the required changes and click 'Update'.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Update isolate

Update isolate

Primary metadata

id: 12676 ⓘ

isolate: M18725 ⓘ

country: USA ⓘ

species: *Neisseria meningitidis* ⓘ

sender: Zhao, Xin (xinzhaoh) ⓘ

curator: Keith Jolley (keith) ⓘ

date entered: 2009-03-24 ⓘ

datestamp: 2020-07-23 ⓘ

region: WI ⓘ

Supports multiple values - enter each one on separate line ⓘ

year: 2009 ⓘ

date sampled: dd/mm/yyyy ⓘ

date received: dd/mm/yyyy ⓘ

non culture: ☐ true ☐ false ⓘ

epidemiological year: ⓘ

age yr: ⓘ

age range: ⓘ

age mth: ⓘ

sex: ⓘ

disease: invasive (unspecified/other) ⓘ

Allele designations can also be updated by clicking within the scheme tree and selecting the ‘Add’ or ‘Update’ link next to a displayed locus.

pubs clubs per week: ⓘ

persons kissed past week: ⓘ

regular partner: ☐ true ☐ false ⓘ

regular partner smokes: ☐ true ☐ false ⓘ

ethnicity: ⓘ

Loci

All loci

Typing

MLST

eMLST (20 locus partial genes)

Locus: 16S\_rDNA

Add/update

MLST

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST	clonal complex
8	105	52	4	9	11	7	7303	ST-1572 complex

Schemes will only appear in the tree if data for at least one of the loci within the scheme has been added. You can additionally add or update allelic designations for a locus by choosing a locus in the drop-down list box and clicking ‘Add/update’.

pubs clubs per week: ⓘ

persons kissed past week: ⓘ

regular partner: ☐ true ☐ false ⓘ

regular partner smokes: ☐ true ☐ false ⓘ

ethnicity: ⓘ

Loci

All loci

Typing

MLST

eMLST (20 locus partial genes)

Locus: abcZ

Add/update

Navigate and select schemes within tree to display allele designations

The allele designation update page allows you to modify an existing designation, or alternatively add additional designations. The sender, status (confirmed/provisional) and method (manual/automatic) needs to be set for each designation (all pending designations have a provisional status). The method is used to differentiate designations that have been determined manually from those determined by an automated algorithm.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Update allele

Update abcZ allele for isolate 12676

Provenance/primary metadata

id: 12676  
isolate: M18725  
strain designation: B: P1,ND,ND: F-ND: ST-7303 (cc1572)  
country: USA  
region: WI  
year: 2009  
disease: invasive (unspecified/other)  
source: CSF  
species: Neisseria meningitidis  
serogroup: B  
capsule group: B  
sender: Xin Zhao  
curator: Julia Bennett  
date entered: 2009-03-24  
datestamp: 2009-03-24

Update other loci:  
Locus: NEIS0421 (ipxL2) [Add/update](#)

Locus: abcZ

Add new allele designation

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

isolate id: 12676  
locus: abcZ  
allele id: 5  
sender: Jolley, Keith (keith)  
status: confirmed  
method: manual  
curator: Keith Jolley (keith)  
datestamp: 2020-07-23  
date entered: 2020-07-23  
comments:

**Action**

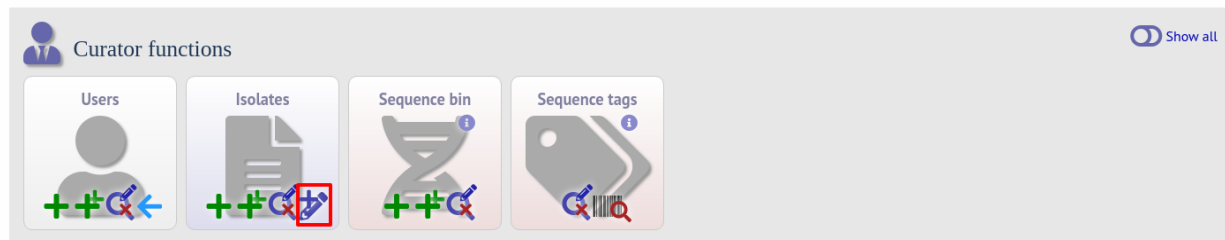
[RESET](#) [SUBMIT](#)

Existing designations

Update	Delete	allele id	sender	status	method	comments
		8	Xin Zhao	confirmed	manual	

## 6.13 Batch updating multiple isolate records

Select 'batch update' isolates link on the curator's index page.



Prepare your update data in 3 columns in a spreadsheet:

1. Unique identifier field
2. Field to be updated
3. New value for field

You should also include a header line at the top - this isn't used so can contain anything but it should be present.

Columns must be tab-delimited which they will be if you copy and paste directly from the spreadsheet.

So, to update isolate id-100 and id-101 to serogroup B you would prepare the following:

id	field	value
100	serogroup	B
101	serogroup	B

Select the field you are using as a unique identifier, in this case id, from the drop-down list box, and paste in the data. If the fields already have values set, you should also check the 'Update existing values' checkbox. Press 'submit'.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch Isolate Update

Help

## Batch isolate update

This page allows you to batch update provenance fields or allele designations for multiple isolates.

- The first line, containing column headings, will be ignored.
- The first column should be the isolate id (or unique field that you are selecting isolates on). If a secondary selection field is used (so that together the combination of primary and secondary fields are unique), this should be entered in the second column.
- The next column should contain the field/locus name and then the final column should contain the value to be entered, e.g.

```
id      field  value
2       country USA
2       abcZ   5
```

- The columns should be separated by tabs. Any other columns will be ignored.
- If you wish to blank a field, enter '<blank>' as the value.

Please enter the field(s) that you are selecting isolates on. Values used must be unique within this field or combination of fields, i.e. only one isolate has the value(s) used. Usually the database id will be used.

Please paste in your data below:

```
id      field  value
100     serogroup B
101     serogroup B
```

Options

Primary selection field:   
Optional selection field:   
☒ Update existing values

Allele designations

☒ Add additional new designation  
☐ Replace existing designations

Multi-value fields

☒ Add additional value  
☐ Replace existing values

Action

A confirmation page will be displayed if there are no problems. If there are problems, these will be listed. Press 'Upload' to upload the changes.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch Isolate Update

Help

## Batch isolate update

The following changes will be made to the database. Please check that this is what you intend and then press 'Update'. If you do not wish to make these changes, press your browser's back button.

Transaction	id	Field	New value	Value(s) currently in database	Action
1	100	serogroup	B	C	update field with new value
2	101	serogroup	B	C	update field with new value

Action

You can also use a secondary selection field such that a combination of two fields uniquely defines the isolate, for example using country and isolate name.

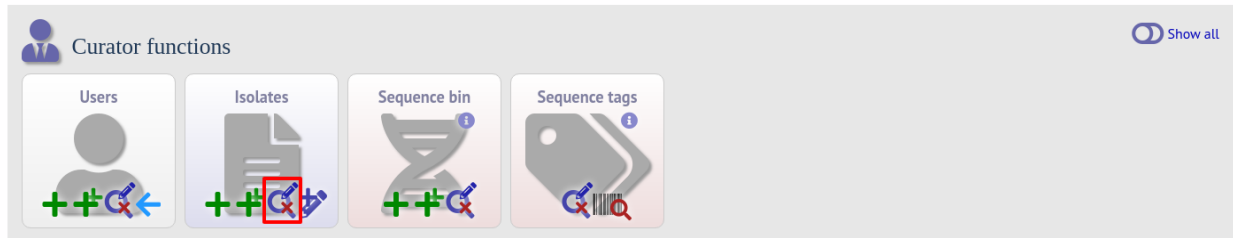
So, for example, to update the serogroups of isolates CN100 and CN103, both from the UK, select the appropriate primary and secondary fields and prepare the data as follows:

isolate	country	field	value
CN100	UK	serogroup	B
CN103	UK	serogroup	B

## 6.14 Deleting multiple isolate records

**Note:** Please note that standard curator accounts may not have permission to delete multiple isolates. Administrator accounts are always able to do this.

Before you can delete multiple records, you need to search for them. From the curator's main page, click the update/delete isolates link:



Enter search criteria that specifically return the isolates you wish to delete. Click 'Delete ALL'.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Query or update isolates

Query or update isolates

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

Combine with: AND

date entered = 2014-03-18

curator (surname) = Jolley

Display/sort options

Order by: id

Display: 25 records per page

Action

RESET SEARCH

3 records returned.

Delete Tag scanning Projects Bookmark query

Delete ALL Scan Select project... Link 2020-07-23:1 Add bookmark

Delete	Update	Sequence bin	New version	Isolate fields							Finotyping antigens			
				id	isolate	aliases	country	year	disease	species	capsule group	PorA VR1	PorA VR2	FetA VR
				28787	M22296		USA			Neisseria meningitidis		5-1	2-81	
				28788	M22553		USA			Neisseria meningitidis		5-2	10-96	
				28789	M22568		USA			Neisseria meningitidis		7-2	4-39	

You will have a final chance to change your mind:

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Delete multiple records

Delete multiple isolate records

Warning

If you proceed, you will delete 3 isolate records. Please confirm that this is your intention.

The identifiers will not be re-assigned if you 'delete and retire'.

Confirm action

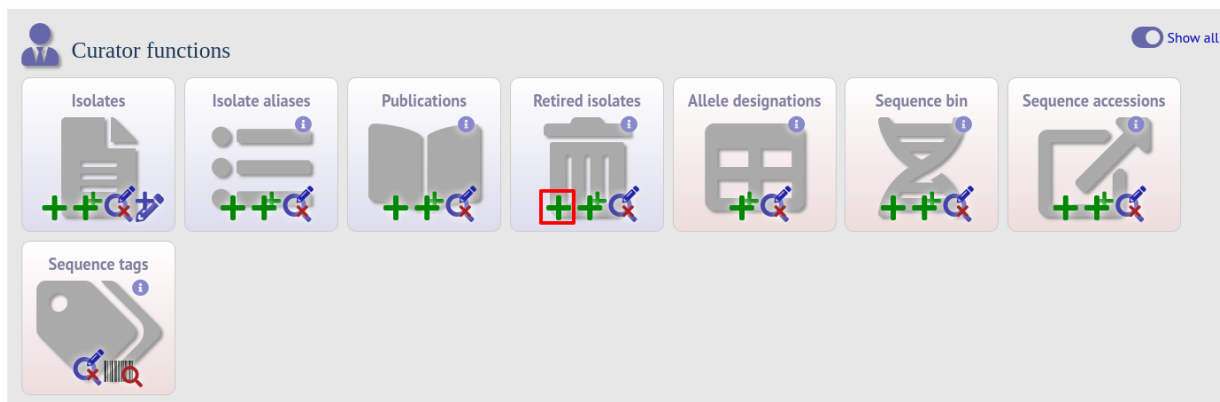
DELETE DELETE AND RETIRE

Click 'Delete'. You can also choose to delete and retire the isolate id. If you do this, the id number will not be re-used. It is possible to set the configuration so that you only have the option to delete and retire.

## 6.15 Retiring isolate identifiers

Sometimes there is a requirement to prevent the automated assignment of a particular isolate identifier number - an isolate with that identifier may have been commonly referred to and has since been removed. Reassignment of the identifier to a new isolate record may lead to confusion, so in this instance, it would be better to prevent this.

You can retire an isolate identifier by clicking the ‘Add’ retired isolates link on the isolates database curators’ page. This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Enter the isolate id to retire and click ‘Submit’.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Add new retired isolate id

Add new retired isolate id

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record	Action
isolate id: 46262 curator: Keith Jolley (keith) timestamp: 2020-07-23	<input type="button" value="RESET"/> <input type="button" value="SUBMIT"/>

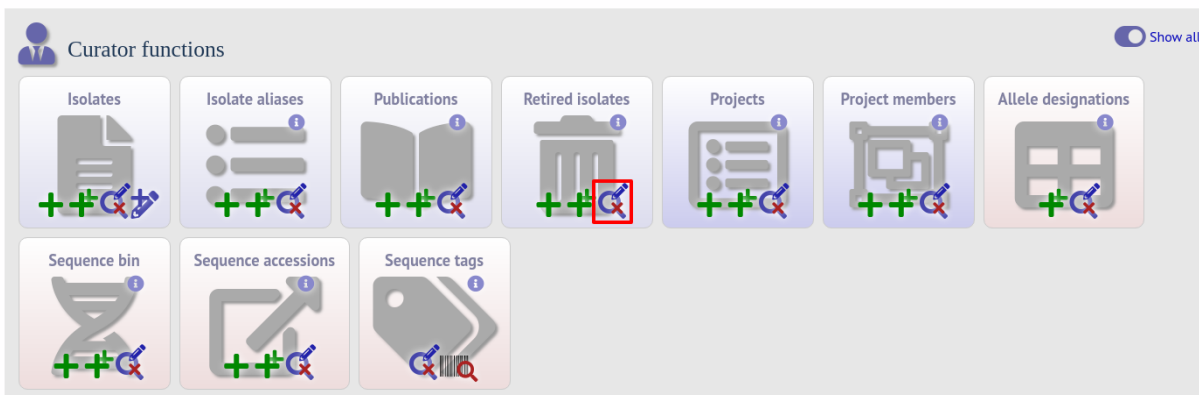
You cannot retire an isolate identifier that already exists, so you must delete it before retiring it. Once an identifier is retired, you will not be able to create a new isolate record using that identifier.

You can also retire an isolate identifier when you *delete an isolate record*.

## 6.16 Un-retiring isolate identifiers

If an isolate identifier has been retired, it is possible to un-retire it so that it can be re-assigned. To do this, you need to remove the identifier from the retired\_isolates table.

First, find the isolate identifier in the retired\_isolates table by clicking the ‘Update/delete’ retired isolates link on the isolate database curators’ page. This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Search by any criteria to find the isolate identifier.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Query retired isolate id information

### Query retired isolate id information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

datestamp = today

**Display**

Order by: isolate id ascending

Display: 25 records per page

**Filter query by**

curator: Jolley, Keith (keith)

**Action**

RESET SEARCH

1 record returned.

Delete	Update	Isolate id	curator	datestamp
		80316	Keith Jolley	2020-08-05

Click the delete link on the identifier to be un-retired.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Query retired isolate id information

### Query retired isolate id information

Please enter your search criteria below (or leave blank and submit to return all records).

**Search criteria**

datestamp = today

**Display**

Order by: isolate id ascending

Display: 25 records per page

**Filter query by**

curator: Jolley, Keith (keith)

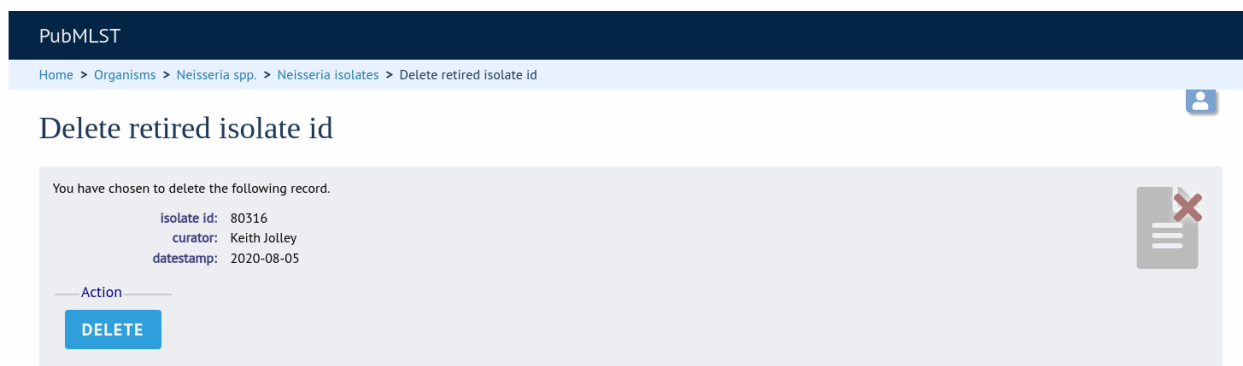
**Action**

RESET SEARCH

1 record returned.

Delete	Update	Isolate id	curator	datestamp
		80316	Keith Jolley	2020-08-05

A confirmation page will be displayed. Click 'Delete' to remove the identifier from the retired isolates table.



The identifier can now be re-assigned when adding a new isolate record.

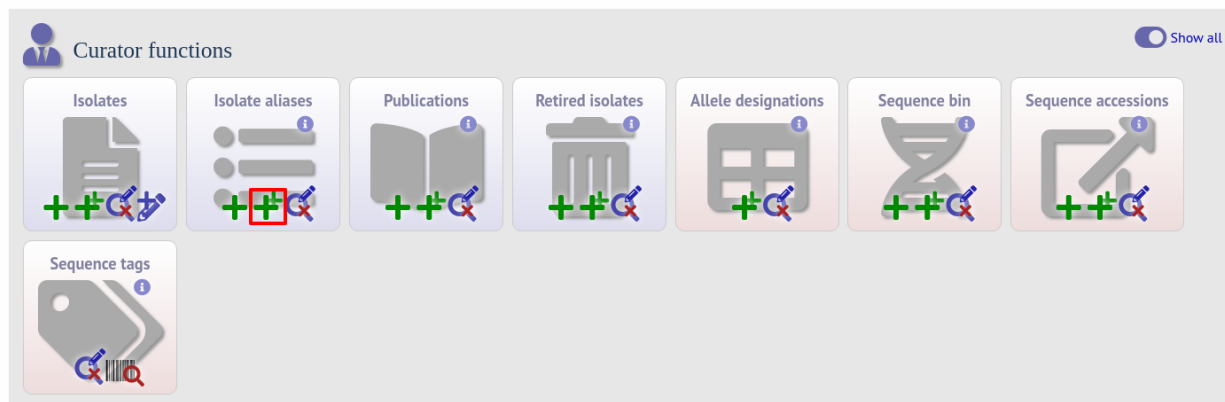
## 6.17 Setting alternative names for isolates (aliases)

Isolates can have any number of alternative names that they are known by. These isolate aliases can be set when isolates are first added to the database or batch uploaded later. When querying by isolate names, the aliases are also searched automatically.

If *adding isolates* singly, add the aliases in to the aliases box (one alias per line):

If batch adding isolates, they can be entered as a semi-colon (;) separated list in the aliases column.

As stated above, aliases can also be batch added. To do this, click the batch add (++) isolate aliases link on the curator's index page. This function is normally hidden, so you may need to click the 'Show all' toggle to display it.



Prepare a list in a spreadsheet using the provided template. This consists of two columns: isolate\_id and alias. For example, to add the aliases 'JHS212' and 'NM11' to isolate id 5473, the values to paste in look like:

PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Batch add isolate alias records](#)

Batch insert isolate aliases

Instructions

This page allows you to upload isolate alias data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

Templates

Check the [description of database fields](#) for help with filling in the template.

Upload

Paste in tab-delimited text (Include a field header line).

isolate\_id

alias

5473

JHS212

5473

MN11

Action

RESET

SUBMIT

A confirmation page will be displayed.

PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Batch add isolate alias records](#)

Batch insert isolate aliases

Import status

No obvious problems identified so far.

Action

IMPORT DATA

Data to be imported

The following table shows your data. Any field with red text has a problem and needs to be checked.

isolate_id	alias	timestamp	curator
5473	JHS212	2020-07-23	2
5473	MN11	2020-07-23	2

Click 'Import data'.

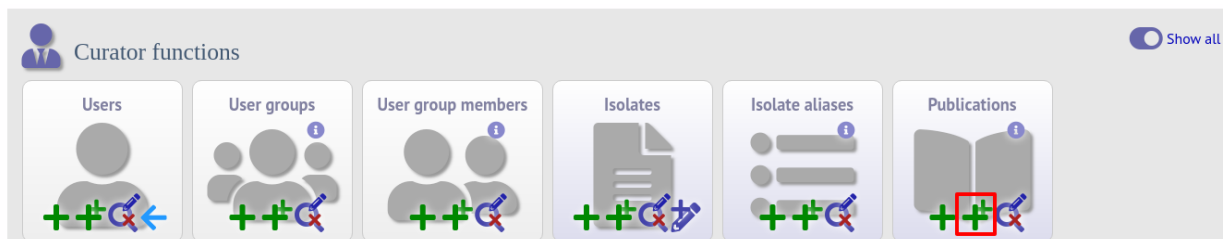
6.17. Setting alternative names for isolates (aliases)

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## 6.18 Linking isolate records to publications

Isolates can be associated with publications by adding PubMed id(s) to the record. This can be done when *adding the isolate*, where lists of PubMed ids can be entered in to the web form.

They can also be associated in batch after the upload of isolate records. Click the PubMed batch add (++) link on the curator's main page. This function is normally hidden, so you may need to click the 'Show all' toggle to display it.



Open the Excel template by clicking the link.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add PubMed link records

Batch insert refs

Instructions

This page allows you to upload PubMed link data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

Templates

Check the [description of database fields](#) for help with filling in the template.

Upload

Paste in tab-delimited text (include a field header line).

Action

RESET SUBMIT

The Excel template has two columns, isolate\_id and pubmed\_id. Simply fill this in with a line for each record and then paste the entire spreadsheet in to the web form and press submit.

PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Batch add PubMed link records](#)

Batch insert refs

Instructions

This page allows you to upload PubMed link data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

Templates

Check the [description of database fields](#) for help with filling in the template.

Upload

Paste in tab-delimited text (Include a field header line).

isolate\_id

pubmed\_id

6160

17517841

6162

17517841

18968

26515523

Action

RESET

SUBMIT

To ensure that publication information is stored locally and available for searching, the references database needs to be *updated regularly*.

## 6.19 Uploading sequence contigs linked to an isolate record

### 6.19.1 Select isolate from drop-down list

To upload sequence data, click the sequences add (+) sequence bin link on the curator's main page.

The screenshot shows the 'Curator functions' section of the BIGSdb interface. It contains three main buttons: 'Isolates' (with a document icon), 'Sequence bin' (with a DNA double helix icon), and 'Sequence tags' (with a tag icon). Each button has a green plus sign and a red minus sign. The 'Sequence bin' button is highlighted with a red rectangular box. To the right of these buttons is a 'Show all' link.

Select the isolate that you wish to link the sequence to from the dropdown list box (or if the database is large and there are too many isolates to list, enter the id in the text box). You also need to enter the person who sent the data. Optionally, you can add the sequencing method used.

Paste sequence contigs in FASTA format in to the form.

6.19. Uploading sequence contigs linked to an isolate record

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## PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Add new sequences](#)


## Upload sequences

This page allows you to upload sequence data for a specified isolate record in FASTA format.

Please note that you can reach this page for a specific isolate by [querying isolates](#) and then clicking 'Upload' within the isolate table.

Please fill in the following fields - required fields are marked with an exclamation mark (!).

Paste in sequences in FASTA format:

```
GGGTATGTAGTAATCAAATTCCTGACTTATCTGTAATACCTTAATTGTAGTTGGGT
TGTCACCTCTTTAATAGAAGTAGTACCAATAACCTTTCTACATCGACAGTCGCATA
TATTGGCCATCAGGAGTCATCGATACGGAGAAGAACTACTTTATTACTTTGAAGTATA
ACCTTCAATTCATTTGGGAGATGGTAAAACTGAACGGTTATTGCAATAGGCTATGG
AAGTCCCTCAAGAACATGCTCAAAGCAGCAGATACCGGTTGCCGTTGTCTCATT
GGTGATATCGAGTAGTACTATTGCTATATTAATTCTGTGTTTACAGCACCTATATT
TTTGATTCTGTAGTAAGCCATCAAGTTCTTTAACTGTCTGGTTGGTATAGCTGCTTG
GCCGCTTCGCTTCGACACGCCCCACAGGCGCTTCCCAAGCGTTGCCACGTTACC
GCACCGTGGCGATTCCCGCGCCGCTTGGCGAGCTGAGTGACCATGACAGTACAACCA
GAAGGATTAGCCATGCAGGTGCTGATAGCTAATTACCGCTGTACCGATCAGCGAGCT
GTCACACTGCGACATAAACCCATAGCTGTTAATCAACATCGGCTGTGTGCCATTA
CGGATATTGCTTATCAAATGGCAGCATCTTATCTCGGATTAGTCATCGACCTGCC
GCATGTGACGGCATAAATCTTGGATGATTTTTCAGTGGGTTTGTGGGCTTCTGC
GGTTGATGCTTTTTCGATTGGTAGGGGTAAGTCAAAATCAAAGCATTATTAACCTAC
GCCACCTCAGCCGATTCGCCGATGATTACATCGCCCGCTTGGTGGCCGACGCTG
CGGCAATAATCTTCGAGTAAGTGAACCTTATGCTTTTCCGATCGTGTAGTGTAGCA
GGGTTTCTGCCGCAAGTATGGATTGAGTACGATTCCCAACTGCTGCGCAATTGCC
CGCTTTTACATTTTCTTGTACCAATCCGTAACACACCCAGCAAGCGTGGGGAAC
TGTTTGGCAACATA
```

## Attributes

isolate id: !

sender: !

method:

run id:

assembly id:

## Options

- ☒ Don't insert sequences shorter than 100 bps. [?](#)
- ☒ Don't insert sequences containing only homopolymers. [?](#)

Link to experiment:

Alternatively upload FASTA file

or enter Genbank accession

Select FASTA file:

Action

Click 'Submit'. A summary of the number of isolates and their lengths will be displayed. To confirm upload, click 'Upload'.

## PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Add new sequences](#)


## Upload sequences

The following sequences will be entered.

Original designation	Sequence length	Comments
180426	26167	NODE_1211_length_26135_cov_16.536217
180427	1240	NODE_619_length_1208_cov_9.455298
180428	1566	NODE_655_length_1534_cov_15.418513
180429	1580	NODE_675_length_1548_cov_17.753876
180430	8422	NODE_31_length_8390_cov_14.525030
180431	2753	NODE_254_length_2721_cov_18.400587
180432	1987	NODE_262_length_1955_cov_8.388747
180433	30823	NODE_252_length_30791_cov_15.767627
180434	568	NODE_189_length_536_cov_31.078358
180435	543	NODE_716_length_511_cov_12.113503
180436	13771	NODE_465_length_13739_cov_15.131669
180437	15920	NODE_38_length_15888_cov_17.174660
180438	2430	NODE_778_length_2398_cov_8.673060
180439	689	NODE_1765_length_657_cov_8.754947
180440	287	NODE_729_length_255_cov_13.007843
180441	16369	NODE_52_length_16337_cov_17.192997
180442	684	NODE_190_length_652_cov_116.434052
180443	3126	NODE_95_length_3094_cov_14.927279
180444	5104	NODE_770_length_5072_cov_12.878943
180445	1255	NODE_263_length_1223_cov_10.451349
180446	4528	NODE_181_length_4496_cov_14.635231
180447	4468	NODE_558_length_4436_cov_14.670198
180448	949	NODE_1179_length_917_cov_13.504908
180449	4065	NODE_527_length_4033_cov_15.608480
180450	2467	NODE_212_length_2435_cov_12.223409
180451	822	NODE_54_length_790_cov_9.398734
180452	12793	NODE_146_length_12761_cov_14.578794

Summary

Number of contigs: 359

Minimum length: 265

Maximum length: 33,563

Total length: 2,059,411

Mean length: 5,736

N50 contig number: 60

N50 contig length (L50): 10,581

N90 contig number: 200

N90 contig length (L50): 3,126

N95 contig number: 241

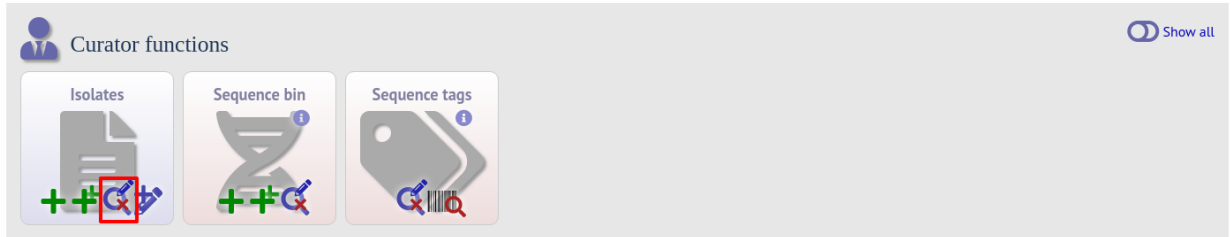
N95 contig length (L50): 1,863

Action

## 6.19.2 Select from isolate query

As an alternative to selecting the isolate from a dropdown list (or entering the id on large databases), it is also possible to upload sequence data following an isolate query.

Click the isolate update/delete link from the curator's main page.



Enter your search criteria. From the list of isolates displayed, click the 'Upload' link in the sequence bin column of the appropriate isolate record.

PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Query or update isolates

Query or update isolates

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

isolate = M00242905

Display/sort options

Order by: id ascending

Display: 25 records per page

Action

RESET SEARCH

1 record returned.

Tag scanning Bookmark query

Scan 2020-07-23:1 Add bookmark

Delete	Update	Sequence bin	New version	Isolate fields							MLST		Finotyping antigens			
				id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
				3	M00242905		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1099		19	15	

The same upload form as detailed above is shown. Instead of a dropdown list for isolate selection, however, the chosen isolate will be pre-selected.

Attributes

isolate id: 3) M00242905

sender: Jolley, Keith (keith)

method:

run id:

assembly id:

Options

☒ Don't insert sequences shorter than 100 bps.

☒ Don't insert sequences containing only homopolymers.

Link to experiment:

Alternatively upload FASTA file or enter Genbank accession

Select FASTA file:

Choose file No file chosen

Action

RESET SUBMIT

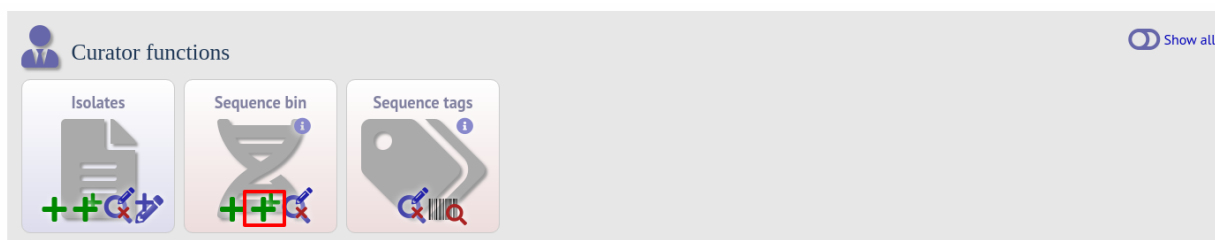
### 6.19.3 Upload options

On the upload form, you can select to filter out short sequences or those containing only homopolymeric repeats (which can be artefactually produced by some assembler software versions) from your contig list.

The screenshot shows the 'Options' section of the upload form. It includes two checked checkboxes: 'Don't insert sequences shorter than 100 bps.' and 'Don't insert sequences containing only homopolymers.' Below these are fields for 'Link to experiment:', 'Alternatively upload FASTA file', and 'or enter Genbank accession'. At the bottom are 'RESET' and 'SUBMIT' buttons.

## 6.20 Batch uploading sequence contigs linked to multiple isolate records

To upload contigs for multiple isolates, click the batch add (++) sequence bin link on the curator's main page.



The first step is to upload the name of the contig file that will be linked to each isolate record. This can be done by pasting two columns in tab-delimited text format (e.g. from a spreadsheet) - the first column contains the isolate identifier, the second contains the filename of the contigs file, which should be in FASTA format.

You can choose which field to use for identifying the isolates, e.g. id (database id) or isolate (name of isolate). The value provided for this field needs to uniquely identify the isolate in the database - please note that only id is guaranteed to be unique.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

Batch upload sequence assemblies to multiple isolate records

This function allows you to upload assembly contig files for multiple records together.

The first step in the upload process is to state which assembly contig FASTA file should be linked to each isolate record. You can use any provenance metadata field that uniquely identifies an isolate.

You can upload up to 100 genomes at a time.

Identifying field name

Field: isolate

Filenames

Paste in tab-delimited text, e.g. copied from a spreadsheet, consisting of two columns. The first column should be the value for the isolate identifier field (specified above), and the second should be the filename that you are going to upload. You need to ensure that you use the full filename, including any suffix such as .fas or .fasta, which may be hidden by your operating system.

```
JB_21292    JB_21292.fasta
JB_21293    JB_21293.fasta
JB_21294    JB_21294.fasta
```

Action

RESET SUBMIT

Click Submit. The system will check to make sure that the isolate records are uniquely identified (if not, you will see an error message informing you of this and you will need to use the database id as the identifier). You will then see a file upload form.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

Batch upload sequence assemblies to multiple isolate records

Please upload the assembly contig files for each isolate record.

remove row	id	isolate	current sequence contigs	bin state total size (bp)	filename	upload status
<input type="checkbox"/>	80309	JB_21292	-	-	JB_21292.fasta	✗
<input type="checkbox"/>	80310	JB_21293	-	-	JB_21293.fasta	✗
<input type="checkbox"/>	80311	JB_21294	-	-	JB_21294.fasta	✗

Remove

3 FASTA files left to upload.

Contig assembly files

Please upload contig assemblies with the filenames as you specified (indicated in the table). Individual filesize is limited to 64 MB. You can upload up to 64 MB in one go, although you can upload multiple times so that the total size of the upload can be larger.

Drop files here or click to upload.

Drag and drop your FASTA format contig files in to the dotted drop area. Provided the filenames exactly match the filename you stated, these will be uploaded to a staging area.

Click 'Validate' to check that these files are valid FASTA format.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

Batch upload sequence assemblies to multiple isolate records

Please upload the assembly contig files for each isolate record.

remove row	id	isolate	current sequence contigs	bin state total size (bp)	filename	upload status
<input type="checkbox"/>	80309	JB_21292	-	-	JB_21292.fasta	✓
<input type="checkbox"/>	80310	JB_21293	-	-	JB_21293.fasta	✓
<input type="checkbox"/>	80311	JB_21294	-	-	JB_21294.fasta	✓

[Remove](#)

All files uploaded. The sequences have not yet been validated. This needs to be done before they can be added to the database.

Action

**VALIDATE**

The files will be checked and a table will be displayed showing the total sequence size and number of contigs found. Select the data sender and, optionally the sequencing method from the dropdown lists. Then click 'Upload validated contigs'.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

Batch upload sequence assemblies to multiple isolate records

Validation

id	isolate	filename	valid FASTA	contigs	total size
80309	JB_21292	JB_21292.fasta	✓	364	2,069,108
80310	JB_21293	JB_21293.fasta	✓	359	2,059,411
80311	JB_21294	JB_21294.fasta	✓	199	2,057,385

You can upload 3 records.

Please do not refresh the page after you click the upload button. Upload may take a short while.

Attributes

sender: Jolley, Keith (keith)

method: Illumina

Options

☒ Don't insert sequences shorter than 100 bps.

☒ Don't insert sequences containing only homopolymers.

Action

**UPLOAD VALIDATED CONTIGS**

You can also choose to filter out short contigs selecting the checkbox and choosing the minimum length from the dropdown box in the options settings. You can also choose to filter out sequences containing only homopolymeric runs which can be produced artefactually by some assembler versions.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

Batch upload sequence assemblies to multiple isolate records

Validation

id	isolate	filename	valid FASTA	contigs	total size
80309	JB_21292	JB_21292.fasta	✓	364	2,069,108
80310	JB_21293	JB_21293.fasta	✓	359	2,059,411
80311	JB_21294	JB_21294.fasta	✓	199	2,057,385

You can upload 3 records.

Please do not refresh the page after you click the upload button. Upload may take a short while.

Attributes

sender: ! Jolley, Keith (keith)   
 method: Illumina

Options

- ☒ Don't insert sequences shorter than 100 bps.
- ☒ Don't insert sequences containing only homopolymers.

Action

**UPLOAD VALIDATED CONTIGS**

A confirmation message will be displayed after clicking the Upload button.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add new sequences

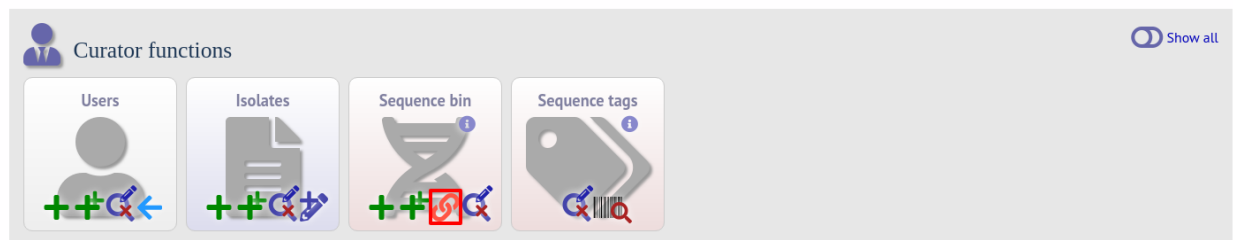
Batch upload sequence assemblies to multiple isolate records

3 sequence assemblies uploaded.

## 6.21 Linking remote contigs to isolate records

If *remote contigs have been enabled*, isolates can be linked to contigs stored in an external BIGSdb database, rather than directly uploaded. These will then be loaded when needed, for example during scanning or data export. This will be marginally slower than hosting contigs within the same database, but minimises duplication of sequence data and associated storage. Contigs need to be accessible via the BIGSdb *RESTful API*.

Click the sequences link icon on the curator's main page.



Either select the isolate id from the dropdown list, or enter it manually (list is disabled if there are >1000 records in the database). Enter the URI for the RESTful API of the parent isolate record, e.g. [http://rest.pubmlst.org/db/pubmlst\\_rmlst\\_isolates/isolates/933](http://rest.pubmlst.org/db/pubmlst_rmlst_isolates/isolates/933). This URI can require authentication if credentials have been *set up*.

Press submit.

PubMLST

Home > Organisms > Organism > Leptospira isolates > Add remote contigs

Add remote contigs

This page allows you to link contigs stored in a remote BIGSdb database to an isolate record. Access to these contigs is via the BIGSdb RESTful API which must be running on the remote database.

Valid URIs are in the form 'http://rest.pubmlst.org/db/{database\_config}/isolates/{isolate\_id}'.

Enter details

isolate id: 1

isolate record URI: http://rest.pubmlst.org/db/pubmlst\_rmlst\_isolates/isolates/933

Action

RESET SUBMIT

Summary information about the number of contigs and their total length will be downloaded from the remote isolate record. You will then be prompted to upload this information to the database, by clicking the 'Upload' button.

PubMLST

Home > Organisms > Organism > Leptospira isolates > Add remote contigs

Add remote contigs

Checking contigs

Downloading isolate record ... done.

Contigs: 25

Total length: 2,697,907 bp

Action

UPLOAD

The contigs will be downloaded in bulk in order to determine their lengths. This information is stored within the local database as it is required for various outputs. Full metadata is not stored at this stage.

PubMLST

Home > Organisms > Organism > Leptospira isolates > Add remote contigs

Add remote contigs

25 remote contigs added.

Please note that so far only links to the contig records have been added to the database. The contigs themselves have not been downloaded and checked. Processing records the length of each contig and stores a checksum within the database so that it is possible to tell if the sequence ever changes. You can either do this now or it can be performed offline by a scheduled task.

Total contigs: 25

Remote contigs: 25 (25 unprocessed)

Total length: 2,697,907

Action

PROCESS CONTIGS NOW

This is all that is required for the contigs to be used as normal. In order to get the full metadata about the contigs (sequencing platform used, sender and datestamp information), you can choose to process the contigs by clicking the 'Process contigs now' button. This will download each contig in turn, and store its provenance metadata locally.

PubMLST

Home > Organisms > Organism > Leptospira isolates > Add remote contigs

Add remote contigs

Processed contigs

Contigs processed: 25  
Total length: 2,697,907 bp

Alternatively, this step can be *performed offline automatically*.

## 6.22 Automated web-based sequence tagging

Sequence tagging, or tag-scanning, is the process of identifying alleles by scanning the sequence bin linked to an isolate record. Defined loci can either have a single reference sequence, that is defined in the locus table, or they can be linked to an external database that contains the sequences for known alleles. The tagging function uses BLAST to identify sequences and will tag the specific sequence region with locus information and an allele designation if a matching allele is identified by reference to an external database.

Select ‘scan’ sequence tags on the curator’s index page.

Curator functions

Show all

Isolates

Sequence bin

Sequence tags

Next, select the isolates whose sequences you wish to scan against. Multiple isolates can be selected by holding down the Ctrl key. All isolates can be selected by clicking the ‘All’ button under the isolate selection list. On database with a large number of isolates, you will need to enter a list of isolate ids rather than pick from a list.

Select either individual loci or schemes (collections of loci) to scan against. Again, multiple selections can be made.

## Sequence tag scan

Please select the required isolate ids and loci for sequence scanning - use Ctrl or Shift to make multiple selections. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. By default, loci are only scanned for an isolate when no allele designation has been made or sequence tagged. You can choose to rescan loci with existing designations or tags by selecting the appropriate options.

Isolates

34

Loci

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
ackA2 (NEIS1727)  
acnA (NEIS1729)  
acnB (NEIS1492)

Schemes

Plasmids  
Typing  
MLST  
Finetyping antigens  
16S  
Antigen genes  
Bexsero Antigen Sequence  
Human-restricted Neisseria

Clear List all

All None Paste list

Parameters

Min % identity: 70  
Min % alignment: 50  
BLASTN word size: 20  
Return up to: 1 partial match(es)  
Stop after: 200 new matches  
Stop after: 5 minute(s)

☐ Scan selected loci together  
☒ Use TBLASTX  
☐ Hunt for nearby start and stop codons  
☐ Return partial matches even when exact matches are found  
☐ Override locus view restrictions  
☐ Rescan even if allele designations are already set  
☐ Rescan even if allele sequences are tagged  
☐ Use only type alleles to identify locus  
☐ Mark missing sequences as provisional allele '0'

Restrict included sequences by

Sequence method:  
Project:  
Experiment:

Action

RESET SCAN

Choose your scan parameters. Lowering the value for BLASTN word size will increase the sensitivity of the search at the expense of time. Using TBLASTX is more sensitive but also much slower. TBLASTX can only be used to identify the sequence region rather than a specific allele (since it will only match the translated sequence and there may be multiple alleles that encode a particular peptide sequence).

By default, for each isolate only loci that have not had either an allele designation made or a sequence region scanned will be scanned again. To rescan in these cases, select either or both the following:

- Rescan even if allele designations are already set
- Rescan even if allele sequences are tagged

You can select to only use type alleles to identify the locus. This will constrain the search space so that allele definitions don't become more variable over time. If a partial match is found to a type allele then a full database lookup will be performed to identify any known alleles. An allele can be given a status of type allele when *defining*.

If fast scanning is enabled, there will also be an option to 'Scan selected loci together'. This can be significantly quicker than a locus-by-locus search against all alleles but is not enabled by default as it can use more memory on the server and requires *exemplar alleles* to be defined.

Options can be returned to their default setting by clicking the 'Defaults' button.

**Parameters**

Min % identity: 70

Min % alignment: 50

BLASTN word size: 20

Return up to: 1  partial match(es)

Stop after: 200  new matches

Stop after: 5  minute(s)

☐ Scan selected loci together

☐ Use TBLASTX

☐ Hunt for nearby start and stop codons

☐ Return partial matches even when exact matches are found

☐ Override locus view restrictions

☐ Rescan even if allele designations are already set

☐ Rescan even if allele sequences are tagged

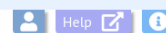
☐ Use only type alleles to identify locus

☐ Mark missing sequences as provisional allele '0'

Press 'Scan'. The system takes approximately 1-2 seconds to identify each sequence (depending on machine speed and size of definitions databases). Alternatively, if 'Scan selected loci together' is available and selected, it may take longer to return initial results but total time should be less (e.g. a 2000 loci cgMLST scheme may be returned in 1-2 minutes). Any identified sequences will be listed in a table, with checkboxes indicating whether allele sequences or sequence regions are to be tagged.

## PubMLST

Home &gt; Organisms &gt; Neisseria spp. &gt; Neisseria isolates &gt; Sequence tag scan



## Sequence tag scan

Isolate	Match	Locus	Allele	% identity	Alignment length	Allele length	E-value	Sequence bin id	Start	End	Predicted start	Predicted end	Orientation	Designate allele	Tag sequence	Flag ⓘ
34) 20	exact	abcZ	1	100.00	433	433	0.0	182791	7064	7496	7064	7496	←	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	adk	3	100.00	465	465	0.0	182750	1392	1856	1392	1856	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	aroE	1	100.00	490	490	0.0	182731	32577	33066	32577	33066	←	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	fumC	1	100.00	465	465	0.0	182815	19783	20247	19783	20247	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	gdh	1	100.00	501	501	0.0	182852	7516	8016	7516	8016	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	pdhC	1	100.00	480	480	0.0	182819	13868	14347	13868	14347	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
34) 20	exact	pgm	3	100.00	450	450	0.0	182831	24559	25008	24559	25008	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>

extract →
extract →
extract →
extract →
extract →
extract →
extract →

Action

Started: Thu Jul 23 15:36:58 2020  
 Finished: Thu Jul 23 15:37:03 2020  
 Elapsed time: 5 seconds  
 Please note that scan results will remain on the server for 7 days.

Individual sequences can be extracted for inspection by clicking the ‘extract →’ link. The sequence (along with flanking regions) will be opened in another browser window or tab.

Checkboxes are enabled against any new sequence region or allele designation. You can also set a flag for a particular sequence to mark an attribute. These will be set automatically if these have been defined within the sequence definition database for an identified allele.

**See also:***Sequence tag flags*

Ensure any sequences you want to tag are selected, then press ‘Tag alleles/sequences’.

If any new alleles are found, a link at the bottom will display these in a format suitable for automatic allele assignment by *batch uploading to sequence definition* database.

**See also:**

Offline curation tools

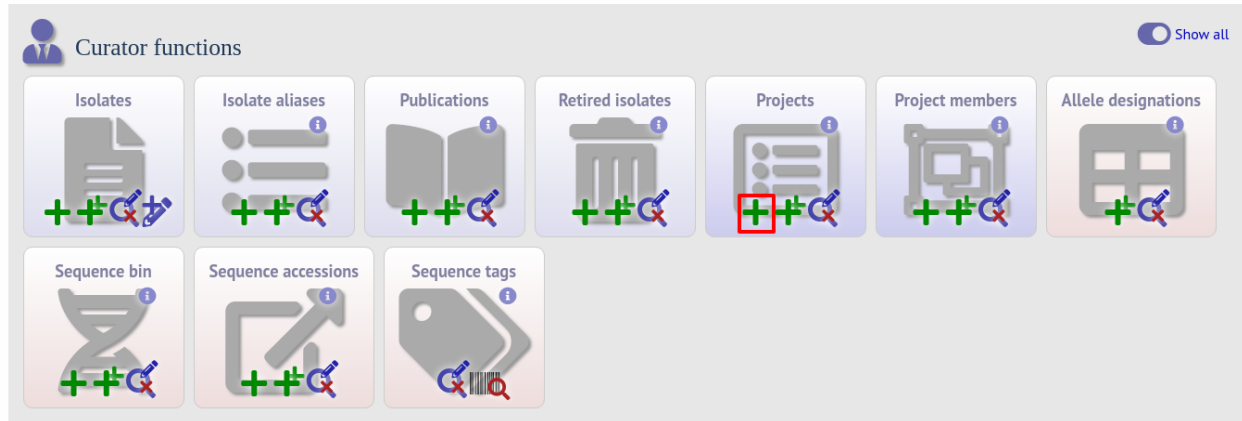
*Automated offline sequence tagging*

## 6.23 Projects

### 6.23.1 Creating the project

The first step in grouping by project is to set up a project.

Click the add (+) project link on the curator’s main page. This function is normally hidden, so you may need to click the ‘Show all’ toggle to display it.



Enter a short description for the project. This is used in drop-down list boxes within the query interfaces, so make sure it is not too long.

You can also enter a full description. If this is added, the project description can be displayed at the top of an isolate information page (but see 'isolate\_display' flag below). The full description can include HTML formatting, including image links.

There are additionally two flags that affect how projects are listed:

- `isolate_display` - Setting this is required for the project and its description to be listed at the top of an isolate record (default: false).
- `list` - Setting this is required for the project to be listed in a page of projects linked from the main contents page.

There are a further two option flags:

- `private` - Setting this makes the project a private *user project*. You will be set as the project owner and will be the only user able to access it by default. You can add additional users or user groups who will be able to access and update the project data later.
- `no_quota` - If set, isolates added to this project will not count against a user's quota of *private records* (only relevant to private projects).

Click 'Submit'.

## PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Add new project description](#)


## Add new project description

Please fill in the fields below - required fields are marked with an exclamation mark (!).

Record

Action

id:!

3

short description:!

MRF Meningococcus Genome Library

!

isolate display:!

☐ true ☒ false

!

list:!

☐ true ☒ false

!

private:!

☐ true ☒ false

!

no quota:!

☒ true ☐ false

!

restrict user:!

☐ true ☒ false

!

restrict usergroup:!

☐ true ☒ false

!

curator:!

Keith Jolley (keith)

datestamp:!

2020-07-23

full description:!

England, the Scottish Haemophilus, Legionella, Meningococcus and Pneumococcus Reference (SHLMRP) Laboratory, The Wellcome Trust Sanger Institute and the University of Oxford, funded by the Meningitis Research Foundation.</p>
 <p>Use of the MRF Genome Library data <a href="/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst\_neisseria\_mrfgenomes">must be cited</a> in any publication or presentation making use of it.</p>
 </div>

!

curate config:!

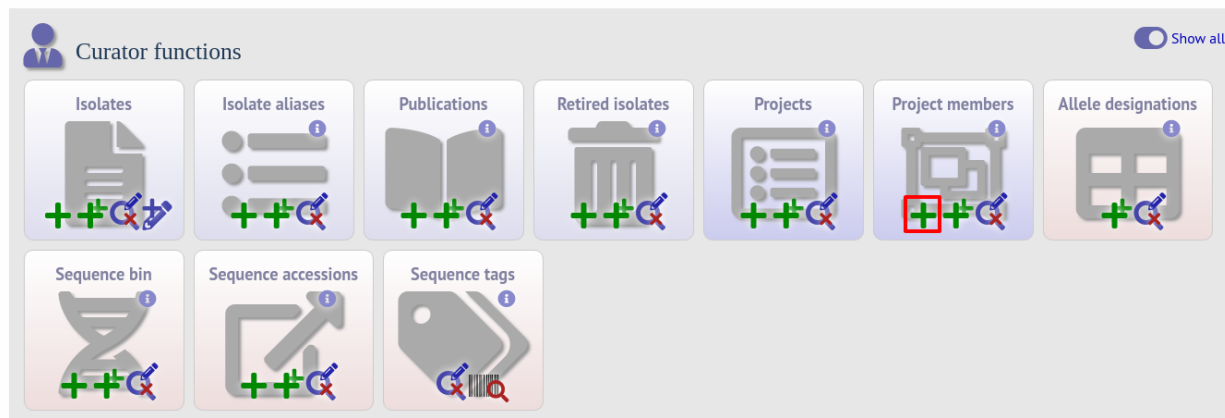
!

RESET

SUBMIT

### 6.23.2 Explicitly adding isolates to a project



Explicitly adding isolates to the project can be done individually or in batch mode. To add individually, click the add (+) project member link on the curator's main page. This function is normally hidden, so you may need to click the 'Show all' toggle to display it.



Select the project from the dropdown list box and enter the id of the isolate that you wish to add to the project. Click 'Submit'.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Add new project member





## Add new project member


Please fill in the fields below - required fields are marked with an exclamation mark (!).


Record	Action
project id: 3) MRF Meningococcus Genome Library isolate id: 18968 curator: Keith Jolley (keith) timestamp: 2020-07-23	<div>RESET</div> <div>SUBMIT</div>


To add isolates in batch mode. Click the batch add (++) project members link on the curator's main page.



Curator functions


Show all



Isolates



Isolate aliases



Publications



Retired isolates



Projects


Project members


Allele designations


Sequence bin



Sequence accessions


Sequence tags

Download an Excel submission template:

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add project member records





## Batch insert project members

### Instructions

This page allows you to upload project member data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

### Templates

Check the [description of database fields](#) for help with filling in the template.


### Upload

Upload	Action
Paste in tab-delimited text (Include a field header line).	<div>RESET</div> <div>SUBMIT</div>

You will need to know the id number of the project - this is the id that was used when you created the project. Fill in the spreadsheet, listing the project and isolate ids. Copy and paste this to the web upload form. Press 'Submit'.

PubMLST

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Batch add project member records](#)





## Batch insert project members

### Instructions

This page allows you to upload project member data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.

### Templates

Check the [description of database fields](#) for help with filling in the template.

### Upload

Paste in tab-delimited text (Include a field header line).

project\_id

isolate\_id

318968

318969

319023

319024

319025

319026

319027

319028

319029

319030

319031

319032

319033

319034

Action

RESET

SUBMIT

**See also:**

Setting up user projects

*User projects*

## 6.24 Isolate record versioning

Versioning enables multiple versions of genomes to be uploaded to the database and be analysed separately. When a new version is created, a copy of the provenance metadata, and publication links are created in a new isolate record. The sequence bin and allele designations are not copied.

By default, old versions of the record are not returned from queries. Most query pages have a checkbox to 'Include old record versions' to override this.

Links to different versions are displayed within an isolate record:

174

Chapter 6. Curator's guide

 Provenance/primary metadata

**genogroup notes:** C backbone: csc fragmented (71.17% cov),cssB fragmented (16.16% cov),cssB fragmented (17.2% cov),ctrA fragmented (88.4% cov),ctrB fragmented (98.45% cov),ctrE fragmented (92.3% cov),ctrF fragmented (15.31% cov),ctrF fragmented (81.43% cov),missing ctrD,missing tex. Prediction code: [https://github.com/ntopaz/characterize\\_neisseria\\_capsule](https://github.com/ntopaz/characterize_neisseria_capsule).

**capsule group:** discrepancy

**sender:** Keith Jolley, University of Oxford,  
 UK  
**curator:** Auto Tagger  
**update history:** [56 updates](#) [show details](#)  
**date entered:** 2012-06-27  
**timestamp:** 2020-02-10

## Secondary metadata

 Vaccines

**Bexsero reactivity:** insufficient data 

◀ notes

 Versions

More than one version of this isolate record exist.

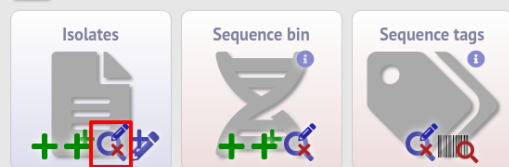
Newer versions: 40500

#### Publication (1)

- Kistulyu AO, Katz LS, Agrawal S, Hagen MS, Conley AB, Jayaraman P, Nelakuditi V, Humphrey JC, Sammons SA, Govil D, Mair RD, Tatti KM, Tondella ML, Harcourt BH, Mayer LW, Jordan IK (2010). A computational genomics pipeline for prokaryotic sequencing projects. *Bioinformatics* 26:1819-26. **13 isolates**

To create a new version of an isolate record, query or browse for the isolate:

 Curator functions

 Show all

## 6.24. Isolate record versioning

## PubMLST

Home &gt; Organisms &gt; Neisseria spp. &gt; Neisseria isolates &gt; Query or update isolates



## Query or update isolates

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

id = Enter value... + ⓘ

Display/sort options

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET

SEARCH

83,414 records returned (1 - 25 displayed).

Tag scanning

Projects

Private records

Bookmark query

Scan

Select project...

Link

Publish

2020-07-23:1

Add bookmark



Delete	Update	Sequence bin	New version	Isolate fields ⓘ								MLST		Finotyping antigens		
				id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
				1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-5
				2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
				3	M00242905		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1099		19	15	
				4	M1027	B43; NIBSC_3076; Z1043	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex			
				5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex	7	16	
				6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
				7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
				8	M00242007		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex		14	
				9	0021/84		Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex			
				10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	18-1	3	F5-1

The isolate record will be displayed. The suggested id number for the new record will be displayed - you can change this. By default, the new record will also be added to any projects that the old record is a member of. Uncheck the 'Add new version to projects' checkbox to prevent this.

Click the 'Create' button.

## PubMLST

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Create new isolate record version



## Create new isolate record version

This page allows you to create a new version of the isolate record shown below. Provenance and publication information will be copied to the new record but the sequence bin and allele designations will not. This facilitates storage of different versions of genome assemblies. The old record will be hidden by default, but can still be accessed when needed, with links from the new record. The update history will be reset for the new record.

Enter new record id	Options	Action
id: <input type="text" value="80312"/>	<input checked="" type="checkbox"/> Add new version to projects	<a href="#">CREATE</a>



## Provenance/primary metadata

id: 7	genogroup: A	sender: Wendell Zollinger, Dept Bacterial Diseases, Walter Reed Army Institute of Research, Washington DC, USA
isolate: 7891	genogroup notes: A backbone: All essential capsule genes intact and present. Prediction code: <a href="https://github.com/ntopaz/characterize_neisseria_capsule">https://github.com/ntopaz/characterize_neisseria_capsule</a> .	curator: Auto Tagger
aliases: B54; NIBSC_2760; Z1054		update history: <a href="#">120 updates</a> <a href="#">show details</a>
strain designation: A: P1.20.9: F3-1: ST-5 (cc5)	capsule group: A	date entered: 2001-02-07
country: Finland	MLEE designation: Subgroup III	timestamp: 2020-04-16
continent: Europe	serotype: 4,21	
year: 1975	sero subtype: P1.9	
disease: invasive (unspecified/other)	ET no: 48	
source: CSF		
epidemiology: epidemic		



## CURATING DATA SUBMITTED VIA THE AUTOMATED SUBMISSION SYSTEM

Data may be submitted by users using the automated submission system if it has been enabled for a specific database. As a curator, you will be notified of pending submissions when you log in to the curator's interface or if you access the 'Manage submissions' links from the standard contents page. Additionally, if your user account has the 'submission\_emails' flag set in the users' table you will also receive E-mail notification of new submissions for which you have sufficient privileges to curate.

BIGSdb

Home > Organisms > Organism > Neisseria typing

*Neisseria* typing database

Query a sequence

- Sequence query**  
Query a single sequence or whole genome assembly to identify allelic matches.
- Batch sequence query**  
Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

- Sequence attribute search**  
Find alleles by matching criteria (all loci together)
- Locus-specific sequence attribute search**  
Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

- Allelic profile query**  
Search, browse or enter list of profiles
- Search by combinations of alleles**  
This can include partial matches to find related profiles.
- Batch profile query**  
Lookup multiple allelic profiles together.

LOG OUT

**SUBMISSIONS** 1

DOWNLOADS

EXPORT

ANALYSIS

CUSTOMISE

INFORMATION

ISOLATES

Any submissions for which you have sufficient privileges to curate will be shown.

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- [alleles](#)
- [MLST profiles](#)
- [Bexsero Antigen Sequence Typing \(BAST\) profiles](#)
- [Conjugative Plasmid profiles](#)
- [Cryptic Plasmid profiles](#)
- [NG MAST profiles](#)
- [beta lactamase plasmid profiles](#)
- [isolates](#) (without assembly files) [Link to isolate database](#)
- [genomes](#) (isolate records with assembly files) [Link to isolate database](#)

### New allele sequence submissions waiting for curation

Your account is authorized to handle the following submissions:

Submission id	Submitted	Updated	Submitter	Locus	Technology	Sequences
BIGSdb_20200723194830_018868_29257	2020-07-23	2020-07-23	<a href="#">Joe Bloggs</a>	NEIS0001 (lpxC)	Illumina	3

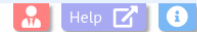
 [Show closed submissions](#)

## 7.1 Alleles

Click the link to the appropriate submission on the ‘Manage submissions’ page.

## BIGSdb

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Submissions



## Manage submissions

## Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- [alleles](#)
- [MLST profiles](#)
- [Bexsero Antigen Sequence Typing \(BAST\) profiles](#)
- [Conjugative Plasmid profiles](#)
- [Cryptic Plasmid profiles](#)
- [NG MAST profiles](#)
- [beta lactamase plasmid profiles](#)
- [isolates \(without assembly files\)](#) [Link to isolate database](#)
- [genomes \(isolate records with assembly files\)](#) [Link to isolate database](#)

## New allele sequence submissions waiting for curation

Your account is authorized to handle the following submissions:

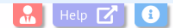
Submission Id	Submitted	Updated	Submitter	Locus	Technology	Sequences
<b>BIGSdb_20200723194830_018868_29257</b>	2020-07-23	2020-07-23	<a href="#">Joe Bloggs</a>	NEIS0001 (lpxC)	Illumina	3

[Show closed submissions](#)

You will see a summary section that describes details about how the sequences were obtained. There should also be [link here](#) to download all the sequences in FASTA format.

## BIGSdb

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Submissions &gt; Curate submission



## Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

## Summary

type: alleles  
 submitter: [Joe Bloggs](#), University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 locus: NEIS0001 (lpxC)  
 sequences: 3 [FASTA](#)  
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

## Sequences

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending	Q	<a href="#">Curate</a>
UK323	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAAATTTGTGGATAA	✓	pending	Q	<a href="#">Curate</a>
UK347	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending	Q	<a href="#">Curate</a>

BATCH CURATE

BATCH QUERY

Mark all:

[Pending](#)[Rejected](#)[Update](#)

## Messages

Message: [Append](#) [Send now](#)

## Archive

Archive of submission and any supporting files:

[Download](#) [TAR](#)

There will also be a table summarizing the sequences in the submission and their current submission status.

BIGSdb


Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Help







## Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

**Summary**

type: alleles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 locus: NEIS0001 (lpxC)  
 sequences: 3   
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

**Sequences**

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAGAAGCTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending		
UK323	924	ATGCTGCAAGAAGCTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending		
UK347	924	ATGCTGCAAGAAGCTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending		


BATCH CURATE    BATCH QUERY    Mark all: [Pending](#) [Rejected](#) [Update](#)

**Messages**

Message: [Append](#) [Send now](#)

**Archive**

Archive of submission and any supporting files:

[Download](#) 

### 7.1.1 Individual allele curation

Individual sequences can be curated singly by clicking the ‘Curate’ links next to the sequence in the table. If you have supporting data attached to the submission, e.g. Sanger trace files then you may need to assess the submission based on the policy of the database.

**BIGSdb**

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

[Help](#) [Info](#)

## Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

**Summary**

type: alleles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 locus: NEIS0001 (lpxC)  
 sequences: 3   
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

**Sequences**

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending		<a href="#">Curate</a>
UK323	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAAATTTGTGGATAA	✓	pending		<a href="#">Curate</a>
UK347	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	pending		<a href="#">Curate</a>

[BATCH CURATE](#)
[BATCH QUERY](#)

Mark all: [Pending](#) [Rejected](#) [Update](#)

**Messages**

Message: [Append](#) [Send now](#)

**Archive**

Archive of submission and any supporting files:

[Download](#)

Clicking this link takes you to the curation interface *single sequence upload page*. The upload form will be filled with details from the submission. You may wish to manually change the status from the dropdown list of values.

**PubMLST**

Home > Organisms > Organism > Neisseria typing > Add new allele sequence

[Help](#) [Info](#)

## Add new allele sequence

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

locus: NEIS0001  
 allele id: 1992  
 sequence: ATCGATTTGCGCGCAATCCTACATCGACGAAATCGCGCGCGCGCACTTTGCGCTTATGCACGAACTGGAA  
 ATGATGCGCGCCACAATCTGGGTTTGGCGGCAATTTGAACAACGCCATCGTGATTGACGACACGGATGCTCTG  
 AATCCTGAAGGCTTGCGCTATCCGATGAGTTTGTGCGCCACAAAATCCTTGATGCCATCGCGGATTGTATATC  
 GTCGGACACCCGATTATCGGTGCGTTTGAAGGCTACAAATCGGGACACGCCATCAACAACGCACTTTGCGCGCG  
 GTTTTGGCAGACGAAACGGCTTACGACCGGGTGAATTTGCCGACAGCGATGATTGCCGACGATTTACGAG  
 CTGAACATCAGAACTTGTGGATAA

status: unchecked  
 sender: Bloggs, Joe (jbloggs)  
 curator: Keith Jolley (keith)  
 date entered: 2020-07-23  
 datestamp: 2020-07-23  
 type allele: ☐ true ☐ false New allele searches can be constrained to use just type alleles in comparisons  
 comments:

Flags: alternative start codon  
 atypical  
 contains IS element  
 downstream fusion

**Action**

[RESET](#)
[SUBMIT](#)

Clicking 'Submit' from this form will define the new allele and add it to the database. A link on the confirmation page will take you back to the submission management page.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new allele sequence

Add new allele sequence

Sequence NEIS0001 (lpxC): 1993 added.  
Don't forget to [close the submission](#)

You will find that the status of the newly assigned sequence has changed in the summary table. The assigned value and status are determined on display and should always reflect the live database values.


PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission



Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

Summary

type: alleles  
submitter: Joe Bloggs, University of Oxford, UK  
datestamp: 2020-07-23  
status: pending  
locus: NEIS0001 (lpxC)  
sequences: 3   
technology: Illumina  
read length: 100-199  
coverage: 20-49x  
assembly: de novo  
assembly software: Spades

Sequences

Identifier	Length	Sequence	Complete CDS	Status	Query / Assigned allele
UK322	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTTGGATAA	✓	assigned	1993
UK323	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTTGGATAA	✓	pending	
UK347	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTTGGATAA	✓	pending	

BATCH CURATE BATCH QUERY


Mark all: [Pending](#) [Rejected](#) [Update](#)

Messages

Message: [Append](#) [Send now](#)

Archive

Archive of submission and any supporting files:

[Download](#) 

## 7.1.2 Batch allele curation

Often, you will want to batch upload submitted sequences. This can be done by clicking the 'Batch curate' button.

**Note:** Batch curation is only available for loci that do not have extended attributes defined. Entries for these loci require additional values set for these additional fields and so need to be handled individually.

PubMLST
Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

Summary

type: alleles  
submitter: Joe Bloggs, University of Oxford, UK  
datestamp: 2020-07-23  
status: pending  
locus: NEIS0001 (lpxC)  
sequences: 3   
technology: Illumina  
read length: 100-199  
coverage: 20-49x  
assembly: de novo  
assembly software: Spades

Sequences

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTGTGGATAA		assigned		1993
UK323	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTGTGGATAA		pending		
UK347	924	ATGCTGCAAAGAACCTTTGGC ... ACATCAGAACTTGTGGATAA		pending		

Mark all: Pending Rejected Update

BATCH CURATE BATCH QUERY

Messages

Message:

Archive

Archive of submission and any supporting files:

Download

This takes you to the *batch FASTA upload page* in the curators' interface.

The upload form will be filled with details from the submission. You may wish to manually change the status from the dropdown list of values.

PubMLST
Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Batch insert sequences

This page allows you to upload allele sequence data in FASTA format. The identifiers in the FASTA file will be used unless you select the option to use the next available id (loci with integer ids only). Do not include the locus name in the identifier in the FASTA file.

Please note that you can not use this page to upload sequences for loci with extended attributes.

Enter parameters

locus: NEIS0001 (lpxC)  
status: unchecked  
sender: Bloggs, Joe (jbloggs)  
sequence (FASTA): >UK323  
ATGCTGCAAAGAACCTTTGGCGAAATCCATCAGCGTTACCGGAGTCGGGCTGCATTCCGGGC  
GAACGCGTCGCGCTGACCTGCACCCGCGCCTGAAAACAGCTGGATTTCTTCCTCCGAAGT  
ACCGATTGGACGGCGAGATGGCGAACAATCAAATGACCCCTATTGTGATCAACGAT  
ACCGCGCTTTCTCCACCATCGTTACCGCAAAAGCGCTGCGCTCGGCACAAATCGAACAC  
ATTATGTCGCGCTGTCGCGCTACGGCATCGAAATGCGCTGATTGAGCTGAACGCGCC  
GAAATCCGATTATGACGGCTCCAGCGCTGCGCTTTATTACCTTTTGCAAGATGCGGGC  
GTGGTCGATCAAAAGGCGCAAAAGCGTTTTTGAAATCCTCAAGCCTGTGAAATCAAA  
GAAGCGGCAAAATGGGTACGCTTTACGCGTATGACGGCTTAAGGTAACGCTGACCATC  
GAATTCACCAATCGGTTTTCAACGCGAGCTGCCCACTTTGAAATTGATTTCGCGCGC

☒ Reject all sequences that are not complete reading frames - these must have a start and in-frame stop codon at the ends and no internal stop codons. Existing sequences are also ignored.  
☐ Override sequence similarity check  
☒ Use next available id (only for loci with integer ids)

Action

RESET CHECK

Click 'Check' on this form will perform some standard checks before allowing you to upload the sequences.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Batch insert sequences

Sequence check

Locus: NEIS0001 (lpxC)

Original designation	Allele id	Status	Action
UK323	1992	OK	<a href="#">UPLOAD VALID SEQUENCES</a>
UK347	1994	OK	

A link on the confirmation page will take you back to the submission management page.

PubMLST

Home > Organisms > Organism > Neisseria typing > Batch insert sequences

Batch insert sequences

Sequences added.

Don't forget to [close the submission!](#)

[←](#) [+](#)

The status of the sequences should reflect their newly assigned status.


PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

Summary

type: alleles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 locus: NEIS0001 (lpxC)  
 sequences: 3   
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

Sequences


Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAGAAGAACTTTGGC ... ACATCAGAACTTTGGGATAA	✓	assigned	Q	1993
UK323	924	ATGCTGCAAGAAGAACTTTGGC ... ACATCAGAAATTTGGGATAA	✓	assigned	Q	1992
UK347	924	ATGCTGCAAGAAGAACTTTGGC ... ACATCAGAACTTTGGGATAA	✓	assigned	Q	1994

Messages

Message: [Append](#) [Send now](#)

Archive

Archive of submission and any supporting files:

[Download](#) 

Action

[CLOSE SUBMISSION](#)

### 7.1.3 Rejecting sequences

Sometimes you may need to reject all, or some of, the sequences in a submission. You can do this by changing the value in the status dropdown box next to each sequence. Click 'Update' to make the change.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

**Summary**

type: alleles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 outcome: accepted - data uploaded  
 locus: NEIS0001 (lpxC)  
 sequences: 3   
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

**Sequences**

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAAGAACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected		
UK323	924	ATGCTGCAAAGAACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected		
UK347	924	ATGCTGCAAAGAACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected		

BATCH CURATE    BATCH QUERY

Mark all: Pending Rejected Update

**Messages**

Message: Append Send now

Archive

Archive of submission and any supporting files:

Download

### 7.1.4 Requesting additional information

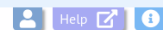
You can send a message to the submitter by entering it in the Messages box and clicking 'Send now'. This will append a message to the submission and send an update to the submitter so that they can respond.

### 7.1.5 Closing the submission

You can add a message to the submitter by entering it in the message box and clicking 'Append'. Once sequences have all been either assigned or rejected, the 'Close submission' button will be displayed. Click this to close the submission. The submitter will be notified of their submission status.

## PubMLST

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Submissions &gt; Curate submission



## Curate submission

Submission: BIGSdb\_20200723194830\_018868\_29257

## Summary

type: alleles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-23  
 status: pending  
 locus: NEIS0001 (lpxC)  
 sequences: 3   
 technology: Illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

## Sequences

Identifier	Length	Sequence	Complete CDS	Status	Query	Assigned allele
UK322	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected	Q	
UK323	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected	Q	
UK347	924	ATGCTGCAAGAAGACTTTGGC ... ACATCAGAACTTGTGGATAA	✓	rejected	Q	

Mark all: [Pending](#) [Rejected](#) [Update](#)

## Messages

Timestamp	User	Message
2020-07-23 21:42:41+00	Keith Jolley	These sequences are not NEIS0001 alleles.

Message: [Append](#) [Send now](#)

## Archive

Archive of submission and any supporting files:

[Download](#)

## Action

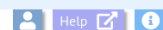
[CLOSE SUBMISSION](#)

## 7.2 Profiles

Click the appropriate submission on the 'Manage submissions' page.

## PubMLST

Home &gt; Organisms &gt; Organism &gt; Neisseria typing &gt; Submissions



## Manage submissions

## Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

## Submission type:

- alleles
- MLST profiles
- Bexsero Antigen Sequence Typing (BAST) profiles
- Conjugative Plasmid profiles
- Cryptic Plasmid profiles
- NG MAST profiles
- beta lactamase plasmid profiles
- isolates (without assembly files) [Link to isolate database](#)
- genomes (isolate records with assembly files) [Link to isolate database](#)

## New allelic profile submissions waiting for curation

Your account is authorized to handle the following submissions:

Submission Id	Submitted	Updated	Submitter	Scheme	Profiles
<b>BIGSdb_20200724071921_021004_01675</b>	2020-07-24	2020-07-24	Joe Bloggs	MLST	3

[Show closed submissions](#)

You will see a table summarizing the profiles in the submission and their current status.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
submitter: Joe Bloggs, University of Oxford, UK  
datestamp: 2020-07-24  
status: pending

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	pending		
UK33	7	56	4	3	2	12	12	pending		
UK34	76	3	5	3	87	43	34	pending		

BATCH CURATE

Mark all: Pending Rejected Update

Messages

Archive

Archive of submission and any supporting files:

Download

Message:

Append

Send now

### 7.2.1 Individual profile curation

Individual profiles can be curated singly by clicking the ‘Curate’ links next to the profile in the table.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
submitter: Joe Bloggs, University of Oxford, UK  
datestamp: 2020-07-24  
status: pending

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	pending		
UK33	7	56	4	3	2	12	12	pending		
UK34	76	3	5	3	87	43	34	pending		

BATCH CURATE

Mark all: Pending Rejected Update

Messages

Archive

Archive of submission and any supporting files:

Download

Message:

Append

Send now

Clicking this link takes you to the curation interface *single profile upload page*. The upload form will be filled with details from the submission.

PubMLST

Home > Organisms > Organism > Neisseria typing > Add new profile

Help

## Add new MLST profile

Please fill in the fields below - required fields are marked with an exclamation mark (!).

**Record**

ST: ! 15581

abcZ: ! 43

adk: ! 2

aroE: ! 12

fumC: ! 32

gdh: ! 32

pdhC: ! 3

pgm: ! 2

sender: ! Bloggs, Joe (jbloggs)

clonal\_complex:

curator: ! Keith Jolley (keith)

date\_entered: 2020-07-24

datestamp: ! 2020-07-24

PubMed ids:

**Action**

RESET SUBMIT


Clicking 'Submit' from this form will define the new profile and add it to the database. A link on the confirmation page will take you back to the submission management page.

PubMLST



Home > Organisms > Organism > Neisseria typing > Add new profile

Help

## Add new MLST profile

 ST-15581 added.

Don't forget to [close the submission!](#)

You will find that the status of the newly assigned profile has changed in the summary table. The assigned value and status are determined on display and should always reflect the live database values.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
submitter: Joe Bloggs, University of Oxford, UK  
timestamp: 2020-07-24  
status: pending

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	assigned		15581
UK33	7	56	4	3	2	12	12	pending		
UK34	76	3	5	3	87	43	34	pending		

Mark all: Pending Rejected Update

**BATCH CURATE**

Messages

Message: Append Send now

Archive

Archive of submission and any supporting files:

Download

## 7.2.2 Batch profile curation

Often, you will want to batch upload submitted profiles. This can be done by clicking the ‘Batch curate’ button.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
submitter: Joe Bloggs, University of Oxford, UK  
timestamp: 2020-07-24  
status: pending

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	assigned		15581
UK33	7	56	4	3	2	12	12	pending		
UK34	76	3	5	3	87	43	34	pending		

Mark all: Pending Rejected Update

**BATCH CURATE**

Messages

Message: Append Send now

Archive

Archive of submission and any supporting files:

Download

This takes you to the *batch profile upload page* in the curators’ interface.

The upload form will be filled with details from the submission.

PubMLST
Home > Organisms > Organism > Neisseria typing > Batch add new MLST profiles - Neisseria typing
Help

## Batch insert MLST profiles

### Instructions

This page allows you to upload profiles as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- You can choose whether or not to include a ST field - if it is omitted, the next available ST will be used automatically. If however, you include it in the header line, then you must also provide it for each profile record.

### Templates

### Upload

Please paste in tab-delimited text (Include a field header line)

abcZ	adk	aroE	fumC	gdh	pdhC	pgm
7	56	4	3	2	12	12
76	3	5	3	87	43	34

#### Parameters

Sender: Bloggs, Joe (jbloggs)

Value will be overridden if you include a sender field in your pasted data.

☐ Ignore previously defined profiles
☐ Ignore duplicate profiles

#### Action

RESET
SUBMIT

After upload, a link on the confirmation page leads back to the submission management page.

PubMLST
Home > Organisms > Organism > Neisseria typing > Batch add new MLST profiles - Neisseria typing
Help

## Batch insert MLST profiles

Profiles added.

Don't forget to [close the submission!](#)

The status of the profiles should reflect their newly assigned status.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Help

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-24  
 status: pending

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	assigned		15581
UK33	7	56	4	3	2	12	12	assigned		15582
UK34	76	3	5	3	87	43	34	assigned		15583

Messages

Archive

Archive of submission and any supporting files:

Download

Action

CLOSE SUBMISSION

### 7.2.3 Rejecting profiles

Sometimes you may need to reject all, or some of, the profiles in the submission. This may be because isolate data had not been made available, against the policy of the database. You can do this by changing the value in the status dropdown box next to each profile. Click 'Update' to make the change.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Help

## Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-24  
 status: pending  
 outcome: accepted - data uploaded

Profiles

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	rejected		
UK33	7	56	4	3	2	12	12	rejected		
UK34	76	3	5	3	87	43	34	rejected		

BATCH CURATE

Mark all: Pending Rejected **Update**

Messages

Archive

Archive of submission and any supporting files:

Download

Message: Append Send now

## 7.2.4 Requesting additional information

You can send a message to the submitter by entering it in the Messages box and clicking ‘Send now’. This will append a message to the submission and send an update to the submitter so that they can respond.

## 7.2.5 Closing the submission

You can add a message to the submitter by entering it in the message box and clicking ‘Append’. Once profiles have all been either assigned or rejected, the ‘Close submission’ button will be displayed. Click this to close the submission. The submitter will be notified of their submission status.

PubMLST

Home > Organisms > Organism > Neisseria typing > Submissions > Curate submission

Help

### Curate submission

Submission: BIGSdb\_20200724071921\_021004\_01675

Summary

type: profiles  
submitter: Joe Bloggs, University of Oxford, UK  
datestamp: 2020-07-24  
status: pending

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
UK32	43	2	12	32	32	3	2	rejected	Q	
UK33	7	56	4	3	2	12	12	rejected	Q	
UK34	76	3	5	3	87	43	34	rejected	Q	

Mark all: Pending Rejected Update

Messages

Timestamp	User	Message
2020-07-24 06:33:44+00	Keith Jolley	Please make a corresponding submission to the isolate database. New STs cannot be assigned without this.

Message: Append Send now

Archive

Action

Archive of submission and any supporting files:

Download TAR

CLOSE SUBMISSION

## 7.3 Isolates

Clicking the appropriate submission on the ‘Manage submissions’ page.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- [isolates](#) (without assembly files)
- [genomes](#) (isolate records with assembly files)

### New isolate submissions waiting for curation

Your account is authorized to handle the following submissions:

Submission id	Submitted	Updated	Submitter	Isolates
<a href="#">BIGSdb_20200724074545_007431_68656</a>	2020-07-24	2020-07-24	Joe Bloggs	2

Show closed submissions

You will see a table summarizing the submission.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions > Curate submission

## Curate submission

### Submission: BIGSdb\_20200724074545\_007431\_68656

#### Summary

type: isolates  
 submitter: [Joe Bloggs](#), University of Oxford, UK  
 datestamp: 2020-07-24  
 status: pending

#### Isolates

isolate	country	year	disease	species	serogroup	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	PorA VR1	PorA VR2	FetA VR	ST (MLST)
UK322	UK	2020	meningitis and septicaemia	Neisseria meningitidis	B	2	3	4	3	8	4	6	5	2	F1-5	11
UK325	UK	2020	septicaemia	Neisseria meningitidis	B	2	3	4	3	8	4	6	5-1	2	F1-5	11

**BATCH CURATE**

Record status: pending **Update**

#### Messages

Archive

Archive of submission and any supporting files:

[Download](#)

Message:  **Append** **Send now**

Click the 'Batch curate' button.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions > Curate submission

## Curate submission

Submission: BIGSdb\_20200724074545\_007431\_68656

**Summary**

type: isolates  
 submitter: Joe Bloggs, University of Oxford, UK  
 datestamp: 2020-07-24  
 status: pending

**Isolates**

isolate	country	year	disease	species	serogroup	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	PorA_VR1	PorA_VR2	FetA_VR	ST (MLST)
UK322	UK	2020	meningitis and septicaemia	Neisseria meningitidis	B	2	3	4	3	8	4	6	5	2	F1-5	11
UK325	UK	2020	septicaemia	Neisseria meningitidis	B	2	3	4	3	8	4	6	5-1	2	F1-5	11

Record status: pending

**BATCH CURATE**

**Messages**

Archive

Archive of submission and any supporting files:

Download

Message:

This will take you to the *batch isolate upload page* in the curators' interface.

The upload form will be filled with details from the submission.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add isolate records

## Batch insert isolates

**Instructions**

This page allows you to upload isolate data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- Optionally enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- Optionally enter references for your isolates as a semi-colon (;) separated list of PubMed ids (non-integer ids will be ignored).
- You can also upload allele fields along with the other isolate data - simply create a new column with the locus name (see the 'allowed\_loci' tab in the Excel template for locus names). These will be added with a confirmed status and method set as 'manual'.
- You can choose whether or not to include an id number field - if it is omitted, the next available id will be used automatically.

**Templates**

Check the [description of database fields](#) for help with filling in the template.

**Upload**

Please select the sender from the list below:

Bloggs, Joe (jbloggs)

Paste in tab-delimited text (Include a field header line).

isolate	country	year	disease	species	serogroup	abcZ	adk	aroE
fumC	gdh	pdhC	pgm	PorA_VR1	PorA_VR2	FetA_VR	Neisseria meningitidis	B
UK322	UK	2020	meningitis and septicaemia	Neisseria meningitidis	B	2	3	4
2	3	4	3	8	4	6	5	2
UK325	UK	2020	septicaemia	Neisseria meningitidis	B	2	3	4
4	3	8	4	6	5-1	2	F1-5	3


Click submit to check and then import if there are no errors.




After upload, a link on the confirmation page leads back to the submission management page.

PubMLST

Home > Organisms > Neisseria spp. > Neisseria isolates > Batch add isolate records

Batch insert isolates

 Database updated.  
Don't forget to [close the submission!](#)

**Note:** Depending on the database policy, definitions of new scheme profiles, e.g. for MLST, may require submission of representative isolate records. Where this is the case, the curator will need to extract the new profile from the submitted record. The tab-delimited isolate text file can be downloaded from the archive of supporting files linked to the submission and used directly for *batch adding new profiles*. Alternatively, the curator could use the *Export functionality* of the database to generate the file required for batch profile definition after upload of the isolate data.

### 7.3.1 Requesting additional information

You can send a message to the submitter by entering it in the Messages box and clicking 'Send now'. This will append a message to the submission and send an update to the submitter so that they can respond.

### 7.3.2 Closing the submission

You can add a message to the submitter by entering it in the message box and clicking 'Append'.

The 'Close submission' button will now appear. Click this to close the submission. The submitter will be notified of their submission status.

## Curate submission


Submission: BIGSdb\_20200724074545\_007431\_68656

## Summary

type: isolates  
 submitter: [Joe Bloggs](#), University of Oxford, UK  
 datestamp: 2020-07-24  
 status: pending  
 outcome: accepted - data uploaded

## Isolates

isolate	country	year	disease	species	serogroup	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	PorA_VR1	PorA_VR2	FetA_VR	ST (MLST)
UK322	UK	2020	meningitis and septicaemia	<i>Neisseria meningitidis</i>	B	2	3	4	3	8	4	6	5	2	F1-5	11
UK325	UK	2020	septicaemia	<i>Neisseria meningitidis</i>	B	2	3	4	3	8	4	6	5-1	2	F1-5	11

Record status: pending  [Update](#)

## Messages

Timestamp	User	Message
2020-07-24 06:59:59+00	Keith Jolley	Isolate 'UK322' uploaded - id: 80312. Isolate 'UK325' uploaded - id: 80313.

## Archive

Archive of submission and any supporting files:

[Download](#) 

## Action

[CLOSE SUBMISSION](#)Message: [Append](#) [Send now](#)

## OFFLINE CURATION TOOLS

### 8.1 Automated offline sequence tagging

Sequence tagging is the process of identifying alleles by scanning the sequence bin linked to an isolate record. Loci need to be defined in an external sequence definition database that contains the sequences for known alleles. The tagging function uses BLAST to identify sequences and will tag the specific sequence region with locus information and an allele designation if a matching allele is identified by reference to an external database.

There is a script called ‘autotag.pl’ in the BIGSdb package. This can be used to tag genome sequences from the command line.

Before autotag.pl can be run for the first time, a log file needs to be created. This can be created if it doesn’t already exist with the following:

```
sudo touch /var/log/bigsdb_scripts.log
sudo chown bigsdb /var/log/bigsdb_scripts.log
```

The autotag.pl script should be installed in /usr/local/bin. It is run as follows:

```
autotag.pl --database <database configuration>
```

where <database configuration> is the name used for the argument ‘db’ when using the BIGSdb application.

If you have multiple processor cores available, use the `--threads` option to set the number of jobs to run in parallel. Isolates for scanning will be split among the threads.

The script must be run by a user that can both write to the log file and access the databases, e.g. the ‘bigsdb’ user (see ‘Setting up the offline job manager’).

A full list of options can be found by typing:

```
autotag.pl --help

NAME
    autotag.pl - BIGSdb automated allele tagger

SYNOPSIS
    autotag.pl --database NAME [options]

OPTIONS
    -0, --missing
        Marks missing loci as provisional allele 0. Sets default word size to 15.
```

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```

-d, --database NAME
    Database configuration name.

-e, --exemplar
    Only use alleles with the 'exemplar' flag set in BLAST searches to identify
    locus within genome. Specific allele is then identified using a database
    lookup. This may be quicker than using all alleles for the BLAST search,
    but will be at the expense of sensitivity. If no exemplar alleles are set
for a locus then all alleles will be used. Sets default word size to 15.

-f --fast
    Perform single BLAST query against all selected loci together. This will
    take longer to return any results but the overall scan should finish
    quicker. This method will also use more memory - this can be used with
    --exemplar to mitigate against this.

-h, --help
    This help page.

-i, --isolates LIST
    Comma-separated list of isolate ids to scan (ignored if -p used).

--isolate_list_file FILE
    File containing list of isolate ids (ignored if -i or -p used).

-I, --exclude_isolates LIST
    Comma-separated list of isolate ids to ignore.

-l, --loci LIST
    Comma-separated list of loci to scan (ignored if -s used).

-L, --exclude_loci LIST
    Comma-separated list of loci to exclude

-m, --min_size SIZE
    Minimum size of seqbin (bp) - limit search to isolates with at least this
    much sequence.

-n, --new_only
    New (previously untagged) isolates only. Combine with --new_max_alleles
if required.

--new_max_alleles ALLELES
    Set the maximum number of alleles that can be designated or sequences
    tagged before an isolate is not considered new when using the --new_only
    option.

-o, --order
    Order so that isolates last tagged the longest time ago get scanned first
    (ignored if -r used).

--only_already_tagged

```

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Only check loci that already have a tag present (but no allele designation). This must be combined **with** the `--already_tagged` option **or** no loci will **match**. This option **is** used to perform a catch-up scan where a curator has previously tagged sequence regions prior to alleles being defined, without the need to scan **all** missing loci.

`-p, --projects LIST`  
Comma-separated **list** of project isolates to scan.

`-P, --exclude_projects LIST`  
Comma-separated **list** of projects whose isolates will be excluded.

`-q, --quiet`  
Only error messages displayed.

`-r, --random`  
Shuffle order of isolate ids to scan.

`--reuse_blast`  
Reuse the BLAST database **for** every isolate (when running `--fast` option). All loci will be scanned rather than just those missing **from an** isolate. Consequently, this may be slower **if** isolates have already been scanned, **and for** the first isolate scanned by a thread. On larger schemes, such **as** wgMLST, **or** when isolates have **not** been previously scanned, setting up the BLAST database can take a significant amount of time, so this may be quicker. This option **is** always selected **if** `--new_only` **is** used.

`-R, --locus_regex REGEX`  
Regex **for** locus names.

`-s, --schemes LIST`  
Comma-separated **list** of scheme loci to scan.

`-t, --time MINS`  
Stop after t minutes.

`--threads THREADS`  
Maximum number of threads to use.

`-T, --already_tagged`  
Scan even when sequence tagged (no designation).

`-v, --view VIEW`  
Isolate database view (overrides value **set in** config.xml).

`-w, --word_size SIZE`  
BLASTN word size.

`-x, --min ID`  
Minimum isolate **id**.

`-y, --max ID`

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Maximum isolate **id**.

## 8.2 Defining exemplar alleles

Exemplar alleles are a subset of the total number of alleles defined for a locus that encompass the known diversity within a specified identity threshold. They can be used to speed up *autotagging* as the BLAST queries are performed against exemplars to identify the locus region in the genome followed by a direct database lookup of the sequence found to identify the exact allele found. This is usually combined with the autotagger `-fast` option.

Once exemplars have been defined you may also wish to set the `fast_scan="yes"` option in the `config.xml` file. This enables their use for scanning within the web curators' interface.

There is a script called 'find\_exemplars.pl' in the BIGSdb scripts/maintenance directory.

A full list of options can be found by typing:

```
find_exemplars.pl --help

NAME
    find_exemplars.pl - Identify and mark exemplar alleles for use
    by tagging functions

SYNOPSIS
    find_exemplars.pl --database NAME    [options]

OPTIONS

--database NAME
    Database configuration name.

--datatype DNA|peptide
    Only define exemplars for specified data type (DNA or peptide)

--exclude_loci LIST
    Comma-separated list of loci to exclude

--help
    This help page.

--loci LIST
    Comma-separated list of loci to scan (ignored if -s used).

--locus_regex REGEX
    Regex for locus names.

--schemes LIST
    Comma-separated list of scheme loci to scan.

--update
    Update exemplar flags in database.
```

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```
--variation DISSIMILARITY
    Value for percentage identity variation that exemplar alleles
    cover (smaller value will result in more exemplars). Default: 10.
```

## 8.3 Automated offline allele definition

There is a script called 'scannew.pl' in the BIGSdb scripts/automation directory. This can be used to identify new alleles from the command line. This can (optionally) upload these to a sequence definition database.

Before scannew.pl can be run for the first time, a log file needs to be created. This can be created if it doesn't already exist with the following:

```
sudo touch /var/log/bigsdb_scripts.log
sudo chown bigsdb /var/log/bigsdb_scripts.log
```

The autotag.pl script should be installed in /usr/local/bin. It is run as follows:

```
scannew.pl --database <database configuration>
```

where <database configuration> is the name used for the argument 'db' when using the BIGSdb application.

If you have multiple processor cores available, use the `--threads` option to set the number of jobs to run in parallel. Loci for scanning will be split among the threads.

The script must be run by a user that can both write to the log file and access the databases, e.g. the 'bigsdb' user (see 'Setting up the offline job manager').

A full list of options can be found by typing:

```
scannew.pl --help

NAME
    scannew.pl - BIGSdb automated allele definer

SYNOPSIS
    scannew.pl --database NAME [options]

OPTIONS
    -a, --assign
        Assign new alleles in definitions database.

    --allow_frameshift
        Allow sequences to contain a frameshift so that the length is not a
        multiple of 3, or an internal stop codon. To be used with
        --coding_sequences option to allow automated curation of pseudogenes.
        New alleles assigned will be flagged either 'frameshift' or 'internal stop
        codon' if appropriate. Essentially, combining these two options only
        checks that the sequence starts with a start codon and ends with a stop
        codon.

    --allow_subsequences
        Allow definition of sub- or super-sequences. By default these will not
```

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```
be assigned.

-A, --alignment INT
    Percentage alignment (default: 100).

-B, --identity INT
    Percentage identity (default: 99).

-c, --coding_sequences
    Only return complete coding sequences.

-d, --database NAME
    Database configuration name.

-h, --help
    This help page.

-i, --isolates LIST
    Comma-separated list of isolate ids to scan (ignored if -p used).

--isolate_list_file FILE
    File containing list of isolate ids (ignored if -i or -p used).

-I, --exclude_isolates LIST
    Comma-separated list of isolate ids to ignore.

-l, --loci LIST
    Comma-separated list of loci to scan (ignored if -s used).

-L, --exclude_loci LIST
    Comma-separated list of loci to exclude.

-m, --min_size SIZE
    Minimum size of seqbin (bp) - limit search to isolates with at least this
    much sequence.

-n, --new_only
    New (previously untagged) isolates only.

-o, --order
    Order so that isolates last tagged the longest time ago get scanned first
    (ignored if -r used).

-p, --projects LIST
    Comma-separated list of project isolates to scan.

-P, --exclude_projects LIST
    Comma-separated list of projects whose isolates will be excluded.

-r, --random
    Shuffle order of isolate ids to scan.
```

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```

-R, --locus_regex REGEX
    Regex for locus names.

-s, --schemes LIST
    Comma-separated list of scheme loci to scan.

-t, --time MINS
    Stop after t minutes.

--threads THREADS
    Maximum number of threads to use.

--type_alleles
    Only use alleles with the 'type_allele' flag set to identify locus.
    If a partial match is found then a full database lookup will be performed
    to identify any known alleles. Using this option will constrain the search
    space so that allele definitions don't become more variable over time. Note
    that you must have at least one allele defined as a type allele for a locus
    if you use this option otherwise you will not find any matches!

-T, --already_tagged
    Scan even when sequence tagged (no designation).

-v, --view VIEW
    Isolate database view (overrides value set in config.xml).

-w, --word_size SIZE
    BLASTN word size.

-x, --min ID
    Minimum isolate id.

-y, --max ID
    Maximum isolate id.

```

## 8.4 Calculating assembly stats

Basic assembly statistics are calculated automatically by the database engine as contigs are added to the sequence bin. These include the number of contigs, total length and the N50 value. Some calculations, such as %GC, number of Ns, and the number of gaps however, require offline analysis since these involve inspecting the nucleotide content of each contig. These can be calculated by running the `update_assembly_stats.pl` script. You can choose to run this against all databases on the system or against a specific database.

Only one copy of the script can run at a time, but it will stop gracefully if it detects another copy running, so it is recommended that the script is run regularly using a CRON job and the `-quiet` option. This ensures that records are updated shortly after they have been uploaded.

Once calculated, all assembly statistics can then be *used in isolate queries*.

A full list of options can be found by typing:

```
update_assembly_stats.pl --help
```

**NAME**

update\_assembly\_stats.pl - Perform/update calculation of assembly GC, N **and** gap stats.

**SYNOPSIS**

update\_assembly\_stats.pl [options]

**OPTIONS**

--database DATABASE CONFIG

Database configuration name. If **not** included then **all** isolate databases defined on the system will be checked.

--exclude CONFIG NAMES

Comma-separated **list** of config names to exclude.

--help

This help page.

--quiet

Only show errors.

--refresh\_days DAYS

Refresh records last analysed longer than the number of days **set**. By default, only records that have **not** been analysed will be checked.

## 8.5 Predicting species based on rMLST analysis

The *rMLST plugin* predicts species based on matches to rMLST alleles exclusively found in a particular species. It uses the PubMLST API to query either a genome sequence or rMLST allele designations to identify the species. When the analysis is run using the plugin, the results are also stored with the isolate record and can then be displayed within the isolate information page. This analysis can also be run offline using the update\_rmlst\_species.pl script.

Only one copy of the script can run at a time, but it will stop gracefully if it detects another copy running, so it is recommended that the script is run regularly using a CRON job and the `-quiet` option. This ensures that records are updated shortly after they have been uploaded.

A full list of options can be found by typing:

```
update_rmlst_species.pl --help
```

**NAME**

update\_rmlst\_species.pl - Perform/update species **id** check

**SYNOPSIS**

update\_rmlst\_species.pl [options]

**OPTIONS**

--database DATABASE CONFIG

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```

Database configuration name. If not included then all isolate databases
defined on the system will be checked.

--exclude CONFIG NAMES
    Comma-separated list of config names to exclude.

--help
    This help page.

--last_run_days DAYS
    Only run for a particular isolate when the analysis was last performed
    at least the specified number of days ago.

--quiet
    Only show errors.

--refresh_days DAYS
    Refresh records last analysed longer that the number of days set. By
    default, only records that have not been analysed will be checked.

```

## 8.6 Cleanly interrupting offline curation

Sometimes you may wish to stop running autotagger or allele autodefiner jobs as they can be run for a long time and as CRON jobs. If these are running in single threaded mode, the easiest way is to simply send a kill signal to the process, i.e. identify the process id using 'top', e.g. 23232 and then

```
kill 23232
```

The scripts should respond to this signal within a couple of seconds, clean up all their temporary files and write the history log (where appropriate). Do not use 'kill -9' as this will terminate the processes immediately and not allow them to clean up.

If these scripts are running using multiple threads, then you need to cleanly kill each of these. The simplest way to terminate all autotagger jobs is to type

```
pkill autotag
```

The parent process will wait for all forked processes to cleanly terminate and then exit itself.

Similarly, to terminate all allele autodefiner jobs, type

```
pkill scannew
```

## 8.7 Uploading contigs from the command line

There is a script called `upload_contigs.pl` in the BIGSdb `scripts/maintenance` directory. This can be used to upload contigs from a local FASTA file for a specified isolate record.

The `upload_contigs.pl` script should be installed in `/usr/local/bin`. It is run as follows:

```
upload_contigs.pl --database <NAME> --isolate <ID> --file <FILE>
                  --curator <ID> --sender <ID>
```

The script must be run by a user who has the appropriate database permissions and the local configuration settings should be modified to match the database user account to be used. The default setting uses the 'apache' user which is used by the BIGSdb web interface.

A full list of options can be found by typing:

```
upload_contigs.pl --help

NAME
    upload_contigs.pl - Upload contigs to BIGSdb isolate database

SYNOPSIS
    upload_contigs.pl --database NAME --isolate ID --file FILE
                      --curator ID --sender ID [options]

OPTIONS
-a, --append
    Upload contigs even if isolate already has sequences in the bin.

-c, --curator ID
    Curator id number.

-d, --database NAME
    Database configuration name.

-f, --file FILE
    Full path and filename of contig file.

-h, --help
    This help page.

-i, --isolate ID
    Isolate id of record to upload to.

-m, --method METHOD
    Method, e.g. 'Illumina', default 'unknown'.

--min_length LENGTH
    Exclude contigs with length less than value.

-s, --sender ID
    Sender id number.
```

## DEFINITION DOWNLOADS

The sequence definition database defines alleles, i.e. links an allele identifier to a sequence. It also defines scheme, e.g. MLST, profiles.

### 9.1 Allele sequence definitions

Click the ‘Allele sequences’ link in the ‘Downloads’ section.

BIGSdb

Home > Organisms > Organism > Neisseria typing

*Neisseria* typing database

Query a sequence

**Sequence query**  
Query a single sequence or whole genome assembly to identify allelic matches.

**Batch sequence query**  
Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

**Sequence attribute search**  
Find alleles by matching criteria (all loci together)

**Locus-specific sequence attribute search**  
Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

**Allelic profile query**  
Search, browse or enter list of profiles

**Search by combinations of alleles**  
This can include partial matches to find related profiles.

**Batch profile query**  
Lookup multiple allelic profiles together.

LOG IN

SUBMISSIONS

DOWNLOADS

Allele sequences  
Allelic profiles

EXPORT

ANALYSIS

CUSTOMISE

INFORMATION

ISOLATES

Depending on the database, you may see either a hierarchical scheme tree or a table of loci. You can choose to display links either by scheme using the scheme tree, as an alphabetical list or a page of all schemes, by selecting the appropriate link at the top of the page.

## 9.1.1 Scheme tree

BIGSdb

Home > Organisms > Organism > Neisseria typing > Download alleles

Help

### Download allele sequences

Select loci by scheme | **Alphabetical list** | All loci by scheme

Click within the tree to display details of loci belonging to schemes or groups of schemes - clicking a group folder will display the loci for all schemes within the group and any subgroups. Click the nodes to expand/collapse.

You can drill down through the tree by clicking branch nodes. Clicking the labels of internal nodes will display tables of all schemes belonging to that scheme group. Clicking the labels of terminal nodes will display that single scheme table.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Download alleles

Help

### Download allele sequences

Select loci by scheme | Alphabetical list | **All loci by scheme**








Click within the tree to display details of loci belonging to schemes or groups of schemes - clicking a group folder will display the loci for all schemes within the group and any subgroups. Click the nodes to expand/collapse.

#### MLST

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison	2020-06-23
adk		DNA	841	Fixed: 465 bp	464	465		O. Harrison	2020-07-14
aroE		DNA	1118	Fixed: 490 bp	489	493		O. Harrison	2020-06-12
fumC		DNA	1184	Fixed: 465 bp	463	467		O. Harrison	2020-06-12
gdh		DNA	1156	Fixed: 501 bp	501	513		O. Harrison	2020-07-03
pdhC		DNA	1096	Fixed: 480 bp	480	503		O. Harrison	2020-06-04
pgm		DNA	1172	Fixed: 450 bp	447	489		O. Harrison	2020-06-12

Click the download link for the required locus

## MLST

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison	2020-06-23
adk		DNA	841	Fixed: 465 bp	464	465		O. Harrison	2020-07-14
aroE		DNA	1118	Fixed: 490 bp	489	493		O. Harrison	2020-06-12
fumC		DNA	1184	Fixed: 465 bp	463	467		O. Harrison	2020-06-12
gdh		DNA	1156	Fixed: 501 bp	501	513		O. Harrison	2020-07-03
pdhC		DNA	1096	Fixed: 480 bp	480	503		O. Harrison	2020-06-04
pgm		DNA	1172	Fixed: 450 bp	447	489		O. Harrison	2020-06-12

Alleles will be downloaded in FASTA format, e.g.

```
>fumC_1
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCGCTGCGGT
TTGGGCGAAATCAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTTCGGCAACGACGTT
ACCATCGGTATGGCGGGCGCGTCGGGCAATTCGAGCTGAACGTCTATATGCCCGTCATC
GCCTACAACCTCTTGCAATCCATCCGCCTGTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCGTCGGCATTAACCCGTACCGGAAAAAATCGACTATTCCTGCACCATTC
CTGATGCTCGTTACCGCGTTAAACCGCAAAAATCGGTTACGAAAAC

>fumC_2
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCGCTGCGGT
TTGGGCGAAATCAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTTCGGCAACGACGTT
ACCATCGGCATGGCGGGCGCGTCGGGCAATTCGAGCTGAACGTCTATATGCCCGTTATC
GCCTACAACCTCTTGCAATCCATCCGCCTCTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCATCGGCATCGAACCCGTACCGGAAAAAATCGACTATTCCTGCACCATTC
CTGATGCTCGTTACCGCGTTAAACCGCAAAAATCGGTTACGAAAAC

>fumC_3
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCGCTGCGGT
TTGGGCGAAATCAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTTCGGCAACGACGTT
ACCATCGGCATGGCGGGCGCGTCGGGCAATTCGAGCTGAACGTCTATATGCCCGTTATC
GCCTACAACCTCTTGCAATCCATCCGCCTGTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCGTCGGCATCGAACCCGTACCGGAAAAAATCGACTATTCCTGCACCATTC
CTGATGCTGGTTACTGCGTTAAACCGTAAAAATCGGCTACGAAAAC
```

## 9.1.2 Alphabetical list

Loci can be displayed in an alphabetical list. Loci will be grouped in to tables by initial letter. If common names are set for loci, they will be listed by both primary and common names.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Download alleles

Help

### Download allele sequences

Select loci by scheme | Alphabetical list | All loci by scheme

2

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Last updated
23S_rRNA		DNA	1101	Variable: No limits set	2884	2966		2019-08-23

A

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
ArsR [NEIS1769]		DNA	195	Variable: No limits set	270	291	ArsR family transcriptional regulator		2020-05-22
AsnC [NEIS1566]		DNA	394	Variable: No limits set	459	471	transcription regulator AsnC		2020-03-20
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison	2020-06-23
abcZ [NEIS1015]		DNA	1263	Variable: No limits set	1890	1944	ABC transporter ATP-binding protein		2020-07-10
aceF [NEIS1279]		DNA	1550	Variable: (1563 min; 1641 max)	1533	1641	dihydropolipamide acetyltransferase (EC 2.3.1.12)		2020-07-10
ackA2 [NEIS1727]		DNA	762	Variable: No limits set	1197	1212	acetate kinase		2020-06-17
acnA [NEIS1729]		DNA	1211	Variable: No limits set	2592	2616	aconitate hydratase 1 (EC 4.2.1.3)		2020-05-20
acnB [NEIS1492]		DNA	1550	Variable: No limits set	2580	2625	aconitate hydratase 2 (EC 4.2.1.3)		2020-06-18
adhA [NEIS0486]		DNA	1532	Variable: No limits set	1035	1047	alcohol dehydrogenase		2020-05-21
adhC [NEIS1741]		DNA	600	Variable: No limits set	1110	1140	alcohol dehydrogenase		2020-05-22

Click the download links for the required locus.

## 9.1.3 All loci by scheme

Loci can also be displayed by scheme with all schemes displayed.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Download alleles

Help

### Download allele sequences

Select loci by scheme | Alphabetical list | All loci by scheme

#### MLST

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison	2020-06-23
adk		DNA	841	Fixed: 465 bp	464	465		O. Harrison	2020-07-14
aroE		DNA	1118	Fixed: 490 bp	489	493		O. Harrison	2020-06-12
fumC		DNA	1184	Fixed: 465 bp	465	467		O. Harrison	2020-06-12
gdh		DNA	1156	Fixed: 501 bp	501	513		O. Harrison	2020-07-03
pdhC		DNA	1096	Fixed: 480 bp	480	503		O. Harrison	2020-06-04
pgm		DNA	1172	Fixed: 450 bp	447	489		O. Harrison	2020-06-12

#### Finotyping antigens

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
PorA_VR1		peptide	360	Variable: No limits set	9	31	PorA variable region 1		2020-06-30
PorA_VR2		peptide	988	Variable: No limits set	5	41	PorA variable region 2		2020-06-15
FetA_VR		peptide	655	Variable: No limits set	20	69		I. Feavers	2020-06-08

#### rplF species








Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
rplF		DNA	257	Fixed: 413 bp	413	413	50S ribosomal protein L6 fragment	E. Watkins	2020-05-18



Click the green download links for the required locus.

## 9.1.4 Download locus table

The locus table can be downloaded in tab-delimited text or Excel formats by clicking the links following table display.

MLST

Locus	Download	Type	Alleles	Length (setting)	Min length	Max length	Full name/product	Curator(s)	Last updated
abcZ		DNA	1077	Fixed: 433 bp	433	434		O. Harrison	2020-06-23
adk		DNA	841	Fixed: 465 bp	464	465		O. Harrison	2020-07-14
aroE		DNA	1118	Fixed: 490 bp	489	493		O. Harrison	2020-06-12
fumC		DNA	1184	Fixed: 465 bp	463	467		O. Harrison	2020-06-12
gdh		DNA	1156	Fixed: 501 bp	501	513		O. Harrison	2020-07-03
pdhC		DNA	1096	Fixed: 480 bp	480	503		O. Harrison	2020-06-04
pgm		DNA	1172	Fixed: 450 bp	447	489		O. Harrison	2020-06-12

## 9.2 Scheme profile definitions

Scheme profiles, e.g. those for MLST, can be downloaded by clicking the appropriate link on the contents page.

BIGSdb

Home > Organisms > Organism > Neisseria typing

### Neisseria typing database

Query a sequence

[Sequence query](#)

Query a single sequence or whole genome assembly to identify allelic matches.

[Batch sequence query](#)

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

[Sequence attribute search](#)

Find alleles by matching criteria (all loci together)

[Locus-specific sequence attribute search](#)

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

[Allelic profile query](#)

Search, browse or enter list of profiles

[Search by combinations of alleles](#)

This can include partial matches to find related profiles.

[Batch profile query](#)

Lookup multiple allelic profiles together.

[LOG IN](#)

[SUBMISSIONS](#)

[DOWNLOADS](#) —

Allele sequences

[Allelic profiles](#)

[EXPORT](#) +

[ANALYSIS](#) +

[CUSTOMISE](#) +

[INFORMATION](#) +

[ISOLATES](#)












If there is only one scheme available, the link will directly download the profiles. If multiple schemes are available, the link will take you to an intermediate page from where you can select the scheme to download.

## BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Download scheme profiles](#)

## Download scheme profiles

Schemes are collections of loci. They may be indexed, in which case they have a primary key field that identifies unique combinations of alleles. The following schemes are indexed.

Name	Download	Profiles	Description	Curator(s)	Last updated
MLST		15,577		Odile Harrison, Keith Jolley	2020-07-14
rpIF species		211		James Bray, Ellie Watkins, Julia Bennett, Kanny Diallo	2019-02-06
Bexsero Antigen Sequence Typing (BAST)		3,755	Scheme designed for the surveillance of the antigen targets included in Bexsero® (fHbp, PorA, NHBA and NadA) for protective immunity. It is based on deduced peptide sequence variants.	Charlene Rodrigues	2020-07-13
Conjugative Plasmid		242		Ana Cehovin	2018-04-25
Cryptic Plasmid		96		Ana Cehovin	2018-05-15
GC OMV peptide typing		2,283	OMV peptide typing based on most abundant components of gonococcal OMVs	Anastasia Unitt, Odile Harrison	2020-03-31
N. gonorrhoeae cgMLST v1.0		8,453			2020-07-14
N. meningitidis cgMLST v1.0		18,679	This is a core genome scheme containing 1605 loci found to be present in >=95% N. meningitidis isolates.	Holly Bratcher	2020-07-14
NG MAST		19,141	N. gonorrhoeae typing scheme using porB and tpbB fragments. In development, please DO NOT USE		2020-06-25
NG STAR		1,933	Neisseria gonorrhoeae Antimicrobial Sequence Type In development, please DO NOT USE	Odile Harrison	2020-07-14
OMV peptide typing		4,046	OMV peptide typing based on the components of the MeNZB vaccine	Hannah Chan, Charlene Rodrigues	2019-05-15

Profiles will be downloaded in tab-delimited format, e.g.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal_complex
1	1	3	1	1	1	1	3	ST-1 complex/subgroup I/II
2	1	3	4	7	1	1	3	ST-1 complex/subgroup I/II
3	1	3	1	1	1	23	13	ST-1 complex/subgroup I/II
4	1	3	3	1	4	2	3	ST-4 complex/subgroup IV
5	1	1	2	1	3	2	3	ST-5 complex/subgroup III
6	1	1	2	1	3	2	11	ST-5 complex/subgroup III
7	1	1	2	1	3	2	19	ST-5 complex/subgroup III
8	2	3	7	2	8	5	2	ST-8 complex/Cluster A4
9	2	3	8	10	8	5	2	ST-8 complex/Cluster A4
10	2	3	4	2	8	15	2	ST-8 complex/Cluster A4
11	2	3	4	3	8	4	6	ST-11 complex/ET-37 complex
12	4	3	2	16	8	11	20	
13	4	10	15	7	8	11	1	ST-269 complex
14	4	1	15	7	8	11	1	ST-269 complex

## DATA RECORDS

Record pages for different types of data can be accessed following a query by clicking appropriate hyperlinks.

### 10.1 Isolate records

An Isolate record page displays everything known about an isolate.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Isolate information](#)
[Help](#) 

## Full information on isolate M10 240474 (id:18968)

 Projects

This isolate is a member of the following project:

## MRF Meningococcus Genome Library



The MRF Meningococcus Genome Library is a collaboration between Public Health England, the Scottish Haemophilus, Legionella, Meningococcus and Pneumococcus Reference (SHLMR) Laboratory, The Wellcome Trust Sanger Institute and the University of Oxford, funded by the Meningitis Research Foundation.

Use of the MRF Genome Library data **must be cited** in any publication or presentation making use of it.

 Provenance/primary metadata

id:	18968	disease:	invasive (unspecified/other)	update history:	<a href="#">223 updates</a> <a href="#">show details</a>
isolate:	M10 240474	species:	Neisseria meningitidis	date entered:	2012-02-15
strain designation:	B: P1.19-1.15-11: F3-9: ST-269 (cc269)	serogroup:	B	datestamp:	2020-02-28
country:	UK [England]	genogroup:	B		
continent:	Europe	capsule group:	B		
region:	South East	ENA run accession:	<a href="#">ERR086224</a> <a href="#">www.ebi.ac.uk</a>		
year:	2010	sender:	Dorothea Hill, University of Oxford, UK		
epidemiological year:	07/2010-06/2011	curator:	Auto Tagger		

 Secondary metadata Vaccines

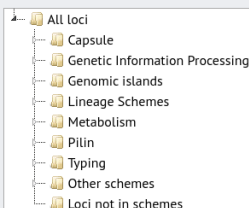
<b>Bexsero reactivity:</b>	cross-reactive 	<b>Trumenba reactivity:</b>	cross-reactive 	<b>Trumenba notes:</b>	fHbp_peptide: 15 is cross-reactive to vaccine variant - data derived from MEASURE assays (PMID:29535195), and SBA assays (PMID:22569484, PMID:22718089, PMID:23352429, PMID:26407272, PMID:26707218, PMID:26803328, PMID:26835974, PMID:27745812, PMID:27846061, PMID:28196734, PMID:28566335, PMID:29236639)
<b>Bexsero notes:</b>	fHbp_peptide: 15 is cross-reactive to vaccine variant - data derived from MATS assays (PMID:23414709, PMID:23588089, PMID:26686998, PMID:26950303, PMID:27355628, PMID:28366725, PMID:30135218, PMID:30592763, PMID:31770063)				

 Publications (4)

- Brehony C, Rodrigues CM, Borrow R, Smith A, Cunney R, Moxon ER, Maiden MC (2016). Distribution of Bexsero® Antigen Sequence Types (BASTs) in invasive meningococcal disease isolates: Implications for immunisation. *Vaccine* **34**:4690-7 [2016 isolates](#)
- Hill DM, Lucidarme J, Gray SJ, Newbold LS, Ure R, Brehony C, Harrison OB, Bray JE, Jolley KA, Bratcher HB, Parkhill J, Tang CM, Borrow R, Maiden MC (2015). Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. *Lancet Infect Dis* **15**:1420-8 [899 isolates](#)
- Rodrigues CMC, Chan H, Vipond C, Jolley K, Harrison OB, Wheeler J, Whiting G, Feavers IM, Maiden MCJ (2018). Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. *Wellcome Open Res* **3**:151 [3505 isolates](#)
- Rodrigues CMC, Lucidarme J, Borrow R, Smith A, Cameron JC, Moxon ER, Maiden MCJ (2018). Genomic Surveillance of 4CMenB Vaccine Antigenic Variants among Disease-Causing Neisseria meningitidis Isolates, United Kingdom, 2010-2016. *Emerg Infect Dis* **24**:673-682 [3066 isolates](#)

 Sequence bin

contigs:	275	N50 contig number:	20	N95 contig number:	97
total length:	2,195,045 bp	N50 length (L50):	34,308	N95 length (L95):	3,513
max length:	109,859 bp	N90 contig number:	74	loci tagged:	2,179
mean length:	7,982 bp	N90 length (L90):	6,405		

[Show sequence bin](#)
 Schemes and loci

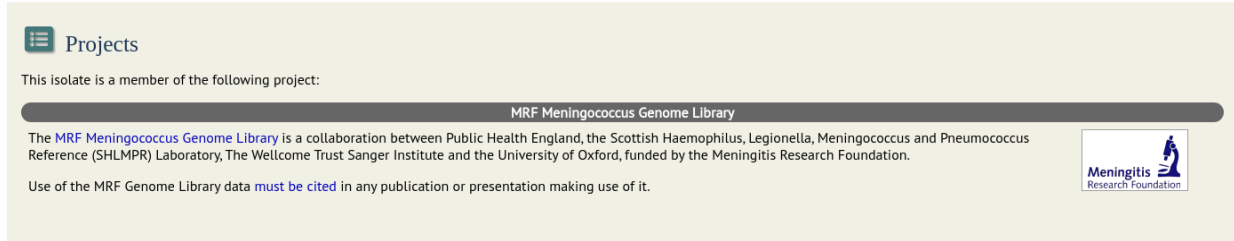
Navigate and select schemes within tree to display allele designations

 Tools

Analysis: [rMLST species id](#) [PCR](#)

Each record will have some or all of the following sections:

### 10.1.1 Projects




**Projects**

This isolate is a member of the following project:

**MRF Meningococcus Genome Library**

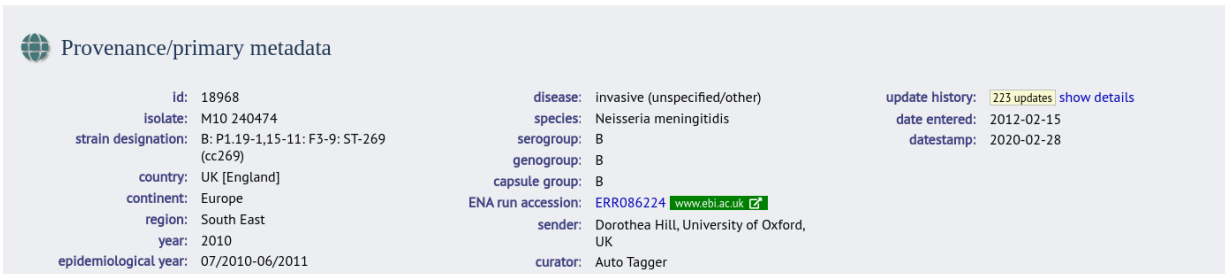
The [MRF Meningococcus Genome Library](#) is a collaboration between Public Health England, the Scottish Haemophilus, Legionella, Meningococcus and Pneumococcus Reference (SHLMRP) Laboratory, The Wellcome Trust Sanger Institute and the University of Oxford, funded by the Meningitis Research Foundation.

Use of the MRF Genome Library data [must be cited](#) in any publication or presentation making use of it.




This displays a list of projects that the isolate is a member of. Only projects that have a full description and the 'isolate\_display' flag in their settings will be displayed.

### 10.1.2 Provenance metadata



**Provenance/primary metadata**

id: 18968	disease: invasive (unspecified/other)	update history: <a href="#">223 updates</a> <a href="#">show details</a>
isolate: M10 240474	species: Neisseria meningitidis	date entered: 2012-02-15
strain designation: B: P1.19-1,15-11: F3-9: ST-269 (cc269)	serogroup: B	timestamp: 2020-02-28
country: UK [England]	genogroup: B	
continent: Europe	capsule group: B	
region: South East	ENA run accession: <a href="#">ERR086224</a> <a href="#">www.ebi.ac.uk</a> 	
year: 2010	sender: Dorothea Hill, University of Oxford, UK	
epidemiological year: 07/2010-06/2011	curator: Auto Tagger	

This section includes:

- provenance fields
- housekeeping data
  - who sent the isolate
  - who last curated
  - record creation times
  - last update times
  - links to update history

The update link displays page with exact times of who and when updated the record.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Isolate information](#)


## Full information on isolate M10 240474 (id:18968)

## Update history

Timestamp	Curator	Action
2020-02-28 12:18	Auto Tagger	NEIS1428: new designation '63' (sequence bin scan) NEIS1428: sequence tagged. Seqbin id: 4957; 28130-30895 (sequence bin scan) NEISp1428: new designation '2' (sequence bin scan) NEISp1428: sequence tagged. Seqbin id: 4957; 28130-30892 (sequence bin scan)
2020-02-28 12:01	Keith Jolley	NEISp1428: designation '2' deleted
2020-02-28 11:55	Keith Jolley	NEIS1428: designation '63' deleted
2019-12-09 14:41	Odile Harrison	NG_porB: designation '34' deleted
2019-08-18 17:48	Auto Tagger	NEIS1338: new designation '1' (sequence bin scan) NEIS1338: sequence tagged. Seqbin id: 4882; 13145-13327 (sequence bin scan)
2019-08-18 17:45	Keith Jolley	NEIS1338: designation '1' deleted
2019-02-16 08:16	Auto Tagger	NG-MAST_porB: new designation '741' (sequence bin scan) NG-MAST_porB: sequence tagged. Seqbin id: 4865; 6602-7091 (sequence bin scan)
2018-12-06 12:57	Holly Bratcher	NEIS2072: sequence tagged. Seqbin id: 4917; -282-311 (sequence bin scan)
2018-10-16 09:36	Auto Tagger	NEIS2583: new designation '71' (sequence bin scan) NEIS2583: sequence tagged. Seqbin id: 4940; 10070-10305 (sequence bin scan) NEIS3171: new designation '12' (sequence bin scan) NEIS3171: sequence tagged. Seqbin id: 4965; 28192-28251 (sequence bin scan)
2018-06-26 10:05	Odile Harrison	NEIS2169: designation '6' deleted
2018-06-16 09:30	Auto Tagger	NEIS2669: new designation '63' (sequence bin scan) NEIS2669: sequence tagged. Seqbin id: 4818; 22479-22907 (sequence bin scan) NEIS2788: new designation '62' (sequence bin scan) NEIS2788: sequence tagged. Seqbin id: 4913; 18651-19082 (sequence bin scan)

## 10.1.3 Publications

## Publications (4)

- Brehony C, Rodrigues CM, Borrow R, Smith A, Cunney R, Moxon ER, Maiden MC (2016). Distribution of Bexsero® Antigen Sequence Types (BASTs) in invasive meningococcal disease isolates: Implications for immunisation. *Vaccine* **34**:4690-7 [2016 isolates](#)
- Hill DM, Lucidarme J, Gray SJ, Newbold LS, Ure R, Brehony C, Harrison OB, Bray JE, Jolley KA, Bratcher HB, Parkhill J, Tang CM, Borrow R, Maiden MC (2015). Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study. *Lancet Infect Dis* **15**:1420-8 [899 isolates](#)
- Rodrigues CMC, Chan H, Vipond C, Jolley K, Harrison OB, Wheeler J, Whiting G, Feavers IM, Maiden MCJ (2018). Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens. *Wellcome Open Res* **3**:151 [3505 isolates](#)
- Rodrigues CMC, Lucidarme J, Borrow R, Smith A, Cameron JC, Moxon ER, Maiden MCJ (2018). Genomic Surveillance of 4CMenB Vaccine Antigenic Variants among Disease-Causing *Neisseria meningitidis* Isolates, United Kingdom, 2010-2016. *Emerg Infect Dis* **24**:673-682 [3066 isolates](#)

This section includes full citation for papers linked to the isolate record. Each citation has a button that will return a dataset of all isolates linked to the paper.

If there are five or more references they will be hidden by default to avoid cluttering the page too much. Click the 'Show/hide' button to display them in this case.

## 10.1.4 Sequence bin summary

## Sequence bin

contigs: 275	N50 contig number: 20	N95 contig number: 97
total length: 2,195,045 bp	N50 length (L50): 34,308	N95 length (L95): 3,513
max length: 109,859 bp	N90 contig number: 74	loci tagged: 2,179
mean length: 7,982 bp	N90 length (L90): 6,405	

[Show sequence bin](#)

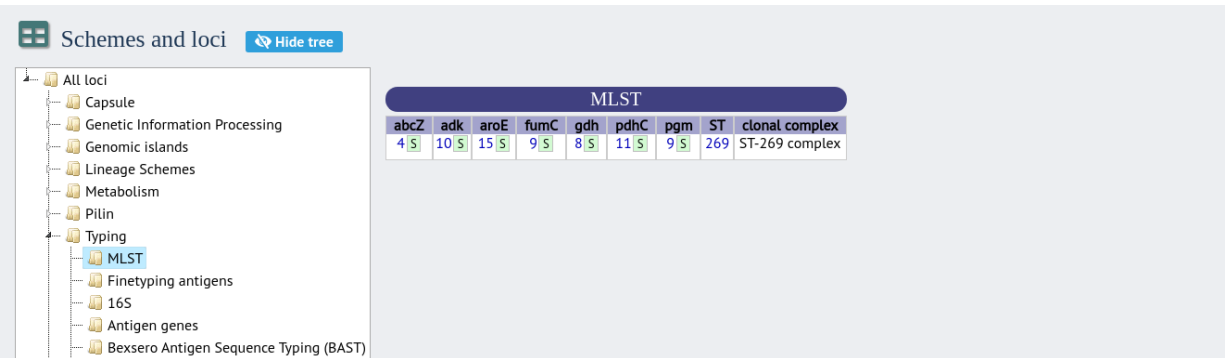
This section contains basic statistics describing the sequence bin. Clicking the 'Show sequence bin' button navigates to the *sequence bin record*.

### 10.1.5 Scheme and locus data

A hierarchical tree displays available schemes. Click within internal nodes to expand them.



Clicking any terminal node will display data available for a scheme or group of schemes.



Click an allele number within the scheme profile, will display the appropriate *allele definition record*. Clicking the green 'S' link will display the appropriate *sequence tag record*.

## 10.2 Allele definition records


An allele definition record displays information about a defined allele in a sequence definition database.

BIGSdb


Home > Organisms > Organism > Neisseria typing > Allele information

Help


## Allele information - abcZ: 2

 Provenance/meta data

locus: [abcZ](#)  
 allele: 2  
 sequence: TTTGATACCG TTGCCGAAGG TTGGGTGAA ATTCGCGATT TATTGGCGCG TTACCACCGC GTCGGCCATG AGTTGGAAAA CGGTTCCGGT GAGGCTTTGT  
 TGAAGAAGCT CAACGAATTA CAACTTGAAA TCGAAGCGAA GGACGGCTGG AAGCTGGATG CGGCAGTCAA GCAGACTTTG GGGGAACTCG GTTTGCCGGA  
 AAACGAAAA ATCGGCAACC TTCCGCGCG TCAGAAAAAG CGTGTGCTCT TGGCGCAGGC TTGGGTGCAG AAGCCGACG TATTGCTGCT GGACGAACCG  
 ACCAACCATT TGGATATCGA CGCGATTATT TGGCTGGAAA ATCTGCTCAA AGCGTTTGAA GGCAGCTTGG TTGTGATTAC CCACGACCGC CGTTTTTTGG  
 ACAATATCGC CACGCGGATT GTCGAACCTG ATC  
 length: 433  
 status: Sanger trace checked  
 date entered: 2001-02-07  
 timestamp: 2009-11-11  
 sender: Keith Jolley, University of Oxford, UK  
 curator: [Man-Suen Chan](#), University of Oxford

 Profiles containing this allele

MLST: [1262 profiles](#)

 Isolate databases

**PubMLST isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [11940 isolates](#)

If the allele is a member of a scheme profile, e.g. MLST, this will be listed. In this case, there will be a button to display all profiles of that scheme that contain the allele.

Similarly, if a *client database* has been setup for the database and the allele has been identified in an isolate, there will be a button to display all isolates that have that allele.

## 10.3 Sequence tag records

BIGSdb
Home > Organisms

NEIS0346 allele sequence: id-18968

Options
Flanking sequence length: 100
Reload

Contig position
sequence bin id: 4956
contig length: 22993
start: 13864
end: 14607
length: 744
orientation: forward
complete: yes
method: Illumina

Sequence

CACTGTACGC GCGCCAGCGG TTCAGCATTG CGGGCAGGCG GAAAACTAT TACCGTACAG CCGACGGTAA AACCGAAGAT GCCGCTCTTA TGGAGAAAA ATGTTAAGCG CGCGCTACCT
CCACCTGCAC GAAGCCTTGG GTTTGGGCCG GATGTGGTTG AAGCGGGGAG CCGTCGTCTT GCCGTCCGCA ACATTGCCGG AAGCCCGAC ACAATCCGC CCGCAAAAGC AAACGCTCCT
CAGCATTCCG CAGCGTCCGT CCGAACAGCA TACCGGTCAG GCACGGCTCA AAACATGAA AGTGTGGAA ACAACCGCG TACATACGC CAAACCCGG CCTGAAACCG AAACGCTCCT
GTCGGGCGTT TCAGACGGCA TCGCCCCGT TCCCGCCGT TCGGGATAA CCAAACTGC CGTTGTGAGC CTGTGCCG CGACCGAGGA TATGTTTAC GGGCAACTGT TCCACGAAA
AGCGGGTGTC CTGCTCGACA ATATACTCAA AGCCGTAGGG CTCGATGCCG CCTATGTCCA CAAACCTGT TGGGTGAAAA CGCCCGCGT CGGCAACCG ATGCCGCTG AAGCGGCAAT
CGCAATGCG CTGGAACAAA CCGCCCGCA ACTCGACGGC TGCGCGCAC CCGCCGTCT GTTCCTCGGA CAGGCGTTT TCAAACCGGA ACGGCAGCG ATGATTGAA CTTGTGCGC
CGCCCGCCCC TTCTTCATCA TCGACCATCC CGCCCGGCTG TTGCGCCAAC CCGAACTCAA AGCCCGGCGC TGGCAGACGC TCAAGCAGCT CAAACGTGTC TTGGCGCAAG GCGCGCGCAG
TTGAAGCGCG CCGCAGCGGG CGGTAGAATC GCAACTGCGT CCAATATCT GACAGAAAGC ACAAATGAC CGATTTCGC CAAGATTTC TTAATTCTC CCTC

Translation

H C T R R T A S A L R A G G K T I T V Q P T V K P K M P S \* W R K Y F1
T V R G A R L Q H C G Q A E K L L P Y S R R \* N R R C R L N G E N F2
L Y A A H G F S I A G R R K N Y Y R T A D G K T E D A V L M E K I F3
1 C A C T G T A C G C G C G C A C G C T T C A G C A T T G C G G G C A G G C G G A A A A C T A T T A C G T A C A G C C G A C G G T A A A C C G A A G A T G C C G T C T T A T G G A G A A A T 100
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
V K R A L P P P A R S L G F G P D V V E A G S R R P A V R N I A G F1
M L S A R Y L H L H E A L G L G P M W L K R G A V V L P S A T L P E F2
C \* A R A T S T C T K P W V W A R C G \* S G E P S S C R P Q H C R F3
101 A G T T A A G C G C G C G C T A C C C A C C T G C A C G A A G C C T T G G G T T T G G G C C C G A T G T G G T T G A A G C G G G A G C C G T C G T C C T G C C G C C G C A A C A T T G C C G G 200
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
K P D T N P P A K A N R P Q H S A A S V R T A Y R S G T A Q N H E F1
S P T Q I R P Q K Q T V L S I P Q R P S E Q H T G Q A R L K T M K F2
K A R H K S A R K S K P S S A F R S V R P N S I P V R H G S K P \* K F3
201 A A A G C C C G A C A A A T C G C C C G C A A A G C A A C C G T C T C A G C A T T C G C A G C G T C C G C C G A A C A G C A T A C C G G T C A G G C A C G G T C A A A C C A T G A A 300
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
S V G N N R R T Y A Q T R A \* N R N A S V R R F R R H R P R S R R F F1
V L E T T A V H T R K P A P E T E T P L S G V S D G I A P V P A A F2
C W K Q P P Y I R A N P R L K P K R L C P A F Q T A S P P F P L F3
301 A G T G T T G G A A C A A C C G C G T A C A T C G C G A A A C C G C G C T G A A A C C G A A C G C C T C T G T C C G G C G T T T C A G A C G C A T C G C C C G T T C C C G C G C T 400
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

A sequence tag record displays information about the location within a contig of a region associated with a locus. The nucleotide sequence will be displayed along with upstream and downstream flanking sequence. The length of these flanking sequences can be modified within the *general options*.

If the tag is for a DNA locus and it is marked as a coding sequence, the three-frame translation will also be displayed.

## 10.4 Profile records

BIGSdb


Home > Organisms > Organism > Neisseria typing > Profile information

Help

### Profile information for ST-11 (MLST)

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
11	2	3	4	3	8	4	6	ST-11 complex

sender: Paula Kriz, Paula Kriz and Keith Jolley  
 curator: [Keith Jolley](#), University of Oxford, UK  
 date entered: 2001-02-07  
 datestamp: 2009-11-11

 Client database

**PubMLST Isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [7315 isolates](#)

A profile record displays information about a scheme, e.g. MLST, profile. Each allele number within the profile will be hyperlinked. Clicking these will take you to the appropriate *allele definition record*.

If a *client database* has been setup for the database and an isolate has the profile, there will be a button to display all isolates that have the profile.

## 10.5 Sequence bin records

BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Isolate info](#) > [Sequence bin](#)
[AIA](#) [Help](#) [i](#)

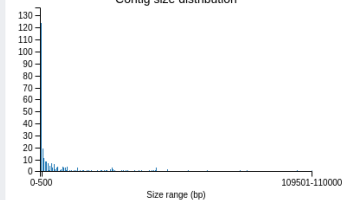
### Sequence bin for M10 240474

#### Contig summary statistics

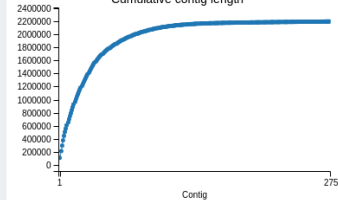
Contigs: 275  
 Total length: 2,195,045  
 Minimum length: 145  
 Maximum length: 109,859  
 Mean length: 7,982  
 N50 contig number: 20  
 N50 length (L50): 34,308  
 N90 contig number: 74  
 N90 length (L90): 6,405  
 N95 contig number: 97  
 N95 length (L95): 3,513



#### Contig size distribution



#### Cumulative contig length



Sequence	Sequencing method	Original designation	Length	Comments	Locus	Start	End	Direction	Annotation
4869	Illumina	NODE_90_length_109787_cov_40.983086	109859		NEIS1151	488	1144	←	EMBL GBK
					NEIS1150	1141	2913	←	
					NEIS1149	3155	3733	→	
					NEIS1148	3896	4513	→	
					NEIS1147	4521	5384	→	
					NEIS1146	5397	5831	←	
					NEIS1145	6141	6869	→	
					NEIS1144	6892	7923	←	
					NEIS1143	8005	8313	←	
					NEIS1142	9288	10541	←	
					NEIS1140	10613	12241	←	
					NEIS1139	12391	12744	→	
					NEIS1138	12824	14362	→	
					NEIS1137	14426	15046	←	
					NEIS1136	15102	15392	←	
					NEIS3082	15504	15569	←	

A sequence bin record contains information about the contigs associated with an isolate record. This includes:

- Number of contigs

- Total length
- Minimum length
- Maximum length
- N50, N90 and N95 values
- Size distribution charts

Charts show the distribution of contig sizes and the cumulative contig length against contig number giving a breakdown indication of contig size.

The record includes an embedded genome browser showing the positions of any loci that have been tagged.

There are also links to download the contigs in FASTA, Genbank or EMBL format, along with annotation in GFF3 format.

Finally there is a table that shows the loci that are tagged on each contig. Individual contigs can also be downloaded in EMBL or Genbank format.

## QUERYING DATA

### 11.1 Querying sequences to determine allele identity

Sequence queries are performed in the sequence definition database. Click ‘Single sequence’ query from the contents page.

The screenshot shows the BIGSdb interface for Neisseria typing. The header includes the BIGSdb logo and a breadcrumb trail: Home > Organisms > Organism > Neisseria typing. The main content area is titled 'Neisseria typing database' and features a grid of query options. The 'Single sequence' option is highlighted with a red box. To the right of the grid is a sidebar with various user actions like LOG IN, SUBMISSIONS, DOWNLOADS, EXPORT, ANALYSIS, CUSTOMISE, INFORMATION, and ISOLATES.

Query a sequence	Find alleles	Search for allelic profiles
<b>Single sequence</b> Query a single sequence or whole genome assembly to identify allelic matches.	<b>By specific criteria</b> Find alleles by matching criteria (all loci together)	<b>By specific criteria</b> Search, browse or enter list of profiles
<b>Batch sequences</b> Query multiple independent sequences in FASTA format to identify allelic matches.	<b>By locus</b> Select, analyse and download specific alleles from a single locus.	<b>By allelic profile</b> This can include partial matches to find related profiles.
		<b>In a batch</b> Look up multiple allelic profiles together.

LOG IN

SUBMISSIONS

DOWNLOADS +

EXPORT +

ANALYSIS +

CUSTOMISE +

INFORMATION +

ISOLATES

Paste your sequence in to the box - there is no need to trim. Often, you can leave the locus setting on ‘All loci’ - the software should identify the correct locus based on your sequence. Sometimes, especially in databases with a large number of defined loci, it may be quicker, however, to select the specific locus or scheme (e.g. MLST) that a locus belongs to.

**Note:** If the locus you are querying is a shorter version of another, e.g. an MLST fragment of a gene where the full length gene is also defined, you will need to select the specific locus or the scheme from the dropdown box. Leaving the selection on ‘All loci’ will return a match to the longer sequence in preference to the shorter one.

Click ‘Submit’.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence query

Help ⓘ

## Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

— Please select locus/scheme — Order results by —

MLST locus

Enter query sequence (single or multiple contigs up to whole genome in size) Alternatively upload FASTA file

Select FASTA file:  
Choose file No file chosen

or enter Genbank accession Action

RESET SUBMIT

```

ACGGTCAGAT TCCCGATATT CCGCCCGATA TTTTCAAAA CTGCGCGCTT GCCTACGATA
TGGTGACGG CTGCGCGGCA AAACCGTTTT TAGATTTTGC ACGACAATCG GGTGCGAAAA
AAACTGCCGA CGGACTGGGT ATGCTAGTCG GTCAGCGCGC GGCTTCCTAC GCCCTCTGGC
GCGGATTTAC GCCCGATATC CGCCCGGTTA TCGAATACAT GAAAGCCCTA TAAACATGTT
CCGCATCATC AAATGGCTGA TTGCCCTGCC CGTCGGCATC TTTATCTTTT TCAATGCCTA
TGTGTACGGC AACATCATT CCTACCGCG

```

If an exact match is found, this will be indicated along with the start position of the locus within your sequence.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence query

Help ⓘ

## Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

— Please select locus/scheme — Order results by —

MLST locus

Enter query sequence (single or multiple contigs up to whole genome in size) Alternatively upload FASTA file

Select FASTA file:  
Choose file No file chosen

or enter Genbank accession Action

RESET SUBMIT

1 exact match found.

Translate query

Locus	Allele	Length	Contig	Start position	End position	Flags	Comments
aroE	2	490	Query	97	586		

📄 📄

If only a partial match is found, the most similar allele is identified along with any nucleotide differences. The varying nucleotide positions are numbered both relative to the pasted in sequence and to the reference sequence. The start position of the locus within your sequence is also indicated.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence query

Help ⓘ ⓘ

## Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

— Please select locus/scheme — Order results by —

MLST locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file:  
Choose file | No file chosen

or enter Genbank accession — Action

RESET SUBMIT

**Translate query**

Closest match: aroE: 64

Show alignment

### Differences

2 differences found. ⓘ

55 A → 151 T  
134 A → 230 C

The locus start point is at position 97 of your query sequence. ⓘ

As an alternative to pasting a sequence in to the box, you can also choose to upload sequences in FASTA format by clicking the file browse button.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence query

Help ⓘ ⓘ

## Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

— Please select locus/scheme — Order results by —

All loci locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file:  
Choose file | No file chosen

or enter Genbank accession — Action

RESET SUBMIT

### 11.1.1 Querying whole genome data

The sequence query is not limited to single genes. You can also paste or upload whole genomes - these can be in multiple contigs. If you select a specific scheme from the dropdown box, all loci belonging to that scheme will be checked (although only exact matches are reported for a locus if one of the other loci has an exact match). If all loci are matched, scheme fields will also be returned if these are defined. This, for example, enables you to identify the MLST sequence type of a genome in one step.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence query

Help ⓘ ⓘ

## Sequence query



Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

Please select locus/scheme Order results by  
 MLST locus


Enter query sequence (single or multiple contigs up to whole genome in size) Alternatively upload FASTA file  
 Select FASTA file:  
 Choose file No file chosen  
 or enter Genbank accession Action  
 RESET SUBMIT

7 exact matches found.

Locus	Allele	Length	Contig	Start position	End position	Flags	Comments
abcZ	2	433	187414	5637	6069		
adk	3	465	187432	8935	9399		
aroE	4	490	187449	4826	5315		
fumC	3	465	187396	4871	5335		
gdh	8	501	187466	7333	7833		
pdhC	4	480	187542	56831	57310		
pgm	6	450	187395	21997	22446		

MLST

 Matching profile  
 ST: 11  
 clonal complex: ST-11 complex

## 11.2 Querying multiple sequences to identify allele identities

You can also query mutiple sequences together. These should be in FASTA format. Click 'Batch sequences' from the contents page.

BIGSdb

Home > Organisms > Organism > Neisseria typing

## Neisseria typing database

Query a sequence

Single sequence

Query a single sequence or whole genome assembly to identify allelic matches.

Batch sequences

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

By specific criteria

Find alleles by matching criteria (all loci together)

By locus

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

By specific criteria

Search, browse or enter list of profiles

By allelic profile

This can include partial matches to find related profiles.

In a batch

Look up multiple allelic profiles together.

LOG IN

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ISOLATES

Paste your sequences (FASTA format) in to the box. Select a specific locus, scheme or 'All loci'.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Batch sequence query

## Batch sequence query

Please paste in your sequences to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

Please select locus/scheme: MLST Order results by: locus

Enter query sequences (FASTA format)

```
>sample_1
GAAGCGAAAAAATCATTGACGAAGGCGGCTTGTTGCGCGACGACATCATTATCGGCATGGTCAAAGAAC
GCATCGCGCAAGACGACTGCAAAAACGGTTTCCTGTTGACGGTTTCCGCGCACATTGGCACAAGCCGA
AGCGATGGTTGAAGCAGGCGTGGATTGGATGCAAGTGGTGAATCGACGTCCTGACAGCGTGATTGTC
GACCGTATGAGCGGCGCGCGTGCATTGGCTTCCGGCGGTAATTACACGTTACCTACAACCGGCCCA
AAGTTGAAGGCAAGACGACGTAACCGCGAAGATTGATTACGCGCGACGACGACAAGAAGAACCCT
```

Alternatively upload FASTA file

Select FASTA file: Choose file | No file chosen

Action

RESET SUBMIT

The best match will be displayed for each sequence in your file. If this isn't an exact match, the differences will be listed.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Batch sequence query

Batch sequence query

Please paste in your sequences to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

Please select locus/scheme: MLST
 Order results by: locus

Enter query sequences (FASTA format)
 Alternatively upload FASTA file

>sample\_1  
 GAAGCGAAAAATCATTGACGAAGCGGCTTGTTGCGCGACGACATCATTATCGGCATGGTCAAAGAAC  
 GCATCGCGCAAGACGACTGCAAAACGGTTTCTGTTGACGGTTTCCGCGGACATTGGCACAAGCCGA  
 AGCGATGGTTGAAGCAGCGCGGATTGGATGCGTGGTTGAAATCGACGTGCTGACAGCGTGAATTGTC  
 GACCGTATGAGCGGCGCGCGCTGCATTGGCTTCGGCCGTACTTACACGTTACCTACAACCCGCCCA  
 AAGTTGAAGGCAAGACGACGTAACCGCGGAAGATTGATTGAGCGGACGACGACAAAGAAGAACCGT

Select FASTA file:  
 Choose file No file chosen

Action

RESET SUBMIT

Contig	Match	Locus	Allele	Differences
sample_1	exact	adk	3	
sample_2	partial	adk	21	1 difference found. <sup>237</sup> T → <sup>237</sup> A
sample_3	partial	adk	27	2 differences found. <sup>230</sup> G → <sup>230</sup> A; <sup>425</sup> A → <sup>425</sup> C

## 11.3 Searching for specific allele definitions

There are two query pages available that allow searching for specific allele definitions. The first allows querying of all loci together by criteria that are common to all. The second is a locus-specific attribute query that can search on any extended attributes that may be defined for a locus. This locus-specific query also allows you to paste in lists of alleles for download or analysis.

### 11.3.1 General (all loci) sequence attribute search

To retrieve specific allele designations, click 'By specific criteria' in the 'Find alleles' section on a sequence definition database contents page.

BIGSdb

Home > Organisms > Organism > Neisseria typing

## Neisseria typing database

Query a sequence

Single sequence

Query a single sequence or whole genome assembly to identify allelic matches.

Batch sequences

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

By specific criteria

Find alleles by matching criteria (all loci together)

By locus

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

By specific criteria

Search, browse or enter list of profiles

By allelic profile

This can include partial matches to find related profiles.

In a batch

Look up multiple allelic profiles together.

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ISOLATES

Enter your query using the dropdown search box - additional terms can be added by clicking the '+' button.

Designations can be queried using *standard operators*.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search

Help ⓘ ⓘ

## Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records). Matching sequences will be returned and you will then be able to update their display and query settings.

**Search criteria**

locus ▾ = ▾ abcZ + ⓘ

**Display**

Order by: locus ▾ ascending ▾

Display: 25 ▾ records per page ⓘ

Filter query by  Action

RESET SEARCH

Click 'Search'.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search

Help ⓘ

### Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records). Matching sequences will be returned and you will then be able to update their display and query settings.

Search criteria

Combine searches with: AND

locus = abcZ

allele id = 5

Filter query by

Action

Display

Order by: locus ascending

Display: 25 records per page

RESET

SEARCH

1 record returned. Click the hyperlink for detailed information.

locus	allele id	sequence	sequence length	type	allele	comments	flags
<a href="#">abcZ</a>	5	TTTGATACCGTTGCC ... TCGTCGAACTCGATC	433				

Click the hyperlinked results to display allele records.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search

Help ⓘ

### Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records). Matching sequences will be returned and you will then be able to update their display and query settings.

Search criteria

Combine searches with: AND

locus = abcZ

allele id = 5

Filter query by

Action

Display

Order by: locus ascending

Display: 25 records per page

RESET

SEARCH

1 record returned. Click the hyperlink for detailed information.

locus	allele id	sequence	sequence length	type	allele	comments	flags
<a href="#">abcZ</a>	<b>5</b>	TTTGATACCGTTGCC ... TCGTCGAACTCGATC	433				

## BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Allele information](#)
[Help](#)

## Allele information - abcZ: 5



## Provenance/meta data

locus: **abcZ**  
 allele: 5  
 sequence: TTTGATACCG TTGCCGAAGG TTGGGGCGAA ATTCGCGATT TATTGCGCCG TTATCATCAT GTCAGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCTTTGT  
 TGAAAGAGCT TAACGAATTG CAACCTTGAAA TCGAAGCGAA GGACGGCTGG AAGCTGGATG CGGCAGTCAA GCAGACTTTG GGTGAACCTG GTTGGCCAGA  
 AAACGAAAA ATCGCAACC TCTCCGGCGG ACAGAAAAAG CGTGTGGCC TAGCGCAGGC TTGGGTGAG AAGCCTGATG TATTGCTGCT GGACGAACCG  
 ACCAACCATT TGGACATTGA CGCGATTATT TGGCTGGAAA ATCTGCTTAA AGCGTTTGAA GGCAGCCTGG TTGTGATTAC CCACGACCGC CGTTTTTTGG  
 ACAATATCGC CACGCGCATC GTCGAACTCG ATC  
 length: 433  
 status: Sanger trace checked  
 date entered: 2001-02-07  
 datestamp: 2009-11-11  
 sender: Keith Jolley, University of Oxford, UK  
 curator: Man-Suen Chan, University of Oxford



## Profiles containing this allele

MLST: **302 profiles**

## Isolate databases

PubMLST isolates: Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. **1578 isolates**

Various search criteria can also be selected by combining with filters. Click the filter heading to display these.

## BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Sequence attribute search](#)
[Help](#)

## Sequence attribute search

Some loci have additional fields which are not searchable from this general page. Search for these at the [locus-specific query](#) page. Use this page also for access to the sequence analysis or export plugins.

Also note that some loci in this database have allele ids defined as text strings. Queries using the '<' or '>' modifiers will work alphabetically rather than numerically unless you filter your search to a locus that uses integer allele ids using the drop-down list.

Please enter your search criteria below (or leave blank and submit to return all records). Matching sequences will be returned and you will then be able to update their display and query settings.

Search criteria

allele id

Filter query by

locus: **abcZ**  
status:   
type allele:   
sender:   
curator:   
allele flag:

Display

Order by:  ascending  
Display: 25 records per page

Action

9 records returned. Click the hyperlinks for detailed information.

locus	allele id	sequence	sequence length	type allele	comments	flags
abcZ	1	TTTGATACTGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	2	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	3	TTTGATACCGTTGCC ... TTGTTGAACTTGACC	433	<input type="checkbox"/>		
abcZ	4	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	5	TTTGATACCGTTGCC ... TCGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	6	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	7	TTTGATACTGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		
abcZ	8	TTTGATACCGTTGCC ... TTGTCGAACTTGACC	433	<input type="checkbox"/>		
abcZ	9	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433	<input type="checkbox"/>		

### 11.3.2 Locus-specific sequence attribute search

Some loci have *extended attribute fields*. To query these, click ‘By locus’ in the ‘Find alleles’ section on a sequence definition database contents page.

The screenshot shows the 'Neisseria typing database' interface. On the right, there is a vertical sidebar with buttons: LOG IN, SUBMISSIONS, DOWNLOADS, EXPORT, ANALYSIS, CUSTOMISE, INFORMATION, and ISOLATES. The main area is divided into three columns: 'Query a sequence', 'Find alleles', and 'Search for allelic profiles'. Under 'Find alleles', the 'By locus' option is highlighted with a red border. Other options include 'By specific criteria' and 'By allelic profile'.

Pick the required locus from the dropdown box.

The screenshot shows the 'Sequence attribute search - PorA\_VR2' interface. At the top, the 'Locus' dropdown is highlighted with a red box, showing 'PorA\_VR2' selected. Below this, there is a section for 'Allele fields' with a dropdown for 'allele id' and an equals sign. To the right, there is a 'Display' section with 'Order by' set to 'ascending' and 'Display' set to '25 records per page'. At the bottom right, there are 'RESET' and 'SEARCH' buttons.

The fields specific for that locus will be added to the dropdown query boxes.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search (locus-specific)

Help ⓘ ⓘ ⓘ

## Sequence attribute search - PorA\_VR2

Locus: PorA\_VR2 Page will reload when changed

- Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

Allele fields

family = 2 ⓘ

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

The query form can be modified by clicking the ‘Modify form options’ tab:

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search (locus-specific)

Help ⓘ ⓘ ⓘ

## Sequence attribute search - abcZ

Locus: abcZ Page will reload when changed

- Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

Allele fields

allele id = ⓘ

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

A list box can be added by clicking the ‘Show’ button for ‘Allele id list box’.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search (locus-specific)

Help ⓘ ⓘ ⓘ

## Sequence attribute search - abcZ

Locus: abcZ Page will reload when changed

- Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

Allele fields

allele id = ⓘ

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Modify form parameters

Click to add or remove additional query terms:

- Allele fields
- Allele id list box
- Filters

Close the form modification tab and you can now enter a list of allele ids for retrieval.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search (locus-specific)

Help ⓘ ⓘ ⚙

### Sequence attribute search - abcZ

Locus: abcZ Page will reload when changed

Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

Allele fields

allele id =  ⓘ

Allele id list

1  
2  
3  
4  
5

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

Various analysis and export options will be available for use on the retrieved sequences. These include FASTA output and *Locus Explorer* analysis.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Sequence attribute search (locus-specific)

Help ⓘ ⓘ ⚙

### Sequence attribute search - abcZ

Locus: abcZ Page will reload when changed

Further information is available for this locus.

Please enter your search criteria below (or leave blank and submit to return all records).

Allele fields

allele id =  ⓘ

Allele id list

1  
2  
3  
4  
5

Display

Order by: allele id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

5 records returned. Click the hyperlinks for detailed information.

locus	allele id	sequence	sequence length	type	allele	comments	flags
abcZ	1	TTTGATACTGTTGCC ... TTGTCGAACTCGATC	433		<input type="checkbox"/>		
abcZ	2	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433		<input type="checkbox"/>		
abcZ	3	TTTGATACCGTTGCC ... TTGTTGAACTTGACC	433		<input type="checkbox"/>		
abcZ	4	TTTGATACCGTTGCC ... TTGTCGAACTCGATC	433		<input type="checkbox"/>		
abcZ	5	TTTGATACCGTTGCC ... TCGTCGAACTCGATC	433		<input type="checkbox"/>		

Analysis tools

Export: FASTA Table

Analysis: Locus Explorer

## 11.4 Browsing scheme profile definitions

If a sequence definition database has schemes defined that include a primary key field, i.e. collections of loci that together create profiles, e.g. for MLST, these can be browsed by clicking the link ‘By specific criteria’ in the ‘Search for allelic profiles’ section.

The screenshot shows the BIGSdb homepage. The navigation bar includes 'Home > Organisms > Organism > Neisseria typing'. The main heading is 'Neisseria typing database'. On the right, there is a sidebar with links: LOG IN, SUBMISSIONS, DOWNLOADS (+), EXPORT (+), ANALYSIS (+), CUSTOMISE (+), INFORMATION (+), and ISOLATES. The main content area is divided into three columns: 'Query a sequence', 'Find alleles', and 'Search for allelic profiles'. Under 'Search for allelic profiles', the 'By specific criteria' option is highlighted with a red box. Other options include 'Single sequence', 'Batch sequences', 'By locus', 'By allelic profile', and 'In a batch'.

Leave query form fields blank (the display of these may vary depending on modification options set by the user). Choose the field to order the results by, the number of results per page to display, and click ‘Search’.

The screenshot shows the 'Search or browse profiles' page. The navigation bar includes 'Home > Organisms > Organism > Neisseria typing > Search or browse profiles'. The main heading is 'Search or browse profiles'. Below the heading, there is a 'Schemes' section with a dropdown menu set to 'MLST' and a 'Select' button. Below this, there is a search form with 'Locus/scheme fields' and 'Display/sort options'. The 'Locus/scheme fields' section has a dropdown set to 'ST' and an equals sign. The 'Display/sort options' section has 'Order by: ST' and 'ascending', and 'Display: 25 records per page'. There are 'RESET' and 'SEARCH' buttons. Below the search form, it says 'Browsing all records. 15,577 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.' Below this, there is a table of results.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
1	1	3	1	1	1	1	3	ST-1 complex
2	1	3	4	7	1	1	3	ST-1 complex
3	1	3	1	1	1	23	13	ST-1 complex
4	1	3	3	1	4	2	3	ST-4 complex
5	1	1	2	1	3	2	3	ST-5 complex
6	1	1	2	1	3	2	11	ST-5 complex
7	1	1	2	1	3	2	19	ST-5 complex

Clicking the hyperlink for any profile will display full information about the profile.

BIGSdb


Home > Organisms > Organism > *Neisseria* typing > Profile information

Help ⓘ ⓘ

## Profile information for ST-11 (MLST)

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
11	2	3	4	5	8	4	6	ST-11 complex

sender: Paula Kriz, Paula Kriz and Keith Jolley  
 curator: Keith Jolley, University of Oxford, UK  
 date entered: 2001-02-07  
 datestamp: 2009-11-11

 Client database

**PubMLST isolates:** Contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample. [7315 isolates](#)

## 11.5 Querying scheme profile definitions

Click the link to ‘By specific criteria’ link in the ‘Search for allelic profiles’ section.

BIGSdb

Home > Organisms > Organism > *Neisseria* typing

## *Neisseria* typing database

Query a sequence

**Single sequence**

Query a single sequence or whole genome assembly to identify allelic matches.

**Batch sequences**

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

**By specific criteria**

Find alleles by matching criteria (all loci together)

**By locus**

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

**By specific criteria**

Search, browse or enter list of profiles

**By allelic profile**

This can include partial matches to find related profiles.

**In a batch**

Look up multiple allelic profiles together.

[LOG IN](#)

[SUBMISSIONS](#)

[DOWNLOADS](#) +

[EXPORT](#) +

[ANALYSIS](#) +

[CUSTOMISE](#) +

[INFORMATION](#) +

[ISOLATES](#)

Enter the search criteria you wish to search on. You can add search criteria by clicking the ‘+’ button in the ‘Locus/scheme fields’ section. These can be combined using ‘AND’ or ‘OR’.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help ⓘ ⚙

## Search or browse profiles

**Schemes**

Please select the scheme you would like to query:

MLST [Select](#)

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Locus/scheme fields** **Display/sort options** **Action**

Combine searches with: AND

date entered >= 2018-03-01 + ⓘ

sender (surname) = Jolley

Order by: ST ascending

Display: 25 records per page ⓘ

[RESET](#) [SEARCH](#)

134 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

⏪ ⏩ 1 2 3 4 5 6 ⏪ ⏩

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
13607	8	5	53	55	10	24	17	ST-41/44 complex
13608	3	6	9	17	17	21	9	ST-41/44 complex
13609	5	496	17	15	30	650	12	ST-198 complex
13610	7	5	6	13	82	53	15	ST-213 complex
13611	3	6	34	5	36	6	9	ST-41/44 complex
13612	9	6	9	17	9	64	9	ST-41/44 complex
13613	59	39	170	237	148	153	65	

Each field can be queried using *standard operators*.

Clicking the hyperlink for any profile will display full information about the profile.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help ⓘ ⚙

## Search or browse profiles

**Schemes**

Please select the scheme you would like to query:

MLST [Select](#)

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Locus/scheme fields** **Display/sort options** **Action**

Combine searches with: AND

date entered >= 2018-03-01 + ⓘ

sender (surname) = Jolley

Order by: ST ascending

Display: 25 records per page ⓘ

[RESET](#) [SEARCH](#)

134 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

⏪ ⏩ 1 2 3 4 5 6 ⏪ ⏩

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
13607	8	5	53	55	10	24	17	ST-41/44 complex
<a href="#">13608</a>	3	6	9	17	17	21	9	ST-41/44 complex
13609	5	496	17	15	30	650	12	ST-198 complex
13610	7	5	6	13	82	53	15	ST-213 complex
13611	3	6	34	5	36	6	9	ST-41/44 complex
13612	9	6	9	17	9	64	9	ST-41/44 complex
13613	59	39	170	237	148	153	65	

Other query options are available by clicking the 'Modify form options' tab.

**BIGSdb**

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help

## Search or browse profiles

### Schemes

Please select the scheme you would like to query:

MLST Select

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Locus/scheme fields Display/sort options Action

ST =  + i Order by: ST ascending Display: 25 records per page i RESET SEARCH

For example, you can enter a list of attributes to query on by clicking the ‘Show’ button next to ‘Attribute values list’.

**BIGSdb**

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help

## Search or browse profiles

### Schemes

Please select the scheme you would like to query:

MLST Select

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Locus/scheme fields Display/sort options Action

ST =  + i Order by: ST ascending Display: 25 records per page i RESET SEARCH

**Modify form parameters**

Click to add or remove additional query terms:

- + Locus/scheme field values
- + **Attribute values list**
- + Filters

A list box will appear within the page. Hide the form modification tab by clicking the ‘X’ in the corner or the purple tab again. Now you can choose the attribute to search on along with a list of values.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help ⓘ ⓘ ⓘ

## Search or browse profiles

### Schemes

Please select the scheme you would like to query:

MLST Select

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Locus/scheme fields** **Attribute values list** **Display/sort options**

ST = + ⓘ **Field:** ST Order by: ST ascending Display: 25 records per page ⓘ

**Action**

RESET SEARCH

4 records returned. Click the hyperlinks for detailed information.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
1	1	3	1	1	1	1	3	ST-1 complex
2	1	3	4	7	1	1	3	ST-1 complex
3	1	3	1	1	1	23	13	ST-1 complex
4	1	3	3	1	4	2	3	ST-4 complex

**Analysis tools**

Analysis: BURST

Export: Profiles Sequences

List values will be combined with any other attributes entered in the query form allowing complex queries can be constructed.

You can also add filters to the form by again clicking the ‘Modify form options’ tab and selecting ‘Filters’.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help ⓘ ⓘ ⓘ

## Search or browse profiles

### Schemes

Please select the scheme you would like to query:

MLST Select

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Locus/scheme fields** **Attribute values list** **Display/sort options**

ST = + ⓘ **Field:** ST Order by: ST Display: 25

**Action**

RESET SEARCH

**Modify form parameters**

Click to add or remove additional query terms:

- ⊖ Locus/scheme field values
- ⊖ Attribute values list
- ⊕ **Filters**

Available filters will vary depending on the database. These will be combined with other query criteria or lists of attributes.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search or browse profiles

Help ⓘ ⓘ ⓘ

## Search or browse profiles

### Schemes

Please select the scheme you would like to query:

MLST Select

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Locus/scheme fields**

ST ▼ = ▼ + ⓘ

**Attribute values list**

Field: ST ▼

1  
2  
3  
4

**Filters**

clonal complex: ST-4 complex ⓘ

**Display/sort options**

Order by: ST ▼ ascending ▼

Display: 25 ▼ records per page ⓘ

**Action**

RESET SEARCH

1 record returned. Click the hyperlink for detailed information.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
4	1	3	3	1	4	2	3	ST-4 complex

### Analysis tools

Export: Profiles Sequences

## 11.6 Identifying allelic profile definitions

For schemes such as MLST you can query allelic combinations to identify the sequence type (or more generically, the primary key of the profile).

Click the ‘By allelic profile’ link in the ‘Search for allelic profiles’ section on a the sequence definition contents page.

BIGSdb

Home > Organisms > Organism > Neisseria typing

## Neisseria typing database

Query a sequence

Single sequence

Query a single sequence or whole genome assembly to identify allelic matches.

Batch sequences

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

By specific criteria

Find alleles by matching criteria (all loci together)

By locus

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

By specific criteria

Search, browse or enter list of profiles

By allelic profile

This can include partial matches to find related profiles.

In a batch

Look up multiple allelic profiles together.

LOG IN

SUBMISSIONS

DOWNLOADS +

EXPORT +

ANALYSIS +

CUSTOMISE +

INFORMATION +

ISOLATES

If multiple schemes are defined in the database you should select the scheme you wish to check.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search by locus combinations

Help ⓘ ⓘ

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST

Please enter your allelic profile below. Blank loci will be ignored.

abcZ	adk	aroE	fumC	gdh	pdhC	pgm

Autofill profile

ST:

Options

Search:

Display/sort options

Order by:

Display:  records per page ⓘ

Action

Enter a combination of allelic values (you can enter a partial profile if you wish).

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search by locus combinations

Help ⓘ ⓘ

## Search by locus combinations

### Schemes

Please select the scheme you would like to query:

MLST

Please enter your allelic profile below. Blank loci will be ignored.

abcZ	adk	aroE	fumC	gdh	pdhC	pgm
2	3	4	3	8	4	6

Autofill profile

ST:

Options

Search:

Display/sort options

Order by:

Display: 25 records per page ⓘ

Action

Alternatively, you can automatically populate a profile by entering a value for the scheme primary key field (e.g. ST) and clicking ‘Autofill’.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search by locus combinations

Help ⓘ ⓘ

## Search by locus combinations

### Schemes

Please select the scheme you would like to query:

MLST

Please enter your allelic profile below. Blank loci will be ignored.

abcZ	adk	aroE	fumC	gdh	pdhC	pgm

Autofill profile

ST:

Options

Search:

Display/sort options

Order by:

Display: 25 records per page ⓘ

Action

To find the closest or exact match, leave the search box on ‘Exact or nearest match’ and click ‘Submit’. The best match will be displayed.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search by locus combinations

Help ⓘ ⓘ

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST Select

Please enter your allelic profile below. Blank loci will be ignored.

abcZ	adk	aroE	fumC	gdh	pdhC	pgm
2	3	4	3	8	4	6

Autofill profile

ST: 11 Autofill

Options

Search: Exact or nearest match

Display/sort options

Order by: ST ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

Exact matches found (7 loci).

1 record returned. Click the hyperlink for detailed information.

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
11	2	3	4	3	8	4	6	ST-11 complex

Analysis tools

Export: Profiles Sequences

Alternatively, if you wish to find all profiles that match the query profile by at least a set number of loci, select the appropriate value in the search dropdown box, e.g. '4 or more matches' will show related profiles that share at least 4 alleles with the query.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Search by locus combinations

Help ⓘ ⓘ

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST Select

Please enter your allelic profile below. Blank loci will be ignored.

abcZ	adk	aroE	fumC	gdh	pdhC	pgm
2	3	4	3	8	4	6

Autofill profile

ST: 11 Autofill

Options

Search: 4 or more matches

Display/sort options

Order by: ST ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

499 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

«
◀
1
2
3
4
5
6
▶
»

ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
10	2	3	4	2	8	15	2	ST-8 complex
11	2	3	4	3	8	4	6	ST-11 complex
50	2	3	19	3	8	4	6	ST-11 complex
51	2	3	4	23	8	6	6	ST-11 complex
52	7	3	4	3	8	4	6	ST-11 complex

## 11.7 Batch profile queries

To lookup scheme definitions, e.g. the sequence type for multiple profiles, click ‘In a batch’ from the ‘Search for allelic profiles’ section of the sequence definition contents page.

The screenshot shows the BIGSdb interface for the Neisseria typing database. The main navigation bar includes 'Home > Organisms > Organism > Neisseria typing'. The page title is 'Neisseria typing database'. The interface is divided into three main sections: 'Query a sequence', 'Find alleles', and 'Search for allelic profiles'. Under 'Search for allelic profiles', there are two columns of options. The first column includes 'Single sequence', 'Batch sequences', and 'By specific criteria'. The second column includes 'By specific criteria', 'By locus', and 'By allelic profile'. The 'In a batch' option under 'By allelic profile' is highlighted with a red box. To the right of these sections is a sidebar with a 'LOG IN' button and a list of actions: 'SUBMISSIONS', 'DOWNLOADS', 'EXPORT', 'ANALYSIS', 'CUSTOMISE', 'INFORMATION', and 'ISOLATES', each with a plus sign to expand the menu.

If multiple schemes are defined in the database you should select the scheme you wish to check.

The screenshot shows the BIGSdb interface for the Batch profile query. The main navigation bar includes 'Home > Organisms > Organism > Neisseria typing > Batch profile query'. The page title is 'Batch profile query'. The interface is divided into two main sections: 'Schemes' and 'Enter allelic profiles'. In the 'Schemes' section, there is a dropdown menu with 'MLST' selected and a 'Select' button. In the 'Enter allelic profiles' section, there is a text area for pasting profiles and a 'Paste in profiles' button. At the bottom, there are 'RESET' and 'SUBMIT' buttons.

Copy and paste data from a spreadsheet. The first column is the record identifier, and the remaining columns are the alleles for each locus in the standard locus order defined for the scheme. There are links to the column order which can be used as a header line for your spreadsheet and to example data.

Click submit after pasting in the data.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Batch profile query

Help

## Batch profile query

### Schemes

Please select the scheme you would like to query:

MLST

Enter allelic profiles below in tab-delimited text format using copy and paste (for example directly from a spreadsheet). Columns can be separated by any amount of whitespace. The first column should be an isolate identifier and the remaining columns should comprise the allele numbers ([show column order](#)). Click here for [example data](#). Non-numerical characters will be stripped out of the query.

Paste in profiles

isolate_1	2	6	9	5	9	6	8
isolate_2	35	24	15	48	6	482	41
isolate_3	7	5	1	13	82	53	17
isolate_4	6	5	53	3	74	8	54
isolate_5	558	43	39	45	65	594	600
isolate_6	8	4	6	17	5	18	16
isolate_7	222	3	58	275	30	3	255
isolate_8	222	1	58	261	263	5	255
isolate_9	662	3	4	3	8	7	6
isolate_10	12	29	2	26	26	65	17

Action

A results table will be displayed.



BIGSdb

Home > Organisms > Organism > Neisseria typing > Batch profile query

Help

## Batch profile query

Isolate	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST	clonal complex	Query
isolate_1	2	6	9	5	9	6	8	3021	ST-41/44 complex	<a href="#">Q</a>
isolate_2	35	24	15	48	6	482	41	7697	ST-192 complex	<a href="#">Q</a>
isolate_3	7	5	1	13	82	53	17	1997	ST-213 complex	<a href="#">Q</a>
isolate_4	6	5	53	3	74	8	54	9403		<a href="#">Q</a>
isolate_5	558	43	39	45	65	594	600	9057	ST-1494 complex (lactamica)	<a href="#">Q</a>
isolate_6	8	4	6	17	5	18	16	4399	ST-103 complex	<a href="#">Q</a>
isolate_7	222	3	58	275	30	3	255	8691	ST-4821 complex	<a href="#">Q</a>
isolate_8	222	1	58	261	263	5	255	11045	ST-4821 complex	<a href="#">Q</a>
isolate_9	662	3	4	3	8	7	6	11161	ST-11 complex	<a href="#">Q</a>
isolate_10	12	29	2	26	26	65	17	2040		<a href="#">Q</a>
isolate_11	9	6	9	9	9	6	653	12841	ST-41/44 complex	<a href="#">Q</a>
isolate_12	16	2	6	25	17	655	22	10137	ST-53 complex	<a href="#">Q</a>
isolate_13	4	10	2	5	3	453	9	7008		<a href="#">Q</a>
isolate_14	3	6	9	60	9	137	9	777	ST-41/44 complex	<a href="#">Q</a>
isolate_15	28	104	9	9	9	6	9	6747	ST-41/44 complex	<a href="#">Q</a>

## 11.8 Investigating allele differences

### 11.8.1 Sequence similarity

To find sequences most similar to a selected allele within a sequence definition database, expand the ‘Analysis’ menu item and click ‘Sequence similarity’ on the contents page.

Enter the locus and allele identifier of the sequence to investigate and the number of nearest matches you’d like to see, then press submit.

A list of nearest alleles will be displayed, along with the percentage identity and number of gaps between the sequences.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Sequence similarity

Help

## Find most similar alleles

This page allows you to find the most similar sequences to a selected allele using BLAST.

Select parameters Action

Locus: abcZ

Allele: 5

Number of results: 10

RESET SUBMIT

abcZ-5

Allele	% Identity	Mismatches	Gaps	Alignment	Compare
abcZ: 729	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 671	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 657	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 453	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 213	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 166	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 114	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 103	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 646	99.769	1	0	433/433	<a href="#">Compare</a>
abcZ: 405	99.769	1	0	433/433	<a href="#">Compare</a>

Click the appropriate ‘Compare’ button to display a list of nucleotide differences and/or a sequence alignment.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Sequence comparison

Help

## Allele sequence comparison

This tool allows you to select two alleles and highlight the nucleotide differences between them.

Select parameters Action

Locus: abcZ

Allele #1: 5

Allele #2: 729

SUBMIT

Nucleotide differences between abcZ: 5 and abcZ: 729

Identity: 99.77 %

Show alignment

Differences: 1

157: G → T

## 11.8.2 Sequence comparison

To directly compare two sequences, expand the ‘Analysis’ section and click ‘Sequence comparison’ on the contents page of a sequence definition database.

BIGSdb

Home > Organisms > Organism > Neisseria typing

## Neisseria typing database

### Query a sequence

**Single sequence**

Query a single sequence or whole genome assembly to identify allelic matches.

**Batch sequences**

Query multiple independent sequences in FASTA format to identify allelic matches.

### Find alleles

**By specific criteria**

Find alleles by matching criteria (all loci together)

**By locus**

Select, analyse and download specific alleles from a single locus.

### Search for allelic profiles

**By specific criteria**

Search, browse or enter list of profiles

**By allelic profile**

This can include partial matches to find related profiles.

**In a batch**

Look up multiple allelic profiles together.

LOG IN

SUBMISSIONS

DOWNLOADS +

EXPORT +

ANALYSIS -

Sequence similarity

**Sequence comparison**

Locus Explorer

CUSTOMISE +

INFORMATION +

ISOLATES

Enter the locus and two allele identifiers to compare. Press submit.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Sequence comparison

Help

## Allele sequence comparison

This tool allows you to select two alleles and highlight the nucleotide differences between them.

Select parameters

Locus:

Allele #1:

Allele #2:

Action

**SUBMIT**

A list of nucleotide differences and/or an alignment will be displayed.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Sequence comparison

Help

## Allele sequence comparison

This tool allows you to select two alleles and highlight the nucleotide differences between them.

Select parameters Action

Locus:

Allele #1:

Allele #2:

SUBMIT

Nucleotide differences between abcZ: 5 and abcZ: 8

Identity: 90.53 %

Show alignment

Differences: 41

72: G → T

78: A → G

79: A → C

81: T → C

82: G → A

83: G → A

87: G → A

88: A → G

89: G → A

90: T → C

93: G → C

See also:

*Locus explorer plugin.*

## 11.9 Browsing isolate data

Isolate records can be browsed by clicking the link to ‘Search database’.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates

## Neisseria isolates database

The Neisseria PubMLST database contains data for a collection of isolates that represent the total known diversity of Neisseria species. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.

Query database

[Search database](#)

Browse, search by any criteria, or enter list of attributes.

[Search by combinations of loci](#)

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

Leave query form fields blank (the display of these may vary depending on modification options set by the user). Choose the field to order the results by, the number of results per page to display, and click ‘Search’.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

66,602 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ								MLST		Finetyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1099		19	15	
4	M1027	B43; NIBSC_3076; Z1043	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex			
5	M00240227		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1100	ST-32 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	1101	ST-22 complex			
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex	20	9	F3-1
8	M00242007		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1102	ST-18 complex		14	
9	0021/84		Czech Republic	1984	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	114	ST-22 complex			
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	18-1	3	F5-1

Clicking the hyperlink for any record will display *full information* about the profile.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

66,602 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ								MLST		Finetyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1099		19	15	
4	M1027	B43; NIBSC_3076; Z1043	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex			
5	M00240227		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1100	ST-32 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	1101	ST-22 complex			
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex	20	9	F3-1
8	M00242007		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1102	ST-18 complex		14	
9	0021/84		Czech Republic	1984	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	114	ST-22 complex			
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	18-1	3	F5-1

## 11.10 Querying isolate data

The ‘Search database’ page of an isolate database allows you to also search by combinations of provenance criteria, scheme and locus data, and more.

To start with, only one provenance field search box is displayed but more can be added by clicking the ‘+’ button (highlighted). These can be linked together by ‘and’ or ‘or’.

After the search has been submitted, the results will be displayed in a table.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* Isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

Combine with: AND ▾

country ▾ = ▾ USA + ⓘ

year ▾ >= ▾ 2000

**Display/sort options**

Order by: id ▾ ascending ▾

Display: 25 ▾ records per page ⓘ

**Action**

RESET SEARCH

2,682 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
341	M7085		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex			
499	MDL01A0601		USA	2001	meningitis	<i>Neisseria meningitidis</i>	Y	1378	ST-23 complex			
500	MDL01A2447		USA	2001	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	Y	1379	ST-23 complex			
866	MDO1227		USA	2001		<i>Neisseria meningitidis</i>		1624	ST-167 complex			
867	MDO1056		USA	2001		<i>Neisseria meningitidis</i>		1625	ST-23 complex			
868	MDO1066		USA	2001		<i>Neisseria meningitidis</i>		1626	ST-269 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
2299	M7257		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	
2316	M7086		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	22	ST-22 complex	6	3	

Each field can be queried using *standard operators*.

More search features are available by clicking the ‘Modify form options’ tab on the top of the screen.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* Isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

Combine with: AND ▾

country ▾ = ▾ USA + ⓘ

year ▾ >= ▾ 2000

**Display/sort options**

Order by: id ▾ ascending ▾

Display: 25 ▾ records per page ⓘ

**Action**

RESET SEARCH

2,682 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
341	M7085		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex			
499	MDL01A0601		USA	2001	meningitis	<i>Neisseria meningitidis</i>	Y	1378	ST-23 complex			
500	MDL01A2447		USA	2001	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	Y	1379	ST-23 complex			
866	MDO1227		USA	2001		<i>Neisseria meningitidis</i>		1624	ST-167 complex			
867	MDO1056		USA	2001		<i>Neisseria meningitidis</i>		1625	ST-23 complex			
868	MDO1066		USA	2001		<i>Neisseria meningitidis</i>		1626	ST-269 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
2299	M7257		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	
2316	M7086		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	22	ST-22 complex	6	3	

A tab will be displayed. Different options will be available here depending on the database. Queries will be combined from the values entered in all form sections. Possible options are:

- Provenance fields
  - Search by combination of provenance field values, e.g. country, year, sender.
- Allele designations/scheme field values
  - Search by combination of allele designations and/or scheme fields e.g. ST, clonal complex information.

- Allele designation status
  - Search by whether allele designation status is confirmed or provisional.
- Tagged sequence status
  - Search by whether tagged sequence data is available for a locus. You can also search by sequence flags.
- Attribute values list
  - Enter a list of values for any provenance field, locus, or scheme field.
- Filters
  - Various filters may be available, including
    - \* Publications
    - \* Projects
    - \* MLST profile completion status
    - \* Clonal complex
    - \* Sequence bin size
    - \* Inclusion/exclusion of *old versions*

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

Combine with: AND ▾

country ▾ = ▾ USA + ⓘ

year ▾ >= ▾ 2000

Display/sort options

Order by: id

Display: 25 ▾ records per page ⓘ

Action

RESET SEARCH

2,682 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ							MLST		Fine		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR	...
341	M7085		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex		
499	MDL01A0601		USA	2001	meningitis	<i>Neisseria meningitidis</i>	Y	1378	ST-23 complex		
500	MDL01A2447		USA	2001	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	Y	1379	ST-23 complex		
866	MDO1227		USA	2001		<i>Neisseria meningitidis</i>		1624	ST-167 complex		
867	MDO1056		USA	2001		<i>Neisseria meningitidis</i>		1625	ST-23 complex		
868	MDO1066		USA	2001		<i>Neisseria meningitidis</i>		1626	ST-269 complex		
2281	M7089		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2 F1-1
2299	M7257		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
2316	M7086		USA	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	22	ST-22 complex	6	3

✕

Modify form parameters

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters

If the interface is modified, a button to save options becomes available within the tab. If this is clicked, the modified form will be displayed the next time you go to the query page.

### 11.10.1 Query by allele designation/scheme field

Queries can be combined with allele designation/scheme field values.

Make sure that the allele designation/scheme field values fieldset is displayed by selecting it in the ‘Modify form options’ tab.

The screenshot shows the BIGSdb search interface. The main search form has two sections: 'Isolate provenance fields' and 'Allele designations/scheme fields'. The 'Isolate provenance fields' section has a dropdown menu for 'id' and a text input for 'Enter value...'. The 'Allele designations/scheme fields' section has a dropdown menu for 'ST (MLST)' and a text input for '11'. The 'Display/sort options' section has a dropdown for 'Order by: id' and a dropdown for 'Display: 25 records per page'. The 'Action' section has 'RESET' and 'SEARCH' buttons. A 'Modify form parameters' dialog box is open on the right, showing a list of fields to be included in the query. The 'Allele designations/scheme field values' field is highlighted with a red box. The dialog box also has a 'Help' button and a 'Filters' button.

Designations can be queried using *standard operators*.

Additional search terms can be combined using the ‘+’ button.

Add your search terms and click ‘Submit’. Allele designation/scheme field queries will be combined with terms entered in other sections.

The screenshot shows the BIGSdb search interface with the search results for the query 'ST (MLST) = 11'. The search results are displayed in a table with columns: Id, Isolate, aliases, country, year, disease, species, capsule group, ST, and MLST. The results show 6,991 records returned (1 - 25 displayed). The table is paginated, showing records 1 through 6. The 'ST' column shows '11' for all records, and the 'MLST' column shows 'ST-11 complex' for all records.

Id	Isolate	aliases	country	year	disease	species	capsule group	ST	MLST
79	160		USA	1993	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
100	638		USA	1994	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
156	00-1008		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
161	00-1050		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
162	00-1122		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
164	00-1245		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
165	00-1257		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
166	00-1263		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	B	11	ST-11 complex
167	00-1264		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex
168	00-1299		UK [Scotland]	2000	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex

## 11.10.2 Query by allele designation count

Queries can be combined with counts of the total number of designations or for individual loci.

Make sure that the allele designation counts fieldset is displayed by selecting it in the ‘Modify form options’ tab.

The screenshot shows the BIGSdb search interface. At the top, there's a navigation bar with 'Home > Organisms > Neisseria spp. > Neisseria isolates > Search or browse database'. Below this is a search bar with the text 'Search or browse database'. To the right of the search bar are icons for Help, Information, and a wrench. Below the search bar is a form with two tabs: 'Isolate provenance fields' and 'Display/sort options'. The 'Isolate provenance fields' tab is active, showing a search criteria field with 'id' selected and a search button. The 'Display/sort options' tab is also visible, showing 'Order by: id' and 'Display: 25 records per page'. A 'Modify form parameters' dialog box is open on the right, showing a list of fields to include or exclude. The 'Allele designation counts' field is highlighted with a red box.

For example, to find all isolates that have designations at >1000 loci, select ‘total designations > 1000’, then click ‘Submit’.

The screenshot shows the BIGSdb search interface. At the top, there's a navigation bar with 'Home > Organisms > Neisseria spp. > Neisseria isolates > Search or browse database'. Below this is a search bar with the text 'Search or browse database'. To the right of the search bar are icons for Help, Information, and a wrench. Below the search bar is a form with two tabs: 'Isolate provenance fields' and 'Allele designation counts'. The 'Allele designation counts' tab is active, showing a search criteria field with 'total designations > 1000' entered. The 'Isolate provenance fields' tab is also visible, showing a search criteria field with 'id' selected and a search button. Below the search bar, the results show 27,528 records returned (1 - 25 displayed). A table of results is displayed below the search bar.

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	18-1	3	F5-1
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-6
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5

You can also search for isolates where any isolate has a particular number of designations. Use the term ‘any locus’ to do this.

Finally, you can search for isolates with a specific number of designations at a specific locus.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... ⓘ

**Allele designation counts**

Count of abcZ > 1 ⓘ

**Display/sort options**

Order by: id ascending ⓘ

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

10 records returned. Click the hyperlinks for detailed information.

Isolate fields ⓘ							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
451	14/1455	NIBSC_2732; Z4717	Russia	1970	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex	20	9	F3-1
887	OX9930357		UK [England]	1999	carrier	<i>Neisseria meningitidis</i>	B	43	ST-41/44 complex	19	15-1	F1-98
3412	OX9931676		UK [England]	1999	carrier	<i>Neisseria meningitidis</i>	B	1228	ST-41/44 complex	7-1	1	
3415	OX9931776		UK [England]	1999	carrier	<i>Neisseria meningitidis</i>	B	1644	ST-213 complex	22	14	F5-5
4193	OX9931563		UK [England]	1999	carrier	<i>Neisseria meningitidis</i>	C	136	ST-41/44 complex	5	2	F1-20
34733	LNP15075		Burkina Faso	1997		<i>Neisseria meningitidis</i>				20	10-1	F3-1
57890	15134		Spain	2002	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W			5-1	10-4	F1-18,F1-7
61162	NmissMen5		Italy	2016		<i>Neisseria meningitidis</i>				12	16-11	F1-5
89074	61/2013		Austria	2013	meningitis	<i>Neisseria meningitidis</i>	B	1193,15334	ST-116 complex	21	10-1,16	F1-5,F4-2
91694	NML2009-301		Canada	2009		<i>Neisseria meningitidis</i>	B	154,9411	ST-41/44 complex	7-2	4	F1-18

Additional search terms can be combined using the ‘+’ button. Designation count queries will be combined with terms entered in other sections.

**Note:** Searches for ‘all loci’ with counts that include zero, e.g. ‘count of any locus = 0’ or with a ‘<’ operator are not supported. This is because such searches have to identify every isolate for which one or more loci are missing. In databases with thousands of loci this can be a very expensive database query.

### 11.10.3 Query by allele designation status

Allele designations can be queried based on their status, i.e. whether they are confirmed or provisional. Queries will be combined from the values entered in all form sections.

Make sure that the allele designation status fieldset is displayed by selecting it in the ‘Modify form options’ tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⓘ ⓘ

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... ⓘ

**Display/sort options**

Order by: id

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

**Modify form parameters**

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status**
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters

Select a locus from the dropdown box and either ‘provisional’ or ‘confirmed’. Additional query fields can be displayed by clicking the ‘+’ button. Click ‘Submit’.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

Allele designation status

id = Enter value... ⓘ

ack is provisional ⓘ

Display/sort options

Action

Order by: id ascending ⓘ

Display: 25 records per page ⓘ

RESET SEARCH

2 records returned. Click the hyperlinks for detailed information.

Isolate fields ⓘ							MLST		Finetyping antigens			
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
14733	NJ9703	BennettTree32	Unknown			Neisseria subflava		10304				
19363	961-5945		Unknown			Neisseria meningitidis	B	153	ST-8 complex	21	16	F5-8

### Analysis tools

Breakdown:

Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis:

BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export:

Dataset Contigs Sequences

Third party:

GrapeTree iTOL PhyloViz Microreact

Provisional allele designations are marked within the results tables with a pink background. Any scheme field designations that depend on the allele in question, e.g. a MLST ST, will also be marked as provisional.

## 11.10.4 Query by annotation status

Isolates can be queried by the annotation status of particular schemes if these have been set up. The idea is that for a well-annotated record the isolate would be expected to have allele designations for all loci in the scheme. Alternatively, different thresholds for number of loci with allele designations can be set up by the scheme administrator to indicate good or bad quality thresholds.

Make sure that the annotation status fieldset is displayed by selecting it in the ‘Modify form options’ tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

**Modify form parameters**

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Annotation status**
- Sequence bin
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters

Additional search terms can be combined using the ‘+’ button. Annotation status queries will be combined with terms entered in other sections.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Annotation status**

Combine with: AND

Ribosomal MLST good + ⓘ

MLST good

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

31,286 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

⏪ ⏩ 1 2 3 4 5 6 ⏪ ⏩

Isolate fields ⓘ										MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR		
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex	5-2	10	F1-5		
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F5-1		
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex	20	9	F3-1		
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	18-1	3	F5-1		
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F3-6		
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F5-1		
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex	7	13-1	F1-5		

### 11.10.5 Query by sequence bin size and number of contigs

Isolates can be queried based on the total length of sequences within the sequence bin, the number of contigs, the N50 and/or the L50 values.

Make sure that the sequence bin fieldset is displayed by selecting it in the ‘Modify form options’ tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

**Modify form parameters**

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Sequence bin**
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters

Additional search terms can be combined using the ‘+’ button. Sequence bin queries will be combined with terms entered in other sections.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Sequence bin**

Combine with: AND

total length (Mbp) > 1.8 + ⓘ

number of contigs <= 50 + ⓘ

**Display/sort options**

Order by: id ascending

Display: 25 records per page ⓘ

RESET SEARCH

573 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« 1 2 3 4 5 6 »

Isolate fields ⓘ									MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR	
30	14	BennettTree10; alpha14	Germany	1999	carrier	<i>Neisseria meningitidis</i>	cnt	53	ST-53 complex	7	30-3	F5-5	
237	H44/76	44/76-3; NIBSC_2724; Z3842	Norway	1976	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	32	ST-32 complex	7	16	F3-3	
240	MC58	BennettTree07; Z7176	UK	1983		<i>Neisseria meningitidis</i>	B	74	ST-32 complex	7	16-2	F1-5	
613	Z2491	BennettTree09; C751; NIBSC_2763; Z6244	The Gambia	1983	meningitis	<i>Neisseria meningitidis</i>	A	4	ST-4 complex	7	13-1	F1-5	
638	G2136	NIBSC_2743; Z6411	UK [England]	1986	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	8	ST-8 complex	5-2	10-1	F3-6	
698	FAM18	BennettTree11; NIBSC_3076; Z4259	USA	1983	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	C	11	ST-11 complex	5	2	F1-30	

## 11.10.6 Query by sequence tag count

Queries can be combined with counts of the total number of tags or for individual loci.

Make sure that the tagged sequence counts fieldset is displayed by selecting it in the ‘Modify form options’ tab.

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Display/sort options**

Order by: id

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

**Modify form parameters**

Click to add or remove additional query terms:

- ☐ Provenance fields
- ☒ Secondary metadata
- ☒ Allele designations/scheme field values
- ☒ Allele designation counts
- ☒ Allele designation status
- ☒ Tagged sequence counts
- ☒ Tagged sequence status
- ☒ Attribute values list
- ☒ Filters

For example, to find all isolates that have sequence tags at >1000 loci, select ‘total tags > 1000’, then click ‘Submit’.

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value... + ⓘ

**Tagged sequence counts**

Count of total tags > 1000 + ⓘ

**Display/sort options**

Order by: id

Display: 25 records per page ⓘ

**Action**

RESET SEARCH

27,521 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

Isolate fields ⓘ								MLST		Finetyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	18-1	3	F5-1
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-6
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5

You can also search for isolates where any isolate has a particular number of sequence tags. Use the term ‘any locus’ to do this.

Finally, you can search for isolates with a specific number of tags at a specific locus.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria Isolates](#) > Search or browse database


## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields** **Tagged sequence counts**

id = Enter value... **Count of BACT000065 (rpmJ) = 2**

**Display/sort options** **Action**

Order by: id ascending

Display: 25 records per page

[RESET](#) [SEARCH](#)

27,187 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.



Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-6
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5
31	10	B269; NIBSC_2825; Z1269	Burkina Faso	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5

Additional search terms can be combined using the ‘+’ button. Sequence tag count queries will be combined with terms entered in other sections.

**Note:** Searches for ‘all loci’ with counts that include zero, e.g. ‘count of any locus = 0’ or with a ‘<’ operator are not supported. This is because such searches have to identify every isolate for which one or more loci are not tagged. In databases with thousands of loci this can be a very expensive database query.

### 11.10.7 Query by tagged sequence status

Sequence tags identify the region of a contig within an isolate’s sequence bin entries that correspond to a particular locus. The presence or absence of these tags can be queried as can whether or not the sequence has an a flag associated with. These flags designate specific characteristics of the sequences. Queries will be combined from the values entered in all form sections.

Make sure that the tagged sequences status fieldset is displayed by selecting it in the ‘Modify form options’ tab.

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

id = Enter value...

Action

RESET SEARCH

Display/sort options

Order by: id

Display: 25 records per page

Modify form parameters

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Tagged sequence counts
- Tagged sequence status**
- Attribute values list
- Filters

Select a specific locus in the dropdown box (or alternatively 'any locus') and a status. Available status values are:

- **untagged**
  - The locus has not been tagged within the sequence bin.
- **tagged**
  - The locus has been tagged within the sequence bin.
- **complete**
  - The locus sequence is complete.
- **incomplete**
  - The locus sequence is incomplete - normally because it continues beyond the end of a contig.
- **flagged: any**
  - The sequence for the locus has a flag set.
- **flagged: none**
  - The sequence for the locus does not have a flag set.
- **flagged: <specific flag>**
  - The sequence for the locus has the specific flag chosen.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields Tagged sequence status

id = Enter value... NEIS0001 (pxC) is flagged: internal stop codon

Display/sort options Action

Order by: id ascending

Display: 25 records per page

RESET SEARCH

1 record returned. Click the hyperlink for detailed information.

Isolate fields ⓘ										MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR		
2077	153	alpha153	Germany	1999	carrier	<i>Neisseria meningitidis</i>	E	60	ST-60 complex	5	2	F1-7		

Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

**See also:***Sequence tag flags*

### 11.10.8 Query by list of attributes

The query form can be modified with a list box in to which a list of values for a chosen attribute can be entered - this could be a list of ids, isolate names, alleles or scheme fields. This list will be combined with any other criteria or filter used on the page.

If the list box is not shown, add it by selecting it in the ‘Modify form options’ tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields Display/sort options

id = Enter value... Order by: id

Display: 25 records per page

Action

RESET SEARCH

✕

Modify form parameters

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters

Select the attribute to query and enter a list of values.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙️

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

id = Enter value... ⓘ

Attribute values list

Field: id

1  
2  
3  
4  
5

Display/sort options

Order by: id ascending

Display: 25 records per page ⓘ

RESET SEARCH

5 records returned. Click the hyperlinks for detailed information.

Isolate fields ⓘ							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	<i>Neisseria meningitidis</i>	A	1	ST-1 complex	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1099		19	15	
4	M1027	B43; NIBSC_3076; Z1043	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex			
5	M00240227		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	1100	ST-32 complex	7	16	

### Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree iTOL PhyloViz Microreact

## 11.10.9 Query filters

There are various filters that can additionally be applied to queries, or the filters can be applied solely on their own so that they filter the entire database.

Make sure that the filters fieldset is displayed by selecting it in the ‘Modify form options’ tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Help ⓘ ⚙️

## Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

id = Enter value... ⓘ

Display/sort options

Order by: id

Display: 25 records per page ⓘ

RESET SEARCH

✕

Modify form parameters

Click to add or remove additional query terms:

- Provenance fields
- Secondary metadata
- Allele designations/scheme field values
- Allele designation counts
- Allele designation status
- Tagged sequence counts
- Tagged sequence status
- Attribute values list
- Filters**

The filters displayed will depend on the database and what has been defined within it. Common filters are:

- Publication - Select one or more publication that has been linked to isolate records.
- Project - Select one or more project that isolates belong to.
- Profile completion - This is commonly displayed for MLST schemes. Available options are:
  - complete - All loci of the scheme have alleles designated.
  - incomplete - One or more loci have not yet been designated.
  - partial - The scheme is incomplete, but at least one locus has an allele designated.
  - started - At least one locus has an allele designated. The scheme may be complete or partial.
  - not started - The scheme has no loci with alleles designated.
- **Provenance fields - Dropdown list boxes of values for specific provenance** fields may be present if set for the database. Users can choose to *add additional filters*.
- **Old record versions - Checkbox which, if selected, will include all record** versions in a query.

### 11.10.10 Querying by allelic profile

If a scheme, such as MLST, has been defined for an isolate database it is possible to query the database against complete or partial allelic profiles. Even if no scheme is defined, queries can be made against all loci.

On the index page, click ‘Search by combinations of loci (profiles)’ for any defined scheme. Enter either a partial (any combination of loci) or complete profile.

The screenshot displays the BIGSdb interface for the Neisseria isolates database. At the top, the header reads 'BIGSdb' and the breadcrumb trail is 'Home > Organisms > Neisseria spp. > Neisseria isolates'. Below this, the title 'Neisseria isolates database' is shown. A descriptive paragraph states: 'The Neisseria PubMLST database contains data for a collection of isolates that represent the total known diversity of Neisseria species. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.'

The main content area is titled 'Query database' and contains two search input fields. The first field is labeled 'Search database' with the instruction 'Browse, search by any criteria, or enter list of attributes.' The second field is labeled 'Search by combinations of loci' with the instruction 'This can include partial matches to find related isolates.' This second field is highlighted with a red rectangular border. To the right of the search area is a vertical sidebar with several navigation buttons: 'LOG IN' (with a key icon), 'SUBMISSIONS' (with an upload icon), 'PROJECTS' (with a list icon and a '+' button), 'EXPORT' (with a document icon and a '+' button), 'ANALYSIS' (with a bar chart icon), 'CUSTOMISE' (with a gear icon and a '+' button), 'INFORMATION' (with an 'i' icon and a '+' button), and 'TYPING' (with a list icon).

If multiple schemes are defined, you may have to select the scheme you wish to query in the ‘Schemes’ dropdown box and click ‘Select’.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search by locus combinations

Help ⓘ

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST

Please enter your allelic profile below. Blank loci will be ignored. Autofill profile by searching remote database

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST:
							<input type="button" value="Autofill"/>

Filters

Project:  ⓘ

☐ Include old record versions

Options

Search:

Display/sort options

Order by:

Display:  records per page ⓘ

Action

Enter the combination of alleles that you want to query for. Fields can be left blank.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search by locus combinations

Help ⓘ ⓘ ⓘ

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST

Please enter your allelic profile below. Blank loci will be ignored. Autofill profile by searching remote database

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST:
2	3	4	3	8	4	6	<input type="button" value="Autofill"/>

Filters

Project:  ⓘ

☐ Include old record versions

Options

Search:

Display/sort options

Order by:

Display:  records per page ⓘ

Action

Alternatively, for scheme profiles, you can enter a primary key value (e.g. ST) and select 'Autofill' to automatically fill in the associated profile.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search by locus combinations

Help ⓘ ⌵

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST Select

Please enter your allelic profile below. Blank loci will be ignored. Autofill profile by searching remote database

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST:
9	6	9	9	9	6	9	44 <span>Autofill</span>

Filters

Project: ⓘ

☐ Include old record versions

Options

Search: Exact or nearest match

Display/sort options

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

Select the number of loci that you'd like to match in the options dropdown box. Available options are:

- Exact or nearest match
- Exact match only
- x or more matches
- y or more matches
- z or more matches

Where x,y, and z will range from n-1 to 1 where n is the number of loci in the scheme.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search by locus combinations

Help ⓘ ⌵

## Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST Select

Please enter your allelic profile below. Blank loci will be ignored. Autofill profile by searching remote database

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST:
9	6	9	9	9	6	9	44 <span>Autofill</span>

Filters

Project: ⓘ

☐ Include old record versions

Options

Search: Exact or nearest match

Display/sort options

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

Click 'Search'.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Search by locus combinations

Help ⓘ ⓘ ⓘ

### Search by locus combinations

Schemes

Please select the scheme you would like to query:

MLST Select

Please enter your allelic profile below. Blank loci will be ignored.

Autofill profile by searching remote database

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST: 44	Autofill
9	6	9	9	9	6	9		

Filters

Project: ⓘ

☐ Include old record versions

Options

Search: Exact or nearest match

Display/sort options

Order by:

id

Display: 25 records per page ⓘ

Action

RESET SEARCH

Exact matches found (7 loci).

195 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

<< < 1 2 3 4 5 6 > >>

Isolate fields ⓘ								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
41	19		Germany	1999	carrier	Neisseria meningitidis	B	44	ST-41/44 complex			
70	38		Germany	1999	carrier	Neisseria meningitidis	NG	44	ST-41/44 complex			
427	NG E30	NIBSC_2804; Z4692	Norway	1988	carrier	Neisseria meningitidis	B	44	ST-41/44 complex	21	16	F1-7
774	99-182		Canada	1999	invasive (unspecified/other)	Neisseria meningitidis	B	44	ST-41/44 complex			
792	99-132		Canada	1999	invasive (unspecified/other)	Neisseria meningitidis	B	44	ST-41/44 complex			
975	0069/93		Czech Republic	1993	carrier	Neisseria meningitidis	B	44	ST-41/44 complex	22	14-4	F1-7
1097	3532	Z7184	The Netherlands	1975		Neisseria meningitidis	B	44	ST-41/44 complex		4	
1603	0213/93		Czech Republic	1993	carrier	Neisseria meningitidis	B	44	ST-41/44 complex	22	14-4	F1-19
1604	0214/93		Czech Republic	1993	carrier	Neisseria meningitidis	B	44	ST-41/44 complex	22	14-4	F1-7
1633	0244/93		Czech Republic	1993	carrier	Neisseria meningitidis	B	44	ST-41/44 complex	22	14-4	F1-7

### 11.11 Bookmarking an isolate query

Once you have made an isolate database query, you can bookmark it so that it can be repeated in the future. You need to have an account and be logged in to the database to be able to bookmark.

Following a query, there will be a ‘Bookmark query’ section in the results header section. Enter a name for the bookmark (a default name based on the date will be shown) and click ‘Add bookmark’.

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Chapter 11. Querying data

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

Combine with: AND

continent = Europe

year >= 2014

**Filters**

Publication: Select options

Project: Select options

MLST profiles: ST-11 complex

Clonal complex (MLST): ST-11 complex

Sequence bin: Sequence bin size >= 2 Mbp

☐ Include old record versions

Add filter: Add

**Display/sort options**

Order by: id ascending

Display: 25 records per page

**Action**

RESET SEARCH

2,302 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

**Your projects**

Select project... Add these records

**Bookmark query**

2020-07-28:1 Add bookmark

<< < 1 2 3 4 5 6 > >>

Isolate fields							MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	FetA VR
30154	M14 240001		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30155	M14 240002		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30156	M14 240007		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30157	M14 240013		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30158	M14 240019		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30159	M14 240022		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	8621	ST-11 complex	5	2
30160	M14 240026		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30161	M14 240029		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2
30162	M14 240031		UK [England]	2014	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2

A new top-right tab will appear when you have saved bookmarks. You can click on this to easily access all saved bookmarks.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id = Enter value...

**Display/sort options**

Order by: id ascending

Display: 25 records per page

**Action**

RESET SEARCH

**Bookmarks**

- 2020-07-28:1

Manage bookmarks

You can also access your bookmarks from the main contents page. A link will appear in the query section once you have saved a bookmark.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

The *Neisseria* PubMLST database contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.

### Query database

[Search database](#)

Browse, search by any criteria, or enter list of attributes.

[Search by combinations of loci](#)

This can include partial matches to find related isolates.

[Bookmarks](#)

Retrieve dataset from bookmarked queries.

LOG OUT

SUBMISSIONS 1

PRIVATE DATA

PROJECTS

EXPORT

ANALYSIS

CUSTOMISE

INFORMATION

TYPING

JOBS 1

This will take you to a page where you can manage your bookmarks.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Bookmarks

## Bookmarks

Please note that only you will be able to access a query defined by a bookmark if it is shown as locked.

Click the padlock icon to make it publicly shareable - you can then copy the URL from the 'Run query' field and share this with colleagues.

Delete	Name	Database configuration	Created	Share	Run query
	2020-07-28:1 pubmlst_neisseria_isolates	2020-07-28			

You can go to a bookmarked search by clicking on the 'Run query' icon. By default, a bookmark can only be used by the logged-in user who created it. This is for privacy reasons to prevent other users from finding out what terms are being used for a search. If, however, you wish to share the URL to the query, you can make it shareable by clicking the padlock icon.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Bookmarks

## Bookmarks

Please note that only you will be able to access a query defined by a bookmark if it is shown as locked.

Click the padlock icon to make it publicly shareable - you can then copy the URL from the 'Run query' field and share this with colleagues.

Delete	Name	Database configuration	Created	Share	Run query
	2020-07-28:1 pubmlst_neisseria_isolates	2020-07-28			

The icon will change to a green open padlock. You can right-click on the ‘Run query’ link to copy the URL if you wish to share it with others.

**BIGSdb**

Home > Organisms > Neisseria spp. > Neisseria isolates > Bookmarks

## Bookmarks

Please note that only you will be able to access a query defined by a bookmark if it is shown as locked.  
Click the padlock icon to make it publicly shareable - you can then copy the URL from the 'Run query' field and share this with colleagues.

Delete	Name	Database configuration	Created	Share	Run query
	2020-07-28:1 pubmlst_neisseria_isolates	2020-07-28			

Bookmarks can be deleted by clicking on the delete icon.

## 11.12 Retrieving isolates by linked publication

Click ‘Analysis’ on the contents page.

**BIGSdb**

Home > Organisms > Neisseria spp. > Neisseria isolates

## Neisseria isolates database

The Neisseria PubMLST database contains data for a collection of isolates that represent the total known diversity of Neisseria species. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.

### Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS

EXPORT

**ANALYSIS**

CUSTOMISE

INFORMATION

TYPING

Click ‘Publication breakdown’

## BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugin summary

## Analysis plugins

Categories - Jump to: [Breakdown](#) | [Analysis](#) | [Third party](#)

## Breakdown

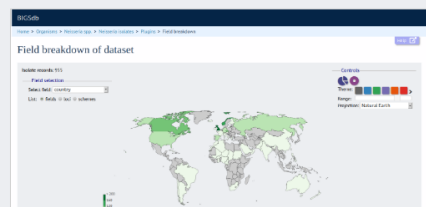
Breakdown plugins - Jump to: [Field Breakdown](#) | [Two Field Breakdown](#) | [Unique Combinations](#) | [Polymorphisms](#) | **[Publication Breakdown](#)** | [Sequence Bin Breakdown](#)

## Field Breakdown

Summary: Breakdown of query results by field

The field breakdown plugin displays the frequency of each value for fields, alleles and schemes. Output is in the form of dynamic charts, maps, and tables. Data can be exported as an Excel file, SVG image, or FASTA file.

Documentation [bigsdb.readthedocs.io](https://bigsdb.readthedocs.io)



Then click ‘Launch Publication Breakdown’.

## Publication Breakdown

Summary: Breakdown of query results by publication

This plugin shows all publications linked to isolates in a query dataset or within the whole database. The results can be filtered by author or year. The output includes full citation details and a link to display all isolates linked to any listed publication.

Documentation [bigsdb.readthedocs.io](https://bigsdb.readthedocs.io)

ID	Author	Title	Year	Isolates
1000000000	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000001	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000002	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000003	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000004	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000005	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000006	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000007	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000008	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10
1000000009	Smith J, Jones K	Genomic analysis of <i>Neisseria meningitidis</i> serotype 4 isolates	2010	10

Launch ‘Publication Breakdown’

## Sequence Bin Breakdown

Summary: Breakdown of sequence bin contig properties

The sequence bin breakdown plugin calculates statistics based on the number and length of contigs in the sequence bin as well as the number of loci tagged for each isolate record. Using this latter metric against a cgMLST scheme can be a good indicator of genome quality. Values for number of contigs, total sequence length, mean contig length and contig length distribution are charted.

Documentation [bigsdb.readthedocs.io](https://bigsdb.readthedocs.io)

A list of publications linked by isolates within the database will be displayed.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > Publications

Help

## Publication breakdown of dataset

Filter query by      Display      Action

Author: All authors      Order by: number of isolates      descending      SUBMIT

Year: All years      Display: 25 records per page

138 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

« < 1 2 3 4 5 6 > »

PubMed id	Year	Citation	Title	Isolates in database
<a href="#">32163580</a>	2020	Harrison OB, Cehovin A, Skett J, Jolley KA, Massari P, Genco CA, Tang CM, Maiden MCJ (2020) <i>J Infect Dis</i> [Epub ahead of print]:	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance.	<a href="#">3705 isolates</a>
<a href="#">30687793</a>	2018	Rodrigues CMC, Chan H, Vipond C, Jolley K, Harrison OB, Wheeler J, Whiting G, Feavers IM, Maiden MCJ (2018) <i>Wellcome Open Res</i> <b>3</b> : 151	Typing complex meningococcal vaccines to understand diversity and population structure of key vaccine antigens.	<a href="#">3505 isolates</a>
<a href="#">29553330</a>	2018	Rodrigues CMC, Lucidarme J, Borrow R, Smith A, Cameron JC, Moxon ER, Maiden MCJ (2018) <i>Emerg Infect Dis</i> <b>24</b> : 673-682	Genomic Surveillance of 4CMenB Vaccine Antigenic Variants among Disease-Causing <i>Neisseria meningitidis</i> Isolates, United Kingdom, 2010-2016.	<a href="#">3066 isolates</a>
<a href="#">27521232</a>	2016	Brehony C, Rodrigues CM, Borrow R, Smith A, Cunney R, Moxon ER, Maiden MC (2016) <i>Vaccine</i> <b>34</b> : 4690-7	Distribution of Bexsero® Antigen Sequence Types (BASTs) in invasive meningococcal disease isolates: Implications for	<a href="#">2016 isolates</a>

These can be filtered by author and/or year, and the sort order changed.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > Publications

Help

## Publication breakdown of dataset

Filter query by      Display      Action

Author: Jolley KA      Order by: number of isolates      descending      SUBMIT

Year: All years      Display: 25 records per page

19 records returned. Click the hyperlinks for detailed information.

PubMed id	Year	Citation	Title	Isolates in database
<a href="#">32163580</a>	2020	Harrison OB, Cehovin A, Skett J, Jolley KA, Massari P, Genco CA, Tang CM, Maiden MCJ (2020) <i>J Infect Dis</i> [Epub ahead of print]:	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance.	<a href="#">3705 isolates</a>
<a href="#">17517841</a>	2007	Taha MK, Vázquez JA, Hong E, Bennett DE, Bertrand S, Bukovski S, Cafferkey MT, Carion F, Christensen JJ, Diggle M, Edwards G, Enriquez R, Fazio C, Frosch M, Heuberger S, Hoffmann S, Jolley KA, Kadlubowski M, Kechrid A, Kesanopoulos K, Kriz P, Lamberts L, Levenet I, Musilek M, Paragi M, Sager A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zorantonelli ML (2007) <i>Antimicrob Agents Chemother</i> <b>51</b> : 2784-92	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> .	<a href="#">1666 isolates</a>
<a href="#">18815379</a>	2008	Buckee CO, Jolley KA, Recker M, Penman B, Kriz P, Gupta S, Maiden MC (2008) <i>Proc Natl Acad Sci U S A</i> <b>105</b> : 15082-7	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> .	<a href="#">1054 isolates</a>
<a href="#">26515523</a>	2015	Hill DM, Lucidarme J, Gray SJ, Newbold LS, Ure R, Brehony C, Harrison OB, Bray JE, Jolley KA, Bratcher HB, Parkhill J, Tang CM, Borrow R, Maiden MC (2015) <i>Lancet Infect Dis</i> <b>15</b> : 1420-8	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study.	<a href="#">899 isolates</a>
<a href="#">15776372</a>	2005	Claus H, Maiden MC, Wilson DJ, McCarthy ND, Jolley KA, Urwin R, Hessler F, Frosch M, Vogel U (2005) <i>J Infect Dis</i> <b>191</b> : 1263-71	Genetic analysis of meningococci carried by children and young adults.	<a href="#">822 isolates</a>

To display the isolate records for any of the displayed publications, click the button to the right of the citation.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > Publications

Help

## Publication breakdown of dataset

Filter query by
Display
Action

Author: Jolley KA
Year: All years
Order by: number of isolates
Display: 25 records per page
SUBMIT

19 records returned. Click the hyperlinks for detailed information.

PubMed id	Year	Citation	Title	Isolates in database
<a href="#">32163580</a>	2020	Harrison OB, Cehovin A, Skett J, Jolley KA, Massari P, Genco CA, Tang CM, Maiden MCJ (2020) <i>J Infect Dis</i> [Epub ahead of print]:	<i>Neisseria gonorrhoeae</i> Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance.	<a href="#">3705 isolates</a>
<a href="#">17517841</a>	2007	Taha MK, Vázquez JA, Hong E, Bennett DE, Bertrand S, Bukovski S, Cafferkey MT, Carlon F, Christensen JJ, Diggle M, Edwards G, Enriquez R, Fazio C, Frosch M, Heuberger S, Hoffmann S, Jolley KA, Kadłubowski M, Kechrid A, Kesanopoulos K, Kriz P, Lambertsen L, Levenet I, Musilek M, Paragi M, Sagner A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zarantonelli ML (2007) <i>Antimicrob Agents Chemother</i> <b>51</b> : 2784-92	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> .	<a href="#">1666 isolates</a>
<a href="#">18815379</a>	2008	Buckee CO, Jolley KA, Recker M, Penman B, Kriz P, Gupta S, Maiden MC (2008) <i>Proc Natl Acad Sci U S A</i> <b>105</b> : 15082-7	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> .	<a href="#">1054 isolates</a>
<a href="#">26515523</a>	2015	Hill DM, Lucidarme J, Gray SJ, Newbold LS, Ure R, Brehony C, Harrison OB, Bray JE, Jolley KA, Bratcher HB, Parkhill J, Tang CM, Borrow R, Maiden MC (2015) <i>Lancet Infect Dis</i> <b>15</b> : 1420-8	Genomic epidemiology of age-associated meningococcal lineages in national surveillance: an observational cohort study.	<a href="#">899 isolates</a>
<a href="#">15776372</a>	2005	Claus H, Maiden MC, Wilson DJ, McCarthy ND, Jolley KA, Urwin R, Hessler F, Frosch M, Vogel U (2005) <i>J Infect Dis</i> <b>191</b> : 1263-71	Genetic analysis of meningococci carried by children and young adults.	<a href="#">822 isolates</a>

The abstract of the paper will be displayed (if available), along with all isolates linked to it.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Publication dataset

Publication dataset
Citation query (PubMed id: 32163580)

Harrison OB, Cehovin A, Skett J, Jolley KA, Massari P, Genco CA, Tang CM, Maiden MCJ (2020) *J Infect Dis* [Epub ahead of print]:  
***Neisseria gonorrhoeae* Population Genomics: Use of the Gonococcal Core Genome to Improve Surveillance of Antimicrobial Resistance.**  
Clustering with cgMLST identified globally distributed, persistent, gonococcal lineages improving understanding of the population biology of gonococci and revealing its population structure. These findings have implications for the emergence of antimicrobial resistance in gonococci and how this is associated with lineages, some of which are more predisposed to developing antimicrobial resistance than others.

3,705 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

1 2 3 4 5 6

id	isolate	aliases	Isolate fields			species	capsule group	MLST		Finotyping antigens		
			country	year	disease			ST	clonal complex	PorA VR1	PorA VR2	FetA VR
<a href="#">2855</a>	FA1090	BennettTree06; NC_002946	USA	1980		<i>Neisseria gonorrhoeae</i>		1899		18-10	43	F1-27
<a href="#">13685</a>	NCCP11945	BennettTree04; NC_011035	South Korea	2005		<i>Neisseria gonorrhoeae</i>		1901		18-10	43	F3-14
<a href="#">14729</a>	M5-11	BennettTree05; NC_022240	USA	1960		<i>Neisseria gonorrhoeae</i>		6959		18-10	43	F4-7
<a href="#">15698</a>	DGI2		USA			<i>Neisseria gonorrhoeae</i>		8421		18-10	43	F3-14
<a href="#">15935</a>	PID24	BennettTree01	USA			<i>Neisseria gonorrhoeae</i>		8418		18-10	43	F1-26
<a href="#">15936</a>	DGI18	BennettTree02	USA			<i>Neisseria gonorrhoeae</i>		8418		18-10	43	F1-26
<a href="#">21065</a>	TCDC-NG08107		Unknown	2008		<i>Neisseria gonorrhoeae</i>		7363		18-10	43	F1-26
<a href="#">21066</a>	PID18		Unknown			<i>Neisseria gonorrhoeae</i>		1926		18-10	43	F1-26
<a href="#">21067</a>	1291		Unknown			<i>Neisseria gonorrhoeae</i>		8422		18-10	43	F4-7

## 11.13 User-configurable options

The BIGSdb user interface is configurable in a number of ways. Choices made are remembered between sessions. If the database requires you to log on, the options are associated with your user account, whereas if it is a public database, that you haven't logged in to, the options are associated with a browser cookie so they will be remembered if you connect from the same computer (using the same browser).

Most options are set by clicking the 'Customise' link on the database contents page. Most of the available options are visible for isolate databases, whereas sequence definition databases have fewer available.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

The *Neisseria* PubMLST database contains data for a collection of isolates that represent the total known diversity of *Neisseria* species. For every allelic profile in the profiles/sequence definition database there is at least one corresponding isolate deposited here. Any isolate may be submitted to this database and consequently it should be noted that it does not represent a population sample.

### Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE -

General options

Locus display

Scheme display

Scheme field display

INFORMATION +

TYPING

### 11.13.1 General options

The general options tab is displayed by default. If another tab is being shown, click the 'General options' header.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > General options

Help

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Display 25 records per page.  
Page bar position: top and bottom  
Display 100 nucleotides per line in sequence alignments.  
Display 100 nucleotides of flanking sequence (where available).  
☐ Display locus aliases if set.  
☒ Enable tooltips (beginner's mode).

SET OPTIONS

Main results table - display options  
Main results table - provenance field selection  
Main results table - secondary metadata selection  
Isolate record display  
Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

The general tab allows the following options to be modified:

- Records per page
- Page bar position
- Nucleotides per line - Some analyses display sequence alignments. This option allows you to set the width of these alignments so suit your display.
- Flanking sequence length - This sets the length of flanking sequence upstream and downstream of a particular locus that is included whenever a sequence is displayed. Flanking sequences are displayed fainter than the locus sequence.
- Locus aliases - Loci can have multiple names (aliases). Setting this option will display all alternative names in results tables.
- Tooltips (beginner's mode) - Most query forms have help available in the form of information tooltips. These can be switched on/off here. They can also be toggled off by clicking the Toggle: 'i' button at the top-right of the display of some pages.

Click 'Set options' to remember any changes you make.

## 11.13.2 Main results table

The ‘main results table’ tab contains options for the display of paged results following a query.

Click the ‘Main results table’ header to display the tab.

BIGSdb
Home > Organisms > Neisseria spp. > Neisseria isolates > General options
Help

### Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Display 25 records per page.  
Page bar position: top and bottom  
Display 100 nucleotides per line in sequence alignments.  
Display 100 nucleotides of flanking sequence (where available).  
☐ Display locus aliases if set.  
☒ Enable tooltips (beginner's mode).

SET OPTIONS

Main results table - display options
Main results table - provenance field selection
Main results table - secondary metadata selection
Isolate record display
Query filters

Reset
Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

The ‘main results table’ tab will scroll up.

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Main results table - display options

☐ Hyperlink allele designations where possible.  
☒ Differentiate provisional allele designations.  
☐ Display information about sequence bin records tagged with locus information (tooltip).  
☐ Display sequence bin size.  
☐ Display contig count.  
☐ Display publications.

SET OPTIONS

Main results table - provenance field selection

Main results table - secondary metadata selection

Isolate record display

Query filters

Reset  
Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.  

RESET ALL TO DEFAULTS

This tab allows the following options to be modified:

- Hyperlink allele designations - Hyperlinks point to an information page about the particular allele definition. Depending on the locus, these may exist on a different website.
- Differentiate provisional allele designations - Allele designations can be set as confirmed or provisional, usually depending on the method of assignment. Selecting this option will display provisional designations in a different colour to confirmed designations.
- Information about sequence bin records - Creates a tooltip that displays details about sequence tags corresponding to a locus.
- Sequence bin records - Displays a tooltip linking to the sequence tag if available.
- Sequence bin size - Displays the size of the sum of all contigs associated with each isolate record.
- Contig count - Displays the number of contigs associated with each isolate record.
- Publications - Displays citations with links to PubMed for each record.

### 11.13.3 Isolate record display

The 'isolate record display' tab contains options for the display of a full isolate record.

Click the 'Isolate record display' tab to display the tab.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > General options

Help

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (*Neisseria* isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Display 25 records per page.  
 Page bar position: top and bottom  
 Display 100 nucleotides per line in sequence alignments.  
 Display 100 nucleotides of flanking sequence (where available).  
☐ Display locus aliases if set.  
☒ Enable tooltips (beginner's mode).

SET OPTIONS

Main results table - display options  
 Main results table - provenance field selection  
 Main results table - secondary metadata selection  
**Isolate record display**  
 Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

The 'Isolate record display' tab will scroll up.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > General options

Help

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (*Neisseria* isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Main results table - display options

Main results table - provenance field selection

Main results table - secondary metadata selection

Isolate record display

☒ Differentiate provisional allele designations.  
☐ Display sender, curator and last updated details for allele designations (tooltip).  
☒ Display information about sequence bin records tagged with locus information (tooltip).  
☐ Display information about whether alleles have flags defined in sequence definition database (shown in sequence detail tooltip).

SET OPTIONS

Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

This tab allows the following options to be modified:

- Differentiate provisional allele designations - Allele designations can be set as confirmed or provisional, usually depending on the method of assignment. Selecting this option will display provisional designations in a different colour to confirmed designations.
- Display sender, curator and last updated records - Displays a tooltip containing sender information next to each allele designation.
- Sequence bin information - Displays a tooltip with information about the position of the sequence if tagged within the sequence bin.
- Allele flags - Displays information about whether alleles have flags defined in sequence definition databases.

### 11.13.4 Provenance field display

The ‘provenance field display’ tab contains checkboxes for fields to display in the main results table.

Click the ‘Provenance field display’ tab to display the tab.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > General options

Help

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

• General options

Display 25 records per page.  
Page bar position: top and bottom  
Display 100 nucleotides per line in sequence alignments.  
Display 100 nucleotides of flanking sequence (where available).  
☐ Display locus aliases if set.  
☒ Enable tooltips (beginner's mode).

SET OPTIONS

• Main results table - display options

• Main results table - provenance field selection

• Main results table - secondary metadata selection

• Isolate record display

• Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

The ‘Provenance field display’ tab will scroll up.

## BIGSdb

Home &gt; Organisms &gt; Neisseria spp. &gt; Neisseria isolates &gt; General options

Help 

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Main results table - display options

Main results table - provenance field selection

Select the isolate provenance fields that you wish to be displayed in the main results table following a query. Settings for displaying locus and scheme data can be made by performing a locus, scheme or scheme field query and then selecting the 'Customize' option.

<input checked="" type="checkbox"/> isolate	<input type="checkbox"/> age_mth	<input type="checkbox"/> penicillin_range	<input type="checkbox"/> azithromycin
<input checked="" type="checkbox"/> aliases	<input type="checkbox"/> sex	<input type="checkbox"/> amoxicillin	<input type="checkbox"/> spectinomycin
<input type="checkbox"/> strain_designation	<input checked="" type="checkbox"/> disease	<input type="checkbox"/> sulphonamide	<input type="checkbox"/> bioproject_accession
<input checked="" type="checkbox"/> country	<input type="checkbox"/> source	<input type="checkbox"/> ceftriaxone	<input type="checkbox"/> biosample_accession
<input type="checkbox"/> continent	<input type="checkbox"/> epidemiology	<input type="checkbox"/> ceftriaxone_range	<input type="checkbox"/> ENA_run_accession
<input type="checkbox"/> region	<input checked="" type="checkbox"/> species	<input type="checkbox"/> chloramphenicol	<input type="checkbox"/> private_project
<input checked="" type="checkbox"/> year	<input type="checkbox"/> serogroup	<input type="checkbox"/> chloramphenicol_range	<input type="checkbox"/> comments
<input type="checkbox"/> date_sampled	<input type="checkbox"/> genogroup	<input type="checkbox"/> cefotaxime	<input type="checkbox"/> sender
<input type="checkbox"/> isoyear_sampled	<input type="checkbox"/> genogroup_notes	<input type="checkbox"/> cefotaxime_range	<input type="checkbox"/> curator
<input type="checkbox"/> week_sampled	<input checked="" type="checkbox"/> capsule_group	<input type="checkbox"/> rifampicin	<input type="checkbox"/> date_entered
<input type="checkbox"/> date_received	<input type="checkbox"/> MLEE_designation	<input type="checkbox"/> rifampicin_range	<input type="checkbox"/> datestamp
<input type="checkbox"/> non_culture	<input type="checkbox"/> serotype	<input type="checkbox"/> ciprofloxacin	
<input type="checkbox"/> epidemiological_year	<input type="checkbox"/> sero_subtype	<input type="checkbox"/> ciprofloxacin_range	
<input type="checkbox"/> age_yr	<input type="checkbox"/> ET_no	<input type="checkbox"/> tetracycline	
<input type="checkbox"/> age_range	<input type="checkbox"/> penicillin	<input type="checkbox"/> cefixime	

ALL

NONE

DEFAULT

SET OPTIONS

Main results table - secondary metadata selection

Isolate record display

Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

Some fields will be checked by default - these are defined during *database setup* (maindisplay option).

Check any fields that you wish to be displayed and then click 'Set options'. You can return to the default selection by clicking 'Default' followed by 'Set options'.

### 11.13.5 Query filters

The 'query filters' tab contains checkboxes for provenance fields and scheme completion status. Checking these results in drop-down list box filters appearing in the query page *filters fieldset*.

Click the 'Query filters' tab to display the tab.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > General options

Help

## Set database options

Here you can set options for your use of the website. Options are remembered between sessions and affect the current database (Neisseria isolates) only. If some of the options don't appear to set when you next go to a query page, try refreshing the page (Shift + Refresh) as some pages are cached by your browser.

General options

Display 25 records per page.  
Page bar position: top and bottom  
Display 100 nucleotides per line in sequence alignments.  
Display 100 nucleotides of flanking sequence (where available).  
☐ Display locus aliases if set.  
☒ Enable tooltips (beginner's mode).

SET OPTIONS

Main results table - display options  
Main results table - provenance field selection  
Main results table - secondary metadata selection  
Isolate record display  
Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

RESET ALL TO DEFAULTS

The 'Query filters' tab will scroll up.

Query filters

Select the fields for which you would like dropdown lists containing known values on which to filter query results. These will be available in the filters section of the query interface.

<input type="checkbox"/> isolate	<input type="checkbox"/> serotype	<input type="checkbox"/> private_project
<input type="checkbox"/> country	<input type="checkbox"/> sero_subtype	<input type="checkbox"/> comments
<input type="checkbox"/> continent	<input type="checkbox"/> ET_no	<input type="checkbox"/> sender
<input type="checkbox"/> region	<input type="checkbox"/> penicillin	<input type="checkbox"/> curator
<input type="checkbox"/> year	<input type="checkbox"/> penicillin_range	<input type="checkbox"/> date_entered
<input type="checkbox"/> date_sampled	<input type="checkbox"/> amoxicillin	<input type="checkbox"/> datestamp
<input type="checkbox"/> isoyear_sampled	<input type="checkbox"/> sulphonamide	<input checked="" type="checkbox"/> MLST profile completion
<input type="checkbox"/> week_sampled	<input type="checkbox"/> ceftriaxone	<input type="checkbox"/> Bexsero Antigen Sequence Typing (BAST) profile completion
<input type="checkbox"/> date_received	<input type="checkbox"/> ceftriaxone_range	<input type="checkbox"/> Conjugative Plasmid profile completion
<input type="checkbox"/> non_culture	<input type="checkbox"/> chloramphenicol	<input type="checkbox"/> Cryptic Plasmid profile completion
<input type="checkbox"/> epidemiological_year	<input type="checkbox"/> chloramphenicol_range	<input type="checkbox"/> GC OMV peptide typing profile completion
<input type="checkbox"/> age_yr	<input type="checkbox"/> cefotaxime	<input type="checkbox"/> N. gonorrhoeae cgMLST v1.0 profile completion
<input type="checkbox"/> age_range	<input type="checkbox"/> cefotaxime_range	<input type="checkbox"/> N. meningitidis cgMLST v1.0 profile completion
<input type="checkbox"/> age_mth	<input type="checkbox"/> rifampicin	<input type="checkbox"/> NG MAST profile completion
<input type="checkbox"/> sex	<input type="checkbox"/> rifampicin_range	<input type="checkbox"/> NG STAR profile completion
<input type="checkbox"/> disease	<input type="checkbox"/> ciprofloxacin	<input type="checkbox"/> OMV peptide typing profile completion
<input type="checkbox"/> source	<input type="checkbox"/> ciprofloxacin_range	<input type="checkbox"/> Ribosomal MLST profile completion
<input type="checkbox"/> epidemiology	<input type="checkbox"/> tetracycline	<input type="checkbox"/> beta lactamase plasmid profile completion
<input type="checkbox"/> species	<input type="checkbox"/> cefixime	<input type="checkbox"/> rplF species profile completion
<input type="checkbox"/> serogroup	<input type="checkbox"/> azithromycin	
<input type="checkbox"/> genogroup	<input type="checkbox"/> spectinomycin	
<input type="checkbox"/> genogroup_notes	<input type="checkbox"/> bioproject_accession	
<input type="checkbox"/> capsule_group	<input type="checkbox"/> biosample_accession	
<input type="checkbox"/> MLEE_designation	<input type="checkbox"/> ENA_run_accession	

ALL
NONE
DEFAULT
SET OPTIONS

A list of possible filters appears. Click any checkbox for a filter you would like to make available. Click 'Set options' when done. You can return to the default selection by clicking 'Default' followed by 'Set options'.

### 11.13.6 Modifying locus and scheme display options

Whether or not loci, schemes or scheme fields are displayed in result tables, isolate records, or within query dropdown boxes can all be set with default options when first defined. These attributes can, however, be overridden by a user, and these selections will be remembered between sessions.

The procedure to modify these attributes is the same for locus, schemes or scheme fields, so the steps for loci will be demonstrated only.

Click the appropriate link in the ‘Customise’ section on the isolate contents page.

The screenshot shows the BIGSdb interface for the Neisseria isolates database. The top navigation bar includes 'BIGSdb' and a breadcrumb trail: 'Home > Organisms > Neisseria spp. > Neisseria isolates'. Below this is the title 'Neisseria isolates database' and a descriptive paragraph about the Neisseria PubMLST database. The main content area is titled 'Query database' and contains two search boxes: 'Search database' (with the instruction 'Browse, search by any criteria, or enter list of attributes.') and 'Search by combinations of loci' (with the instruction 'This can include partial matches to find related isolates.'). On the right side, there is a sidebar with a 'LOG IN' button and a list of menu items: 'SUBMISSIONS', 'PROJECTS', 'EXPORT', 'ANALYSIS', 'CUSTOMISE', 'INFORMATION', and 'TYPING'. The 'CUSTOMISE' menu item is expanded, showing a 'General options' section with three sub-items: 'Locus display', 'Scheme display', and 'Scheme field display'. These three sub-items are highlighted with a red rectangular box.

Either select the locus id by querying for it directly.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Query locus information

Help ⓘ ⓘ

## Query locus information

Please enter your search criteria below (or leave blank and submit to return all records). Matching loci will be returned and you will then be able to update their display and query settings.

Search criteria

id
=
abcZ
+ ⓘ

Display

Order by:
id
ascending
Display: 25 records per page ⓘ

Filter query by
Action

RESET SEARCH

1 record returned. Click the hyperlink for detailed information.

Customize

Locus options

id	data type	locus type	allele id format	length	length varies	coding sequence	isolate display*	main display*	query field*	analysis*	view
abcZ	DNA	partial CDS	integer	433	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

\* Default values are displayed for this field. These may be overridden by user preference.

Designations can be queried using *standard operators*.

Alternatively, you can search by filtering loci by schemes. Click the ‘Filter query by’ header and select the scheme in the dropdown box.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Query locus information](#)
[Help](#) [🔗](#) [i](#)

## Query locus information

Please enter your search criteria below (or leave blank and submit to return all records). Matching loci will be returned and you will then be able to update their display and query settings.

**Search criteria**

id  =  [+](#) [i](#)

**filter query by**

data type:

locus type:

allele id format:

length varies:  [i](#)

coding sequence:

complete cds:  [i](#)

orf:

match longest:  [i](#)

pcr filter:  [i](#)

probe filter:  [i](#)

introns:

isolate display:

main display:  [i](#)

query field:  [i](#)

analysis:  [i](#)

submission template:  [i](#)

view:

curator:  [i](#)

scheme: **MLST** [i](#)

**Display**

Order by:  ascending

Display: 25 records per page [i](#)

**Action**

[RESET](#) [SEARCH](#)

7 records returned. Click the hyperlinks for detailed information.

[Customize](#)[Locus options](#)

id	data type	locus type	allele id format	length	length varies	coding sequence	isolate display*	main display*	query field*	analysis*	view
<a href="#">abcZ</a>	DNA	partial CDS	integer	433	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">adk</a>	DNA	partial CDS	integer	465	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">aroE</a>	DNA	partial CDS	integer	490	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">fumC</a>	DNA	partial CDS	integer	465	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">gdh</a>	DNA	partial CDS	integer	501	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">pdhC</a>	DNA	partial CDS	integer	480	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">pgm</a>	DNA	partial CDS	integer	450	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	

\* Default values are displayed for this field. These may be overridden by user preference.

Once loci have been selected, click Customize 'locus options'.

scheme: **MLST** [i](#)

7 records returned. Click the hyperlinks for detailed information.

[Customize](#)[Locus options](#)

id	data type	locus type	allele id format	length	length varies	coding sequence	isolate display*	main display*	query field*	analysis*	view
<a href="#">abcZ</a>	DNA	partial CDS	integer	433	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">adk</a>	DNA	partial CDS	integer	465	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">aroE</a>	DNA	partial CDS	integer	490	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">fumC</a>	DNA	partial CDS	integer	465	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">gdh</a>	DNA	partial CDS	integer	501	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">pdhC</a>	DNA	partial CDS	integer	480	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
<a href="#">pgm</a>	DNA	partial CDS	integer	450	<input type="checkbox"/>	<input checked="" type="checkbox"/>	allele only	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	

\* Default values are displayed for this field. These may be overridden by user preference.

You can then choose to add or remove individual loci from the selection by clicking the appropriate checkboxes. At the bottom of the page are a number of attributes that you can change - clicking 'Change' will affect all selected loci.

Possible options for loci are:

- isolate\_display - Sets how the locus is displayed within an isolate record:
  - allele only - display only identifier
  - sequence - display the full sequence

- hide - don't show at all
- main\_display - Sets whether the locus is displayed in the main results table following a query.
- query\_field - Sets whether the locus appears in dropdown list boxes to be used within queries.
- analysis - Sets whether the locus can be used in data analysis functions.

---

**Note:** Settings for loci can be overridden by those set for schemes that they are members of. For example, if you set a locus to be displayed within a main results table, but that locus is a member of a scheme and you set that scheme not to be displayed, then the locus will not be shown. Conversely, if you set a scheme to be displayed, but set its member locus not to be shown, then that locus will not be displayed (but other loci and scheme fields may be, depending on their independent settings).

---

## USER PROJECTS

If user projects are enabled, authenticated users are able to set up their own projects in order to group isolates for analysis. If private data and user quotas are enabled, these projects can include private records that can then be shared with other user accounts. Note, that simply adding a record to a user project does not make the record itself private.

**Note:** User projects can be enabled by an administrator by setting ‘user\_projects=”yes”’ in the *config.xml* file for the database.

To create a new project, go to the isolate database contents page and expand the ‘Projects’ section. Click ‘Your projects’.


The screenshot displays the BIGSdb interface for the Neisseria isolates database. At the top, the header shows 'BIGSdb' and a breadcrumb trail: 'Home > Organisms > Neisseria spp. > Neisseria isolates'. Below this, the title 'Neisseria isolates database' is followed by a descriptive paragraph about the database's content. The main area is titled 'Query database' and contains two search boxes: 'Search database' (with a description: 'Browse, search by any criteria, or enter list of attributes.') and 'Search by combinations of loci' (with a description: 'This can include partial matches to find related isolates.'). On the right side, there is a vertical sidebar with several navigation buttons: 'LOG IN', 'SUBMISSIONS', 'PROJECTS' (which is expanded to show 'Public projects' and 'Your projects', with 'Your projects' highlighted by a red box), 'EXPORT', 'ANALYSIS', 'CUSTOMISE', 'INFORMATION', and 'TYPING'.

Enter the name of your project (this must be unique on the system - you will be told if the name is already used). You can optionally include a description - if you do this, this will appear within *isolate records* when accessed from your account. Click ‘Create’.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > User projects

User projects

 New private projects

Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

New project

Name:

Description:

Action

Existing projects

You do not own or are a member of any projects.

You can either add isolates to your project directly following a query or by manually editing a list of ids.

## 12.1 Adding isolates to a user project following a query

Perform an isolate database query. If you have set up a project, there will be a link in the results header box. Select your project and click ‘Add these records’.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance fields

Combine with: AND

country = UK

year = 2016

capsule group = W

Allele designations/scheme fields

ST (MLST) = 11

Display/sort options

Order by: id ascending

Display: 25 records per page

Action

196 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Your projects

UK group W ST-11 2016

Bookmark query

2020-07-29:1

1 2 3 4 5 6

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
42451	M16 240077		UK	2016		<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
42475	M16 240003		UK [England]	2016	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
42478	M16 240008		UK [England]	2016	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
42480	M16 240010		UK [England]	2016	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-1
42481	M16 240011		UK [England]	2016	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	11	ST-11 complex	5	2	F1-146

The records will be added to the project. Please note that it doesn't matter whether any of the records have been previously added.


## 12.2 Adding or removing isolates belonging to a user project by editing a list

From the user projects page, click the ‘Add/remove records’ link for the project that you wish to modify.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > User projects

User projects

 New private projects





Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

Name:   
 Description:

[New project](#)
[Action](#)
[CREATE](#)

Your projects

Delete	Add/remove records	Modify users	Project	Description	Administrator	Isolates	Browse
			UK group W ST-11 2016	Group W ST-11 isolates from the UK in 2016.	<input checked="" type="checkbox"/>	196	

You can also add isolates to projects from the results of a [query](#).

Note that deleting a project will not delete its member isolates.

Edit the list of ids of records belonging to the list. You can copy and paste this list if you wish to prepare it in a spreadsheet or text editor. Click ‘Update’ when finished.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > User projects

User projects

Project: UK group W ST-11 2016

Group W ST-11 isolates from the UK in 2016.

The list below contains id numbers for isolate records belonging to this project. You can add and remove records to this project by modifying the list of isolate ids. This only affects which records belong to the project - you will not remove isolate records from the database by removing them from this list.

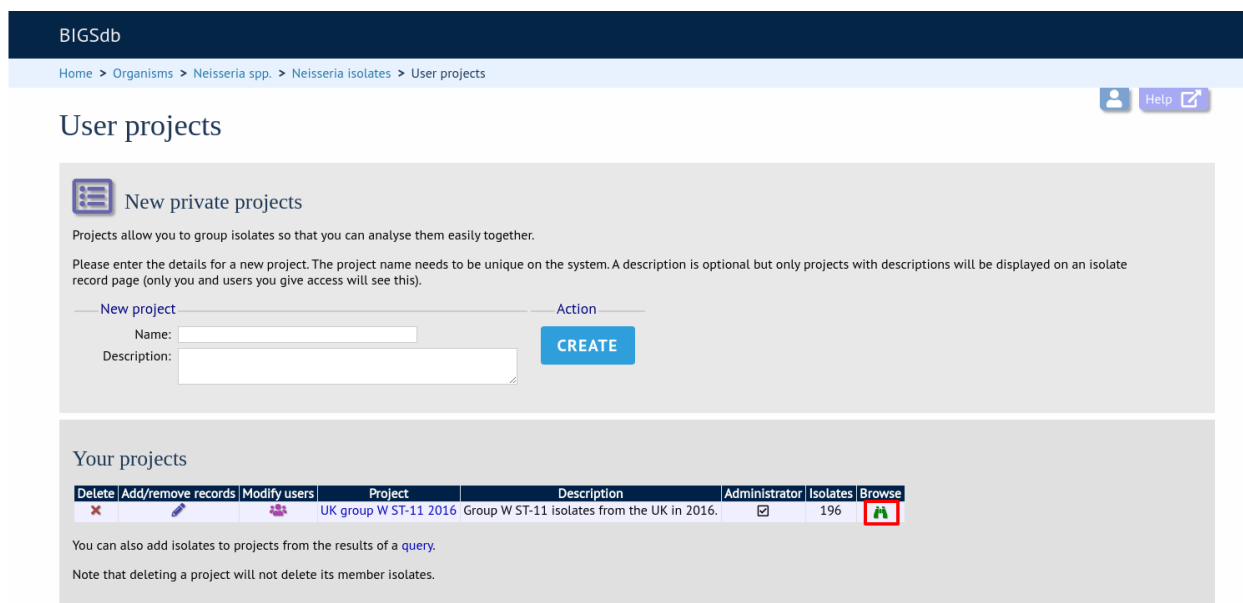
Isolate ids:   
 Action: [RESET](#) [UPDATE](#)

42451  
 42475  
 42478  
 42480  
 42481  
 42482  
 42483  
 42484  
 42485  
 42486

You can also add isolate records to this project from the results of a [query](#).

## 12.3 Accessing project isolates

To browse isolate records belonging to a project, go to the user projects page and click the ‘Browse’ link for the project.



**User projects**

**New private projects**

Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

**New project** **Action**

Name:

Description:

**CREATE**

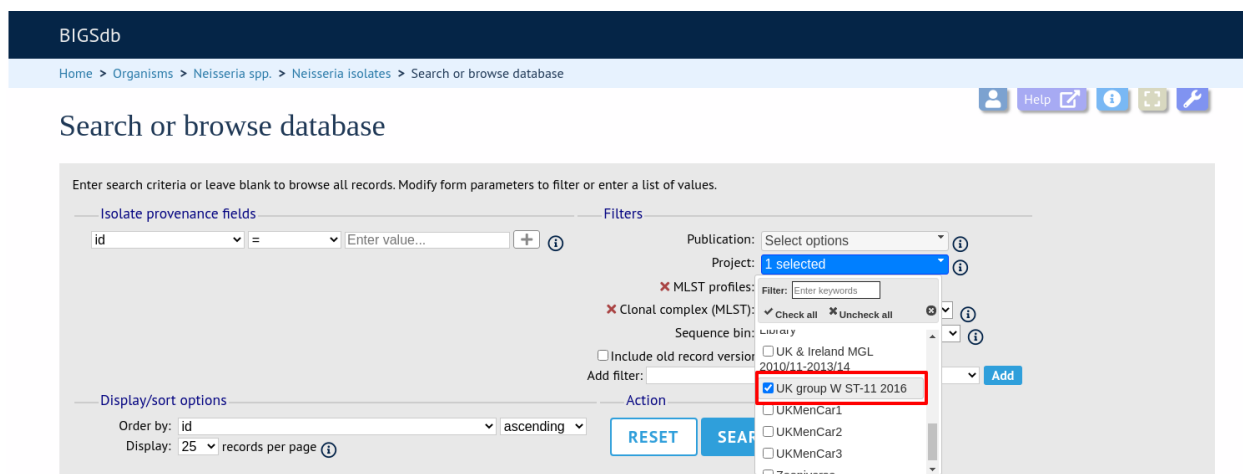
**Your projects**

Delete	Add/remove records	Modify users	Project	Description	Administrator	Isolates	Browse
			UK group W ST-11 2016	Group W ST-11 isolates from the UK in 2016.		196	

You can also add isolates to projects from the results of a [query](#).

Note that deleting a project will not delete its member isolates.

Alternatively, you can select the project from the *projects filter* on the isolate query page. This would enable you to combine the project with additional search criteria



**Search or browse database**

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

**Isolate provenance fields**

id  =  Enter value...

**Filters**

Publication: Select options

Project: 1 selected

MLST profiles:  Filter:

Clonal complex (MLST): ☒ Check all  ☐ Uncheck all

Sequence bin: ☐ Include old record version

Add filter:

**Display/sort options**

Order by: id  ascending

Display: 25  records per page

**Action**

UK group W ST-11 2016

UKMenCar1

UKMenCar2

UKMenCar3

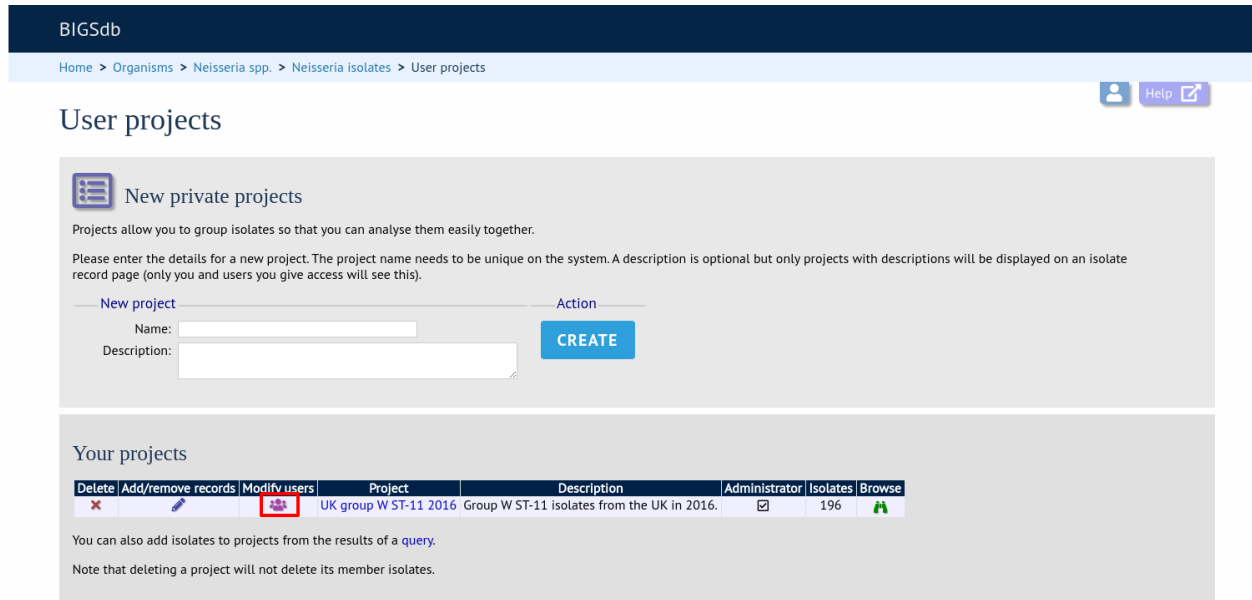
Zooniverse

Please note that you will only see your project in the filter list if you are logged in. As a private project, only you will see it.

## 12.4 Allowing other users to share your project

You can share a project that you own with any other user. In order to do this, you must know the username that they use to log in with. They will see the project in their own list of private projects and in the query interface projects filter.

From the user projects page, click the ‘Modify users’ link for the specified project:



**User projects**

**New private projects**

Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

**New project** **Action**

Name:

Description:

**CREATE**

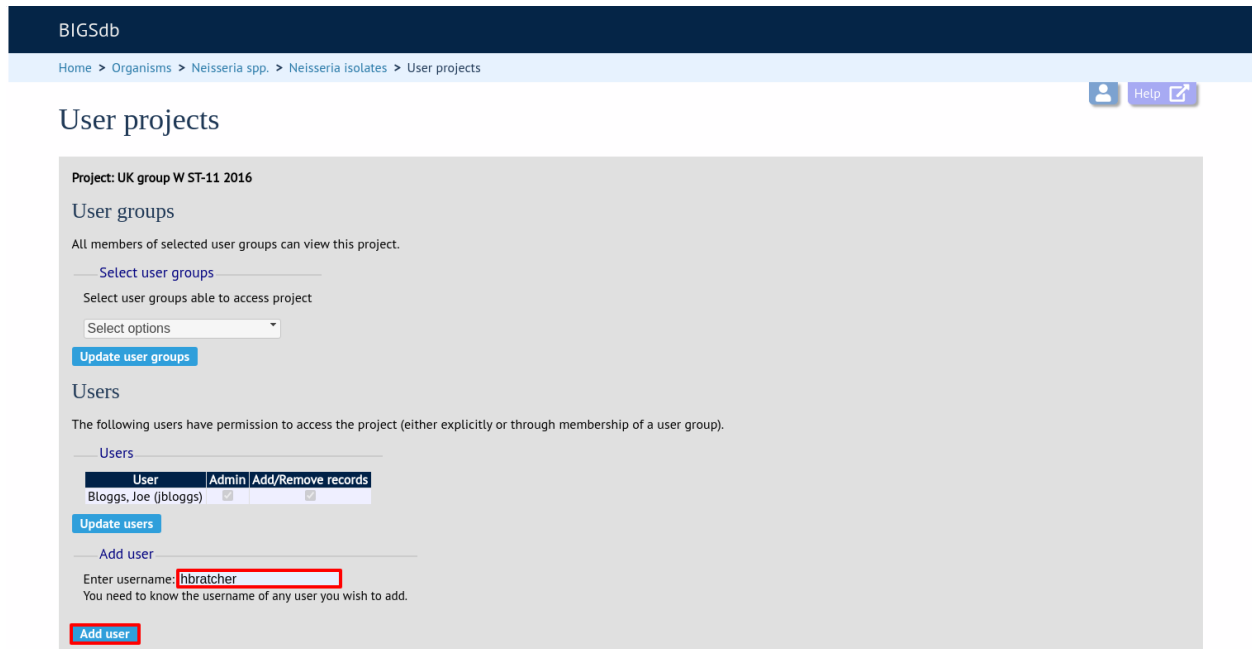
**Your projects**

Delete	Add/remove records	Modify users	Project	Description	Administrator	Isolates	Browse
			UK group W ST-11 2016	Group W ST-11 isolates from the UK in 2016.	<input checked="" type="checkbox"/>	196	

You can also add isolates to projects from the results of a [query](#).

Note that deleting a project will not delete its member isolates.

Enter the username of the person you wish to share with and click ‘Add user’:



**Project: UK group W ST-11 2016**

**User groups**

All members of selected user groups can view this project.

**Select user groups**

Select user groups able to access project

Select options

**Update user groups**

**Users**

The following users have permission to access the project (either explicitly or through membership of a user group).

**Users**

User	Admin	Add/Remove records
Bloggs, Joe (jbloggs)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

**Update users**

**Add user**

Enter username:

You need to know the username of any user you wish to add.

**Add user**

If user groups are in use, you can also share your project with all members of a user group from the same page.

Once a user has been added, you can give them permission to administer (add other users, modify the description or delete) or add/remove records to the project:

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > User projects

User projects

Project: UK group W ST-11 2016

User groups

All members of selected user groups can view this project.

Select user groups

Select user groups able to access project

Select options

Update user groups

Users

The following users have permission to access the project (either explicitly or through membership of a user group).

Users

Remove	User	Admin	Add/Remove records
	Bloggs, Joe (jbloggs)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/>	Bratcher, Holly (hbratcher)	<input type="checkbox"/>	<input type="checkbox"/>

Update users

Add user

Enter username: hbratcher

You need to know the username of any user you wish to add.

Add user

## 12.5 Deleting a user project

You can delete a project from the user projects page by clicking the 'Delete' link next to the project in question.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > User projects

User projects

New private projects

Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

New project

Name:

Description:

Action

CREATE

Your projects

Delete	Add/remove records	Modify users	Project	Description	Administrator	Isolates	Browse
<input checked="" type="checkbox"/>			UK group W ST-11 2016	Group W ST-11 isolates from the UK in 2016.	<input checked="" type="checkbox"/>	196	

You can also add isolates to projects from the results of a [query](#).

Note that deleting a project will not delete its member isolates.

If the project contains any isolates you will be asked for confirmation. Click the 'Delete project' button.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > User projects

Help

## User projects

This project contains 196 isolates. Please confirm that you wish to remove the project (the isolates in the project will not be deleted).

[X Delete project](#)

### New private projects

Projects allow you to group isolates so that you can analyse them easily together.

Please enter the details for a new project. The project name needs to be unique on the system. A description is optional but only projects with descriptions will be displayed on an isolate record page (only you and users you give access will see this).

[New project](#) [Action](#)

Name:

Description:

[CREATE](#)

### Your projects

Delete	Add/remove records	Modify users	Project	Description	Administrator	Isolates	Browse
			UK group W ST-11 2016	Group W ST-11 isolates from the UK in 2016.	<input checked="" type="checkbox"/>	196	

You can also add isolates to projects from the results of a [query](#).

Note that deleting a project will not delete its member isolates.

If the project contains no isolates, the confirmation page is skipped and the project is removed immediately.

**Note:** Removing a project does not delete the isolate records belonging to it. A project is simply a means of grouping records.



## PRIVATE RECORDS

Users with a status of ‘submitter’, ‘curator’, or ‘admin’ can upload private isolate records that will be hidden from public view. A quota needs to be set for the user by an admin before they are able to do this.

### 13.1 Uploading private records

In order to upload private records, you need to make sure that you are logged in. If your account has a quota, there will be a menu item called ‘Private data’. Click the ‘Upload/manage records’ link.


The screenshot shows the BIGSdb interface for the Neisseria isolates database. At the top, there is a dark blue header with the text 'BIGSdb'. Below it, a light blue breadcrumb trail reads 'Home > Organisms > Neisseria spp. > Neisseria isolates'. The main content area is titled 'Neisseria isolates database'. On the left, there is a 'Query database' section with two search boxes: 'Search database' (with subtext 'Browse, search by any criteria, or enter list of attributes.') and 'Search by combinations of loci' (with subtext 'This can include partial matches to find related isolates.'). On the right, there is a vertical sidebar with several buttons: 'LOG OUT' (with a red icon), 'SUBMISSIONS', 'PRIVATE DATA' (highlighted with a red box), 'PROJECTS', 'EXPORT', 'ANALYSIS', 'CUSTOMISE', 'INFORMATION', and 'TYPING'. Each button has a small icon and a '+' sign next to it.

You will see an overview of your quota and links to upload and edit your records. Click the ‘Upload private isolate records’ link (assuming you have quota available).

BIGSdb


Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Private records

Private records


 Limits

Accounts have a quota for the number of private records that they can upload. Uploading of private data to some registered projects may not count against your quota.

Records (total): 0  
Records (quota): 0  
Quota: 100  
You can upload: 100

 Upload

[Upload private isolate records](#)

 Curate

[Update private records](#) [Curator's interface](#)


**Note:** This link takes you to the standard curator's interface. If you upload here, then your data will **not be private**. Either use the 'Upload' link above to upload private records to your quota (if you have any available), or use the upload link on the individual projects listed below to upload to those projects.

You will then be taken to a curator page that allows you to upload data copy and pasted from a spreadsheet. There is a link to an Excel template that you will need to use to prepare your data - this is the same template used if you were to submit your data to a curator.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Batch add isolate records

Batch insert isolates

 Private data upload

These isolates will count against your quota of private data.



Quota available: 100

Instructions

This page allows you to upload isolate data as tab-delimited text or copied from a spreadsheet.

- Field header names must be included and fields can be in any order. Optional fields can be omitted if you wish.
- Optionally enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- Optionally enter references for your isolates as a semi-colon (;) separated list of PubMed ids (non-integer ids will be ignored).
- You can also upload allele fields along with the other isolate data - simply create a new column with the locus name (see the 'allowed\_loci' tab in the Excel template for locus names). These will be added with a confirmed status and method set as 'manual'.
- You can choose whether or not to include an id number field - if it is omitted, the next available id will be used automatically.

Templates

Check the [description of database fields](#) for help with filling in the template.

Upload

Paste in tab-delimited text (Include a field header line).

Action

[RESET](#) [SUBMIT](#)

See *batch adding isolate records* for details of the upload process.

## 13.2 Modifying private records

Click the ‘Private data’ link on the contents page.

Now click the ‘Update private records’ link. You will be taken to the *curators’ interface*, where you will be able to use the standard curator tools.

Use the *curators’ interface* to make any changes to your isolate records, including *uploading genome data*.

## 13.3 Sharing access to private records

If *user projects* are enabled on the database, you can share access to your private isolates by adding them in to a user project and then sharing this.

See *user projects* for more details.

## DATA ANALYSIS PLUGINS

### 14.1 BLAST

The BLAST plugin enables you to BLAST a sequence against any of the genomes in the database, displaying a table of matches and extracting matching sequences.

The function can be accessed by selecting the ‘Analysis’ section on the main contents page.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates

### Neisseria isolates database

#### Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

**ANALYSIS**

CUSTOMISE +

INFORMATION +

TYPING

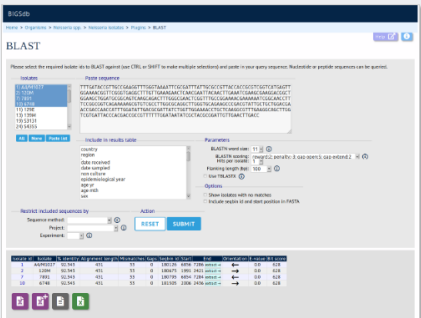
Jump to the ‘Analysis’ category, follow the link to BLAST, then click ‘Launch BLAST’.

**BLAST**

Summary: BLAST a query sequence against selected isolate data

The BLAST plugin enables you to BLAST a sequence against any of the genomes in the database, displaying a table of matches which can be downloaded in Excel format. In addition, the matched sequence regions are made available for download in FASTA format, either with or without surrounding flanking sequence.

[Documentation](#) [bigsdbs.readthedocs.io](#)



Launch 'BLAST'

Alternatively, it can be accessed following a query by clicking the 'BLAST' button in the Analysis list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Navigation: << < 1 2 3 4 5 6 > >>

#### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Publications](#) [Sequence bin](#)

Analysis: [Codons](#) [Gene Presence](#) [Genome Comparator](#) **[BLAST](#)** [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Select the isolate records to analyse (on large databases you will need to enter a list of ids). These will be pre-selected if you accessed the plugin following a query. Paste in a sequence to query - this be either a DNA or peptide sequence.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Plugins](#) > [BLAST](#)
[Help](#) [🔗](#) [i](#)

## BLAST

Please select the required isolate ids to BLAST against (use CTRL or SHIFT to make multiple selections) and paste in your query sequence. Nucleotide or peptide sequences can be queried.

**Isolates**  
1  
2  
3  
4  
5  
6  
7  
[Clear](#) [List all](#)

**Paste sequence**  
GAAGCCTTAGGCGGACGCGATGCCGCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCGGCAAGCCTGAA  
TAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCGCGTTGCGGTTTGGGCGAAATCAAATCCCCG  
AAACGAGCCGGGTTGTCCTCATGCGCGGCAAGTCAACCGGACCAATGGGCAAGCAATGACGATGGTG  
TGCTGCCAAGTGTTCGGCAACGACGTTACCATCGGTATGGCGGGCGGTCGGGCAATTCGAGCTGAACGT  
CTATATGCCGTTATCGCCTACACCTCTTGCAATCCATCCGCTCTTGGGCGACGCGTGAACAGCTTCA  
ACGAACACTGCGCCATCGGCATCGAACCCGTACCGGAAAAATCGACTATTCTCGCACCATTCCCTGATG  
CTCGTTACCGCGTTAAACCGCAAAATCGGTTACGAAAAAC

**Include in results table**  
country  
region  
year  
date sampled  
isoyear sampled  
week sampled  
date received  
non culture  
epidemiological year  
age yr

**Parameters**  
BLASTN word size: 11  
BLASTN scoring: reward:2; penalty:-3; gap open:5; gap extend:2  
Hits per isolate: 1  
Flanking length (bp): 100  
☐ Use TBLASTX  
**Options**  
☐ Show isolates with no matches  
☐ Include seqin id and start position in FASTA

**Restrict included sequences by**  
Sequence method:  
Project:  
Experiment:

**Action**  
[RESET](#) [SUBMIT](#)

Click submit. If you are querying against 10 or fewer genomes then the results are run immediately, otherwise the job is sent to the job queue.

A table of BLAST results will be displayed.

## BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Job status viewer

## Job status viewer



## Status

Job id: BIGSdb\_009799\_1596036810\_89173  
 Submit time: 2020-07-29 15:33:30  
 Status: finished  
 Start time: 2020-07-29 15:36:21  
 Progress: 100%  
 Stop time: 2020-07-29 15:36:29  
 Total time: 7 seconds

## Output

Isolate id	Isolate	% Identity	Alignment length	Mismatches	Gaps	Seqbin id	Start	End	Orientation	E-value	Bit score
1	A4/M1027	98.280	465	8	0	180177	19444	19908 extract →	→	0.0	803
2	120M	98.280	465	8	0	180583	4782	5246 extract →	←	0.0	803
7	7891	98.280	465	8	0	180965	19869	20333 extract →	→	0.0	803
10	6748	98.280	465	8	0	181406	36669	37133 extract →	→	0.0	803
11	129E	98.280	465	8	0	181867	35889	36353 extract →	→	0.0	803
13	139M	98.280	465	8	0	182004	36775	37239 extract →	→	0.0	803
19	S3131	98.280	465	8	0	182318	19090	19554 extract →	→	0.0	803
24	S4355	98.280	465	8	0	215673	4534	4998 extract →	←	0.0	803
30	14	99.355	465	3	0	8	1363524	1363988 extract →	→	0.0	825
31	10	98.280	465	8	0	182380	5559	6023 extract →	→	0.0	803
34	20	98.280	465	8	0	182815	19783	20247 extract →	→	0.0	803
35	26	98.280	465	8	0	182880	18879	19343 extract →	→	0.0	803
52	243	98.280	465	8	0	183381	4532	4996 extract →	←	0.0	803
61	393	98.280	465	8	0	183648	7217	7681 extract →	→	0.0	803
64	254	98.280	465	8	0	183818	4716	5180 extract →	←	0.0	803
67	S5611	98.280	465	8	0	184143	4804	5268 extract →	←	0.0	803
82	11-004	98.280	465	8	0	184297	19518	19982 extract →	→	0.0	803
84	IAL2229	98.280	465	8	0	184635	4530	4994 extract →	←	0.0	803
90	CN100	98.280	465	8	0	184814	5350	5814 extract →	←	0.0	803

## Files



FASTA



FASTA with flanking



Table (tab-delimited text)



Table (Excel format)



Tar file containing all output files

Please note that job results will remain on the server for 7 days.

Clicking any of the ‘extract’ buttons to display the matched sequence.

## Output

Isolate id	Isolate	% identity	Alignment length	Mismatches	Gaps	Seqbin id	Start	End	Orientation	E-value	Bit score
1	A4/M1027	98.280	465	8	0	180177	19444	19908 extract →	→	0.0	803
2	120M	98.280	465	8	0	180583	4782	5246 extract →	←	0.0	803
7	7891	98.280	465	8	0	180965	19869	20333 extract →	→	0.0	803
10	6748	98.280	465	8	0	181406	36669	37133 extract →	→	0.0	803
11	129E	98.280	465	8	0	181867	35889	36353 extract →	→	0.0	803
13	139M	98.280	465	8	0	182004	36775	37239 extract →	→	0.0	803
19	S3131	98.280	465	8	0	182318	19090	19554 extract →	→	0.0	803
24	S4355	98.280	465	8	0	215673	4534	4998 extract →	←	0.0	803
30	14	99.355	465	3	0	8	1363524	1363988 extract →	→	0.0	825
31	10	98.280	465	8	0	182380	5559	6023 extract →	→	0.0	803
34	20	98.280	465	8	0	182815	19783	20247 extract →	→	0.0	803

The extracted sequence is shown along with a translated sequence and flanking sequences.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria Isolates](#) > [Extracted sequence](#)

## Extracted sequence: Seqbin id#:180965 (19869-20333)

Sequence position

sequence bin id: 180965  
sequence method: Solexa  
start: 19869  
end: 20333  
length: 465  
orientation: →

Options

Flanking sequence length: 100

Reload

Sequence

```

CGGCACGGGT TTGAACAGCC ATCCCGAATA CGCCGAAAAA GCGCGCGCCA AACTCGCCGA ATTGTCCGGC TTGCCGTTTG TCAGCGCGCC GAACAAATTT GAAGCCTTGG GCGGACGCGA
TGCCCGCGTT GCCGTTTCGG GCGCATTGAA AACGCTGGGG GCAAGCCTGA ATAAAAATCG CAACGACATC CGCTGGCTGG CAAGCGGCC GCGCTGCGGT TTGGGCGAAA TCAAAATCCC
CGAAAAACGAG CCGGGTTTCGT CCATCATGCC GGGCAAAGTC AACCCGACCC AATGCGAAGC GATGACCATG GTGTGCTGCC AAGTGTTCGG CAACGACGTT ACCATCGGTA TGGCGGGCGC
GTCGGGCAAT TTCGAGCTGA AGTCTATAT GCCCGTCATC GCCTACAACC TCTTGAATC CATCCGCTG TTGGGCGACG CGTGCAACAG CTTCAACGAA CACTGCGCCG TCGGCATTGA
ACCCGTACCG GAAAAATCG ACTATTTCCT GCACCATTC CTGATGCTCG TTACCGCGTT AAACCGCAAA ATCGGTTACG AAAACGCGC CAAAGTCGCC AAAACCGCCT ACAAACAA
CAATCGTTG CGCGAAACCG CCGTTGAGTT GGGCTTGCTG ACGGCGGAAG AATTGACGA ACTGG

```

Translation

```

R H G F E Q P S R I R R K S R R Q T R R I V R L A V C O R A E Q I * F1
G T G L N S H P E Y A E K A A A K L A E L S G L P F V S A P N K F F2
A R V * T A I P N T P K K P P P N S P N C P A C R L S A R R T N L F3
1 CGGCACGGGTTTGAACAGCATCCCGAATACGCCGAAAAAGCGCCGCAAACTCGCGAATTGCGCGTTGCCGTTTGTGACGCGCGCGAACAAATTT 100
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
S L G R T R C R R C R F G R I E N A G G K P E * N R Q R H P L A G F1
E A L G G R D A A V A A S G A L K T L A A S L N K I A N D I R W L A F2
K P W A D A M P P L P L R A H * K R W R O A * I K S P T T S A G W F3
101 GAAGCCTTGGGCGGACGCGATGCCGCGTTGCGGCTTCGGGCGCATTGAAAACGCTGGCGGCAAGCCTGAATAAAATCGCAACGACATCCGCTGGCTGG 200
-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

```

At the bottom of the results table are links to export the matching sequences in FASTA format, (optionall) including flanking sequences. You can also export the table in tab-delimited text or Excel formats.

67	S5611	98.280	465	8	0	184143	4804	5268	extract →	←	0.0	803
82	11-004	98.280	465	8	0	184297	19518	19982	extract →	→	0.0	803
84	IAL2229	98.280	465	8	0	184635	4530	4994	extract →	←	0.0	803
90	CN100	98.280	465	8	0	184814	5350	5814	extract →	←	0.0	803

Files

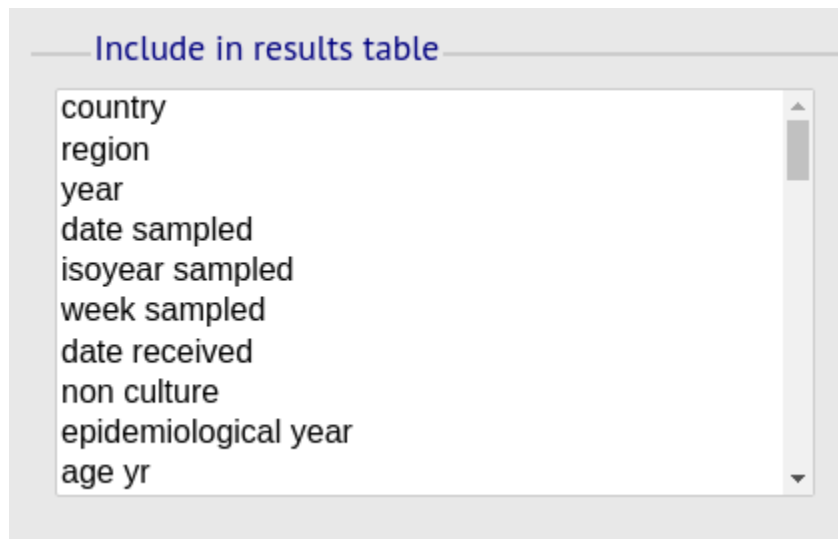
FASTA
 FASTA with flanking
 Table (tab-delimited text)

Table (Excel format)
 Tar file containing all output files

Please note that job results will remain on the server for 7 days.

### 14.1.1 Include in results table fieldset

This selection box allows you to choose which isolate provenance fields will be included in the results table.



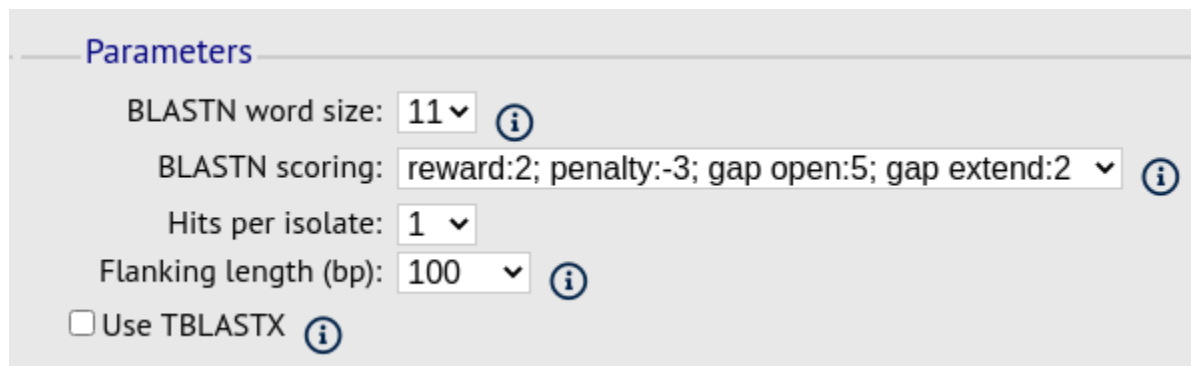
Include in results table

- country
- region
- year
- date sampled
- isoyear sampled
- week sampled
- date received
- non culture
- epidemiological year
- age yr

Multiple values can be selected by clicking while holding down Ctrl.

### 14.1.2 Parameters fieldset

This section allows you to modify BLAST parameters. This affects sensitivity and speed.



Parameters

BLASTN word size: 11 ⓘ

BLASTN scoring: reward:2; penalty:-3; gap open:5; gap extend:2 ⓘ

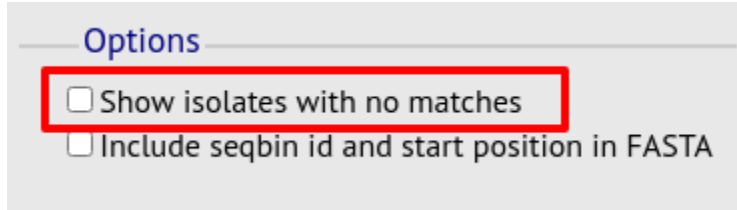
Hits per isolate: 1

Flanking length (bp): 100 ⓘ

☐ Use TBLASTX ⓘ

- **BLASTN word size** - This is the length of the initial identical match that BLAST requires before extending a match (default: 11). Increasing this value improves speed at the expense of sensitivity.
- **BLASTN scoring** - This is a dropdown box of combinations of identical base rewards; mismatch penalties; and gap open and extension penalties. BLASTN has a constrained list of allowed values which reflects the available options in the list.
- **Hits per isolate** - By default, only the best match is shown. Increase this value to the number of hits you'd like to see per isolate.
- **Flanking length** - Set the size of the upstream and downstream flanking sequences that you'd like to include.
- **Use TBLASTX** - This compares the six-frame translation of your nucleotide query sequence against the six-frame translation of the contig sequences. This is significantly slower than using BLASTN.

### 14.1.3 No matches



Options

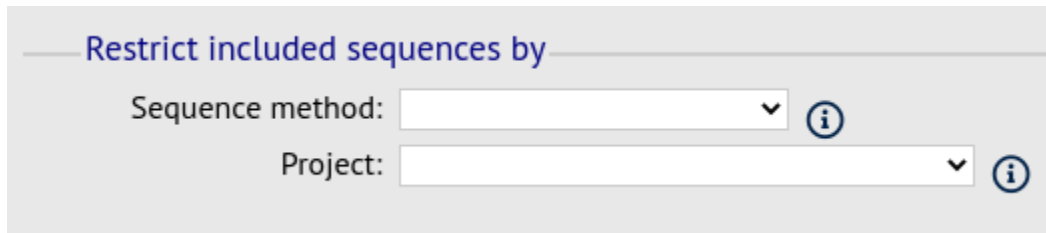
☐ Show isolates with no matches

☐ Include seqbin id and start position in FASTA

Click this option to create a row in the table indicating that a match was not found. This can be useful when screening a large number of isolates.

### 14.1.4 Filter fieldset

This section allows you to further filter your collection of isolates and the contig sequences to include.



Restrict included sequences by

Sequence method:  ⓘ

Project:  ⓘ

Available options are:

- Sequence method - Choose to only analyse contigs that have been generated using a particular method. This depends on the method being set when the contigs were uploaded.
- Project - Only include isolates belonging to the chosen project. This enables you to select all isolates and filter to a project.

## 14.2 BURST

BURST is an algorithm used to group MLST-type data based on a count of the number of profiles that match each other at specified numbers of loci. The analysis is available for both sequence definition database and isolate database schemes that have primary key fields set. The algorithm has to be *specifically enabled* by an administrator. Analysis is limited to 1000 or fewer records.

The plugin can be accessed following a query by clicking the 'BURST' button in the Analysis list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex	7	16	
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: **[BURST](#)** [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

If there multiple schemes that can be analysed, these can then be selected along with the group definition.

BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Plugins](#) > [BURST](#)

[Help](#)

## BURST analysis

This is the original BURST algorithm, developed by Ed Feil, first implemented by Man-Suen Chan. This version has been adapted for use as a plugin for the BIGSdb database software by Keith Jolley.

BURST analysis can be used to:

- Divide strains into groups according to their allelic profiles.
- Count the number of Single Locus Variants (SLV), Double Locus Variants (DLV) and Satellites (SAT) for each sequence type (ST).
- Identify the potential Ancestral Type (AT). These are shown with an asterisk next to their names in the results table.

Graphic representations of BURST groups can be saved in SVG format. This is a vector image format that can be manipulated and scaled in drawing packages, including the freely available [Inkscape](#).

**Options**

Select scheme: MLST

Group definition: profiles match at n-2 loci to any other member of the group [n = number of loci in scheme].

☒ Shade variant rings  
☐ Hide variant names (useful for overview if names start to overlap)

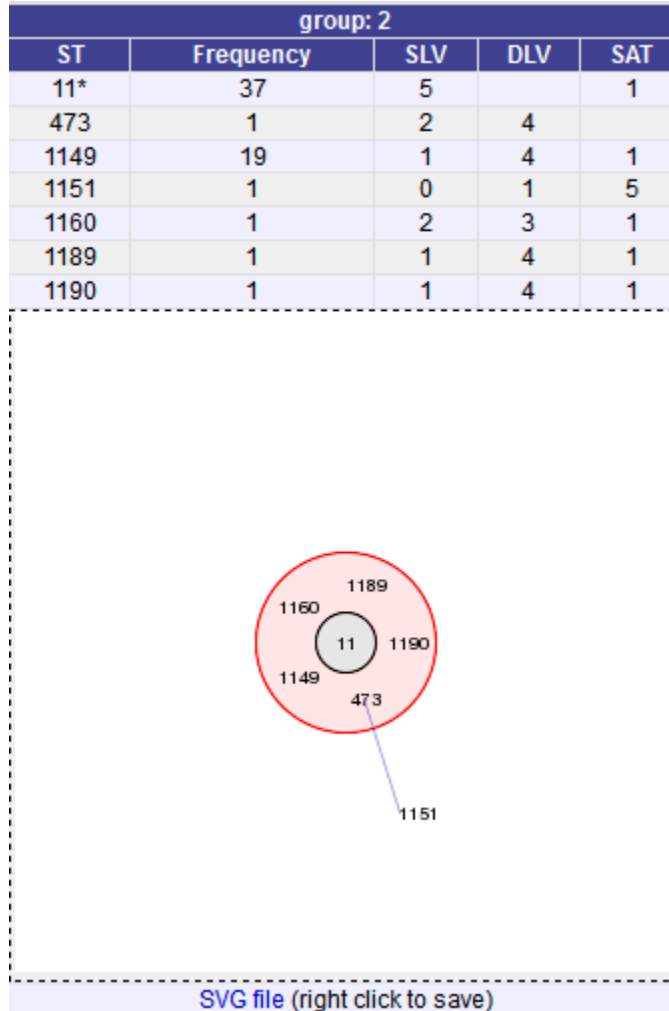
**Action**

SUBMIT

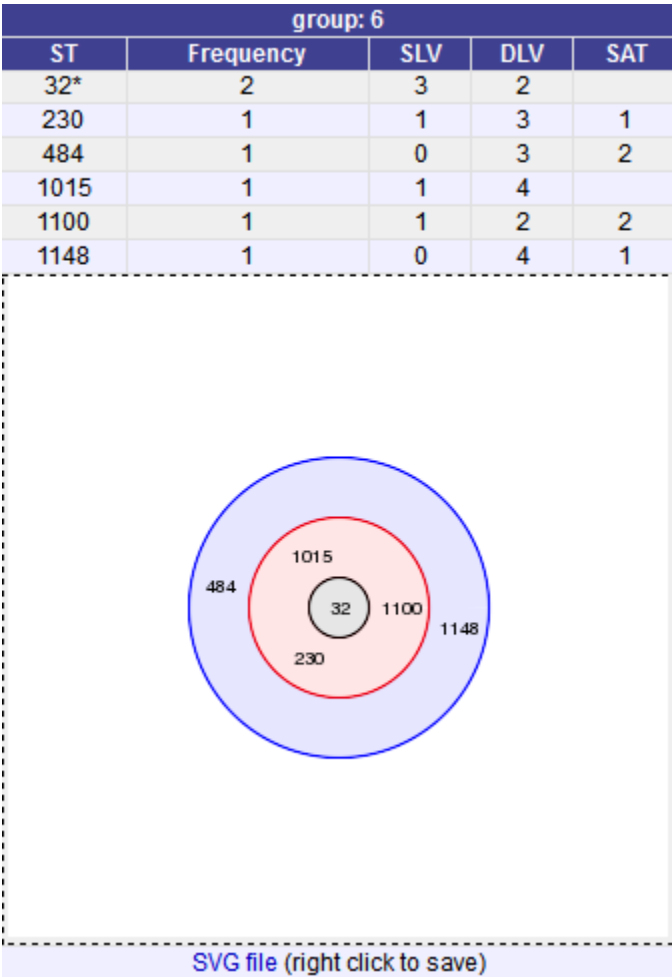
Modifying the group definition affects the size of groups and how they link together. By default, the definition is n-2 (where n is the number of loci), so for example on a 7 locus MLST scheme groups contain STs that match at 5 or more loci to any other member of the group.

Click Submit.

A series of tables will be displayed indicating the groups of profiles. Where one profile can be identified as a central genotype, i.e. the profile that has the greatest number of other profiles that are single locus variants (SLV), double locus variants (DLV) and so on, a graphical representation will be displayed. The central profile is indicated with an asterisk.



SLV profiles that match the central profile are shown within a red circle surrounding the central profile. Most distant profiles (triple locus variants) may be linked with a line. Larger groups may additionally have DLV profiles. These are shown in a blue circle.



Groups can get very large, where linked profiles form sub-groups and an attempt is made to depict these.

The codon usage plugin for isolate databases calculates the absolute and relative synonymous codon usage by isolate and by locus.

### 14.3. Codon usage

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

**ANALYSIS**

CUSTOMISE +

INFORMATION +

TYPING

Jump to the ‘Analysis’ category, follow the link to ‘Codon Usage’, then click ‘Launch Codon Usage’.

The function can be selected by clicking the ‘Codon usage’ link in the Analysis section of the main contents page.

### Analysis

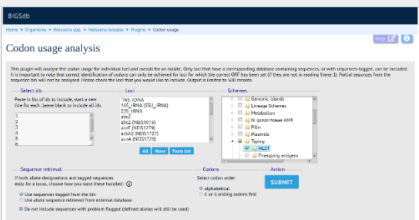
Analysis plugins - Jump to: [Codon Usage](#) | [Gene Presence](#) | [Genome Comparator](#) | [BLAST](#) | [rMLST species identity](#) | [PCR](#)

#### Codon Usage

Summary: Determine codon usage for specified loci for an isolate database query

The codon usage plugin calculates the absolute and relative synonymous codon usage by isolate and by locus for any dataset or the whole database. Specific loci or the loci that are members of a particular scheme can be chosen for analysis.

Documentation [bigsdb.readthedocs.io](https://bigsdb.readthedocs.io)



Launch 'Codon Usage'

Alternatively, it can be accessed following a query by clicking the ‘Codons’ button in the Analysis list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

Enter the ids of the isolate records to analyse - these will be already entered if you accessed the plugin following a query. Select the loci you would like to analyse, either from the dropdown loci list, and/or by selecting one or more schemes.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Codon usage

Help

Codon usage analysis

This plugin will analyse the codon usage for individual loci and overall for an isolate. Only loci that have a corresponding database containing sequences, or with sequences tagged, can be included. It is important to note that correct identification of codons can only be achieved for loci for which the correct ORF has been set (if they are not in reading frame 1). Partial sequences from the sequence bin will not be analysed. Please check the loci that you would like to include. Output is limited to 500 records.

Select ids

1

2

3

4

5

16S\_rDNA

16S\_rRNA (SSU\_rRNA)

23S\_rRNA

abcZ (NEIS1015)

aceF (NEIS1279)

All

None

Paste list

Loci

16S\_rDNA

16S\_rRNA (SSU\_rRNA)

23S\_rRNA

abcZ (NEIS1015)

aceF (NEIS1279)

Schemes

Plasmids

Typing

MLST

Finotyping antigens

16S

Antigen genes

Bexsero Antigen Sequence

Human-restricted Neisseria

Sequence retrieval

If both allele designations and tagged sequences exist for a locus, choose how you want these handled:

☒ Use sequences tagged from the bin

☐ Use allele sequence retrieved from external database

☒ Do not include sequences with problem flagged (defined alleles will still be used)

Codons

Select codon order:

☒ alphabetical

☐ C or G ending codons first

Action

SUBMIT

Click submit. The job will be submitted to the queue and will start running shortly.

Output files will be created in both tab-delimited text and Excel formats for the following:

- Absolute frequency of codon usage by isolate
- Absolute frequency of codon usage by locus
- Relative synonymous codon usage by isolate
- Relative synonymous codon usage by locus


14.3. Codon usage

313

BIGSdb




Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Job status viewer




## Job status viewer





**Status**

Job id: BIGSdb\_004053\_1596101846\_94417  
 Submit time: 2020-07-30 09:37:26  
 Status: finished  
 Start time: 2020-07-30 09:37:35  
 Progress: 100%  
 Stop time: 2020-07-30 09:38:00  
 Total time: 24 seconds

**Output**  
 Files

 Absolute frequency of codon usage by isolate (text)
  Absolute frequency of codon usage by locus (text)
  Relative synonymous codon usage (RSCU) by isolate (text)

 Relative synonymous codon usage (RSCU) by locus (text)
  Absolute frequency of codon usage by isolate (Excel)
  Absolute frequency of codon usage by locus (Excel)

 Relative synonymous codon usage (RSCU) by isolate (Excel)
  Relative synonymous codon usage (RSCU) by locus (Excel)
  Tar file containing all output files

Please note that job results will remain on the server for 7 days.

## 14.4 Field breakdown

The field breakdown plugin for isolate databases displays the frequency of each value for fields, alleles and schemes. The function can be accessed by selecting the ‘Analysis’ section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

Query database

Search database  
 Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci  
 This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

**ANALYSIS**

CUSTOMISE +

INFORMATION +

TYPING

In the ‘Breakdown’ category, follow the link to ‘Field Breakdown’, then click ‘Launch Field Breakdown’.

The breakdown function can be selected for the whole database by clicking the ‘Single field’ link in the Breakdown section of the main contents page.

**Breakdown**

Breakdown plugins - Jump to: [Field Breakdown](#) | [Two Field Breakdown](#) | [Unique Combinations](#) | [Polymorphisms](#) | [Publication Breakdown](#) | [Sequence Bin Breakdown](#)

**Field Breakdown**

Summary: Breakdown of query results by field

The field breakdown plugin displays the frequency of each value for fields, alleles and schemes. Output is in the form of dynamic charts, maps, and tables. Data can be exported as an Excel file, SVG image, or FASTA file.

[Documentation](#) [bigsd.readthedocs.io](#)



[Launch 'Field Breakdown'](#)

Alternatively, a breakdown can be displayed of the dataset returned from a query by clicking the ‘Fields’ button in the Breakdown list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



#### Analysis tools

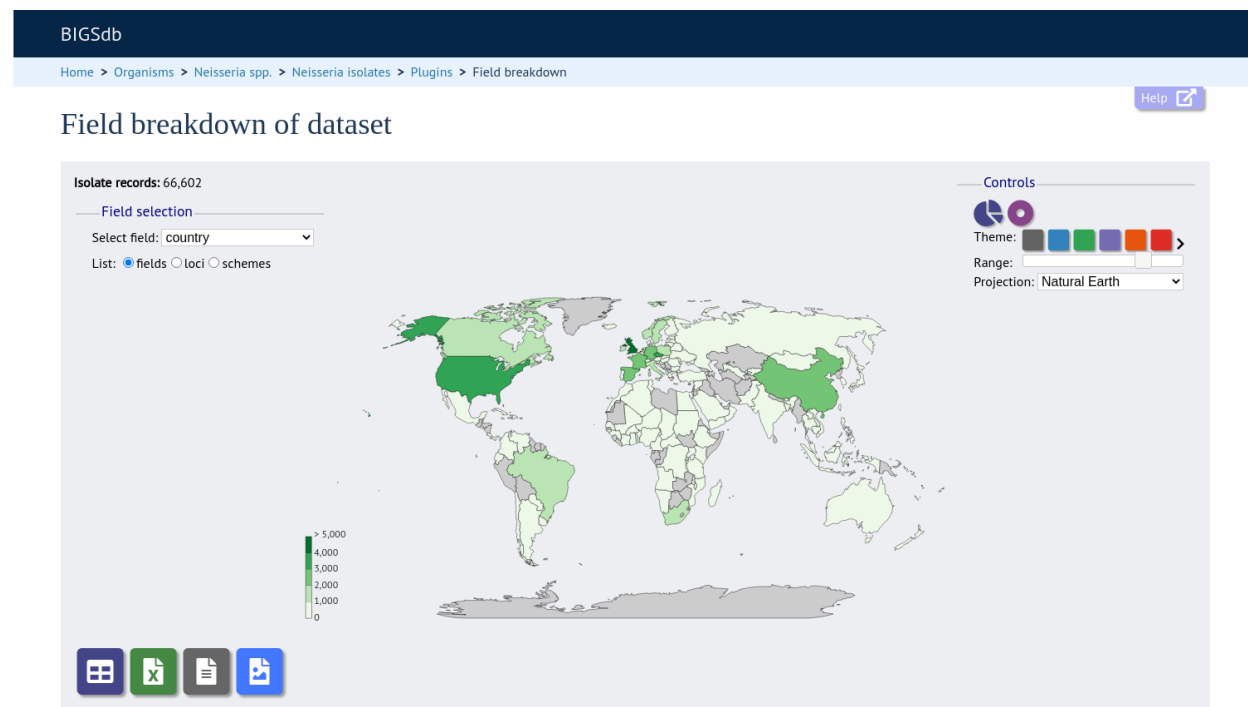
Breakdown: **Fields** | Two Field | Combinations | Publications | Sequence bin

Analysis: Codons | Gene Presence | Genome Comparator | BLAST | rMLST species id | PCR

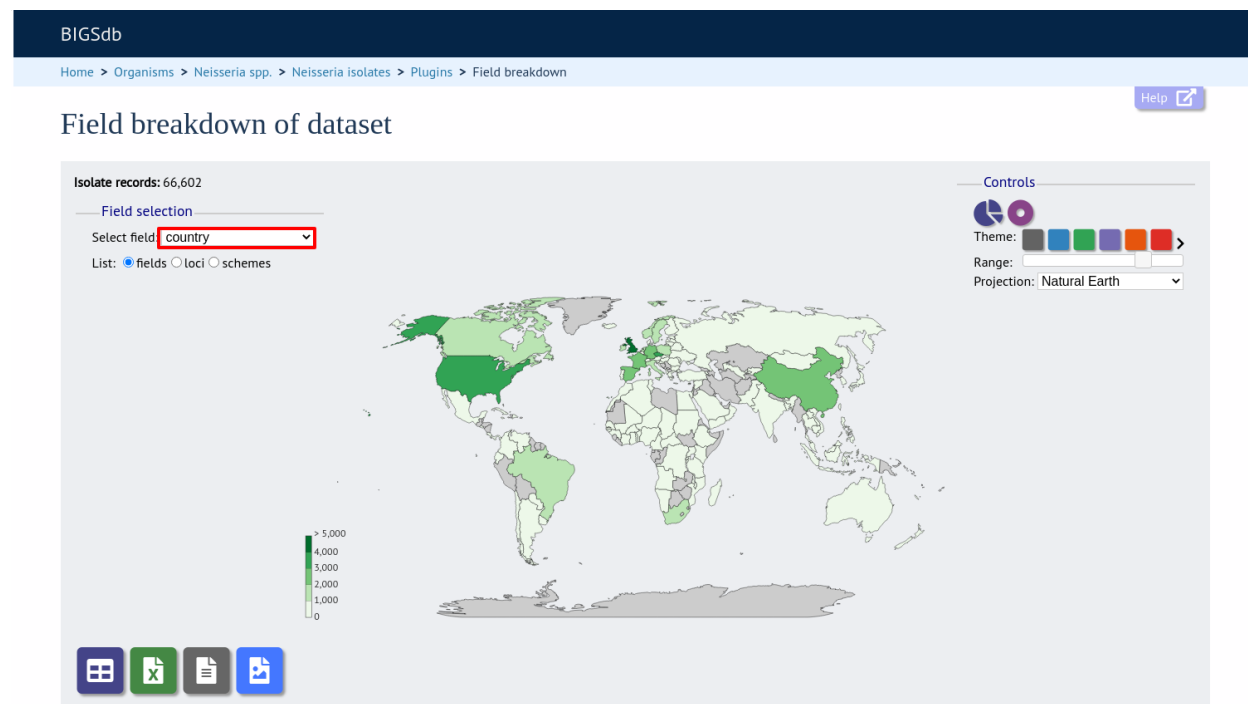
Export: Dataset | Contigs | Sequences

Third party: GrapeTree | PhyloViz

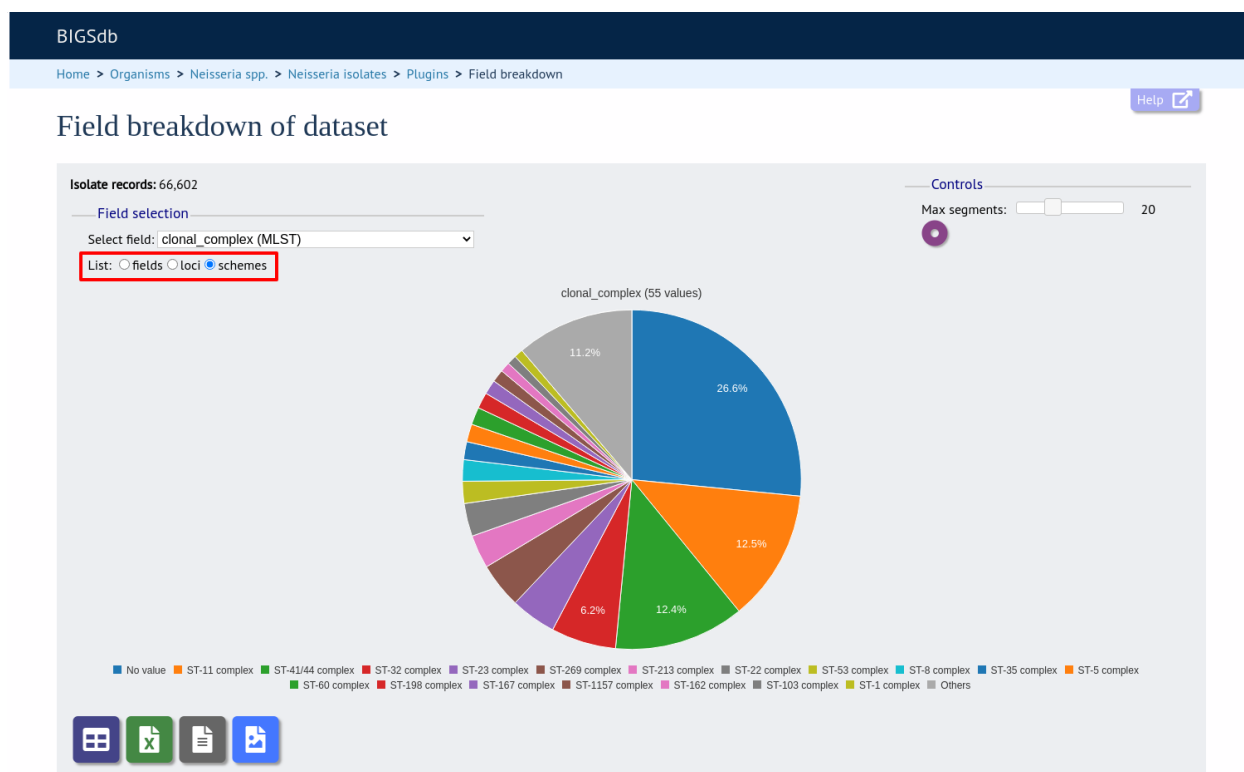
A chart will be displayed for the first field. Depending on the field type, this may be either a world map (for country or continent fields), pie chart, or bar chart.



Other fields can be chosen by selecting them in the dropdown list box.



You can also breakdown loci and schemes by clicking the appropriate button. This will re-populate the dropdown list.

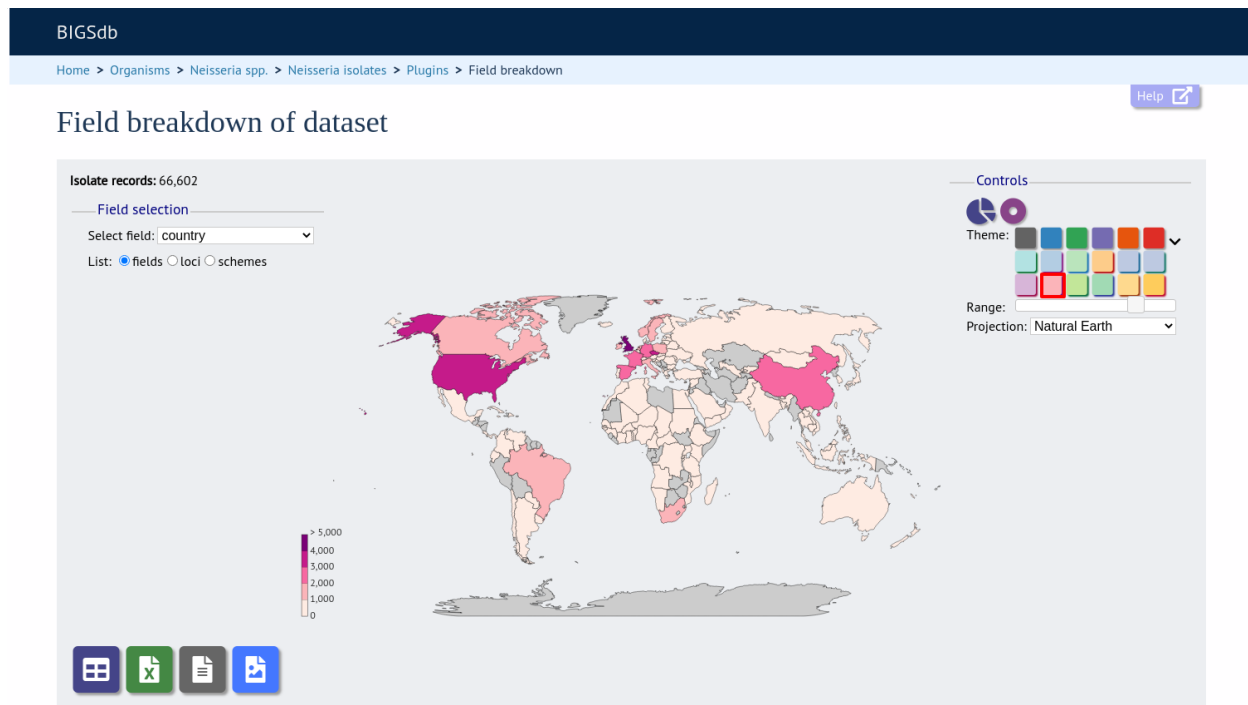


The charts are dynamic and you can manipulate some aspects of them using controls shown on the screen.

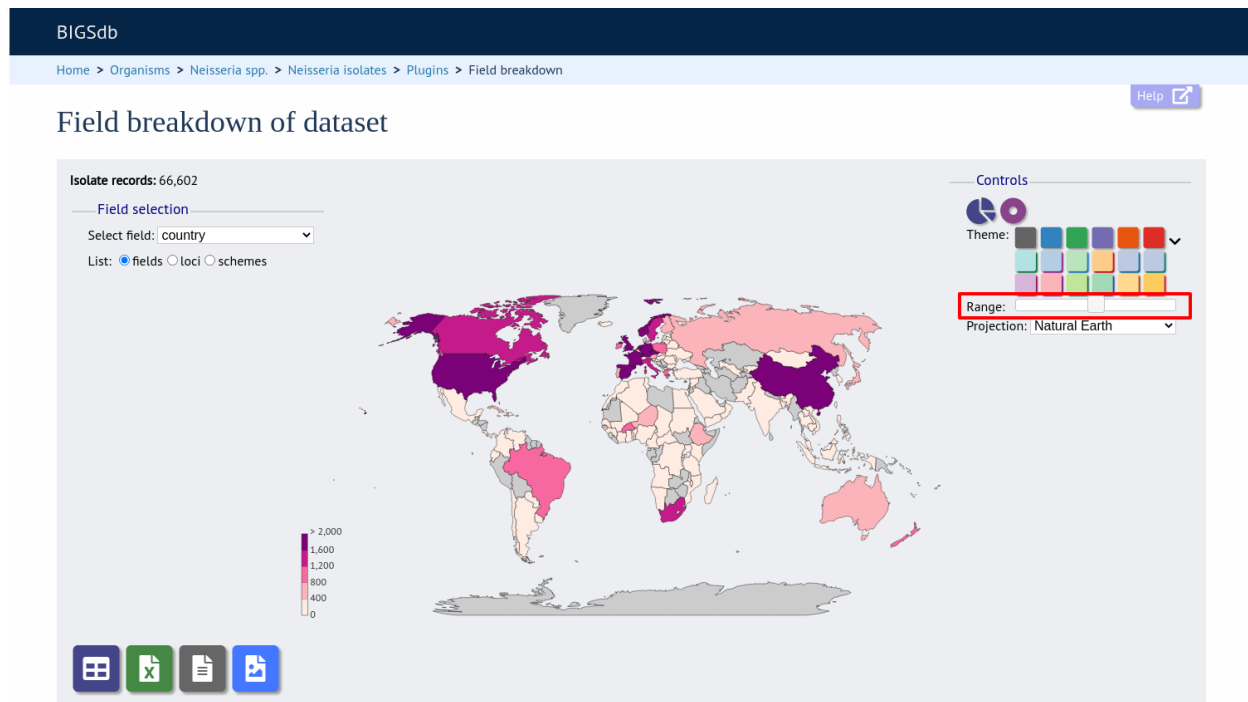
#### 14.4.1 Maps

World maps are shown for country and continent fields (provided standardized country names are used in the database). The maps can be modified in a number of ways.

The colour theme can be changed by clicking the appropriate coloured square. Additional themes are available by clicking the '>' link.

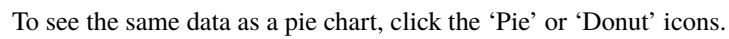


The range that is used to decide the colour boundaries can be changed by using the range slider.

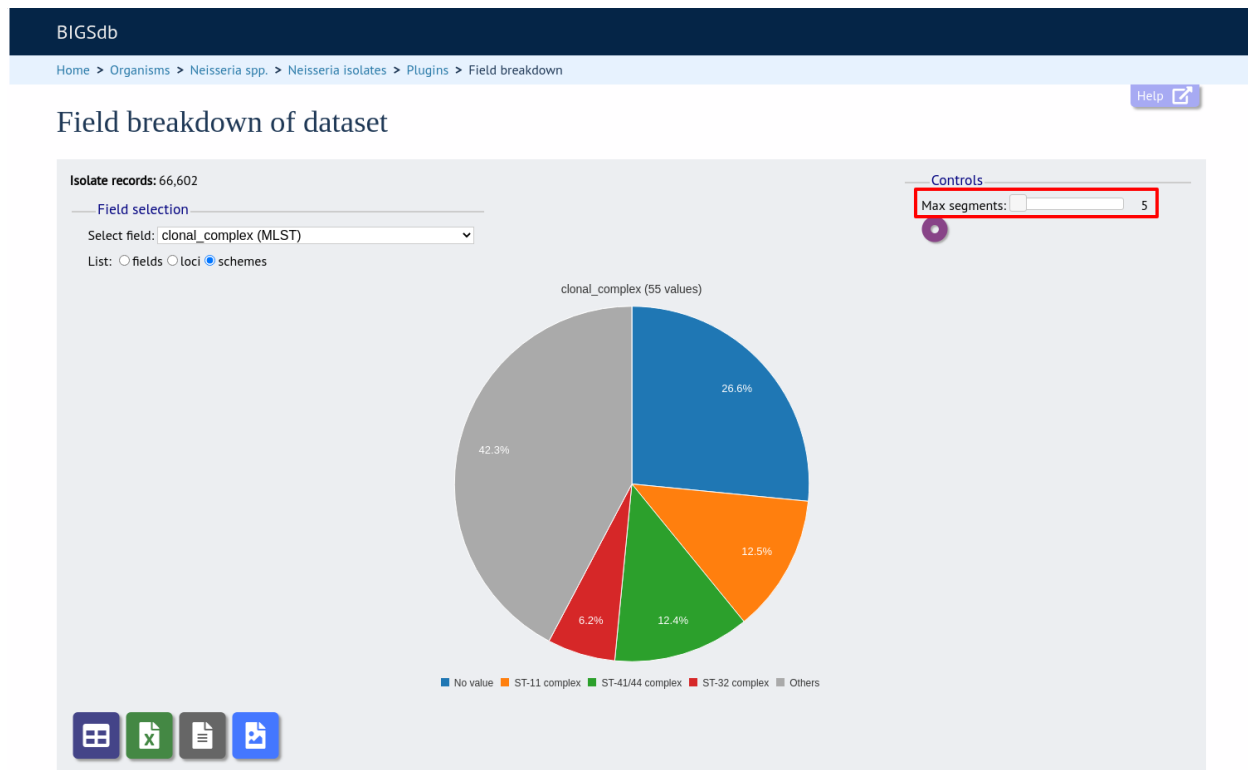


Finally the map projection can be changed. The default ‘Natural Earth’ provides a reasonable display for most latitudes but you may prefer others such as ‘Mercator’.

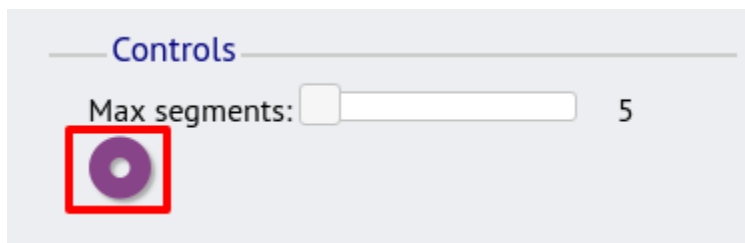
Help 



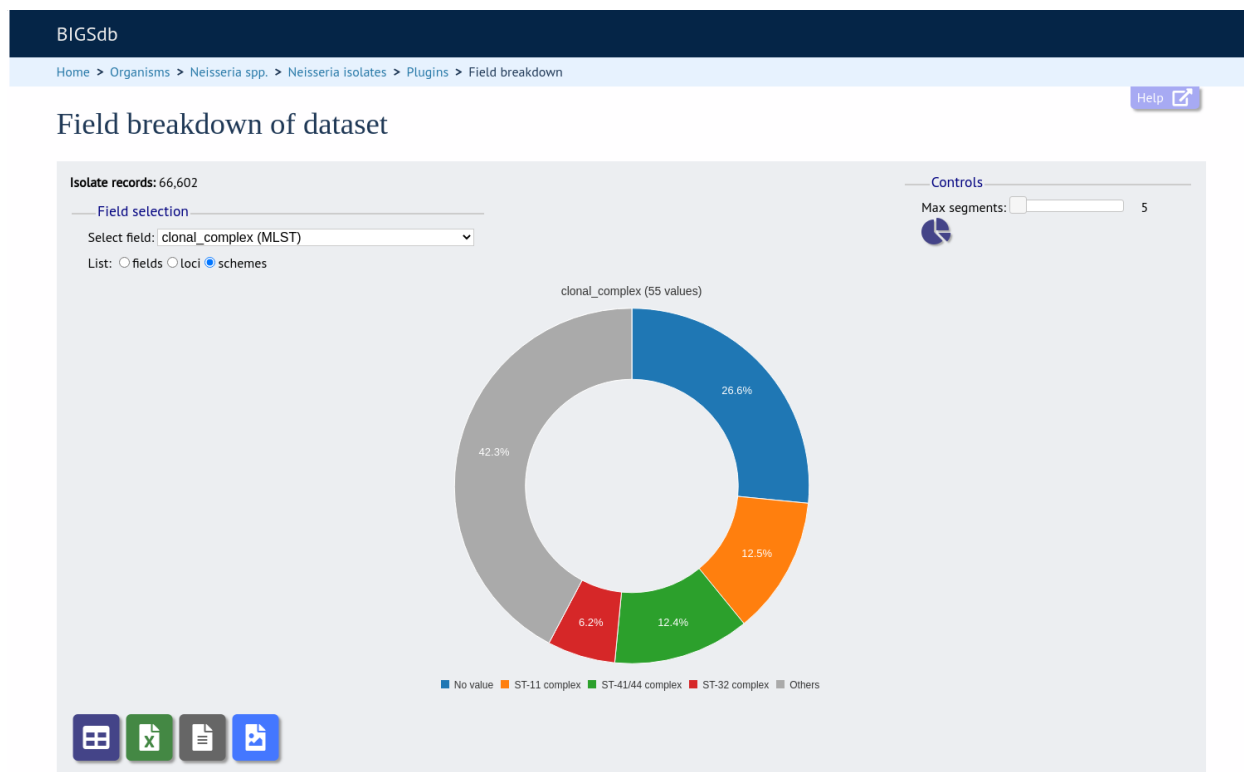
#### 14.4. Field breakdown



The chart can be transformed into a donut chart by clicking the donut icon.



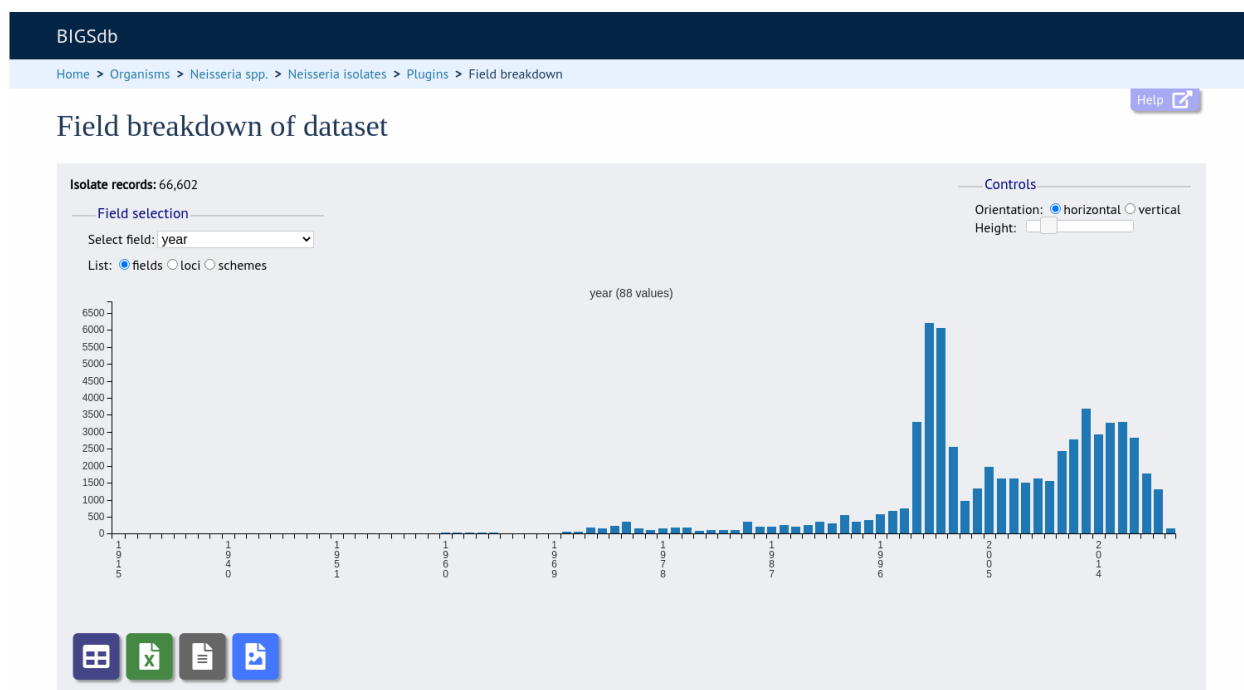
The icon changes to a pie chart image (clicking this will return to the pie chart).



Values can also be removed from the analysis by clicking their label in the legend below the chart. The percentages of the other values will be recalculated. Clicking the label again will re-add the value.

### 14.4.3 Bar charts

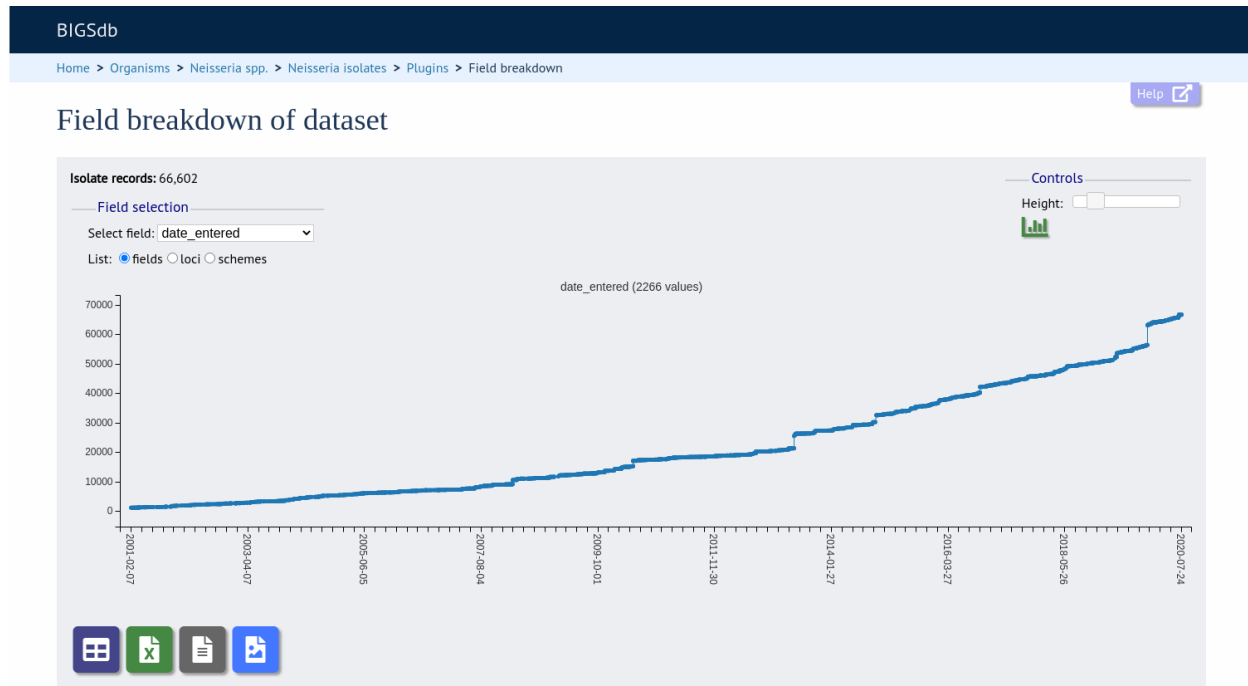
Integer fields will be displayed as a bar chart.



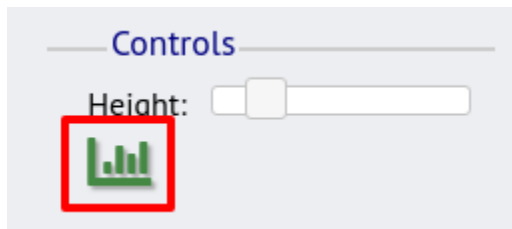
You can modify the height and the orientation of the chart using the controls.

### 14.4.4 Line charts

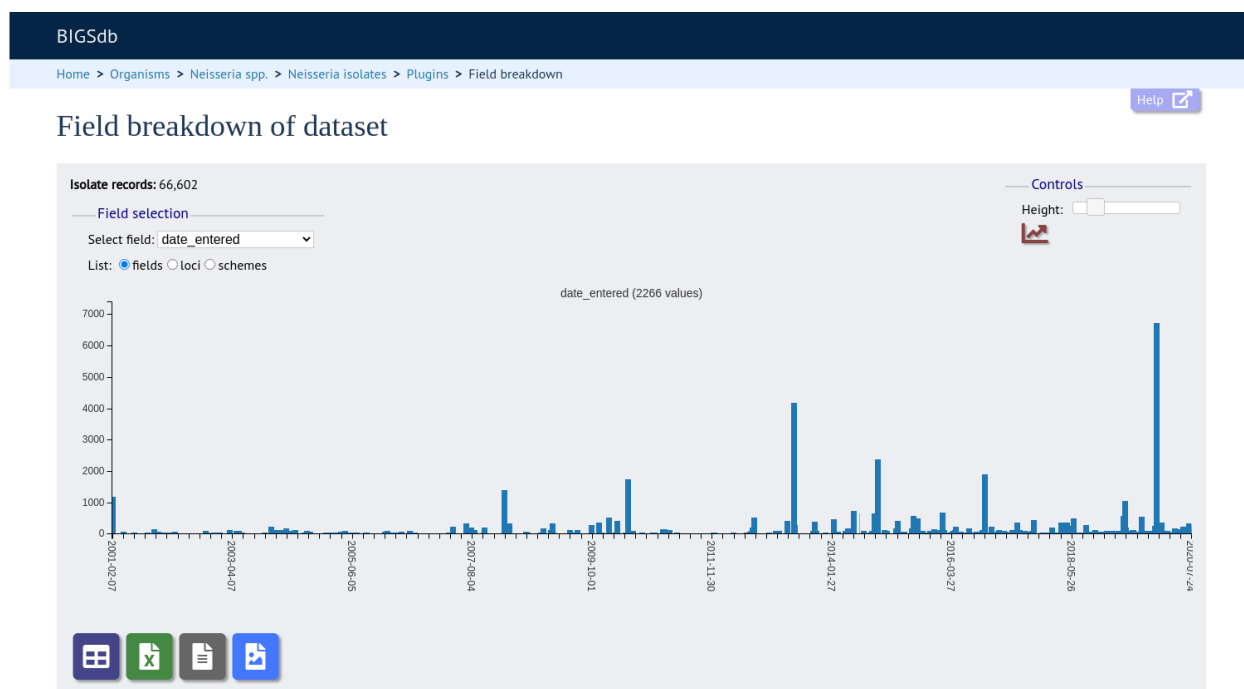
Date fields will be displayed as a line chart. By default this shows the cumulative values.



The chart can be converted in to a bar chart showing discrete values by clicking the bar chart icon.

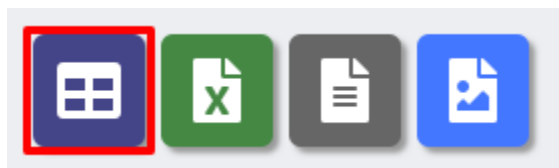


The icon changes to a line chart image (clicking this will return to the line chart).



#### 14.4.5 Summary tables

The field breakdown can be displayed as a summary table containing values and percentages of all values. This can be selected by clicking the table icon below the displayed chart.



The table can be re-ordered by clicking any of the headings.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Field breakdown

Help

### Breakdown by country

131 values.

country	Frequency	Percentage
UK [England]	12836	19.27
UK [Scotland]	5228	7.85
UK	3730	5.60
USA	3263	4.90
Czech Republic	3112	4.67
France	2983	4.48
Germany	2769	4.16
Spain	2273	3.41
China	2185	3.28
Norway	1819	2.73
The Netherlands	1752	2.63
UK [Wales]	1670	2.51
Sweden	1540	2.31
Canada	1477	2.22
South Africa	1321	1.98
Italy	1285	1.93
Ireland	1193	1.79

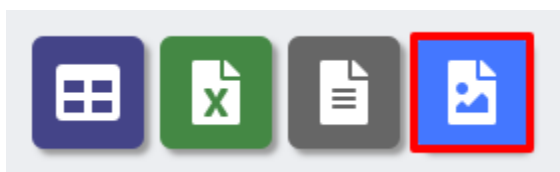
The same table can be exported as an Excel file by clicking the Excel icon.



Alternatively, it can be exported as a tab-delimited text file by clicking the text file icon.

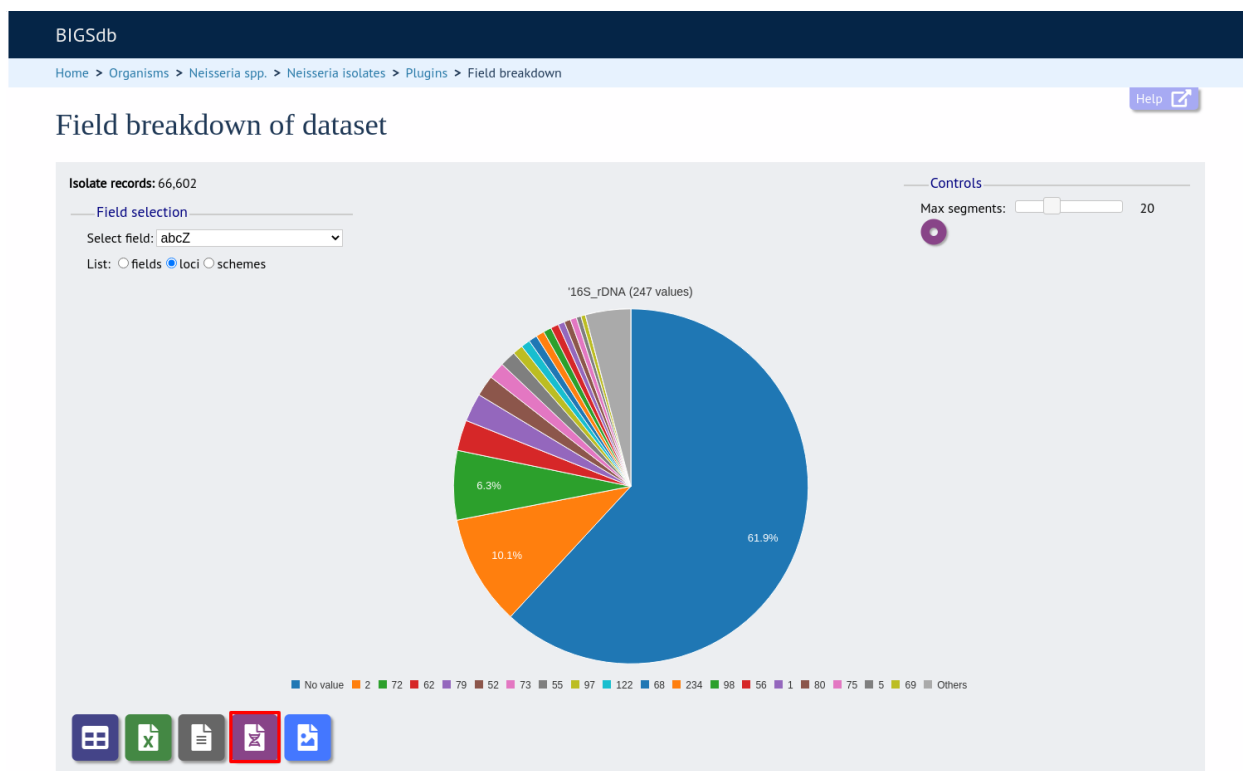


The chart image can also be saved as a SVG file, suitable for manipulation in a graphics program.



### 14.4.6 Exporting allele sequences

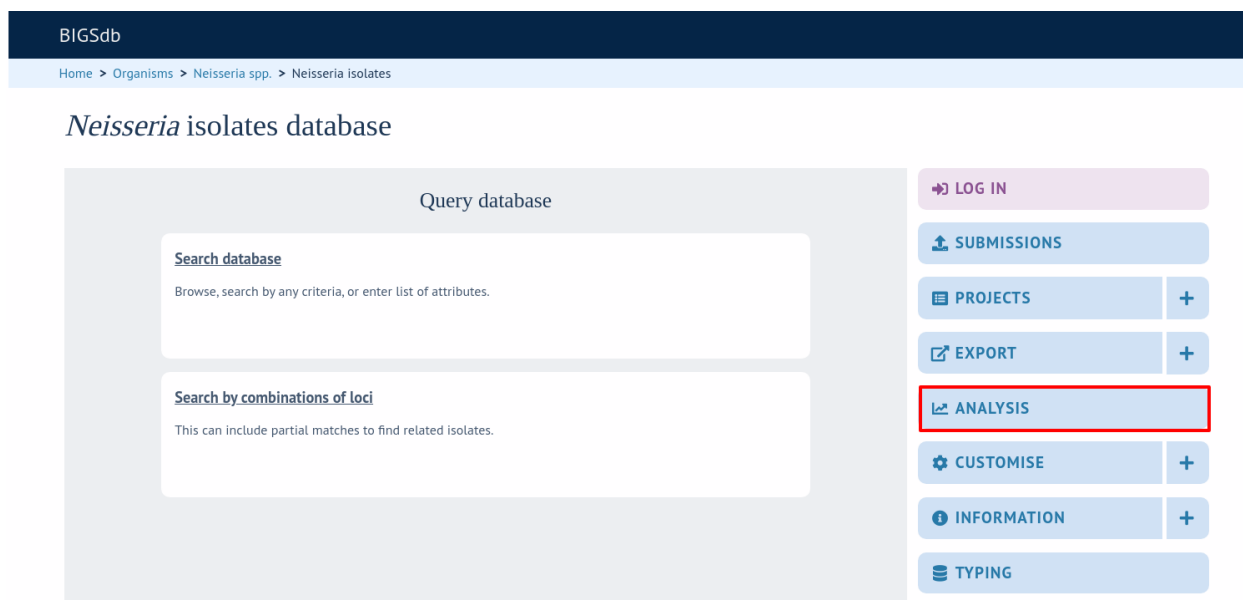
If a locus breakdown is being display, you can choose to export the allele sequences in FASTA format by clicking the FASTA file icon.



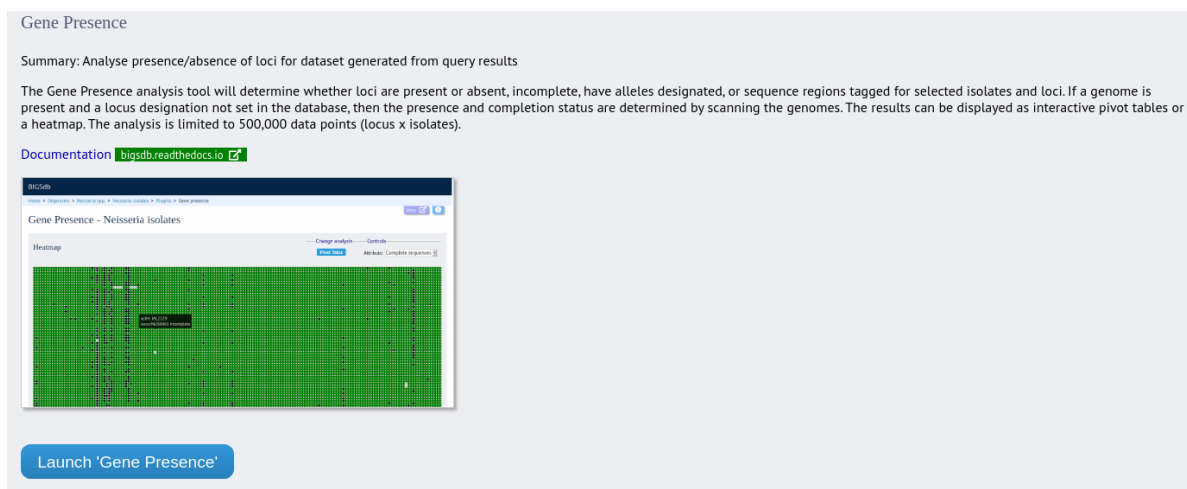
## 14.5 Gene Presence

The Gene Presence analysis tool will determine whether loci are present or absent, incomplete, have alleles designated, or sequence regions tagged for selected isolates and loci. If a genome is present and a locus designation not set in the database, then the presence and completion status are determined by scanning the genomes. The results can be displayed as interactive pivot tables or a heatmap. The analysis is limited to 500,000 data points (locus x isolates).

The function can be accessed by selecting the ‘Analysis’ section on the main contents page.



Jump to the ‘Analysis’ category, follow the link to ‘Gene Presence’, then click ‘Launch Gene Presence’.



Alternatively, it can be accessed following a query by clicking the ‘Gene Presence’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the plugin interface.

61	393	B392; NIBSC_2823; Z1392	Greece	1968	carrier	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
64	254	B439; NIBSC_2812; Z1439	Djibouti	1966	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F1-7
67	S5611	B466; NIBSC_2765; Z1466	Australia	1977	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
82	11-004	B503; NIBSC_2826; Z1503	China	1984	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-8
84	IAL2229	B506; NIBSC_2816; Z1506	Brazil	1976		Neisseria meningitidis	A	5	ST-5 complex	20	9	F2-1
90	CN100	B534; NIBSC_2768; Z1534	UK [England]	1941	invasive (unspecified/other)	Neisseria meningitidis	A	21		5-2	10	F3-9
120	F4698	NIBSC_2731; Z3515	Saudi Arabia	1987	carrier	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
128	F6124	NIBSC_2730; Z3524	Chad	1988	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
160	1014	NIBSC_2821; Z3667	Sudan	1985	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
210	H1964	NIBSC_2796; Z3771	UK	1987	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
237	H44/76	44/76-3; NIBSC_2724; Z3842	Norway	1976	invasive (unspecified/other)	Neisseria meningitidis	B	32	ST-32 complex	7	16	F3-3
238	153	NIBSC_2733; Z3905	China	1966	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1



### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

Select the isolates to include. Analysis can be performed on any selection of loci, or more conveniently, you can select a scheme in the scheme selector to include all loci belonging to that scheme. You can also select a recommended scheme if these have been defined.

The parameters of the BLAST query used to determine presence or absence can be modified, but in most cases the default options should work well. Click ‘Submit’ to start the analysis.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Gene presence

Help

## Gene Presence - Neisseria isolates

Please select the required isolate ids and loci for comparison - use CTRL or SHIFT to make multiple selections in list boxes. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description.

Interactive analysis is limited to 500,000 data points (isolates x loci). If you select more than this then output will be restricted to static tables.

Isolates

1  
2  
7  
10  
11  
13  
19

Clear List all

User genomes

Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome):

Choose file No file chosen

Loci

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)

All None Paste list

Recommended schemes

Select one or more schemes below or use the full schemes list.

MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0

Clear

Schemes

All loci  
Capsule  
Genetic Information Processing  
Genomic islands  
Lineage Schemes  
Metabolism  
N. gonorrhoeae AMR  
Pilin  
Plasmids

Parameters / options

Min % identity: 70  
Min % alignment: 50  
BLASTN word size: 20

Action

RESET SUBMIT

The job will be sent to the job queue. When it has finished, you will have two options to display the output: ‘Pivot Table’ or ‘Heatmap’.


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Chapter 14. Data analysis plugins

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Job status viewer

## Job status viewer





**Status**

Job id: BIGSdb\_017561\_1596120664\_37507  
 Submit time: 2020-07-30 14:51:04  
 Status: finished  
 Start time: 2020-07-30 14:51:13  
 Progress: 100%  
 Stop time: 2020-07-30 14:52:46  
 Total time: 1 minute and 32 seconds

**Output**

[Pivot Table](#)
[Heatmap](#)

Files

 Presence/absence (Excel)
  Presence/absence (text)
  Tar file containing all output files

Please note that job results will remain on the server for 7 days.

### 14.5.1 Pivot Table

Clicking the ‘Pivot Table’ button will display an interactive pivot table. The default display shows the number of isolates for which each locus is present or absent.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Gene presence

Help ⓘ

## Gene Presence - Neisseria isolates

121,980 data points (isolates x loci) used

Please note that table updates may be slow if you try to combine id (or isolate) with locus. Any other combination of fields is fine, e.g. locus vs presence, id vs presence.

**Pivot table**

Drag and drop fields on to the table axes. Multiple fields can be combined.

Table ▾
 id ▾ isolate ▾ complete ▾ known allele ▾ designated ▾ tagged ▾

Count ▾ : --
 presence ▾

locus ▾

	presence	absent	present	Totals
locus				
NEIS0001			76	76
NEIS0004			76	76
NEIS0005			76	76
NEIS0006			76	76
NEIS0007			76	76
NEIS0008			76	76
NEIS0009			76	76
NEIS0010			76	76

Change analysis ▾

[Heatmap](#)

You can break down any combination of fields by dragging them from the field area at the top of the table to either of the axes. For example, to show how many isolates have alleles designated and sequence regions tagged for each locus, drag the ‘designated’ and ‘tagged’ fields to the x-axis selector.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Gene presence

Help

## Gene Presence - Neisseria isolates

121,980 data points (isolates x loci) used

Please note that table updates may be slow if you try to combine id (or isolate) with locus. Any other combination of fields is fine, e.g. locus vs presence, id vs presence.

**Pivot table**

Drag and drop fields on to the table axes. Multiple fields can be combined.

Table: Count

Fields: id, isolate, complete, known allele, designated, tagged

Row field: locus

Column field: presence

locus	presence	absent	present	Totals
NEIS0001			76	76
NEIS0004			76	76
NEIS0005			76	76
NEIS0006			76	76
NEIS0007			76	76
NEIS0008			76	76
NEIS0009			76	76
NEIS0010			76	76

Change analysis

Heatmap

The table will be re-drawn including these fields.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Gene presence

Help

## Gene Presence - Neisseria isolates

121,980 data points (isolates x loci) used

Please note that table updates may be slow if you try to combine id (or isolate) with locus. Any other combination of fields is fine, e.g. locus vs presence, id vs presence.

**Pivot table**

Drag and drop fields on to the table axes. Multiple fields can be combined.

Table: Count

Fields: id, isolate, complete, known allele

Row field: locus

Column field: presence, designated, tagged

locus	presence		absent		present		Totals
	designated	not designated	designated	not designated	designated	not designated	
	tagged	untagged	tagged	untagged	tagged	untagged	
NEIS0001					76		76
NEIS0004					67	9	76
NEIS0005					71	5	76
NEIS0006					76		76
NEIS0007					76		76
NEIS0008					76		76

Change analysis

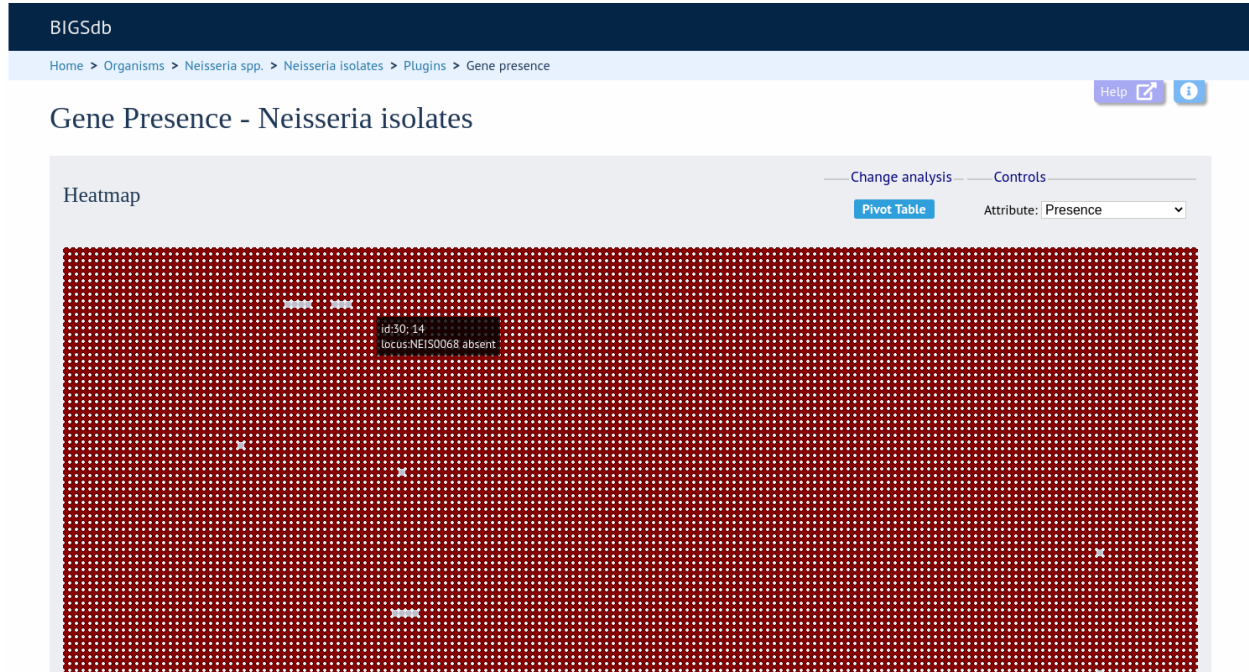
Heatmap

**Note:** If your dataset has more than 100,000 data points (locus x isolates), then be aware that combining both id (or isolate) and locus within the table will result in sluggish performance. Any other combination of fields should be fine.

## 14.5.2 Heatmap

Clicking the ‘Heatmap’ button will display an interactive heatmap. By default the display shows the presence or absence of a locus for each isolate.

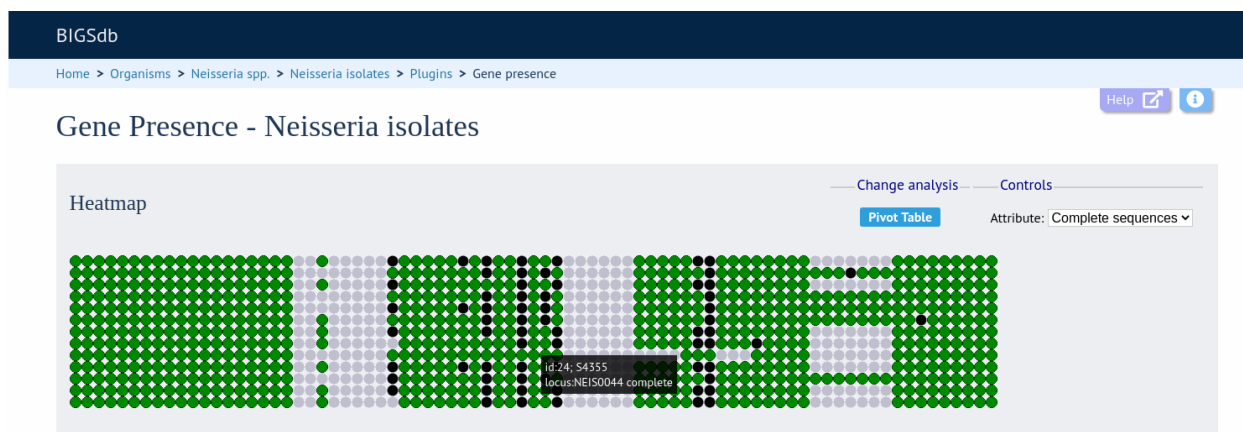
Hovering the mouse cursor or touching a region will identify the isolate and locus in a tooltip.



Change the attribute that is displayed by changing the selection in the attribute dropdown box:



The heatmap does scale to the number of records required to be displayed. If you find individual points to be too small, then choose a smaller subset of data to display:

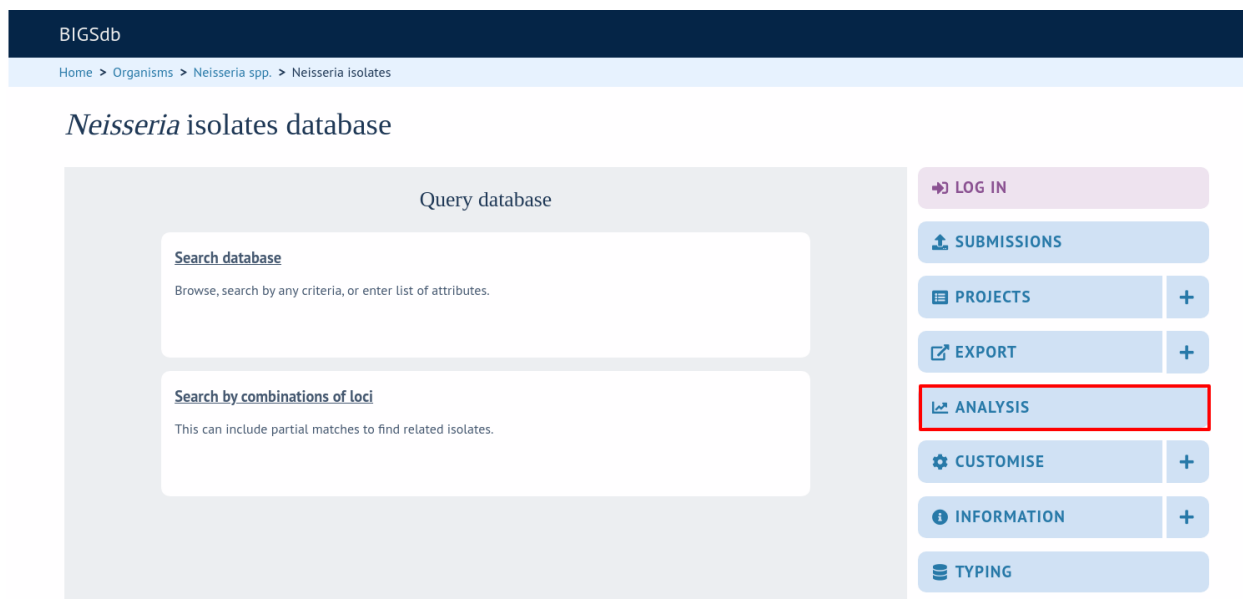


## 14.6 Genome comparator

Genome Comparator is an optional plugin that can be enabled for specific databases. It is used to compare whole genome data of isolates within the database using either the database defined loci or the coding sequences of an annotated genome as the comparator.

Output is equivalent to a whole genome MLST profile, a distance matrix calculated based on allelic differences and a NeighborNet graph generated from this distance matrix.

Genome Comparator can be accessed by selecting the 'Analysis' section on the main contents page.



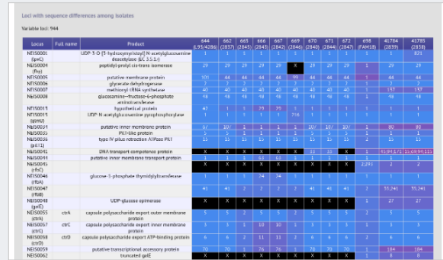
Jump to the 'Analysis' category, follow the link to 'Genome Comparator', then click 'Launch Genome Comparator'.

## Genome Comparator

Summary: Compare genomes at defined loci or against loci defined in a reference genome

Genome Comparator is used to compare whole genome data of isolates within the database using either the database defined loci or the coding sequences of an annotated genome as the comparator. Output is equivalent to a whole genome MLST profile, a distance matrix calculated based on allelic differences and a NeighborNet graph generated from this distance matrix. The analysis facilitates the determination of precisely which loci vary among isolates. Additionally, user-uploaded genomes that are not contained in the database can be analysed alongside genomes that are.

Documentation [bigssdb.readthedocs.io](https://bigssdb.readthedocs.io)



Alternatively, it can be accessed following a query by clicking the 'Genome Comparator' button at the bottom of the results table. Isolates with sequence data returned in the query will be automatically selected within the Genome Comparator interface.

14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



## Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

## 14.6.1 Analysis using defined loci

Select the isolate genomes that you wish to analyse. These will either be in a dropdown list or, if there are too many in the database, a text input where a list can be entered. You can also upload your own genomes for analysis - these should be either a single file in FASTA format (if you have just one genome), or a zip file containing multiple FASTA files. Select either the loci from the list or a set of schemes (either from the schemes box or from a list of recommended schemes if these have been set up). Press submit.

BIGSdb
Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Genome comparator
Help ⓘ ⓘ

## Genome Comparator - Neisseria isolates

Selecting 'All loci' will produce an artefactual analysis because this database contains different kinds of loci that are not equivalent (complete genes, MLST fragments, peptide variable regions, intergenic regions etc.). You are advised to select one of the recommended schemes.

Please select the required isolate ids and loci for comparison - use CTRL or SHIFT to make multiple selections in list boxes. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

### Isolates

644  
662  
665  
666  
667  
669  
670

Clear List all

### User genomes

Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome): ⓘ

Choose file No file chosen

### Loci

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)

All None Paste list

### Include in identifiers

isolate  
country  
region  
year  
date sampled  
isoyear sampled  
week sampled  
date received  
non culture

### Recommended schemes

Select one or more schemes below or use the full schemes list.

MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0

Clear

### Schemes

Genomic islands  
Lineage Schemes  
Metabolism  
N. gonorrhoeae AMR  
Pilin  
Plasmids  
Typing  
MLST  
Finotyping antigens

### Annotated reference genome

Enter accession number: ⓘ  
or choose annotated genome: ⓘ  
or upload Genbank/EMBL/FASTA file: ⓘ  

Choose file No file chosen

### Parameters / options

Min % identity: 70 ⓘ  
Min % alignment: 50 ⓘ  
BLASTN word size: 20 ⓘ  
☐ Rescan undesigned loci ⓘ

### Distance matrix calculation

With incomplete loci:  
☐ Completely exclude from analysis  
☐ Treat as distinct allele  
☒ Ignore in pairwise comparison  
☐ Exclude pairwise missing loci  
☒ Exclude loci paralogous in all  
☒ Exclude pairwise paralogous loci

### Alignments

☐ Produce alignments ⓘ  
☒ Include ref sequences in alignment  
☐ Align all loci (not only variable)  
☐ Create alignment stats  
Aligner: MAFFT

### Core genome analysis

Core threshold (%): 90 ⓘ  
☐ Calculate mean distances ⓘ

### Filter by

Sequence method: ⓘ  
Project: ⓘ  
Experiment: ⓘ

### Action

RESET SUBMIT

The job will be submitted to the job queue and will start running shortly.

There will be a series of tables displaying variable loci, colour-coded to indicate allelic differences. Finally, there will be links to a distance matrix which can be loaded in to SplitsTree for further analysis and to a NeighborNet chart showing relatedness of isolates. Due to processing constraints on the web server, this NeighborNet is only calculated if 200 or fewer genomes are selected for analysis, but this can be generated in the stand-alone version of SplitsTree using the distance matrix if required.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Job status viewer](#)

## Job status viewer



## Status

Job id: BIGSdb\_024566\_1596186459\_13471  
 Submit time: 2020-07-31 09:07:39  
 Status: finished  
 Start time: 2020-07-31 09:07:42  
 Progress: 100%  
 Stop time: 2020-07-31 09:07:46  
 Total time: 4 seconds

## Output

## Analysis against defined loci

## All loci

Allele numbers are used where these have been defined, otherwise sequences will be marked as 'New#1', 'New#2' etc. Missing alleles are marked as 'X'. Incomplete alleles (located at end of contig) are marked as 'I'.

Locus	Full name	Product	644 (L93/4286)	662 (2837)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)	41784 (2839)	41785 (2838)
abcZ			2	2	2	2	2	7	2	2	2	2	2	2
adk			3	3	3	3	3	3	3	3	3	3	3	3
aroE			4	19	4	4	4	4	19	19	19	4	4	4
fumC			3	3	24	23	23	3	3	3	3	3	3	3
gdh			8	8	8	8	8	8	8	8	8	8	8	8
pdhC			4	4	4	6	6	4	4	4	4	4	4	4
pgm			6	6	6	6	6	6	6	6	6	6	6	6

## Loci with sequence differences among isolates

Variable loci: 4

Locus	Full name	Product	644 (L93/4286)	662 (2837)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)	41784 (2839)	41785 (2838)
abcZ			2	2	2	2	2	7	2	2	2	2	2	2
aroE			4	19	4	4	4	4	19	19	19	4	4	4
fumC			3	3	24	23	23	3	3	3	3	3	3	3
pdhC			4	4	4	6	6	4	4	4	4	4	4	4

## Exactly matching loci

These loci are identical in all isolates.

Matches: 3

Locus	Full name	Product	644 (L93/4286)	662 (2837)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)	41784 (2839)	41785 (2838)
adk			3	3	3	3	3	3	3	3	3	3	3	3
gdh			8	8	8	8	8	8	8	8	8	8	8	8
pgm			6	6	6	6	6	6	6	6	6	6	6	6

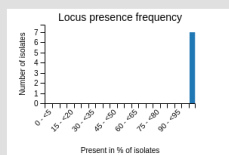
## Unique strains

Unique strains: 5

Strain 1	Strain 2	Strain 3	Strain 4	Strain 5
662 (2837)	644 (L93/4286)	666 (2843)	669 (2846)	665 (2845)
670 (2840)	698 (FAM18)	667 (2842)		
671 (2844)	41784 (2839)			
672 (2847)	41785 (2838)			

## Charts

Click to enlarge.



## Files

Text output file

Excel format output

Distance matrix (Nexus format) - Suitable for loading in to SplitsTree. Distances between taxa are calculated as the number of loci with different allele sequences

Locus presence frequency (text)

Tar file containing all output files

Splits graph (Neighbour-net; SVG format)

(click to enlarge)

Please note that job results will remain on the server for 7 days.

## 14.6.2 Analysis using annotated reference genome

Select the isolate genomes that you wish to analyse and then either enter a Genbank accession number for the reference genome, or select from the list of reference genomes (this list will only be present if the administrator has *set it up*). Selecting reference genomes will hide the locus and scheme selection forms.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Genome comparator

Help ⓘ

### Genome Comparator - Neisseria isolates

Selecting 'All loci' will produce an artefactual analysis because this database contains different kinds of loci that are not equivalent (complete genes, MLST fragments, peptide variable regions, intergenic regions etc). You are advised to select one of the recommended schemes.

Please select the required isolate ids and loci for comparison - use CTRL or SHIFT to make multiple selections in list boxes. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

**Isolates**

644  
662  
665  
666  
667  
669  
670

Clear List all

**User genomes**

Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome): ⓘ

Choose file No file chosen

**Include in identifiers**

isolate  
country  
region  
year  
date sampled  
isoyear sampled  
week sampled  
date received  
non culture

**Annotated reference genome**

Enter accession number: ⓘ

or choose annotated genome: FAM18 (Nm) ⓘ

or upload Genbank/EMBL/FASTA file: ⓘ

Choose file No file chosen ⓘ

**Parameters / options**

Min % identity: 70 ⓘ

Min % alignment: 50 ⓘ

BLASTN word size: 20 ⓘ

☐ Rescan undesigned loci ⓘ

**Distance matrix calculation**

With incomplete loci:

☐ Completely exclude from analysis

☐ Treat as distinct allele

☒ Ignore in pairwise comparison

☐ Exclude pairwise missing loci

☒ Exclude loci paralogous in all

☒ Exclude pairwise paralogous loci

**Alignments**

☐ Produce alignments ⓘ

☒ Include ref sequences in alignment

☐ Align all loci (not only variable)

☐ Create alignment stats

Aligner: MAFFT ⓘ

**Core genome analysis**

Core threshold (%): 90 ⓘ

☐ Calculate mean distances ⓘ

**Filter by**

Sequence method: ⓘ

Project: ⓘ

Experiment: ⓘ

**Action**

RESET SUBMIT

Output is similar to when comparing against defined loci, but this time every coding sequence in the annotated reference will be BLASTed against the selected genomes. Because allele designations are not defined, the allele found in the reference genome is designated allele 1, the next different sequence is allele 2 etc.

### Output

#### Analysis by reference genome

accession: AM421808  
version: 1  
type: dna  
length: 2194961  
description: Neisseria meningitidis serogroup C FAM18 complete genome.  
coding regions: 1975

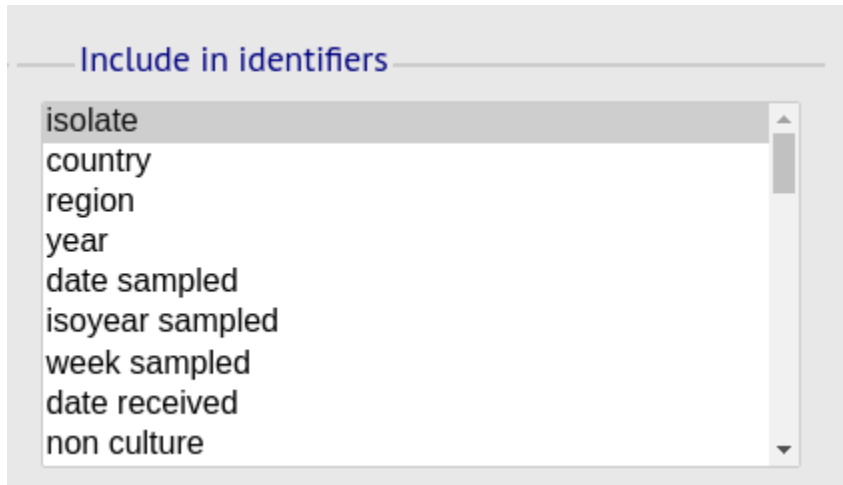
#### All loci

Each unique allele is defined a number starting at 1. Missing alleles are marked as 'X'. Incomplete alleles (located at end of contig) are marked as 'I'.

Locus	Product	Sequence length	Genome position	Reference genome	644 (L93/4286)	662 (2837)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)	41784 (2839)	41785 (2838)
NMC0001 lpxC envA	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	924	1261	1	1	1	1	1	1	1	1	1	1	1	1	2
NMC0002 pilS1	pilin (fragment)	291	3341	1	1	1	1	1	1	1	1	1	1	1	2	1
NMC0003 pilS2	truncated pilin	366	3675	1	2	2	2	2	2	2	2	2	2	2	1	2
NMC0004 fbp	peptidyl-prolyl cis-trans isomerase	330	4069	1	2	2	2	2	2	2	2	2	2	2	1	2
NMC0005	putative membrane protein	219	4476	1	2	3	3	3	3	4	3	5	3	1	3	3
NMC0006	putative glycerate dehydrogenase	954	4816	1	2	2	2	2	2	2	2	2	2	2	1	2
NMC0007 metG	methionyl-tRNA synthetase	2058	5843	1	2	2	2	2	2	2	2	2	2	2	1	5
NMC0008 glmS	glucosamine-fructose-6-phosphate aminotransferase [isomerizing]	1839	8016	1	2	2	2	2	2	2	2	2	2	2	1	2
NMC0009	putative lipoprotein	519	10290	1	1	1	1	1	1	1	1	1	1	1	1	1

### 14.6.3 Include in identifiers fieldset

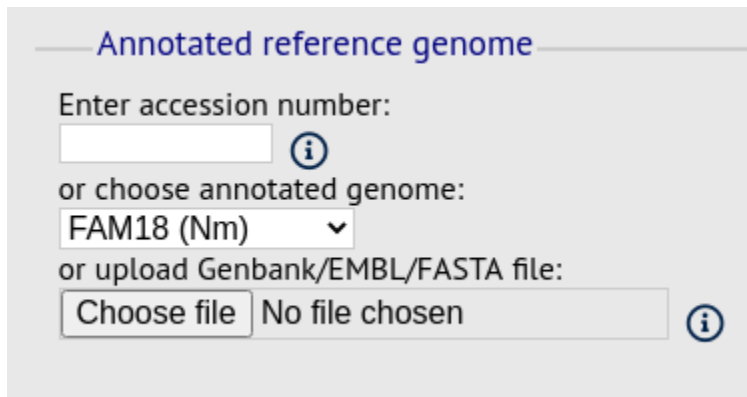
This selection box allows you to choose which isolate provenance fields will be included in the results table. This does not affect the output of the alignments as taxa names are limited in length by the alignment programs.



Multiple values can be selected by clicking while holding down Ctrl.

### 14.6.4 Reference genome fieldset

This section allows you to choose a reference genome to use as the source of comparator sequences.



There are three possibilities here:

1. Enter accession number - Enter a Genbank accession number of an annotated reference and Genome Comparator will automatically retrieve this from Genbank.
2. Select from list - The administrator may have selected some genomes to offer for comparison. If these are present, simply select from the list.
3. Upload genome - Click 'Browse' and upload your own reference. This can either be in Genbank, EMBL or FASTA format. Ensure that the filename ends in the appropriate file extension (.gb, .embl, .fas) so that it is recognized.

### 14.6.5 Parameters/options fieldset

This section allows you to modify BLAST parameters. This affects sensitivity and speed.

- **Min % identity** - This sets the threshold identity that a matching sequence has to be in order to be considered (default: 70%). Only the best match is used.
- **Min % alignment** - This sets the percentage of the length of reference allele sequence that the alignment has to cover in order to be considered (default: 50%).
- **BLASTN word size** - This is the length of the initial identical match that BLAST requires before extending a match (default: 20). Increasing this value improves speed at the expense of sensitivity. The default value gives good results in most cases. The default setting used to be 15 but the new default of 20 is almost as good (there was 1 difference among 2000 loci in a test run) but the analysis runs twice as fast.

### 14.6.6 Distance matrix calculation fieldset

This section provides options for the treatment of incomplete and paralogous loci when generating the distance matrix.

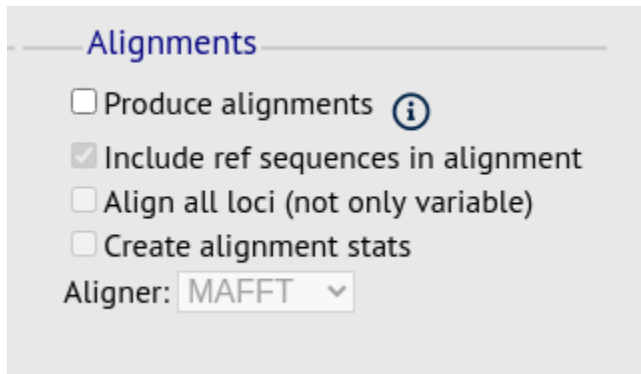
For incomplete loci, i.e. those that continue beyond the end of a contig so are incomplete you can:

- **Completely exclude from analysis** - Any locus that is incomplete in at least one isolate will be removed from the analysis completely. Using this option means that if there is one bad genome with a lot of incomplete sequences in your analysis, a large proportion of the loci may not be used to calculate distances.
- **Treat as a distinct allele** - This treats all incomplete sequences as a specific allele 'I'. This varies from any other allele, but all incomplete sequences will be treated as though they were identical.
- **Ignore in pairwise comparison (default)** - This is probably the best option. In this case, incomplete alleles are only excluded from the analysis when comparing the particular isolate that has it. Other isolates with different alleles will be properly included. The effect of this option will be to shorten the distances of isolates with poorly sequenced genomes with the others.

Paralogous loci, i.e. those with multiple good matches, can be excluded from the analysis (default). This is the safest option since there is no guarantee that differences seen between isolates at paralogous loci are real if the alternative matches are equally good. NB: Loci are also only classed as paralogous when the alternative matches identify different sequences, otherwise multiple contigs of the same sequence region would result in false positives.

### 14.6.7 Alignments fieldset

This section enables you to choose to produce alignments of the sequences identified.



**Alignments**

☐ Produce alignments ⓘ

☒ Include ref sequences in alignment

☐ Align all loci (not only variable)

☐ Create alignment stats

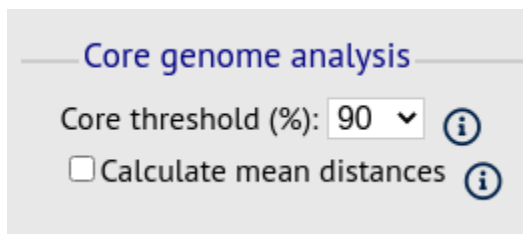
Aligner: MAFFT ▾

Available options are:

- Produce alignments - Selecting this will produce the alignment files, as well as XMFA and FASTA outputs of aligned sequences. This will result in the analysis taking longer to run.
- Include ref sequences in alignment - When doing analysis using an annotated reference, selecting this will include the reference sequence in the alignment files.
- Align all loci - By default, only loci that vary among the isolates are aligned. You may however wish to align all if you would like the resultant XMFA and FASTA files to include all coding sequences.
- Aligner - There are currently two choices of alignment algorithm (provided they have both been installed)
  - MAFFT (default) - This is the preferred option as it is significantly quicker than MUSCLE, uses less memory, and produces comparable results.
  - MUSCLE - This was originally the only choice. It is still included to enable previous analyses to be re-run and compared but it is recommended that MAFFT is used otherwise.

### 14.6.8 Core genome analysis fieldset

This section enables you to modify the inclusion threshold used to calculate whether or not a locus is part of the core genome (of the dataset).



**Core genome analysis**

Core threshold (%): 90 ⓘ

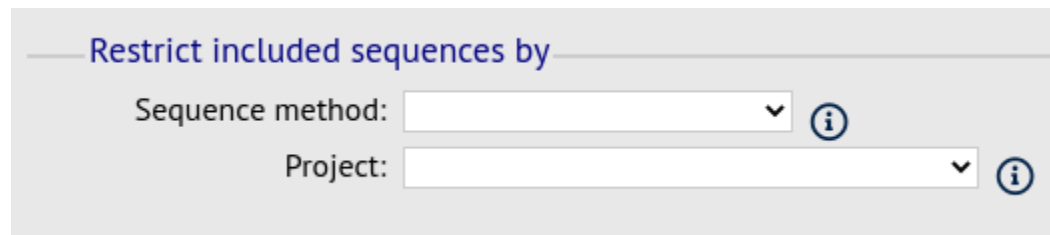
☐ Calculate mean distances ⓘ

The default setting of 90% means that a locus is counted as core if it appears within 90% or more of the genomes in the dataset.

There is also an option to calculate the mean distance among sequences of the loci. Selecting this will also select the option to produce alignments.

### 14.6.9 Filter fieldset

This section allows you to further filter your collection of isolates and the contigs to include.



Available options are:

- Sequence method - Choose to only analyse contigs that have been generated using a particular method. This depends on the method being set when the contigs were uploaded.
- Project - Only include isolates belonging to the chosen project. This enables you to select all isolates and filter to a project.

### 14.6.10 Understanding the output

#### Distance matrix

The distance matrix is simply a count of the number of loci that differ between each pair of isolates. It is generated in NEXUS format which can be used as the input file for [SplitsTree](#). This can be used to generate NeighborNet, Split decomposition graphs and trees offline. If 200 isolates or fewer are included in the analysis, a Neighbor network is automatically generated from this distance matrix.

#### Unique strains

The table of unique strains is a list of isolates that are identical at every locus. Every isolate is likely to be classed as unique if a whole genome analysis is performed, but with a constrained set of loci, such as those for MLST, this will group isolates that are indistinguishable at that level of resolution. nce matrix calculated based on allelic differences and a NeighborNet graph generated from this distance matrix.

## 14.7 GrapeTree

GrapeTree is a tool for generating and visualising minimum spanning trees. It has been developed to handle large datasets (in the region of 1000s of genomes) and works with 1000s of loci as used in cgMLST. It uses an improved minimum spanning algorithm that is better able to handle missing data than alternative algorithms and is able to produce publication quality outputs. Datasets can include metadata which allows nodes in the resultant tree to be coloured interactively.

GrapeTree can be accessed by selecting the 'Analysis' section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

### Query database

#### Search database

Browse, search by any criteria, or enter list of attributes.

#### Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

Jump to the ‘Third party’ category, follow the link to GrapeTree, then click ‘Launch GrapeTree’.

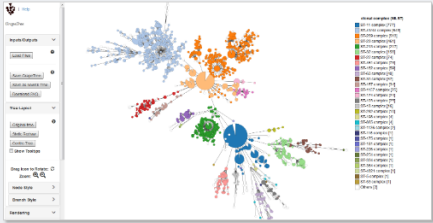
GrapeTree can be accessed from the contents page by clicking the ‘GrapeTree’ link.

### GrapeTree

Summary: Visualization of genomic relationships

GrapeTree is a tool for generating and visualising minimum spanning trees (Zhou *et al.* 2018 *Genome Res* 28:1395-1404). It has been developed to handle large datasets (in the region of 1000s of genomes) and works with 1000s of loci as used in cgMLST. It uses an improved minimum spanning algorithm that is better able to handle missing data than alternative algorithms and is able to produce publication quality outputs. Datasets can include metadata which allows nodes in the resultant tree to be coloured interactively.

Documentation [bigsd.readthedocs.io](https://bigsd.readthedocs.io)



Launch 'GrapeTree'

Alternatively, it can be accessed following a query by clicking the ‘GrapeTree’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the GrapeTree interface.

19958	M10 240476	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	9812	ST-215 complex	22	14	F5-5
19959	M10 240499	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	275	ST-269 complex	22	9	F5-12
19960	M10 240500	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	41	ST-41/44 complex	7-2	4	F1-5
19961	M10 240502	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	340	ST-41/44 complex	7-2	4	F1-5
19962	M10 240503	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	23	ST-23 complex	5-1	2-2	F1-96
19963	M10 240505	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	1655	ST-23 complex	5-1	10-10	F4-1
19964	M10 240507	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	183	ST-23 complex	21	16-5	deleted
19965	M10 240508	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1575		7-2	13-1	F1-7
19966	M10 240511	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	4713		22	9	F5-12
19967	M10 240512	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	41	ST-41/44 complex	7-1	1	F1-5
19968	M10 240514	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex	5	2	F1-1
19969	M10 240515	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	B	269	ST-269 complex	5-1	2-2	F5-1
19970	M10 240520	UK [England]	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	1655	ST-23 complex	5-1	10-1	F4-1



### Analysis tools

Breakdown: **Fields** Two Field Combinations Publications Sequence bin

Analysis: **Codons** Gene Presence Genome Comparator **BLAST** rMLST species id PCR

Export: Dataset **Contigs** Sequences

Third party: **GrapeTree** PhytoViz

Select the isolates to include. The tree can be generated from allelic profiles of any selection of loci, or more conveniently, you can select a scheme in the scheme selector, or choose from recommended schemes if these have been set, to include all loci belonging to that scheme.

Additional fields can be selected to be included as metadata for use in colouring nodes - select any fields you wish to include. Multiple selections can be made by holding down shift or ctrl while selecting. Click 'Submit' to start the analysis.

## BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > GrapeTree

Help ⓘ

## GrapeTree: Visualization of genomic relationships - Neisseria isolates



This plugin generates a minimum-spanning tree and visualizes within GrapeTree:

GrapeTree is developed by: Zheming Zhou (1), Nabil-Fareed Ali Khan (1), Martin J. Sergeant (1), Nina Luhmann (1), Cátia Vaz (2,5), Alexandre P. Francisco (2,4), João André Carriço (3) and Mark Achtman (1)

1. Warwick Medical School, University of Warwick, UK
2. Instituto de Engenharia de Sistemas e Computadores: Investigação e Desenvolvimento (INESC-ID), Lisboa, Portugal
3. Universidade de Lisboa, Faculdade de Medicina, Instituto de Microbiologia e Instituto de Medicina Molecular, Lisboa, Portugal
4. Instituto Superior Técnico, Universidade de Lisboa, Lisboa, Portugal
5. ADEETC, Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, Lisboa, Portugal

Publication: Zhou *et al.* (2018) GrapeTree: Visualization of core genomic relationships among 100,000 bacterial pathogens. *Genome Res* 28:1395-1404.

Selecting 'All loci' will produce an artefactual analysis because this database contains different kinds of loci that are not equivalent (complete genes, MLST fragments, peptide variable regions, intergenic regions etc.). You are advised to select one of the recommended schemes.

This tool will generate minimum spanning trees from allelic profiles. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 50,000 records.

Isolates

18968  
18969  
19823  
19824  
19825  
19826  
19827

Clear List all

Loci

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)

All None Paste list

Recommended schemes

Select one or more schemes below or use the full schemes list.

MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0

Clear

Schemes

MLST  
Finotyping antigens  
16S  
Antigen genes  
Bexsero Antigen Sequence  
Human-restricted Neisseria  
N. gonorrhoeae cgMLST v1  
N. meningitidis cgMLST v1  
Nf MLST

Include fields

Select additional fields to include in GrapeTree metadata.

ciprofloxacin range  
clonal complex (MLST)  
cluster (GC OMV peptide typing)  
comments  
continent  
country

Parameters / options

☐ Rescan undesignated loci ⓘ

Action

SUBMIT

The job will be sent to the job queue. When it has finished, click the button marked 'Launch GrapeTree'.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Job status viewer](#)

## Job status viewer


**Status**

Job id: BIGSdb\_001935\_1596193067\_67514

Submit time: 2020-07-31 10:57:47

Status: finished

Start time: 2020-07-31 10:57:50

Progress: 100%

Stop time: 2020-07-31 11:19:38

Total time: 21 minutes and 47 seconds

**Output**

[Launch GrapeTree](#)

**Files**


[Profiles \(TSV format\) \(18.7 MB\)](#)



[MS Tree \(Newick format\)](#)


[Metadata \(TSV format\)](#)


[Tar file containing all output files \(only files <10MB included - download larger files separately\)](#)

Please note that job results will remain on the server for 7 days.

The generated tree will be rendered in the GrapeTree application page.


[Help](#)

**GrapeTree**

**Inputs/Outputs**

[Load Files](#)

[Save GrapeTree](#)

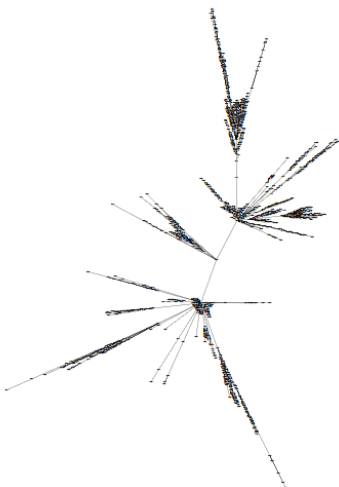
[Save as Newick Tree](#)

[Download SVG](#)

**Tree Layout**

**Rendering**

**Context Menu**



**isolate**

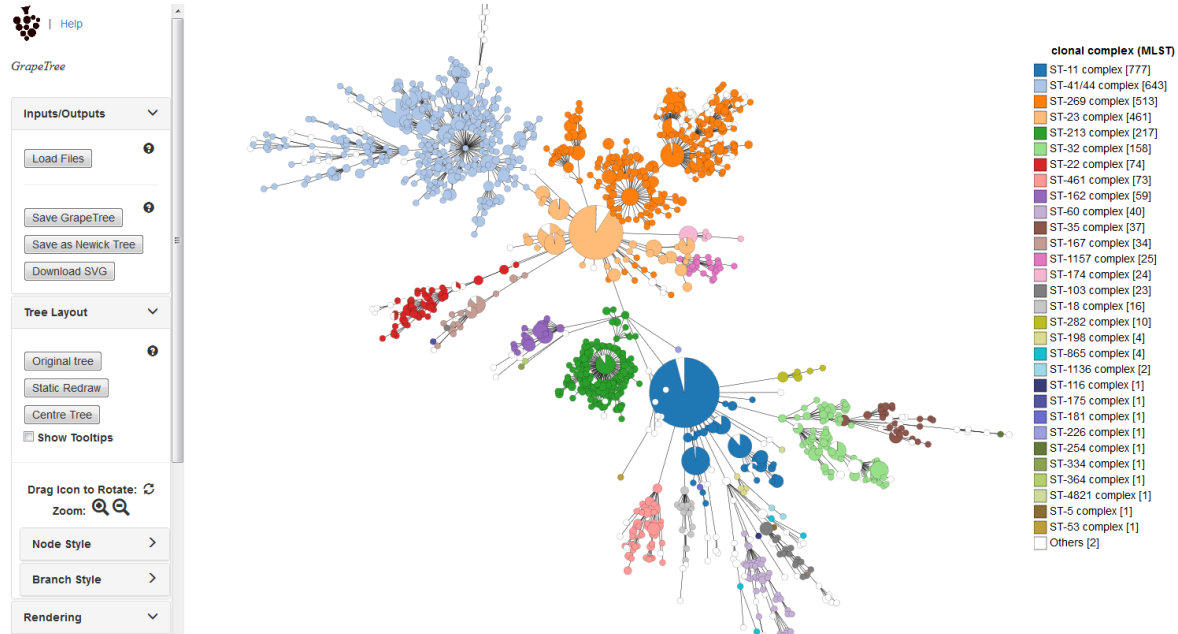
- 09.1126.Y [1]
- 09.1208.P [1]
- 09.1211.Y [1]
- 09.1292.T [1]
- 09.1331.Y [1]
- 09.1347.W [1]
- 09.1368.F [1]
- 09.1385.H [1]
- 09.1402.B [1]
- 09.1453.F [1]
- 09.1507.Q [1]
- 09.1514.A [1]
- 09.1557.B [1]
- 09.1580.V [1]
- 09.1595.J [1]
- 09.1619.R [1]
- 09.1857.M [1]
- 09.1858.V [1]
- 09.1893.P [1]
- 09.1936.F [1]
- 09.1976.T [1]
- 09.1999.X [1]
- 09.2014.G [1]
- 09.2045.J [1]
- 09.2061.P [1]
- 09.2082.C [1]
- 09.2204.A [1]

The image can be manipulated in various ways. These include modifying the tree layout, customising node labels and size, modifying branch lengths and collapsing branches. The image can be saved in SVG format which can be further edited in image publishing software such as Inkscape.

As an example, the default cgMLST tree (above) has been modified (below) as follows:

- Nodes coloured by clonal complex
- Labels removed

- Branches collapsed where  $\leq 100$  loci different
- Node size set to 200%
- Kurtosis (node size relative to number of isolates) set to 75%
- Dynamic rendering allowed to run to fan out nodes



Full details can be found in the [GrapeTree manual](#).

**Note:** GrapeTree has been described in the following publication:

Z Zhou, NF Alikhan, MJ Sergeant, N Luhmann, C Vaz, AP Francisco, JA Carrico, M Achtman (2018) GrapeTree: Visualization of core genomic relationships among 100,000 bacterial pathogens. [Genome Res 28:1395-1404](#).

## 14.8 In silico PCR

This is a tool that can be used to simulate PCR reactions run against genomes stored in the database. This is useful for designing and testing primers. The plugin uses the [exonerate](#) [ipccress](#) program to perform its simulation.

The tool can be accessed by selecting the 'Analysis' section on the main contents page.

## BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates*Neisseria* isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

Jump to the ‘Analysis’ category, follow the link to BLAST, then click ‘Launch PCR’.

PCR

Summary: *In silico* PCR tool for designing and testing primers

The *in silico* PCR tool can be used to simulate PCR reactions run against genomes stored in the database. This is useful for designing and testing primers. The plugin uses the exonerate ipress program to perform its simulation. Primers can contain wobble bases and the number of allowed mismatches for each primer can be set independently. The output is a table of predicted products, showing the number of products and their positions within a contig. It is also possible to export the predicted product sequence.

Documentation [bigsd.readthedocs.io](https://bigsd.readthedocs.io)

Output

ID	Accession	PCR name	Genome	Contig	Start	End	Forward	Reverse
1	AA001234	✓	1	100000	100000	100000	Forward	Reverse
2	12345	✓	1	100000	100000	100000	Forward	Reverse
3	12345	✓	1	100000	100000	100000	Forward	Reverse
4	12345	✓	1	100000	100000	100000	Forward	Reverse

Files

Test format summary file

Export format summary file

HTML file of predicted product sequences

For file containing all output files

Launch ‘PCR’

Alternatively, it can be accessed following a query by clicking the ‘PCR’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the analysis interface.

10	6748	B394; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	18-1	3	F5-1
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5
31	10	B269; NIBSC_2825; Z1269	Burkina Faso	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
34	20	B275; NIBSC_2767; Z1275	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-7
35	26	B278; NIBSC_2764; Z1278	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
52	243	B362; NIBSC_2779; Z1362	Cameroon	1966		Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
61	393	B392; NIBSC_2823; Z1392	Greece	1968	carrier	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
64	254	B439; NIBSC_2812; Z1439	Djibouti	1966	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F1-7
67	S5611	B466; NIBSC_2765; Z1466	Australia	1977	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
82	11-004	B503; NIBSC_2826; Z1503	China	1984	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-8
84	IAL2229	B506; NIBSC_2816; Z1506	Brazil	1976		Neisseria meningitidis	A	5	ST-5 complex	20	9	F2-1
90	CN100	B534; NIBSC_2768; Z1534	UK [England]	1941	invasive (unspecified/other)	Neisseria meningitidis	A	21		5-2	10	F3-9

## Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id **PCR**

Export: Dataset Contigs Sequences

Third party: GrapeTree ITOL PhyloViz Microreact

Select the isolates to include. These will be pre-populated if you arrive here following a search.

Enter your forward and reverse primer sequences in the appropriate boxes. These may contain wobble bases if necessary. You can also specify how many mismatches are allowed for each primer. Finally, you can restrict the reported length to only those products that fall between a minimum and maximum length range.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > In silico PCR

Help ⓘ ⓘ

## In silico PCR

Use this tool to simulate PCR reactions run using genomes stored in the database. This is useful for designing and testing primers. The plugin is a wrapper for the exonerate [ipress](#) program written by Guy Slater.

Please select the required isolate ids to run the PCR reaction against. These isolate records must include genome sequences.

Isolates	Primer 1	Primer 2	Reported products	Action
<div> 1 2 7 10 11 13 19 </div>	<div>TGTTCCGCTTCGACTGCCAAC</div> <div>Allowed mismatches: 0</div>	<div>TCCCCGTCGTAAAAACAATC</div> <div>Allowed mismatches: 0</div>	<div>Min length: 0</div> <div>Max length: 10000</div> <div><input type="checkbox"/> Export sequences</div>	<div>SUBMIT</div>


Clear List all

Click ‘Submit’. The job will be sent to the job queue. The output will be a table of predicted products, showing the number of products and their positions within a contig. A summary of this table is also available to download in tab-delimited text or Excel formats.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Job status viewer](#)

## Job status viewer


**Status**

Job id: BIGSdb\_028633\_1596197976\_78216

Submit time: 2020-07-31 12:19:36

Status: finished

Start time: 2020-07-31 12:19:39

Progress: 100%


Stop time: 2020-07-31 12:19:41


Total time: 2 seconds


**Output**


id	isolate	PCR +ve	products	contig	length	start	end	description
1	A4/M1027	✓	1	180126	898	6772	7669	forward
2	120M	✓	1	180675	898	1608	2505	reverse
7	7891	✓	1	180795	898	6770	7667	forward
10	6748	✓	2	181299	898	1614	2511	reverse
				181505	898	1623	2520	reverse
11	129E	✓	1	181720	898	1620	2517	reverse
13	139M	✓	1	182116	898	6790	7687	forward
19	S3131	✓	1	182225	898	1620	2517	reverse
24	S4355	✓	1	215556	898	6774	7671	forward
30	14	✓	1	8	898	983430	984327	forward
31	10	✓	1	182398	898	1620	2517	reverse
34	20	✓	1	182791	898	6982	7879	forward
35	26	✓	1	182948	898	1913	2810	reverse
52	243	✓	1	183322	898	1624	2521	reverse
61	393	✓	1	183655	898	6767	7664	forward
64	254	✓	1	183761	898	1616	2513	reverse
67	S5611	✓	1	184197	898	1619	2516	reverse
82	11-004	✓	1	184337	898	1911	2808	reverse
84	IAL2229	✓	1	184525	898	6770	7667	forward
90	CN100	✓	1	184677	898	7208	8105	forward

**Files**

 Text format summary file

 Excel format summary file

 FASTA file of predicted product sequences

 Tar file containing all output files

Please note that job results will remain on the server for 7 days.

It is also possible to export the predicted product sequence. You can do this by selecting the ‘Export sequences’ checkbox on the options form.

**Reported products**

Min length:

Max length:

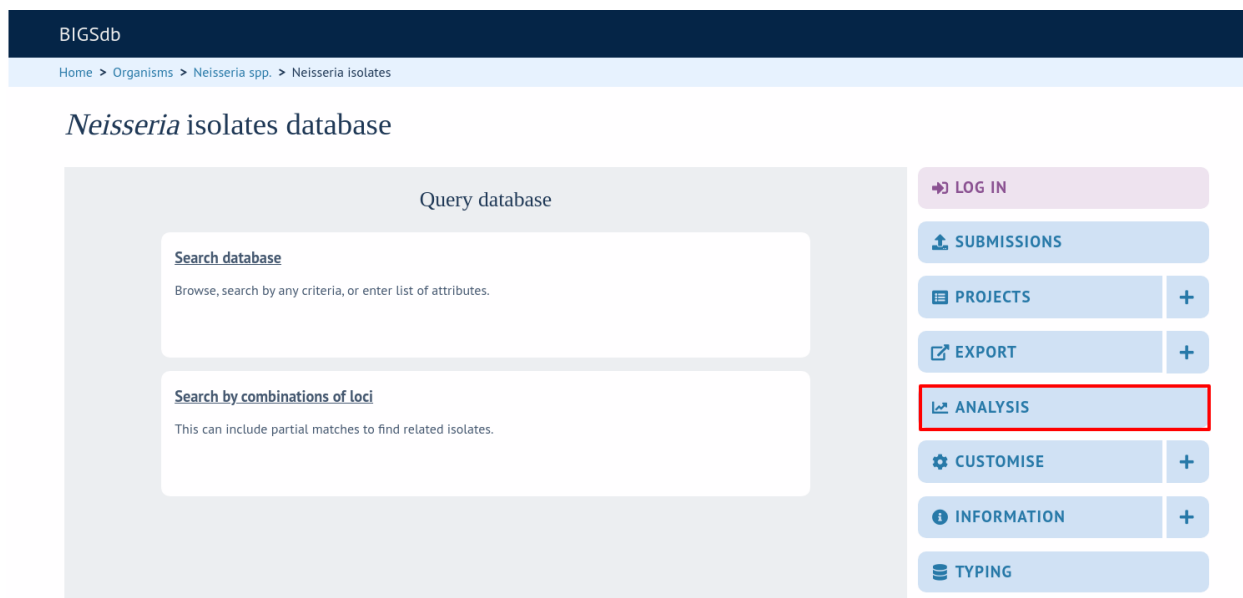
☒ Export sequences

**Note:** The exported sequences will include the primer regions. It is important to note that, unlike a real PCR reaction, these sequences represent the sequence within this region in the genome. In a real PCR reaction, the primers are themselves incorporated in to the product, so even if there was a mismatch in the primer region, the product sequence would include the primer sequence.

## 14.9 Interactive Tree of Life (iTOL)

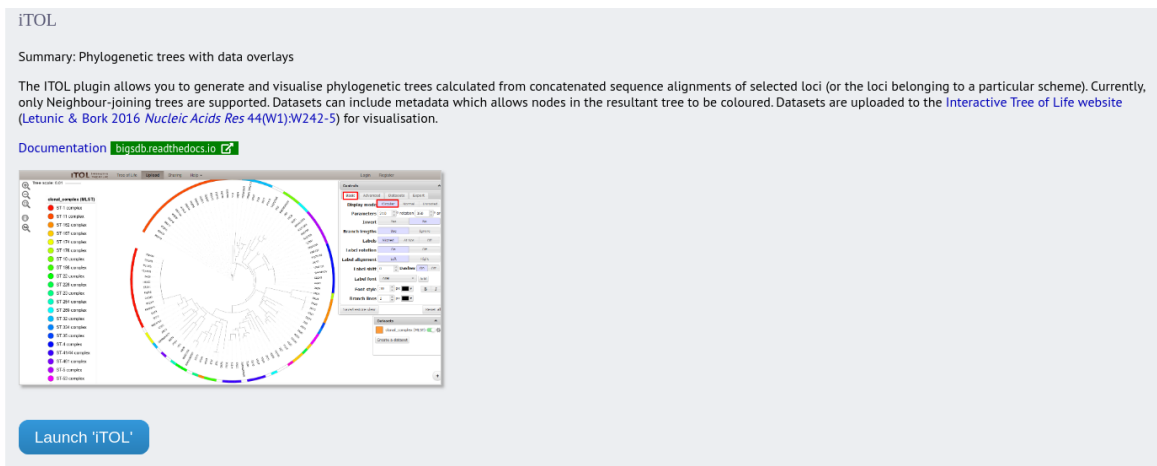
The iTOL plugin allows you to generate and visualise phylogenetic trees calculated from concatenated sequence alignments of selected loci (or the loci belonging to a particular scheme). Currently, only Neighbour-joining trees are supported. Datasets can include metadata which allows nodes in the resultant tree to be coloured.

iTOL can be accessed by selecting the ‘Analysis’ section on the main contents page.



Jump to the ‘Third party’ category, follow the link to iTOL, then click ‘Launch iTOL’.

iTOL can be accessed from the contents page by clicking the ‘iTOL’ link.



Alternatively, it can be accessed following a query by clicking the ‘iTOL’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the iTOL interface.

14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: **Fields** Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree **iTOL** PhyloViz Microreact

Select the isolates to include. The tree can be generated from concatenated sequences of any selection of loci, or more conveniently, you can select a scheme in the scheme selector, or in the list of recommended schemes if these have been set up, to include all loci belonging to that scheme.

Additional fields can be selected to be included as metadata for use in colouring nodes - select any fields you wish to include in the 'iTOL datasets' list. Multiple selections can be made by holding down Shift or Ctrl while selecting. You can also choose how nodes are labeled by metadata - either by colouring the labels or using coloured strips.

Click 'Submit' to start the analysis.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > iTOL

[Help](#) [?](#)

## iTOL - Interactive Tree of Life - Neisseria isolates

This plugin uploads data for analysis within the Interactive Tree of Life online service:

iTOL is developed by: Ivica Letunic (1) and Peer Bork (2,3,4)

1. Biobyte solutions GmbH, Bothestr 142, 69126 Heidelberg, Germany
2. European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany
3. Max Delbrück Centre for Molecular Medicine, 13125 Berlin, Germany
4. Department of Bioinformatics, Biocenter, University of Würzburg, 97074 Würzburg, Germany

Web site: <https://itol.embl.de/>

Publication: Letunic & Bork (2016) Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. *Nucleic Acids Res* 44(W1):W242-5.

This tool will generate neighbor-joining trees from concatenated nucleotide sequences. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA and peptide loci with genome sequences, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 2,500 records or 110,000 sequences (records x loci).

**Isolates**

1  
2  
3  
4  
5  
6  
7

[Clear](#) [List all](#)

**User genomes**

Optionally include data not in the database.

Upload assembly FASTA file (or zip file containing multiple FASTA files - one per genome): [?](#)

[Choose file](#) No file chosen

**Loci**

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)

[All](#) [None](#) [Paste list](#)

**Recommended schemes**

Select one or more schemes below or use the full schemes list.

MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0

[Clear](#)

**Schemes**

Plasmids  
Typing  
Finetyping antigens  
16S  
Antigen genes  
Bexsero Antigen Sequence  
Human-restricted Neisseria

**iTOL datasets**

Select to create data overlays (Use Ctrl to select multiple) [?](#)

tetracycline  
cefixime  
azithromycin  
spectinomycin  
bioproject accession  
biosample accession  
ST (MLST)  
clonal complex (MLST)

**iTOL data type**

☐ text labels ☒ **coloured strips**

**ACTION**

[SUBMIT](#)


The job will be sent to the job queue. When it has finished, the generated tree and associated metadata will be uploaded

to the Interactive Tree of Life website (<https://itol.embl.de/>). Click the button marked ‘Launch iTOL’.

**BIGSdb**

Home > Organisms > Neisseria spp. > Neisseria isolates > Job status viewer

### Job status viewer


 **Status**

Job id: BIGSdb\_027908\_1596206761\_04985

Submit time: 2020-07-31 14:46:01

Status: finished

Start time: 2020-07-31 14:46:05

Progress: 100% 


Stop time: 2020-07-31 14:46:25


Total time: 20 seconds


**Output**


[Launch iTOL](#)

**Files**

 Concatenated FASTA

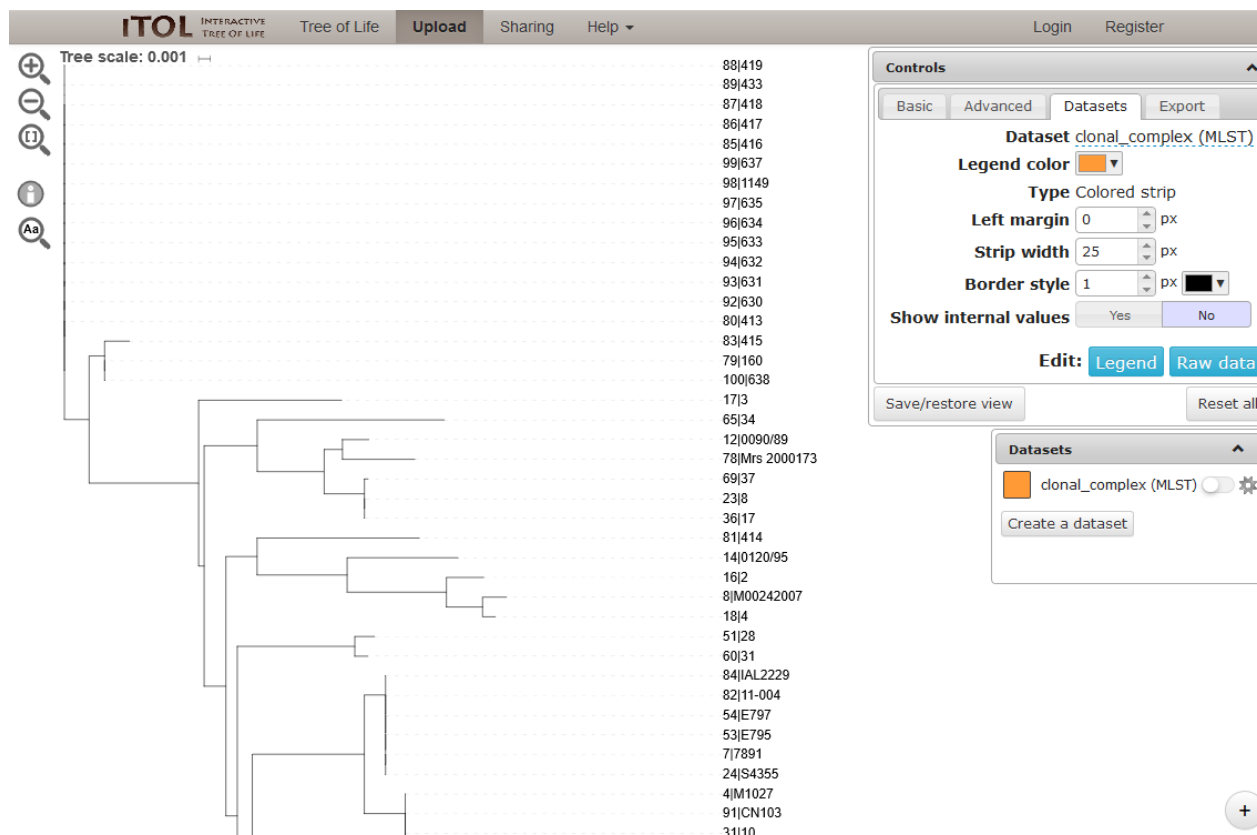
 NJ tree (Newick format)

 iTOL datasets (Zip format)

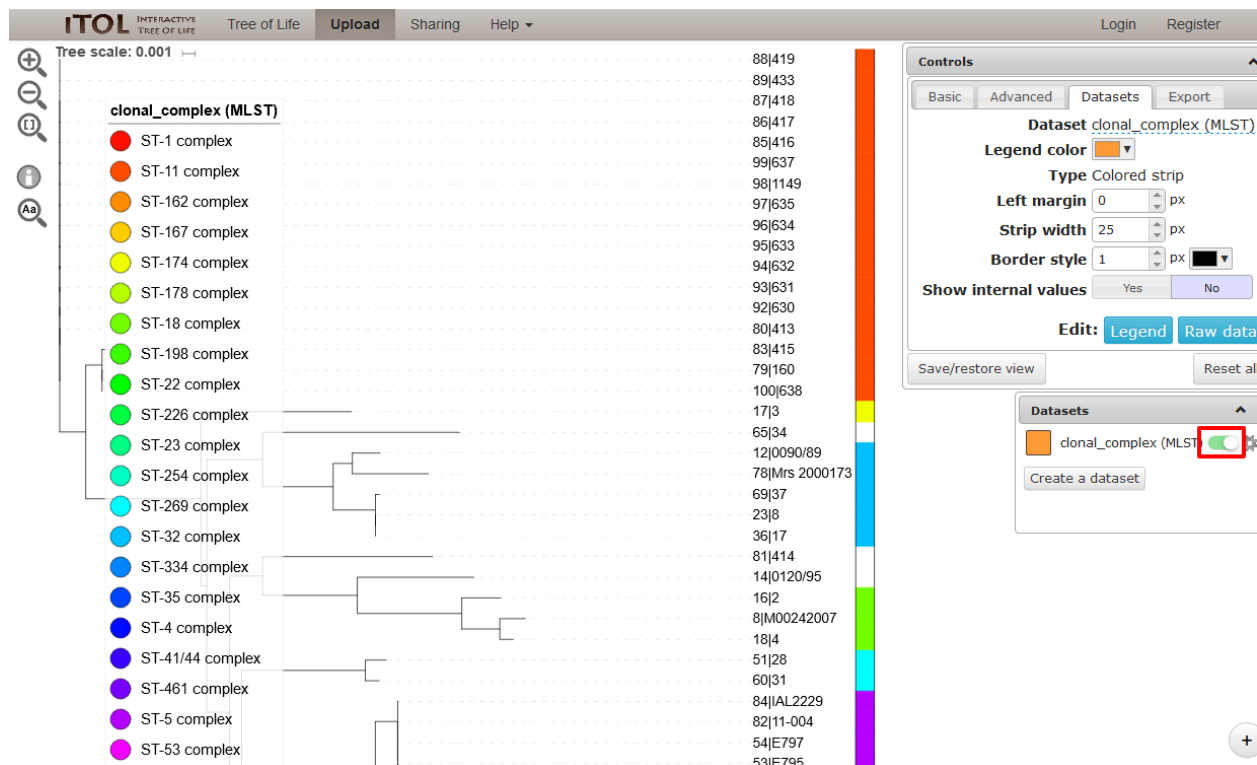
 Tar file containing all output files

Please note that job results will remain on the server for 7 days.

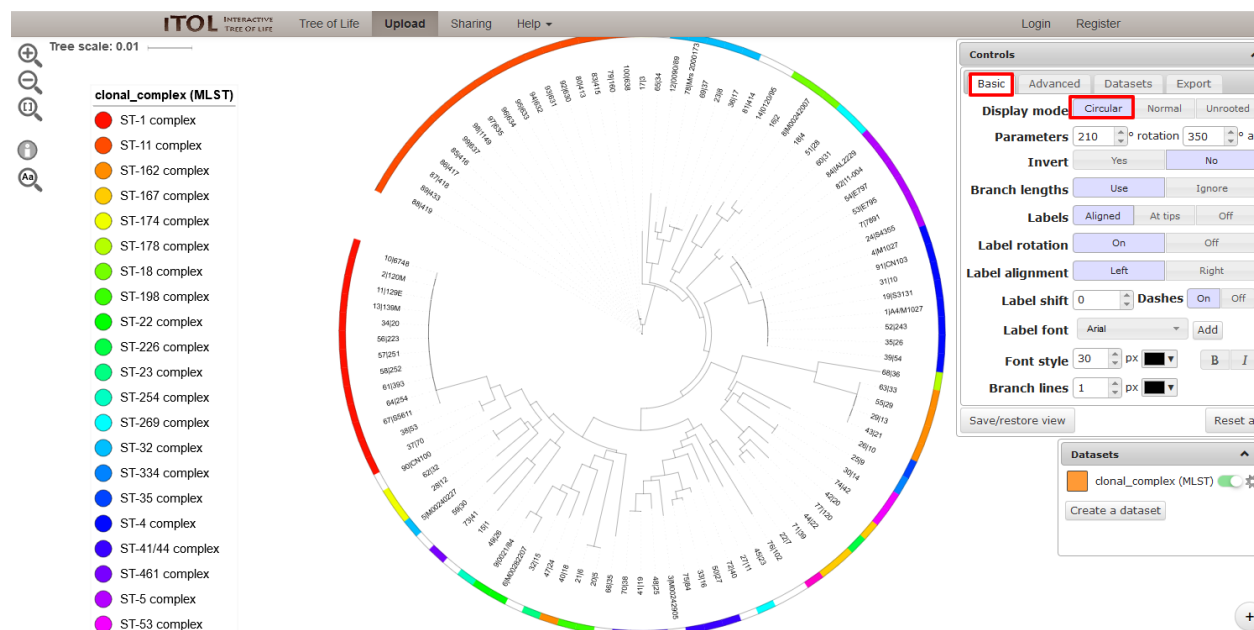
Your browser will open the iTOL website with your tree.



You can manipulate the tree in the browser, and display metadata by selecting the appropriate toggle.



The tree layout can be changed by clicking the 'Basic tab' and, for example, selecting a circular display mode.



See the [detailed documentation on the iTOL website](#) for more information about manipulating and exporting trees.

## 14.10 Locus explorer

The locus explorer is a sequence definition database plugin. It can create schematics showing the polymorphic sites within a locus, calculate the GC content and generate aligned translated sequences.

Expand the 'Analysis' section on the main contents page of a sequence definition database and click 'Locus Explorer'.

The screenshot shows the BIGSdb Locus Explorer interface. The top navigation bar includes 'BIGSdb' and the path 'Home > Organisms > Organism > Neisseria typing'. The main content area is titled 'Neisseria typing database' and features a grid of search and analysis options:

- Query a sequence**
  - Single sequence**: Query a single sequence or whole genome assembly to identify allelic matches.
  - Batch sequences**: Query multiple independent sequences in FASTA format to identify allelic matches.
- Find alleles**
  - By specific criteria**: Find alleles by matching criteria (all loci together).
  - By locus**: Select, analyse and download specific alleles from a single locus.
- Search for allelic profiles**
  - By specific criteria**: Search, browse or enter list of profiles.
  - By allelic profile**: This can include partial matches to find related profiles.
  - In a batch**: Look up multiple allelic profiles together.

On the right sidebar, there is a 'LOG IN' button and a list of actions: SUBMISSIONS, DOWNLOADS, EXPORT, ANALYSIS, CUSTOMISE, INFORMATION, and ISOLATES. The 'ANALYSIS' section is expanded, showing 'Sequence similarity', 'Sequence comparison', and 'Locus Explorer' (highlighted with a red box).

## 14.10.1 Polymorphic site analysis

Select the locus you would like to analyse in the Locus dropdown box. The page will reload.

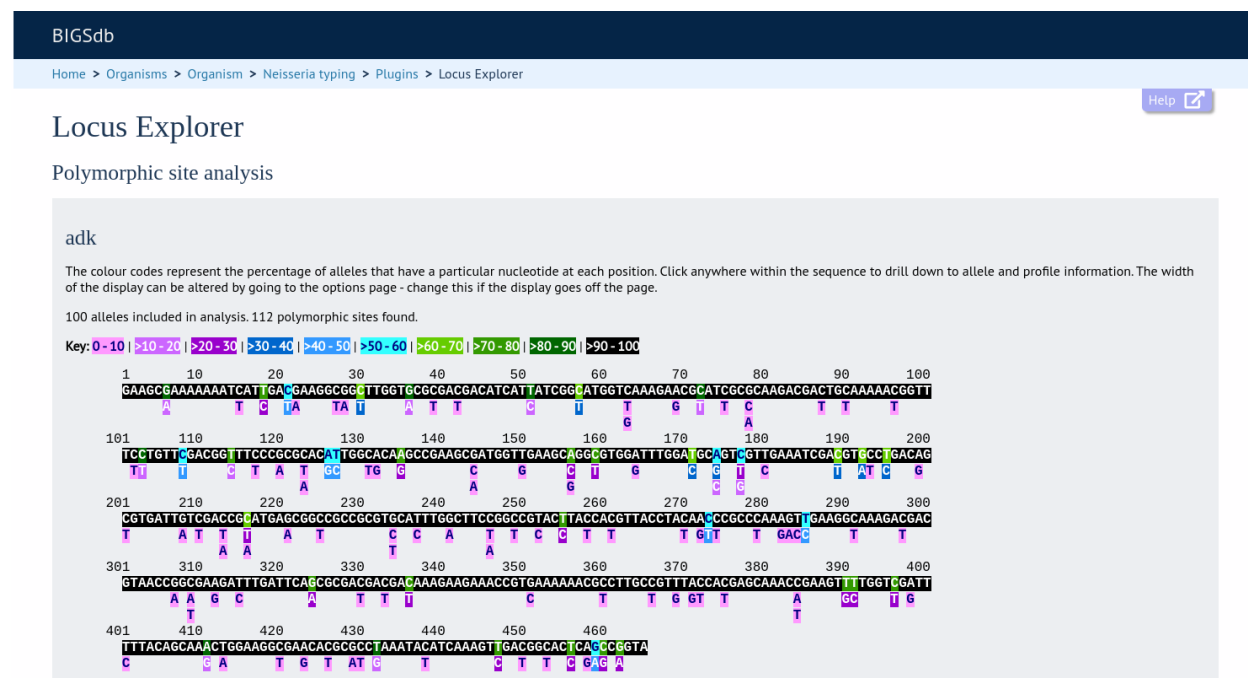
The screenshot shows the BIGSdb Locus Explorer interface. At the top, the breadcrumb navigation is 'Home > Organisms > Organism > Neisseria typing > Plugins > Locus Explorer'. The main heading is 'Locus Explorer'. Below this, there is a section 'Please select locus for analysis:' with a dropdown menu showing 'adk'. To the right of the dropdown, it says 'Page will reload when changed'. Below the dropdown, there are two tabs: 'Select sequences' and 'Select analysis'. Under 'Select sequences', there is a list of numbers 1 through 6, and buttons 'All' and 'None'. Under 'Select analysis', there are three radio button options: 'Polymorphic Sites - Display polymorphic site frequencies and sequence schematic' (which is selected), 'Codon - Calculate G+C content and codon usage', and 'Translate - Translate DNA to peptide sequences'. To the right of these options is a blue 'SUBMIT' button.

Select the alleles that you would like to include in the analysis. Variable length loci are limited to 2000 sequences or fewer since these need to be aligned. Select 'Polymorphic Sites' in the Analysis selection and click 'Submit'.

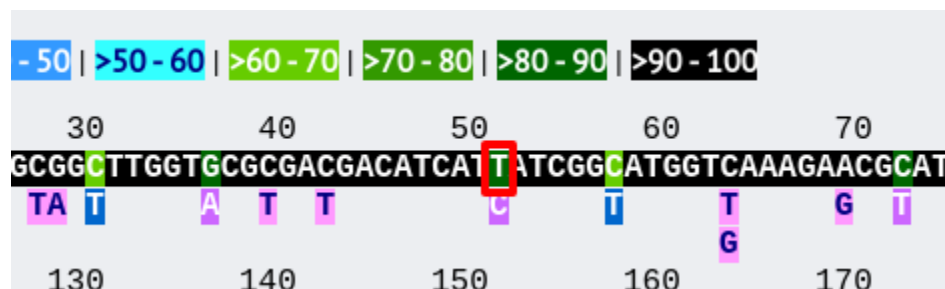
This screenshot shows the same BIGSdb Locus Explorer interface, but with changes. The 'Locus' dropdown still shows 'adk'. In the 'Select sequences' tab, the list of numbers now shows 98, 99, 100, 101, 102, and 103. In the 'Select analysis' tab, the 'Polymorphic Sites - Display polymorphic site frequencies and sequence schematic' option remains selected. The 'SUBMIT' button is still present.

If an alignment is necessary, the job will be submitted to the job queue and the analysis performed. If no alignment is necessary, then the analysis is shown immediately.

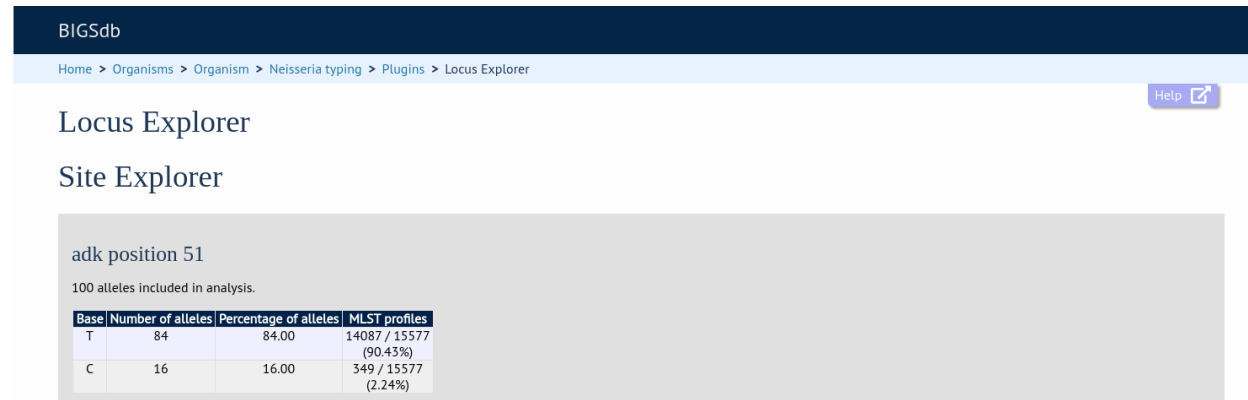
The first part of the page shows the schematic.



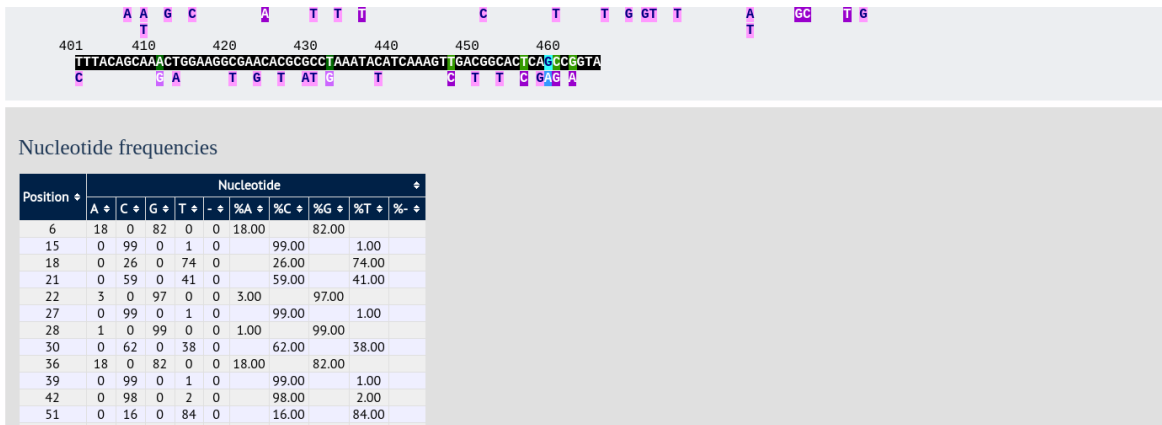
Clicking any of the sequence bases will calculate the exact frequencies of the different nucleotides at that position.



Along with the nucleotide frequencies, it will also show the percentage of allelic profiles containing each nucleotide at that position if the locus is part of a scheme such as MLST.



The second part of the page shows a table listing nucleotide frequencies at each of the variable positions.



See also:

- *Investigating allele differences.*
- *Polymorphism analysis following isolate query.*

## 14.10.2 Codon usage

Select the alleles that you would like to include in the analysis. Again, variable length loci are limited to 200 sequences or fewer since these need to be aligned. Click 'Codon'.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Locus Explorer

Locus Explorer

Please select locus for analysis:

Locus:  Page will reload when changed

Select sequences:

Select analysis:

☒ Codon - Calculate G+C content and codon usage

☐ Polymorphic Sites - Display polymorphic site frequencies and sequence schematic

☐ Translate - Translate DNA to peptide sequences

Submit

All None

The GC content of the alleles will be determined and a table of the codon frequencies displayed.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Locus Explorer

Help

## Locus Explorer

### Codon Usage

adk

ORF used: 1

100 alleles included in analysis.

GC content

Coding: GC 52.33%  
1st letter: GC 65.43%  
2nd letter: GC 31.66%  
3rd letter: GC 59.91%

Codons

Fraction: Proportion of usage of a given codon among its redundant set (i.e. the set of codons which code for this codon's amino acid).  
Frequency: Usage of given codon per 1000 codons.

Codon	Amino acid	Fraction	Frequency	Number
GCA	A	0.265	17.484	271
GCC	A	0.235	15.484	240
GCG	A	0.399	26.323	408
GCT	A	0.101	6.645	103
TGC	C	0.970	6.323	98
TGT	C	0.030	0.194	3
GAC	D	0.745	91.097	1412
GAT	D	0.255	31.226	484
GAA	E	0.924	83.355	1292
GAG	E	0.076	6.839	106
TTC	F	0.614	15.806	245
TTT	F	0.386	9.935	154
GGA	G	0.005	0.387	6
GGC	G	0.740	57.355	889
GGG	G	0.000	0.000	0

### 14.10.3 Aligned translations

If a DNA coding sequence locus is selected, an aligned translation can be produced.

Select the alleles that you would like to include in the analysis. Again, variable length loci are limited to 200 sequences or fewer since these need to be aligned. Click 'Translate'.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Locus Explorer

Help

## Locus Explorer

Please select locus for analysis:

Locus:  Page will reload when changed

Select sequences

1

2

3

4

5

6

All None

Select analysis

☐ Polymorphic Sites - Display polymorphic site frequencies and sequence schematic  
☐ Codon - Calculate G+C content and codon usage  
☒ Translate - Translate DNA to peptide sequences

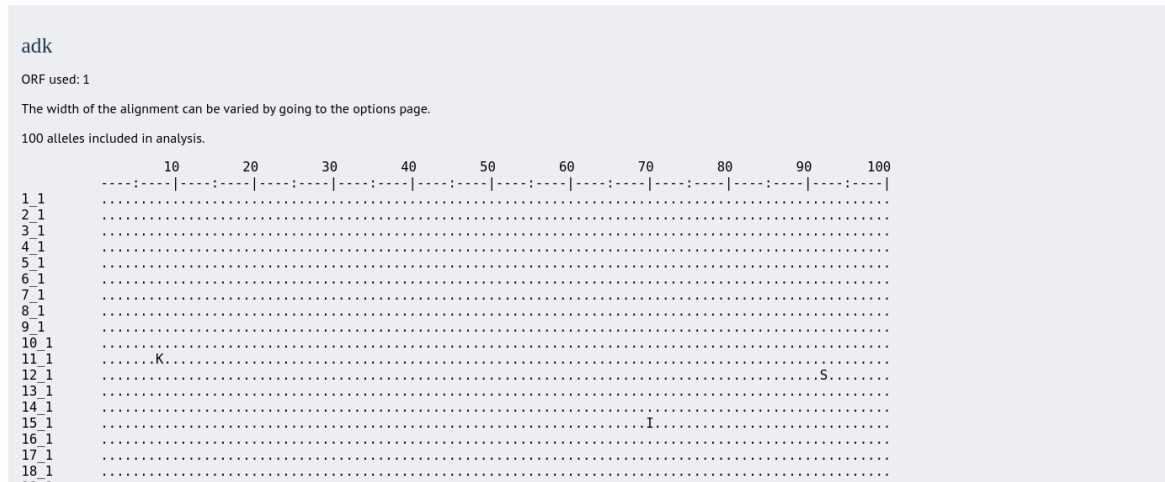
Action

SUBMIT

An aligned amino acid sequence will be displayed.

## Locus Explorer

## Translate - aligned protein sequences



If there appear to be a lot of stop codons in the translation, it is possible that the orf value in the *locus definition* is not set correctly.

## 14.11 Microreact

Microreact is a tool for visualising genomic epidemiology and phylogeography. Individual nodes on a displayed tree are linked to nodes on a geographical map and/or timeline, making any spatial and temporal relationships between isolates apparent.

The Microreact plugin generates Neighbour-joining trees from concatenated sequences for any selection of loci or schemes and uploads these, together with country and year field values to the [Microreact website](#) for display.

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**Note:** While Microreact itself is able to display isolates using GPS coordinates, the BIGSdb plugin is currently limited to the level of country.

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Microreact can be accessed by selecting the ‘Analysis’ section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

### Query database

#### Search database

Browse, search by any criteria, or enter list of attributes.

#### Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

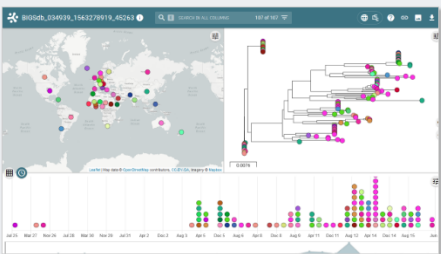
Jump to the ‘Third party’ category, follow the link to BLAST, then click ‘Launch Microreact’.

### Microreact

Summary: Open data visualization and sharing for genomic epidemiology

Microreact is a tool for visualising genomic epidemiology and phylogeography (Argimón *et al* 2016 *Microb Genom* 2:e000093). Individual nodes on a displayed tree are linked to nodes on a geographical map and/or timeline, making any spatial and temporal relationships between isolates apparent. The Microreact plugin generates Neighbour-joining trees from concatenated sequences for any selection of loci or schemes and uploads these, together with country and year field values, to the [Microreact website](#) for display.

Documentation [bigsdbradthetdocs.io](#)



Launch 'Microreact'

Alternatively, it can be accessed following a query by clicking the ‘Microreact’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the Microreact plugin interface.

35	26	B278; NIBSC_2764; Z1278	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
52	243	B362; NIBSC_2779; Z1362	Cameroon	1966		Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
61	393	B392; NIBSC_2823; Z1392	Greece	1968	carrier	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
64	254	B439; NIBSC_2812; Z1439	Djibouti	1966	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F1-7
67	S5611	B466; NIBSC_2765; Z1466	Australia	1977	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
82	11-004	B503; NIBSC_2826; Z1503	China	1984	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-8
84	IAL2229	B506; NIBSC_2816; Z1506	Brazil	1976		Neisseria meningitidis	A	5	ST-5 complex	20	9	F2-1
90	CN100	B534; NIBSC_2768; Z1534	UK [England]	1941	invasive (unspecified/other)	Neisseria meningitidis	A	21		5-2	10	F3-9
120	F4698	NIBSC_2731; Z3515	Saudi Arabia	1987	carrier	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
128	F6124	NIBSC_2730; Z3524	Chad	1988	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
160	1014	NIBSC_2821; Z3667	Sudan	1985	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
210	H1964	NIBSC_2796; Z3771	UK	1987	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
237	H44/76	44/76-3; NIBSC_2724; Z3842	Norway	1976	invasive (unspecified/other)	Neisseria meningitidis	B	32	ST-32 complex	7	16	F3-3
238	153	NIBSC_2733; Z3905	China	1966	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1



### Analysis tools

Breakdown: **Fields** Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree iTOL PhyloViz **Microreact**

Select the isolates to include. The tree can be generated from allelic profiles of any selection of loci, or more conveniently, you can select a scheme in the scheme selector, or from a list of recommended schemes if these have been set, to include all loci belonging to that scheme.

Additional fields can be selected to be included as metadata for use in colouring nodes - select any fields you wish to include. Multiple selections can be made by holding down shift or ctrl while selecting. Click 'Submit' to start the analysis.

## BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Microreact

Help

## Microreact - Neisseria isolates



This plugin uploads data for analysis within the Microreact online service:

Microreact is developed at the [The Centre for Genomic Pathogen Surveillance](https://microreact.org) by a team led by David Aanensen.

Web site: <https://microreact.org>

Publication: Argimón *et al.* (2016) Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. *Microb Genom* 2:e000093.

This tool will generate neighbor-joining trees from concatenated nucleotide sequences. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA and peptide loci with genome sequences, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 3,000 records or 120,000 sequences (records x loci).

Isolates

1

2

7

10

11

13

19

Clear List all

Loci

16S\_rDNA

16S\_rRNA (SSU\_rRNA)

23S\_rRNA

abcZ

abcZ (NEIS1015)

aceF (NEIS1279)

All None Paste list

Recommended schemes

Select one or more schemes below or use the full schemes list.

MLST

Ribosomal MLST

N. meningitidis cgMLST v1.0

N. gonorrhoeae cgMLST v1.0

Clear

Schemes

Plasmids

Typing

MLST

Finotyping antigens

16S

Antigen genes

Bexsero Antigen Sequence

Human-restricted Neisseria

Descriptions

Modify the values below - these will be displayed within the created Microreact project.

Title:

Description: Neisseria isolates

Include fields

Select additional fields to include in Microreact data table - (isolate, country and year are always included).

continent

region

date sampled

isoyear sampled

week sampled

date received

Action

SUBMIT

The job will be sent to the job queue. When it has finished, click the button marked 'Launch Microreact'.

14.11. Microreact

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BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Job status viewer

## Job status viewer

**Status**

Job id: BIGSdb\_032220\_1596269633\_79872  
Submit time: 2020-08-01 08:13:53  
Status: finished  
Start time: 2020-08-01 08:14:00  
Progress: 100%  
Stop time: 2020-08-01 08:14:08  
Total time: 8 seconds

**Output**

Launch Microreact

Files

Concatenated FASTA

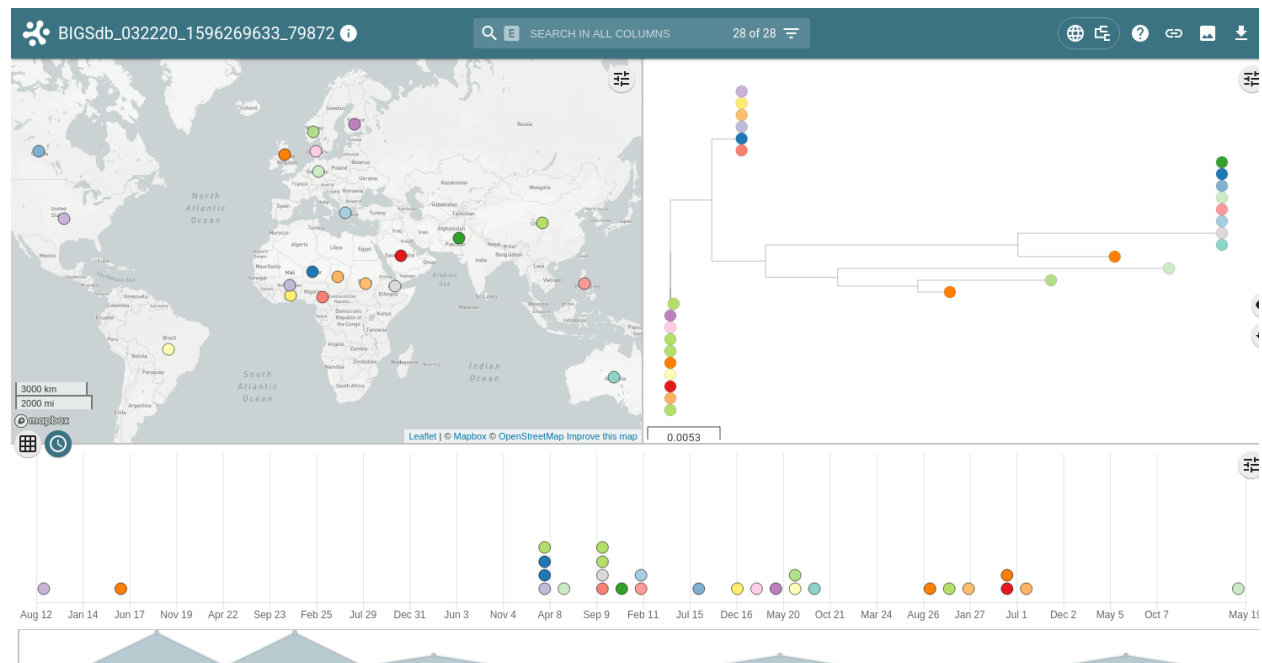
NJ tree (Newick format)

Microreact TSV file

Tar file containing all output files

Please note that job results will remain on the server for 7 days.

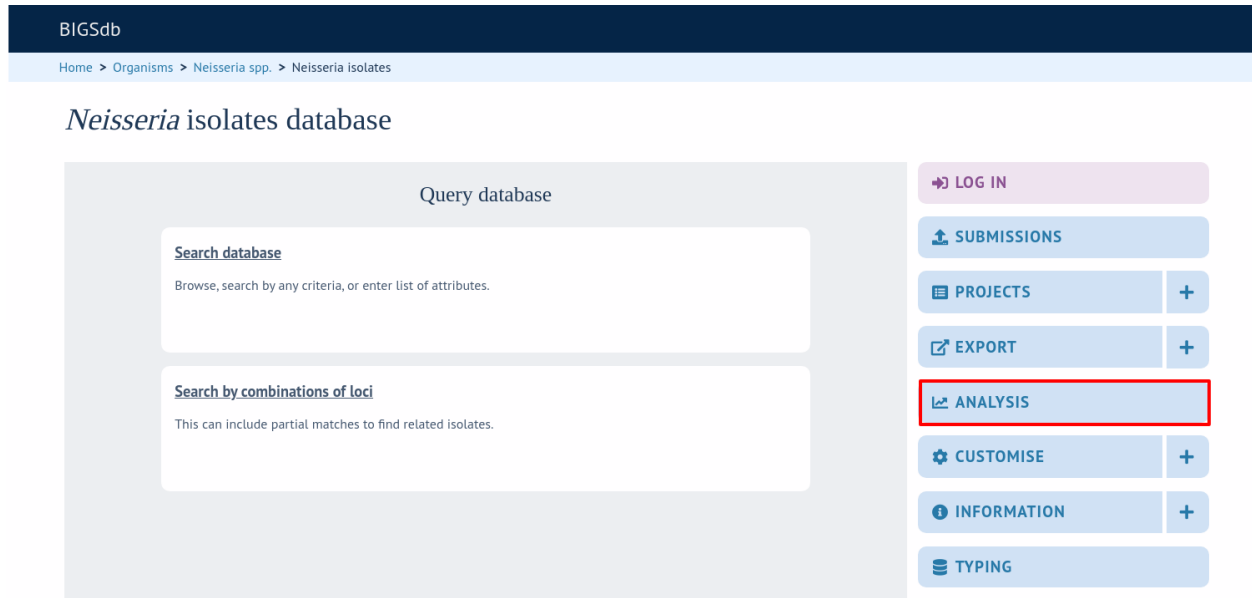
The generated tree will be uploaded to the Microreact website and displayed. Clicking any node will show its position(s) within the tree, map and timeline. A node on the map may correspond to multiple nodes in the tree or timeline.



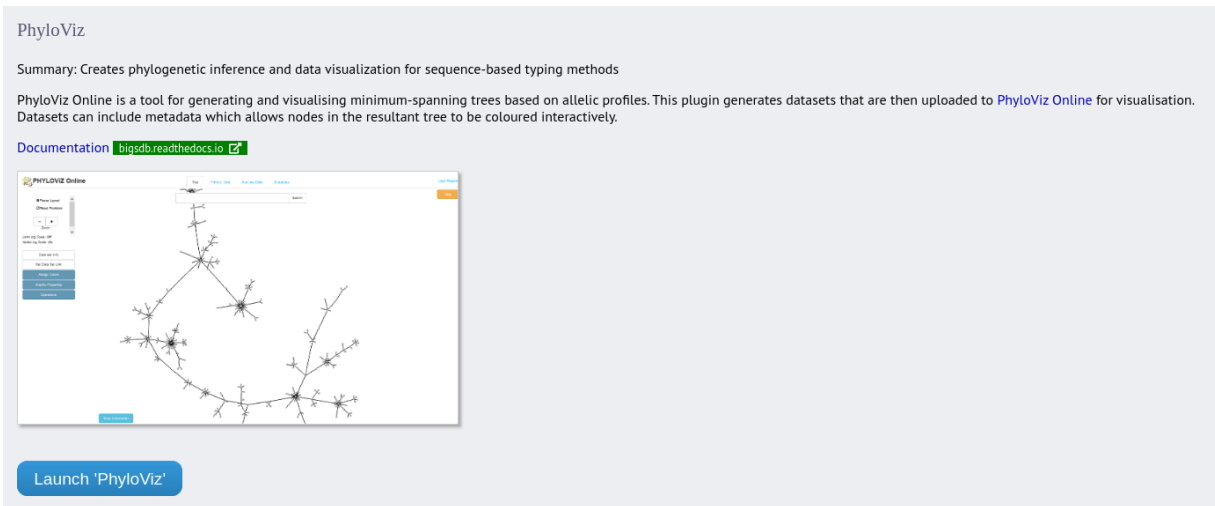
## 14.12 PhyloViz

PhyloViz Online is a tool for generating and visualising minimum-spanning trees. Datasets can include metadata which allows nodes in the resultant tree to be coloured interactively.

PhyloViz can be accessed by selecting the ‘Analysis’ section on the main contents page.



Jump to the ‘Third party’ category, follow the link to PhyloViz, then click ‘Launch PhyloViz’.



Alternatively, it can be accessed following a query by clicking the ‘PhyloViz’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the PhyloViz interface.

15	1		Germany	1999	carrier	Neisseria meningitidis	E	864			
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex		
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex		
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex		
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1 F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex		
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex		
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex		
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex		
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9 F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex		



### Analysis tools

Breakdown: **Fields** Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

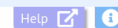
Third party: GrapeTree iTOL **PhyloViz** Microreact

Select the isolates to include. The tree can be generated from allelic profiles of any selection of loci, or more conveniently, you can select a scheme in the scheme selector to include all loci belong to that scheme.

Provenance fields can be selected to be included as metadata for use in colouring nodes - select any fields you wish to include. Multiple selections can be made by holding down Shift or Ctrl while selecting. Click 'Submit' to start the analysis.

## BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > PhyloViz



## PhyloViz: phylogenetic tree vizualisation - Neisseria isolates



This plugin uploads data for analysis within the PhyloViz online service:

PHYLOVIZ Online is developed by: Bruno Gonçalves (1), João André Carriço (1), Alexandre P. Francisco (2,3), Cátia Vaz (2,4) and Mário Ramirez (1)

1. Instituto de Microbiologia, Instituto de Medicina Molecular, Faculdade de Medicina, Universidade de Lisboa, Lisboa, Portugal
2. INESC-ID, R. Alves Redol 9, 1000-029 Lisboa, Portugal
3. Instituto Superior Técnico, Universidade de Lisboa, Lisboa, Portugal
4. Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, 007 Lisboa, Portugal

Web site: <https://online.phyloviz.net/>

Optionally select provenance fields to include in the dataset. This allows you to colour nodes based on field values. Analysis is limited to 10,000 isolates.

**Select ids**

Paste in list of ids to include, start a new line for each. Leave blank to include all ids.

1  
2  
3  
4  
5

**Provenance fields**

id  
isolate  
country  
continent  
region  
year  
date sampled  
isoyear sampled

Alt None

**Loci**

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)

Alt None Paste list

**Schemes**

metagenomics  
N. gonorrhoeae AMR  
Pilin  
Plasmids  
Typing  
MLST  
Finotyping antigens  
16S  
Antigen genes

Action

SUBMIT

The necessary files will be generated immediately. When this has finished, click the button launch 'Launch PhyloViz'.

## BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > PhyloViz

PhyloViz: phylogenetic tree vizualisation - *Neisseria* isolates

This plugin uploads data for analysis within the PhyloViz online service:

PHYLOVIZ Online is developed by: Bruno Gonçalves (1), João André Carriço (1), Alexandre P. Francisco (2,3), Cátia Vaz (2,4) and Mário Ramirez (1)

1. Instituto de Microbiologia, Instituto de Medicina Molecular, Faculdade de Medicina, Universidade de Lisboa, Lisboa, Portugal
2. INESC-ID, R. Alves Redol 9, 1000-029 Lisboa, Portugal
3. Instituto Superior Técnico, Universidade de Lisboa, Lisboa, Portugal
4. Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, 007 Lisboa, Portugal

Web site: <https://online.phyloviz.net/>

Please wait for processing to finish (do not refresh page).

Data are being processed and sent to PhyloViz Online.

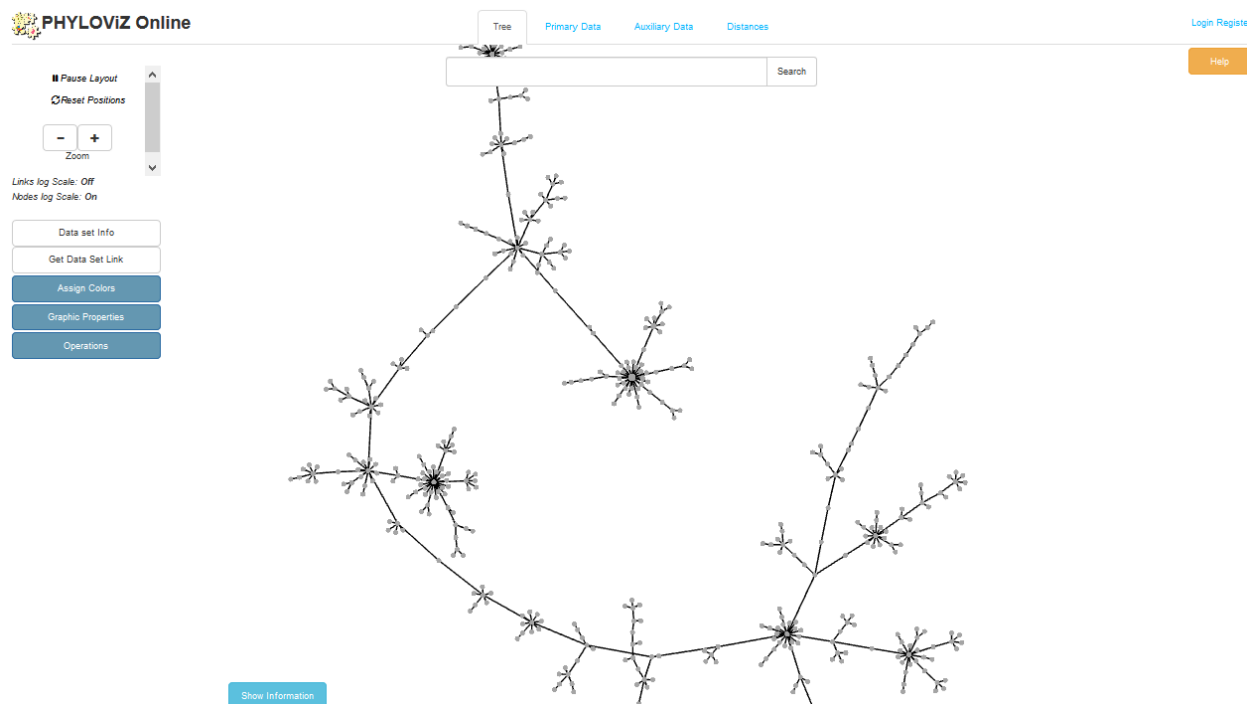
Generating profile data file ... ✓

Generating auxiliary file ... ✓

Sending data to PhyloViz online ... ✓

[Launch PhyloViz](#)

The tree will be sent to and rendered within the PhyloViz website.

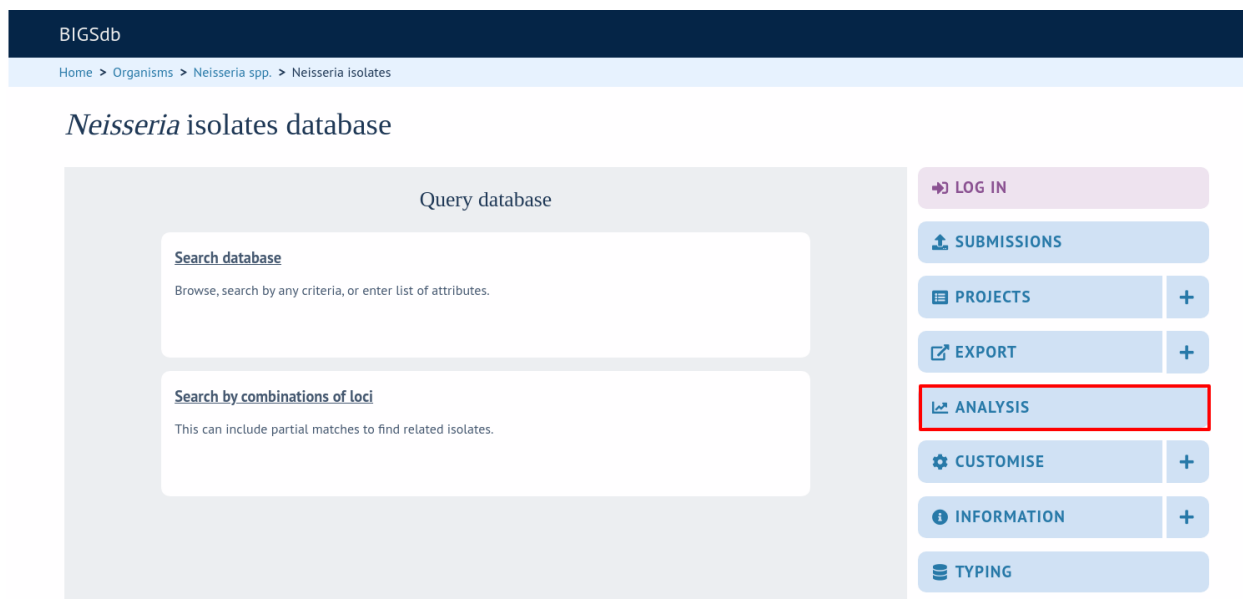


See more information about manipulating the tree on the [PhyloViz website](#).

## 14.13 Polymorphisms

The Polymorphisms plugin generates a *Locus Explorer* polymorphic site analysis on the alleles designated in an isolate dataset following a query.

The analysis can be accessed by selecting the ‘Analysis’ section on the main contents page.



Jump to the ‘Breakdown’ category, follow the link to Polymorphisms, then click ‘Launch Polymorphisms’.

Polymorphisms

Summary: Tool for analysing polymorphic sites for particular locus in an isolate dataset

This plugin generates a schematic of the selected locus showing all the polymorphic sites present in the selected dataset. These are also shown in a tabular form with precise frequencies for each nucleotide at every position.

Documentation [bigsdb.readthedocs.io](https://bigsdb.readthedocs.io)

The screenshot shows the 'Polymorphic site analysis' tool interface. It displays a schematic of the selected locus with polymorphic sites highlighted. Below the schematic is a table titled 'Nucleotide frequencies' showing the frequency of each nucleotide (A, C, G, T) at each position (1 to 100). The table has columns for 'Position', 'A', 'C', 'G', 'T', and 'Total'. The data is as follows:

Position	A	C	G	T	Total
1	1	1	1	1	4
2	1	1	1	1	4
3	1	1	1	1	4
4	1	1	1	1	4
5	1	1	1	1	4
6	1	1	1	1	4
7	1	1	1	1	4
8	1	1	1	1	4
9	1	1	1	1	4
10	1	1	1	1	4
11	1	1	1	1	4
12	1	1	1	1	4
13	1	1	1	1	4
14	1	1	1	1	4
15	1	1	1	1	4
16	1	1	1	1	4
17	1	1	1	1	4
18	1	1	1	1	4
19	1	1	1	1	4
20	1	1	1	1	4
21	1	1	1	1	4
22	1	1	1	1	4
23	1	1	1	1	4
24	1	1	1	1	4
25	1	1	1	1	4
26	1	1	1	1	4
27	1	1	1	1	4
28	1	1	1	1	4
29	1	1	1	1	4
30	1	1	1	1	4
31	1	1	1	1	4
32	1	1	1	1	4
33	1	1	1	1	4
34	1	1	1	1	4
35	1	1	1	1	4
36	1	1	1	1	4
37	1	1	1	1	4
38	1	1	1	1	4
39	1	1	1	1	4
40	1	1	1	1	4
41	1	1	1	1	4
42	1	1	1	1	4
43	1	1	1	1	4
44	1	1	1	1	4
45	1	1	1	1	4
46	1	1	1	1	4
47	1	1	1	1	4
48	1	1	1	1	4
49	1	1	1	1	4
50	1	1	1	1	4
51	1	1	1	1	4
52	1	1	1	1	4
53	1	1	1	1	4
54	1	1	1	1	4
55	1	1	1	1	4
56	1	1	1	1	4
57	1	1	1	1	4
58	1	1	1	1	4
59	1	1	1	1	4
60	1	1	1	1	4
61	1	1	1	1	4
62	1	1	1	1	4
63	1	1	1	1	4
64	1	1	1	1	4
65	1	1	1	1	4
66	1	1	1	1	4
67	1	1	1	1	4
68	1	1	1	1	4
69	1	1	1	1	4
70	1	1	1	1	4
71	1	1	1	1	4
72	1	1	1	1	4
73	1	1	1	1	4
74	1	1	1	1	4
75	1	1	1	1	4
76	1	1	1	1	4
77	1	1	1	1	4
78	1	1	1	1	4
79	1	1	1	1	4
80	1	1	1	1	4
81	1	1	1	1	4
82	1	1	1	1	4
83	1	1	1	1	4
84	1	1	1	1	4
85	1	1	1	1	4
86	1	1	1	1	4
87	1	1	1	1	4
88	1	1	1	1	4
89	1	1	1	1	4
90	1	1	1	1	4
91	1	1	1	1	4
92	1	1	1	1	4
93	1	1	1	1	4
94	1	1	1	1	4
95	1	1	1	1	4
96	1	1	1	1	4
97	1	1	1	1	4
98	1	1	1	1	4
99	1	1	1	1	4
100	1	1	1	1	4

Launch 'Polymorphisms'

The analysis is accessed by clicking the ‘Polymorphic sites’ button in the Breakdown list at the bottom of a results table following a query.

15	1		Germany	1999	carrier	Neisseria meningitidis	E	804			
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex		
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex		
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex		
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex		
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex		
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex		
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex		
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex		



### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [ITOL](#) [PhyloViz](#) [Microreact](#)

Select the locus that you would like to analyse from the list.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Polymorphic sites

Help ⓘ

## Polymorphic site analysis

This tool will analyse the polymorphic sites in the selected locus for the current isolate dataset.

If more than 100 sequences have been selected, the job will be run by the offline job manager which may take a few minutes (or longer depending on the queue). This is because sequences may have gaps in them and consequently need to be aligned which is a processor- and memory- intensive operation.

Loci

Options

Action

16S\_rDNA  
16S\_rRNA (SSU rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
ackA2 (NEIS1727)  
acnA (NEIS1729)

If both allele designations and tagged sequences exist for a locus, choose how you want these handled: ⓘ

☒ Use allele sequence retrieved from external database

☐ Use sequences tagged from the bin

☒ Analyse single example of each unique sequence

☒ Exclude incomplete sequences

ANALYSE

Click 'Analyse'.

A schematic of the locus is generated showing the polymorphic sites. A full description of this can be found in the *Locus Explorer polymorphic site analysis* section.

## Polymorphic site analysis

The colour codes represent the percentage of alleles that have a particular nucleotide at each position. Click anywhere within the sequence to drill down to allele and profile information. The width of the display can be altered by going to the options page - change this if the display goes off the page.

17 alleles included in analysis. 81 polymorphic sites found.

Key: 0-10 | >10-20 | >20-30 | >30-40 | >40-50 | >50-60 | >60-70 | >70-80 | >80-90 | >90-100



## Nucleotide frequencies

Position	Nucleotide										%
	A	C	G	T	-	%A	%C	%G	%T	%-	
9	0	14	0	3	0		82.35		17.65		
24	1	0	16	0	0	5.88		94.12			
27	0	10	0	7	0		58.82		41.18		
28	4	0	13	0	0	23.53		76.47			
30	16	0	1	0	0	94.12		5.88			
36	0	14	0	3	0		82.35		17.65		
45	1	0	16	0	0	5.88		94.12			
54	0	6	0	11	0		35.29		64.71		
57	0	6	0	11	0		35.29		64.71		
59	11	0	6	0	0	64.71		35.29			
60	0	7	0	10	0		41.18		58.82		
63	0	16	0	1	0		94.12		5.88		
64	11	0	6	0	0	64.71		35.29			
66	0	13	0	4	0		76.47		23.53		
72	0	0	14	3	0		82.35		17.65		
78	15	0	2	0	0	88.24		11.76			
79	14	3	0	0	0	82.35	17.65				
81	0	9	0	8	0		52.94		47.06		
82	3	0	14	0	0	17.65		82.35			

## 14.14 Species identification

The species identification tool extracts ribosomal MLST alleles from genomes and determines the species based on the count of alleles that are uniquely found within a single species (or higher taxonomic rank if alleles unique to a species are not found). This is done by making a query to the rMLST genome database.

The tool can be accessed by selecting the 'Analysis' section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## Neisseria isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

Jump to the ‘Analysis’ category, follow the link to rMLST species identity, then click ‘Launch rMLST species identity’. The tool can be accessed from the front page of an isolate database.

rMLST species identity

Summary: Use rMLST to identify species from bacterial genome assemblies

The species identification tool extracts ribosomal MLST alleles from genomes and determines the species based on the count of alleles that are uniquely found within a single species (or higher taxonomic rank if alleles unique to a species are not found). This is done by making a query via the PubMLST RESTful API to the rMLST typing database.

Documentation [bigsd.readthedocs.io](https://bigsd.readthedocs.io)

Output

Isolate	Accession	Species	Function	From identifier (rMLST)	From isolate to genome	Isolate	Species	From isolate to genome
1	AA94227	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	1	AA94227	Neisseria meningitidis
2	12804	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	2	12804	Neisseria meningitidis
3	12804	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	Neisseria meningitidis	3	12804	Neisseria meningitidis

Launch 'rMLST species identity'

Alternatively, it can be accessed following a query by clicking the ‘rMLST species id’ button at the bottom of the results table. Isolates returned from the query will be automatically selected within the species id interface (note that only isolates with a genome assembly will be able to be checked).

14.14. Species identification

365

Sequence bin: Sequence bin size >= 2 Mbp ⓘ

☐ Include old record versions

Add filter:  Add

Display/sort options

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET SEARCH

7 records returned. Click the hyperlinks for detailed information.

Isolate fields ⓘ								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	capsule group	ST	clonal complex	PorA_VR1	PorA_VR2	FetA_VR
1	A4/M1027	B1; NIBSC_2803; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-5
2	120M	B35; NIBSC_2822; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
7	7891	B54; NIBSC_2760; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-1
10	6748	B73; NIBSC_2784; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	18-1	3	F5-1
11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-6
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5

### Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST **rMLST species id** PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree iTOL PhyloViz Microreact

Finally, the analysis is also possible directly from an isolate record, if the isolate has a genome assembly associated with it.

Multiple sequence typing (MLST) of **108 isolates**

- Bratcher HB, Corton C, Jolley KA, Parkhill J, Maiden MC (2014). A gene-by-gene population genomics platform: de novo assembly, annotation and genealogical analysis of 108 representative *Neisseria meningitidis* genomes. *BMC Genomics* **15**:1138 **108 isolates**
- Didelot X, Urwin R, Maiden MC, Falush D (2009). Genealogical typing of *Neisseria meningitidis*. *Microbiology* **155**:176-86 **93 isolates**

Sequence bin

contigs: 364  
total length: 2,069,108 bp  
max length: 50,093 bp  
mean length: 5,685 bp

N50 contig number: 44  
N50 length (L50): 15,404  
N90 contig number: 146  
N90 length (L90): 3,907

N95 contig number: 180  
N95 length (L95): 2,305  
loci tagged: 2,174

Show sequence bin

Schemes and loci

Navigation and select schemes within tree to display allele designations

- All loci
- Capsule
- Genetic Information Processing
- Genomic islands
- Lineage Schemes
- Metabolism
- Pilin
- Typing
- Other schemes
- Loci not in schemes

Tools

Analysis: **rMLST species id** PCR

The tool interface consists of a list of isolate ids to check. This will be pre-populated if accessed following a query or directly from an isolate record. If the rMLST scheme is defined on the system, you will have a choice as to whether to BLAST the genome sequences to identify the rMLST alleles, or just use the designations that are tagged in the database. The latter is much quicker but relies on the record having been scanned and annotated with the rMLST loci.

Click 'Submit'.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Plugins](#) > [Species identification](#)
[Help](#)  

## rMLST species identification

This analysis attempts to identify exact matching rMLST alleles within selected isolate sequence record(s). A predicted taxon will be shown where identified alleles have been linked to validated genomes in the rMLST database.

Please select the required isolate ids to run the species identification for. These isolate records must include genome sequences.

**Isolates**  

1  
2  
7  
10  
11  
13  
19

**Options**  
Scan genome or use allele designations already stored  
☐ Scan genomes  
☒ Use stored allele designations

**Action**  

SUBMIT

Clear

List all


The job will be sent to the job queue.

Results will be displayed in a table as they are generated. The table will display the highest taxonomic rank that can be reliably identified, e.g. species, the taxon and its full taxonomy. An indication of the confidence for the result will also be displayed - this is based on the proportion of alleles found that are unique to a taxon.

Output

Id	Isolate	Rank	Taxon	Prediction from identified rMLST alleles linked to genomes			Identified rSTs	
				Taxonomy	Support	Matches	rST	Species
1	A4/M1027	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2504	<i>Neisseria meningitidis</i>
2	120M	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2532	<i>Neisseria meningitidis</i>
7	7891	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2434	<i>Neisseria meningitidis</i>
10	6748	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2530	<i>Neisseria meningitidis</i>
11	129E	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2528	<i>Neisseria meningitidis</i>
13	139M	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2433	<i>Neisseria meningitidis</i>
19	S3131	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2285	<i>Neisseria meningitidis</i>

Files

 Report file (JSON format)

Please note that job results will remain on the server for 7 days.

Clicking the '+' icon on any row will display further details about the matches.

Id	Isolate	Prediction from identified rMLST alleles linked to genomes					Identified rSTs	
		Rank	Taxon	Taxonomy	Support	Matches	rST	Species
1	A4/M1027	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2504	<i>Neisseria meningitidis</i>
2	120M	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2532	<i>Neisseria meningitidis</i>
7	7891	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	+	2434	<i>Neisseria meningitidis</i>
10	6748	SPECIES	<i>Neisseria meningitidis</i>	<i>Proteobacteria</i> > <i>Betaproteobacteria</i> > <i>Neisseriales</i> > <i>Neisseriaceae</i> > <i>Neisseria</i> > <i>Neisseria meningitidis</i>	100%	-	2530	<i>Neisseria meningitidis</i>

53 loci matched (rMLST uses 53 in total)

Locus	Allele	Length	Contig	Start position	End position	Linked data values
BACT000001	174	1680	181603	52429	34108	species: <i>Neisseria meningitidis</i> [n=1830]
BACT000002	9	729	181098	6971	7699	species: <i>Neisseria meningitidis</i> [n=694]
BACT000003	1	693	181315	13840	14532	species: <i>Neisseria meningitidis</i> [n=1772]
BACT000003	1	693	181474	5814	6506	species: <i>Neisseria meningitidis</i> [n=1772]
BACT000004	2	621	181315	5569	6189	species: <i>Neisseria meningitidis</i> [n=7822]; <i>Neisseria</i> sp. [n=1]
BACT000005	1	519	181315	9345	9863	species: <i>Neisseria meningitidis</i> [n=17221]; <i>Neisseria gonorrhoeae</i> [n=1]; <i>Neisseria</i> sp. [n=1]
BACT000005	1	519	181474	10483	11001	species: <i>Neisseria meningitidis</i> [n=17221]; <i>Neisseria gonorrhoeae</i> [n=1]; <i>Neisseria</i> sp. [n=1]
BACT000006	5	369	181603	53216	53584	species: <i>Neisseria meningitidis</i> [n=2053]; <i>Neisseria</i> sp. [n=1]
BACT000007	1	471	181145	2253	2723	species: <i>Neisseria meningitidis</i> [n=14753]; <i>Neisseria</i> sp. [n=1]
BACT000007	1	471	181374	2271	2741	species: <i>Neisseria meningitidis</i> [n=14753]; <i>Neisseria</i> sp. [n=1]
BACT000008	2	393	181315	10796	11188	species: <i>Neisseria meningitidis</i> [n=7491]
BACT000009	1	393	181193	16935	17327	species: <i>Neisseria meningitidis</i> [n=3125]
BACT000009	1	393	181591	20941	21333	species: <i>Neisseria meningitidis</i> [n=3125]
BACT000010	1	312	181315	19833	20144	species: <i>Neisseria meningitidis</i> [n=926]
BACT000010	1	312	181474	202	513	species: <i>Neisseria meningitidis</i> [n=926]
BACT000011	2	396	181315	6209	6604	species: <i>Neisseria gonorrhoeae</i> [n=15852]; <i>Neisseria meningitidis</i> [n=7271]; <i>Neisseria</i> sp. [n=1]
BACT000012	1	372	181145	2841	3212	species: <i>Neisseria meningitidis</i> [n=1337]; <i>Neisseria gonorrhoeae</i> [n=3]
BACT000012	1	372	181374	2859	3230	species: <i>Neisseria meningitidis</i> [n=1337]; <i>Neisseria gonorrhoeae</i> [n=3]
BACT000013	1	363	181315	6624	6986	species: <i>Neisseria meningitidis</i> [n=19291]; <i>Neisseria</i> sp. [n=1]

**Note:** Ribosomal MLST was first described in Jolley et al. 2012. Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. *Microbiology* 158:1005-15

## 14.15 Sequence bin breakdown

The sequence bin breakdown plugin calculates statistics based on the number and length of contigs in the sequence bin as well as the number of loci tagged for an isolate record.

The function can be accessed by selecting the 'Analysis' section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

Neisseria isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

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TYPING

Jump to the 'Breakdown' category, follow the link to Sequence Bin Breakdown, then click 'Launch Sequence Bin Breakdown'.

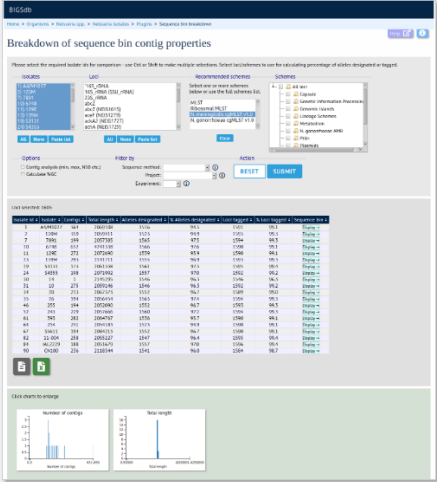
The function can be selected by clicking the ‘Sequence bin’ link on the Breakdown section of the main contents page.

**Sequence Bin Breakdown**

Summary: Breakdown of sequence bin contig properties

The sequence bin breakdown plugin calculates statistics based on the number and length of contigs in the sequence bin as well as the number of loci tagged for each isolate record. Using this latter metric against a cgMLST scheme can be a good indicator of genome quality. Values for number of contigs, total sequence length, mean contig length and contig length distribution are charted.

[Documentation](#) [bigsd.readthedocs.io](#)



Launch ‘Sequence Bin Breakdown’

Alternatively, it can be accessed following a query by clicking the ‘Sequence bin’ button in the Breakdown list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5
31	10	B269; NIBSC_2825; Z1269	Burkina Faso	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
34	20	B275; NIBSC_2767; Z1275	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-7
35	26	B278; NIBSC_2764; Z1278	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
52	243	B362; NIBSC_2779; Z1362	Cameroon	1966		Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
61	393	B392; NIBSC_2823; Z1392	Greece	1968	carrier	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
64	254	B439; NIBSC_2812; Z1439	Djibouti	1966	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F1-7
67	S5611	B466; NIBSC_2765; Z1466	Australia	1977	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
82	11-004	B503; NIBSC_2826; Z1503	China	1984	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-8
84	IAL2229	B506; NIBSC_2816; Z1506	Brazil	1976		Neisseria meningitidis	A	5	ST-5 complex	20	9	F2-1
90	CN100	B534; NIBSC_2768; Z1534	UK [England]	1941	invasive (unspecified/other)	Neisseria meningitidis	A	21		5-2	10	F3-9

### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

Select the isolate records to analyse - these will be pre-selected if you accessed the plugin following a query. You can also select loci and/or schemes which will be used to calculate the totals and percentages of loci designated and tagged. This may be useful as a guide to assembly quality if you use a scheme of core loci where a good assembly would be expected to include all member loci. To determine the total of all loci designated or tagged, click ‘All loci’ in the scheme tree.

There is also an option to determine the mean G+C content and various assembly stats of the sequence bin of each isolate. Note that selecting these will make the analysis run much slower since each contig needs to be examined.

Click submit.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Sequence bin breakdown

Help ⓘ

### Breakdown of sequence bin contig properties

Please select the required isolate ids for comparison - use Ctrl or Shift to make multiple selections. Select loci/schemes to use for calculating percentage of alleles designated or tagged.

**Isolates**  
1  
2  
7  
10  
11  
13  
19  
Clear List all

**Loci**  
16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
All None Paste list

**Recommended schemes**  
Select one or more schemes below or use the full schemes list.  
MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0  
Clear

**Schemes**  
Bexsero Antigen Sequence  
Human-restricted Neisseria  
N. gonorrhoeae cgMLST v1  
**N. meningitidis cgMLST v1**  
NG MAST  
OMV peptide typing  
Ribosomal MLST  
eMLST (20 locus partial ge  
eMLST (20 locus whole ge

**Options**  
☐ Contig analysis (min, max, N50 etc.)  
☐ Calculate %GC

**Filter by**  
Sequence method: ⓘ  
Project: ⓘ  
Experiment: ⓘ

**Action**  
RESET SUBMIT

If there are fewer than 100 isolates selected, the table will be generated immediately. Otherwise it will be submitted to the job queue.

A table of sequence bin stats will be generated.

**Isolates**  
1  
2  
7  
10  
11  
13  
19  
Clear List all

**Loci**  
16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
All None Paste list

**Recommended schemes**  
Select one or more schemes below or use the full schemes list.  
MLST  
Ribosomal MLST  
N. meningitidis cgMLST v1.0  
N. gonorrhoeae cgMLST v1.0  
Clear

**Schemes**  
All loci  
Capsule  
Genetic Information Processing  
Genomic islands  
Lineage Schemes  
Metabolism  
N. gonorrhoeae AMR  
Pilin  
Plasmids

**Options**  
☐ Contig analysis (min, max, N50 etc.)  
☐ Calculate %GC

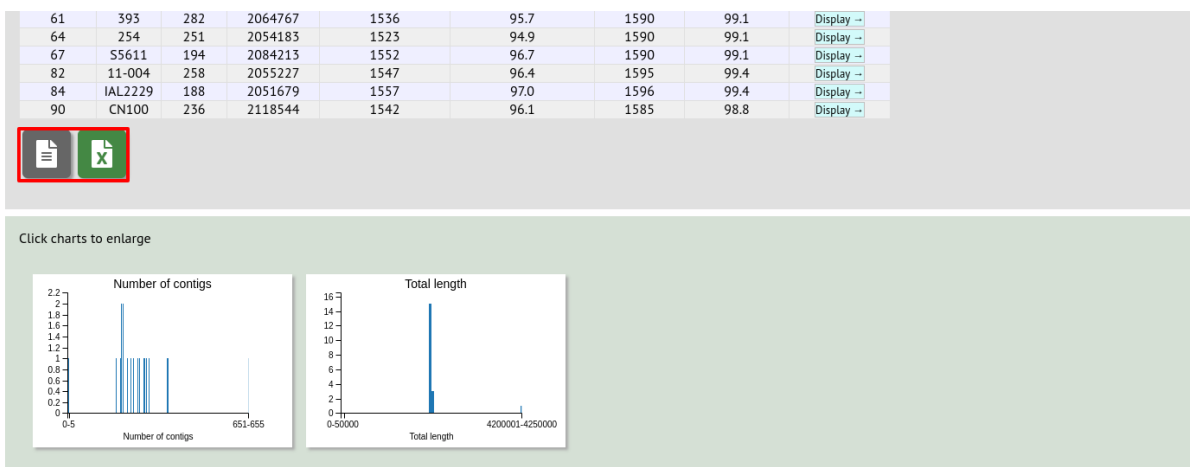
**Filter by**  
Sequence method: ⓘ  
Project: ⓘ  
Experiment: ⓘ

**Action**  
RESET SUBMIT

Loci selected: 1605

Isolate id	Isolate	Contigs	Total length	Alleles designated	% Alleles designated	Loci tagged	% Loci tagged	Sequence bin
1	A4/M1027	364	2069108	1516	94.5	1591	99.1	<a>Display</a>
2	120M	359	2059411	1523	94.9	1593	99.3	<a>Display</a>
7	7891	199	2057385	1565	97.5	1594	99.3	<a>Display</a>
10	6748	652	4241338	1566	97.6	1590	99.1	<a>Display</a>

You can choose to export the data in tab-delimited text or Excel formats by clicking the appropriate link at the bottom of the table.



*Sequence bin records* can also be accessed by clicking the ‘Display’ button for each row of the table.

Experiment:  ⓘ

Loci selected: 1605

Isolate Id	Isolate	Contigs	Total length	Alleles designated	% Alleles designated	Loci tagged	% Loci tagged	Sequence bin
1	A4/M1027	364	2069108	1516	94.5	1591	99.1	Display --
2	120M	359	2059411	1523	94.9	1593	99.3	Display --
7	7891	199	2057385	1565	97.5	1594	99.3	Display --
10	6748	652	4241338	1566	97.6	1590	99.1	Display --
11	129E	272	2072690	1539	95.9	1590	99.1	Display --
13	139M	293	2141711	1555	96.9	1593	99.3	Display --
19	S3131	173	2061338	1561	97.3	1595	99.4	Display --
24	S4355	198	2071992	1557	97.0	1592	99.2	Display --
30	14	1	2145295	1547	96.4	1547	96.4	Display --
31	10	275	2059146	1546	96.3	1592	99.2	Display --
34	20	213	2067373	1552	96.7	1589	99.0	Display --
35	26	194	2056454	1563	97.4	1594	99.3	Display --
52	243	229	2057666	1560	97.2	1594	99.3	Display --
61	393	282	2064767	1536	95.7	1590	99.1	Display --
64	254	251	2054183	1523	94.9	1590	99.1	Display --
67	S5611	194	2084213	1552	96.7	1590	99.1	Display --
82	11-004	258	2055227	1547	96.4	1595	99.4	Display --
84	IAL2229	188	2051679	1557	97.0	1596	99.4	Display --
90	CN100	236	2118544	1542	96.1	1585	98.8	Display --

## 14.16 Two field breakdown

The two field breakdown plugin displays a table breaking down one field against another, e.g. breakdown of serogroup by year.

The analysis can be accessed by selecting the ‘Analysis’ section on the main contents page.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates

## *Neisseria* isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT +

**ANALYSIS**

CUSTOMISE +

INFORMATION +

TYPING

Jump to the ‘Breakdown’ category, follow the link to Two Field Breakdown, then click ‘Launch Two Field Breakdown’.

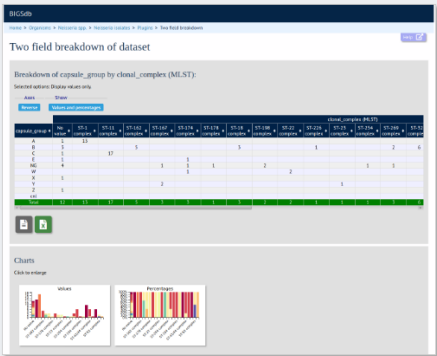
The analysis can be selected for the whole database by clicking the ‘Two field breakdown’ link on the main contents page.

### Two Field Breakdown

Summary: Breakdown of one field against another

The two field breakdown plugin generates a table breaking down the frequencies of one field against another. This is analogous to a spreadsheet pivot table. Any primary metadata field, locus, or scheme field can be used and the output can be exported as an Excel spreadsheet.

[Documentation](#) [bigsd.readthedocs.io](#)



Launch 'Two Field Breakdown'

Alternatively, a two field breakdown can be displayed of the dataset returned from a query by clicking the ‘Two field’ button in the Breakdown list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex	7	16	
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: [Fields](#) **[Two Field](#)** [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

Select the two fields you wish to breakdown and how you would like the values displayed (percentage/absolute values and totaling options).

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Two field breakdown

[Help](#)

## Two field breakdown of dataset

Here you can create a table breaking down one field by another, e.g. breakdown of serogroup by year.

**Isolates**

1  
2  
3  
4  
5  
6  
7

[Clear](#) [List all](#)

**Select fields**

Field 1: clonal complex (MLST)

Field 2: capsule group

**Action**

[RESET](#) [SUBMIT](#)

**Display**

☒ values only

☐ values and percentages

☐ percentages only

**Calculate percentages by**

☒ dataset

☐ row

☐ column

Click submit. The breakdown will be displayed as a table. Bar charts will also be displayed provided the number of returned values for both fields are fewer than 30.

## Two field breakdown of dataset

Breakdown of clonal\_complex (MLST) by capsule\_group:

Selected options: Display values only.

[Axes](#)
[Show](#)

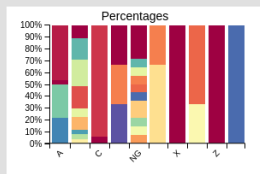
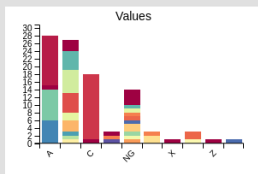
[Reverse](#)
[Values and percentages](#)

clonal_complex (MLST) ▾	capsule_group ▾											Total ▾
	A ▾	B ▾	C ▾	E ▾	NG ▾	W ▾	X ▾	Y ▾	Z ▾	cnl ▾		
No value	1	3	1	1	4		1		1		12	
ST-1 complex	13										13	
ST-11 complex			17								17	
ST-162 complex		5									5	
ST-167 complex					1			2			3	
ST-174 complex				1	1	1					3	
ST-178 complex					1						1	
ST-18 complex		3									3	
ST-198 complex					2						2	
ST-22 complex						2					2	
ST-226 complex		1									1	
ST-23 complex								1			1	
ST-254 complex					1						1	
ST-269 complex		2			1						3	
ST-32 complex		6									6	
ST-334 complex		1									1	
ST-35 complex					1						1	
ST-4 complex	8										8	
ST-41/44 complex		5			1						6	
ST-461 complex		1									1	
ST-5 complex	6										6	
ST-53 complex					1				1		2	
ST-60 complex				1							1	
Total	28	27	18	3	14	3	1	3	1	1	99	



## Charts

Click to enlarge



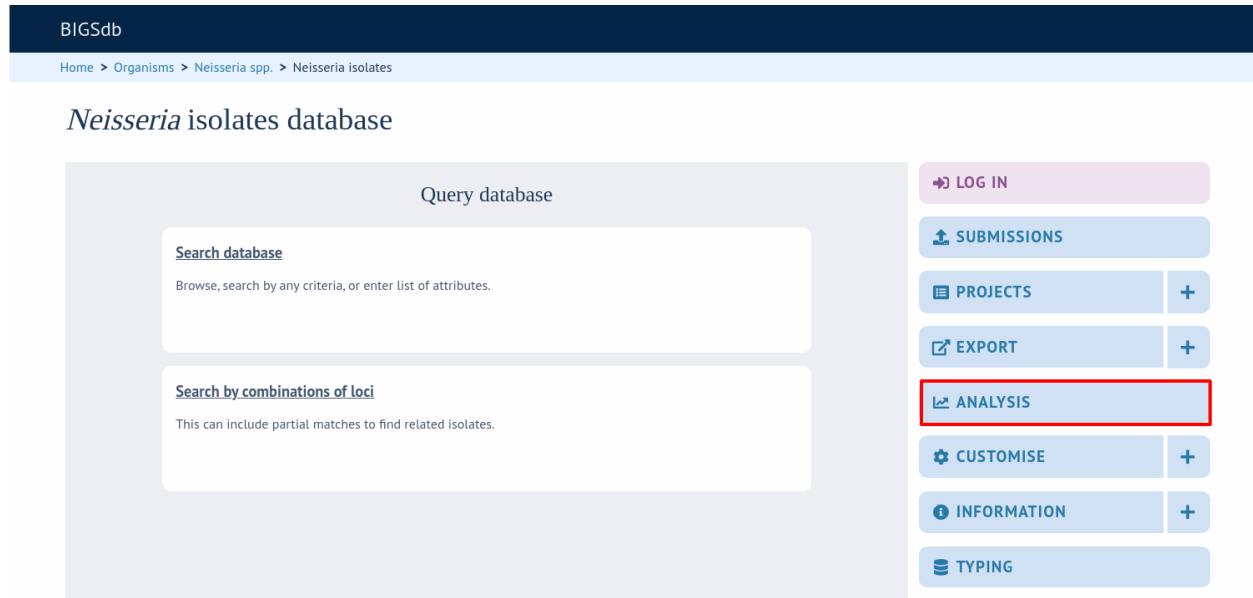
The table values can be exported in a format suitable for copying in to a spreadsheet by clicking ‘Download as tab-delimited text’ underneath the table.

**Note:** The job will be submitted to the offline job queue if the query returns 10,000 or more isolates. In this case, the buttons to reverse the axes or to change whether values or percentages are shown will not be available.

## 14.17 Unique combinations

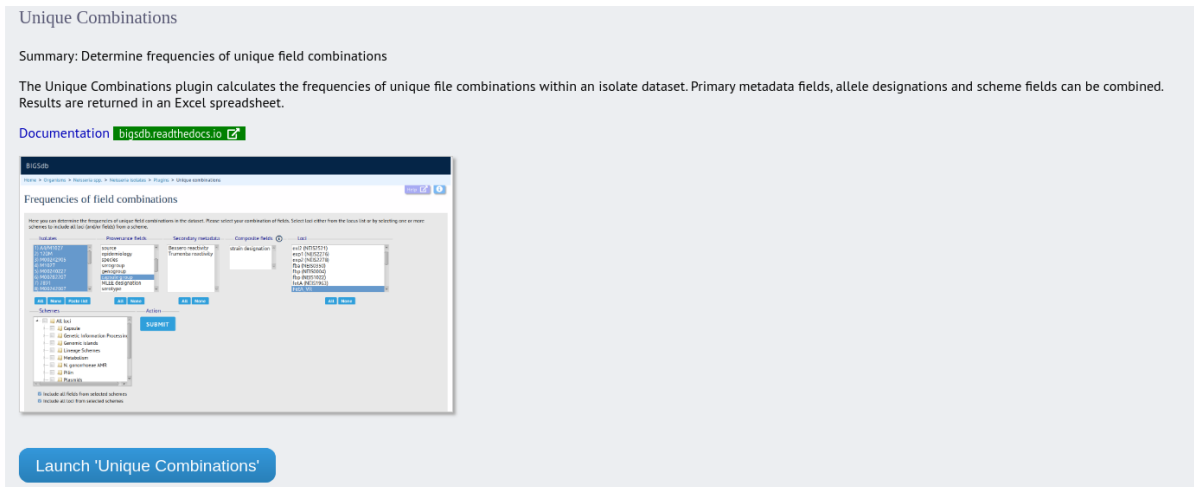
The Unique Combinations plugin calculates the frequencies of unique file combinations within an isolate dataset. Provenance fields, composite fields, allele designations and scheme fields can be combined.

The function can be accessed by selecting the ‘Analysis’ section on the main contents page.



Jump to the ‘Breakdown’ category, follow the link to Unique Combinations, then click ‘Launch Unique Combinations’.

The function can be selected by clicking the ‘Unique combinations’ link in the Breakdown section of the main contents page. This will run the analysis on the entire database.



Alternatively, it can be accessed following a query by clicking the ‘Combinations’ button in the Breakdown list at the bottom of the results table. This will run the analysis on the dataset returned from the query. Please note that the list of functions here may vary depending on the setup of the database.

13	139M	B99; NIBSC_2793; Z1099	Philippines	1908		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-1
14	0120/95		Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117			14	
15	1		Germany	1999	carrier	Neisseria meningitidis	E	864				
16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: **Fields** Two Field **Combinations** Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree iTOL PhyloViz Microreact

Select the combination of fields to analyse, e.g. serogroup and finotyping antigens.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Unique combinations

Help ⓘ ⓘ

### Frequencies of field combinations

Here you can determine the frequencies of unique field combinations in the dataset. Please select your combination of fields. Select loci either from the locus list or by selecting one or more schemes to include all loci (and/or fields) from a scheme.

Isolates: 1 2 3 4 5 6 7

Provenance fields: source epidemiology species serogroup genogroup genogroup notes capsule group MLEE designation

Secondary metadata: Bexsero reactivity Bexsero notes Trumenba reactivity Trumenba notes

Composite fields: strain designation

Loci: '16S\_rDNA 16S\_rRNA (SSU\_rRNA) 23S\_rRNA abcZ abcZ (NEIS1015) aceF (NEIS1279)

Schemes: Plasmids Typing MLST **Finotyping antigens** 16S Antigen genes Bexsero Antigen Sequence Human-restricted Neisseria

Include all fields from selected schemes ☒ Include all loci from selected schemes ☒

SUBMIT

Click submit. The job will be submitted to the job queue. Once analysis has completed, you will be able to download the results in tab-delimited text or Excel formats.

BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > Job status viewer

## Job status viewer



### Status

Job id: BIGSdb\_003448\_1596272602\_28728  
Submit time: 2020-08-01 09:03:22  
Status: finished  
Start time: 2020-08-01 09:03:26  
Progress: 100%  
Stop time: 2020-08-01 09:03:28  
Total time: 2 seconds

### Output

Number of unique combinations: 105

#### Files

[Combinations table \(text\)](#)[Combinations table \(Excel\)](#)[Tar file containing all output files](#)

Please note that job results will remain on the server for 7 days.



## DATA EXPORT PLUGINS

### 15.1 Contig export

The contig export plugin can be accessed by expanding the ‘Export’ section and clicking the ‘Contigs’ link in the contents page of isolate databases.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates

*Neisseria* isolates database

Query database

Search database

Browse, search by any criteria, or enter list of attributes.

Search by combinations of loci

This can include partial matches to find related isolates.

LOG IN

SUBMISSIONS

PROJECTS +

EXPORT -

Export dataset

Contigs

Sequences

ANALYSIS

CUSTOMISE +

INFORMATION +

TYPING

Alternatively, it can be accessed following a query by clicking the ‘Contigs’ button in the Export section at the bottom of the results table.

11	129E	B92; NIBSC_2828; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F3-6
13	139M	B99; NIBSC_2795; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
30	14	BennettTree10; alpha14	Germany	1999	carrier	Neisseria meningitidis	cnl	53	ST-53 complex	7	30-3	F5-5
31	10	B269; NIBSC_2825; Z1269	Burkina Faso	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
34	20	B275; NIBSC_2767; Z1275	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A			5-2	10	F1-7
35	26	B278; NIBSC_2764; Z1278	Niger	1963	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
52	243	B362; NIBSC_2779; Z1362	Cameroon	1966		Neisseria meningitidis	A	4	ST-4 complex	7	13	F1-5
61	393	B392; NIBSC_2823; Z1392	Greece	1968	carrier	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
64	254	B439; NIBSC_2812; Z1439	Djibouti	1966	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F1-7
67	S5611	B466; NIBSC_2765; Z1466	Australia	1977	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex	5-2	10	F5-1
82	11-004	B503; NIBSC_2826; Z1503	China	1984	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	20	9	F3-8
84	IAL2229	B506; NIBSC_2816; Z1506	Brazil	1976		Neisseria meningitidis	A	5	ST-5 complex	20	9	F2-1
90	CN100	B534; NIBSC_2768; Z1534	UK [England]	1941	invasive (unspecified/other)	Neisseria meningitidis	A	21		5-2	10	F3-9

### Analysis tools

Breakdown: [Fields](#) [Two Field](#) [Combinations](#) [Polymorphic sites](#) [Publications](#) [Sequence bin](#)

Analysis: [BURST](#) [Codons](#) [Gene Presence](#) [Genome Comparator](#) [BLAST](#) [rMLST species id](#) [PCR](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Third party: [GrapeTree](#) [iTOL](#) [PhyloViz](#) [Microreact](#)

Select the isolates for which you wish to export contig data for. In databases with a large number of isolates you will need to enter the id numbers rather than select from a list. If the export function was accessed following a query, isolates returned in the query will be pre-selected.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Plugins > Contigs

[Help](#) [?](#) [i](#)

### Contig analysis and export

Please select the required isolate ids from which contigs are associated - use Ctrl or Shift to make multiple selections. Please note that the total length of tagged sequence is calculated by adding up the length of all loci tagged within the contig - if these loci overlap then the total tagged length will be reported as being longer than it really is but it won't exceed the length of the contig.

**Isolates**

1  
2  
7  
10  
11  
13  
19

Clear
List all

**Options**

Identify contigs with >= 0 % of sequence untagged

FASTA header line: original designation

**Action**

RESET
SUBMIT

**Filter by**

Sequence method:  

Project:  

Experiment:  

Minimum length:

At its simplest, press submit.

A table will be produced with download links. Clicking these will produce the contigs in FASTA format.

11  
13  
19

Minimum length:  ⓘ

Action

Clear List all RESET SUBMIT

Contigs with  $\geq 0\%$  sequence length untagged

id	isolate	contigs	matching contigs		non-matching contigs	
			count	download	count	download
1	A4/M1027	364	364		0	
2	120M	359	359		0	
7	7891	199	199		0	
10	6748	652	652		0	
11	129E	272	272		0	
13	139M	293	293		0	
19	S3131	173	173		0	
24	S4355	198	198		0	
30	14	1	1		0	
31	10	275	275		0	
34	20	213	213		0	
35	26	194	194		0	
52	243	229	229		0	
61	393	282	282		0	
64	254	251	251		0	
67	S5611	194	194		0	
82	11-004	258	258		0	
84	IAL2229	188	188		0	
90	CN100	236	236		0	

You can also download all the data in a tar file by clicking the ‘Batch download’ link.

11  
13  
19

Minimum length:  ⓘ

Action

Clear List all RESET SUBMIT

Contigs with  $\geq 0\%$  sequence length untagged

id	isolate	contigs	matching contigs		non-matching contigs	
			count	download	count	download
1	A4/M1027	364	364		0	
2	120M	359	359		0	
7	7891	199	199		0	
10	6748	652	652		0	
11	129E	272	272		0	
13	139M	293	293		0	
19	S3131	173	173		0	
24	S4355	198	198		0	
30	14	1	1		0	
31	10	275	275		0	
34	20	213	213		0	
35	26	194	194		0	
52	243	229	229		0	
61	393	282	282		0	
64	254	251	251		0	
67	S5611	194	194		0	
82	11-004	258	258		0	
84	IAL2229	188	188		0	
90	CN100	236	236		0	

### 15.1.1 Filtering by tagged status of contigs

You can also export contigs based on the percentage of the sequence that has been tagged. This is useful to find sequences to target for gene discovery.

In order to export contigs where at least half the sequence has been tagged (and also the remaining contigs in a separate file), select '50' in the dropdown box for %untagged.

**Options**

Identify contigs with  $\geq$   % of sequence untagged

FASTA header line:  ⓘ

The resulting table has two download links for each isolate, one for contigs matching the condition, and one for contigs that don't match.

11  
13  
19

Minimum length:

Action

[Clear](#) [List all](#) [RESET](#) [SUBMIT](#)

Contigs with  $\geq$ 50% sequence length untagged

id	isolate	contigs	matching contigs		non-matching contigs	
			count	download	count	download
1	A4/M1027	364	141		223	
2	120M	359	60		299	
7	7891	199	38		161	
10	6748	652	377		275	
11	129E	272	55		217	
13	139M	293	164		129	
19	S3131	173	35		138	
24	S4355	198	45		153	
30	14	1	0		1	
31	10	275	52		223	
34	20	215	34		179	
35	26	194	32		162	
52	243	229	45		184	
61	393	282	49		233	
64	254	251	47		204	
67	S5611	194	42		152	
82	11-004	258	37		221	
84	IAL2229	188	30		158	
90	CN100	236	46		190	

## 15.2 Isolate record export

You can export the entire isolate recordset by expanding the Export section on the main contents page and clicking the ‘Export dataset’ link.

Alternatively, you can export the recordsets of isolates returned from a database query by clicking the ‘Dataset’ button in the Export list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

16	2		Germany	1999	carrier	Neisseria meningitidis	B	854	ST-18 complex			
17	3		Germany	1999	carrier	Neisseria meningitidis	W	174	ST-174 complex			
18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Select the isolate ids (if they have not been pre-selected from your query), isolate fields and schemes to include.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Export dataset

Help ⓘ

## Export dataset

This script will export the dataset in tab-delimited text and Excel formats. Select which fields you would like included. Select loci either from the locus list or by selecting one or more schemes to include all loci (and/or fields) from a scheme.

**Isolates**

1	
2	
3	
4	
5	
6	
7	

Clear List all

**Provenance fields**

id isolate aliases country continent region year date sampled

All None

**Secondary metadata**

Bexsero reactivity Bexsero notes Trumenba reactivity Trumenba notes

All None

**Composite fields** ⓘ

strain designation

**References**

☐ references  
☒ PubMed id  
☐ Full citation

**Loci**

16S\_rDNA  
 16S\_rRNA (SSU\_rRNA)  
 23S\_rRNA  
 abcZ  
 abcZ (NEIS1015)  
 aceF (NEIS1279)  
 ...

All None

**Schemes**

Metagenomics  
 N. gonorrhoeae AMR  
 Pilin  
 Plasmids  
 Typing  
 MLST  
 Finotyping antigens  
 16S  
 Antigen genes

☒ Include all fields from selected schemes  
☒ Include all loci from selected schemes

**Classification schemes**

Nm\_cgc\_200  
 Nm\_cgc\_100  
 Nm\_cgc\_50  
 Nm\_cgc\_25  
 Ng\_cgc\_500  
 Ng\_cgc\_400  
 Ng\_cgc\_300  
 Ng\_cgc\_200

All None

**Options**

☐ Indicate sequence status if no allele defined ⓘ  
☐ Include locus common names  
☒ Export allele numbers  
☐ Use one row per field  
☐ Include isolate field in row (used only with 'one row' option)  
☐ Export full allele designation record (used only with 'one row' option)

**Molecular weights**

☐ Export protein molecular weights  
☒ GTG/TTG at start codes for methionine

**Action**

SUBMIT

Click Submit.

You can then download the data in tab-delimited text or Excel formats.

BIGSdb



Home > Organisms > Neisseria spp. > Neisseria isolates > Plugins > Export dataset

Help ⓘ

## Export dataset

Please wait for processing to finish (do not refresh page).

Output files being generated ..... done

Export jobs for larger datasets will be sent to the job queue.

### 15.2.1 Advanced options

Options

- ☐ Indicate sequence status if no allele defined ⓘ
- ☐ Include locus common names
- ☒ Export allele numbers
- ☐ Use one row per field
- ☐ Include isolate field in row (used only with 'one row' option)
- ☐ Export full allele designation record (used only with 'one row' option)

The options fieldset has the following options.

- Include locus common names - any common name for the locus is displayed in parentheses following the primary name.
- Export allele numbers - the allele designation is included for any locus included.
- Use one row per field - this is an alternative output format where instead of each locus and field having a separate column, each field is export on a separate row.
- Include isolate field in row - the name of the isolate is included as a separate column when exporting in 'one row per field' format.
- Export full allele designation record - export sender, curator and timestamp information as separate rows when exporting allele designation data.

### 15.2.2 Molecular weight calculation

The plugin can also calculate the predicted molecular weight of the gene product of any allele designated in the dataset.

Molecular weights

- ☐ Export protein molecular weights
- ☒ GTG/TTG at start codes for methionine

Click the 'Export protein molecular weight' checkbox. Additional columns (or rows depending on the output format) will be created to include the molecular weight data.

## 15.3 Profile export

You can export the allelic profiles for any indexed scheme (those containing a primary key field) defined in the sequence definition database.

The profile export function can be accessed by expanding the 'Export' section and clicking the 'Profiles' link on the contents page.

BIGSdb
Home > Organisms > Organism > Neisseria typing

## Neisseria typing database

Query a sequence

Single sequence

Query a single sequence or whole genome assembly to identify allelic matches.

Batch sequences

Query multiple independent sequences in FASTA format to identify allelic matches.

Find alleles

By specific criteria

Find alleles by matching criteria (all loci together)

By locus

Select, analyse and download specific alleles from a single locus.

Search for allelic profiles

By specific criteria

Search, browse or enter list of profiles

By allelic profile

This can include partial matches to find related profiles.

In a batch

LOG IN
SUBMISSIONS
DOWNLOADS +
EXPORT -

Locus sequences
Profiles
Profile sequences

ANALYSIS +
CUSTOMISE +
INFORMATION +
ISOLATES

Alternatively, you can access this function by clicking the ‘Profiles’ button in the Export list at the bottom of a results table. Please note that the list of functions here may vary depending on the setup of the database.

14	4	1	15	7	8	11	1	ST-269 complex
15	13	3	16	1	3	11	9	ST-364 complex
16	15	9	9	13	8	19	15	ST-4240/6688 complex
17	8	3	13	1	11	12	4	
18	7	8	10	19	10	1	2	ST-18 complex
19	7	8	10	19	8	1	2	ST-18 complex
20	6	8	10	17	10	1	2	ST-18 complex
21	1	5	1	1	2	16	17	
22	11	5	18	8	11	24	21	ST-22 complex
23	10	5	18	9	11	9	17	ST-23 complex
24	2	5	2	7	15	20	5	ST-750 complex
25	6	5	2	12	6	13	14	

<< < 1 2 3 4 5 6 > >>

### Analysis tools

Export: Profiles Sequences

This will take you to a form with a list box in which the identifiers of the profile definitions you wish to include can be entered. Following a query, these values will be pre-entered. If the box is left empty then all profiles will be included. You can optionally include provenance information (sender, curator and datestamps) by selecting the appropriate checkboxes.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Plugins > Profiles

Help

## Export allelic profiles - Neisseria typing

Schemes

Please select the scheme you would like to query:

MLST [Select](#)

This script will export allelic profiles in tab-delimited text and Excel formats.

Select STs

Paste in list of ids to include, start a new line for each. Leave blank to include all ids.

1  
2  
3  
4  
5

Provenance

☐ Include sender details

☐ Include curator details

☐ Include timestamps

Action

[SUBMIT](#)

Click submit.

The export job will be submitted to the job queue.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Job status viewer

## Job status viewer

Status

Job id: BIGSdb\_022243\_1596292027\_18737

Submit time: 2020-08-01 14:27:07

Status: finished

Start time: 2020-08-01 14:27:21

Progress: 100%

Stop time: 2020-08-01 14:27:33

Total time: 12 seconds

Output

Files

Profiles - Tab-delimited text (text)

Profiles - Excel format (Excel)

Tar file containing all output files

Please note that job results will remain on the server for 7 days.

The profiles will be exported in tab-delimited text and Excel formats.

## 15.4 Sequence export

You can export the sequences for any set of loci designated in isolate records, or belonging to scheme profiles in the sequence definition database.

The sequence export function can be accessed by expanding the ‘Export’ section and clicking the ‘Sequences’ link on the contents page of isolate databases, or the ‘Profile sequences’ link on the contents page of sequence definition databases.

The screenshot shows the BIGSdb interface for the 'Neisseria isolates database'. On the left, there's a 'Query database' section with search options. On the right, a sidebar contains navigation links: LOG IN, SUBMISSIONS, PROJECTS, EXPORT, ANALYSIS, CUSTOMISE, INFORMATION, and TYPING. The 'EXPORT' link is expanded, showing 'Export dataset' with options for 'Contigs' and 'Sequences' (highlighted with a red box).

Alternatively, you can access this function by clicking the ‘Sequences’ button in the Export list at the bottom of the results table. Please note that the list of functions here may vary depending on the setup of the database.

18	4		Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex			
19	S3131	B213; NIBSC_2813; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex	7	13-1	F1-5
20	5		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	Neisseria meningitidis	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	Neisseria meningitidis	E	60	ST-60 complex			
23	8		Germany	1999	carrier	Neisseria meningitidis	B	32	ST-32 complex			
24	S4355	B227; NIBSC_2806; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			



### Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs **Sequences**

Third party: GrapeTree iTOL PhyloViz Microreact

Select the isolate or profile records to analyse - these will be pre-selected if you accessed the plugin following a query. Select the loci to include either directly within the loci list and/or using the schemes tree.

This script will export allele sequences in Extended Multi-FASTA (XMFA) format suitable for loading into third-party applications, such as ClonalFrame. It will also produce concatenated FASTA files. Only DNA loci that have a corresponding database containing allele sequence identifiers, or DNA and peptide loci with genome sequences tagged, can be included. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme. If a sequence does not exist in the remote database, it will be replaced with gap characters.

Aligned output is limited to 200 records; total output (records x loci) is limited to 1,000,000 sequences.

Please be aware that if you select the alignment option it may take a long time to generate the output file.

**Select ids**

Paste in list of ids to include, start a new line for each. Leave blank to include all ids.

1  
2  
3  
4  
5

**Include in identifier**

isolate  
country  
region  
year  
date sampled  
isoyear sampled  
week sampled  
date received  
non culture

**Loci**

16S\_rDNA  
16S\_rRNA (SSU\_rRNA)  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
...

All None Paste list

**Schemes**

Plasmids  
Typing  
MLST  
Finotyping antigens  
16S  
Antigen genes  
Bexsero Antigen Sequence  
Human-restricted Neisseria

**Options**

If both allele designations and tagged sequences exist for a locus, choose how you want these handled: ⓘ

☒ Use sequences tagged from the bin  
☐ Use allele sequence retrieved from external database

☒ Do not include sequences with problem flagged (defined alleles will still be used)  
☒ Do not include incomplete sequences

Include: 0 bp flanking sequence ⓘ

☐ Align sequences  
Aligner: MAFFT  
☐ Translate sequences

**Action**

SUBMIT

Click submit. The job will be submitted to the job queue.

Sequences will be export in XMFA and FASTA file formats.

## BIGSdb

[Home](#) > [Organisms](#) > [Neisseria spp.](#) > [Neisseria isolates](#) > [Job status viewer](#)

## Job status viewer

**Status**

Job id: BIGSdb\_029655\_1596295569\_17972

Submit time: 2020-08-01 15:26:09

Status: finished

Start time: 2020-08-01 15:26:13

Progress: 100%

Stop time: 2020-08-01 15:26:19

Total time: 6 seconds

**Output**

Files

XMFA output file (not aligned)

Concatenated FASTA (not aligned)

Tar file containing all output files

Please note that job results will remain on the server for 7 days.

### 15.4.1 Aligning sequences

By default, sequences will be exported unaligned - this is very quick since no processing is required. You can choose to align the sequences by checking the 'Align sequences' checkbox.

#### Options

If both allele designations and tagged sequences exist for a locus, choose how you want these handled: ⓘ

☒ Use sequences tagged from the bin  
☐ Use allele sequence retrieved from external database

☒ Do not include sequences with problem flagged (defined alleles will still be used)  
☒ Do not include incomplete sequences

Include  bp flanking sequence ⓘ

☒ Align sequences  
Aligner:

☐ Translate sequences  
☐ Concatenate in frame

You can also choose to use MUSCLE or MAFFT as the aligner. MAFFT is the default choice and is usually much quicker than MUSCLE. Both produce comparable results.

## SUBMITTING DATA USING THE SUBMISSION SYSTEM

The automated submission system allows users to submit data (new alleles, profiles, or isolates) to the database curators for assignment and upload to the database. The submission system is enabled on a per-database basis so will not always be available.

If the system is enabled, new submissions can be made by clicking the ‘Manage submissions’ link on the database front page.

The screenshot shows the BIGSdb interface for the *Neisseria* typing database. At the top, there is a dark blue header with the text "BIGSdb". Below it is a light blue breadcrumb trail: "Home > Organisms > Organism > Neisseria typing". The main content area is titled "*Neisseria* typing database". It features a grid of search and query options under three main categories: "Query a sequence", "Find alleles", and "Search for allelic profiles". The "SUBMISSIONS" link is highlighted with a red border in the right-hand sidebar. Other links in the sidebar include "LOG IN", "DOWNLOADS", "EXPORT", "ANALYSIS", "CUSTOMISE", "INFORMATION", and "ISOLATES".

**BIGSdb**

Home > Organisms > Organism > Neisseria typing

*Neisseria* typing database

**Query a sequence**

- Sequence query**  
Query a single sequence or whole genome assembly to identify allelic matches.
- Batch sequence query**  
Query multiple independent sequences in FASTA format to identify allelic matches.

**Find alleles**

- Sequence attribute search**  
Find alleles by matching criteria (all loci together)
- Locus-specific sequence attribute search**  
Select, analyse and download specific alleles from a single locus.

**Search for allelic profiles**

- Allelic profile query**  
Search, browse or enter list of profiles
- Search by combinations of alleles**  
This can include partial matches to find related profiles.
- Batch profile query**  
Lookup multiple allelic profiles together.

**LOG IN**

**SUBMISSIONS**

**DOWNLOADS** +

**EXPORT** +

**ANALYSIS** +

**CUSTOMISE** +

**INFORMATION** +

**ISOLATES**

### 16.1 Registering a user account

You must have an account for the appropriate database in order to use the submission system. On systems utilizing site-wide databases, such as PubMLST, this can be done automatically via the web. Other sites may require you to contact a curator to set this up.

## 16.2 Allele submission

New allele data can only be submitted from within the appropriate sequence definition database. Submissions consist of one or more new allele sequences for a single locus. You will need to create separate submissions for each locus - this is because different loci may be handled by different curators.

### 16.2.1 Start

Click the ‘alleles’ link under submission type on the submission management page.

### 16.2.2 Select the submission locus

Select the locus from the locus list box:

The locus list may be very long in some databases. It may be possible to filter these to those belonging to specific schemes. If the scheme tree is shown, select the appropriate scheme, e.g. ‘MLST’ and click ‘Filter’.

**BIGSdb**

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

**Manage submissions**

**Submit new alleles**

You need to make a separate submission for each locus for which you have new alleles - this is because different loci may have different curators. You can submit any number of new sequences for a single locus as one submission. Sequences should be trimmed to the correct start/end sites for the selected locus.

**Filter loci by scheme**

- All loci
  - Strain typing
  - Capsule
  - Genetic Information Processing
  - Genomic islands
  - Lineage Schemes
  - Metabolism
  - N. gonorrhoeae AMR
  - Plasmids
  - Typing**
    - MLST**
    - Finotyping antigens
    - rplF species
    - Antigen genes
    - Bexsero Antigen Sequence Typing (BAST)
    - Human-restricted Neisseria cgMLST v1.0
    - N. gonorrhoeae cgMLST v1.0
    - N. meningitidis cgMLST v1.0
    - NG MAST
    - OMV peptide typing
    - eMLST (20 locus partial genes)
    - eMLST (20 locus whole genes)
    - Other schemes
    - Loci not in schemes

**Select locus**

**Filter**

- 16S\_rDNA
- 23S\_rDNA
- abcZ
- abcZ (NEIS1015)
- aceF (NEIS1279)
- ackA2 (NEIS1727)
- acnA (NEIS1729)
- acnB (NEIS1492)

**Sequence details**

technology: Illumina

read length: 200-299

coverage: 20-49x

assembly: de novo

assembly software: Velvet

☐ Sequence length outside usual range ⓘ

**FASTA or single sequence**

**Action**

**SUBMIT**

The locus list is now constrained making selection easier.

**BIGSdb**

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

**Manage submissions**

**Submit new alleles**

You need to make a separate submission for each locus for which you have new alleles - this is because different loci may have different curators. You can submit any number of new sequences for a single locus as one submission. Sequences should be trimmed to the correct start/end sites for the selected locus.

**Filter loci by scheme**

- All loci
  - Strain typing
  - Capsule
  - Genetic Information Processing
  - Genomic islands
  - Lineage Schemes
  - Metabolism
  - N. gonorrhoeae AMR
  - Plasmids
  - Typing**
    - MLST**
    - Finotyping antigens
    - rplF species
    - Antigen genes
    - Bexsero Antigen Sequence Typing (BAST)
    - Human-restricted Neisseria cgMLST v1.0
    - N. gonorrhoeae cgMLST v1.0
    - N. meningitidis cgMLST v1.0
    - NG MAST
    - OMV peptide typing

**Select locus**

**Filter**

- abcZ
- adk
- aroE
- fumC
- gdh
- pdhC
- pgm

**Sequence details**

technology: Illumina

read length: 200-299

coverage: 20-49x

assembly: de novo

assembly software: Velvet

☐ Sequence length outside usual range ⓘ

**FASTA or single sequence**

**Action**

**SUBMIT**

### 16.2.3 Enter details of sequencing method

There are a number of fields that must be filled in so that the curator knows how the sequence was obtained:

- technology - the sequencing platform used, allowed values are:
  - 454
  - Illumina
  - Ion Torrent
  - PacBio
  - Oxford Nanopore
  - Sanger
  - Solexa
  - SOLiD
  - other
  - unknown
- read length - this is the length of sequencing reads. This is a required field for Illumina data, and not relevant to Sanger sequencing. Allowed values are:
  - <100
  - 100-199
  - 200-299
  - 300-499
  - >500
- coverage - the mean number of reads covering each nucleotide position of the sequence. This is not relevant to Sanger sequencing. Allowed values are:
  - <20x
  - 20-49x
  - 50-99x
  - >100x
- assembly - the means of generating the submitted sequence from the sequencing reads. Allowed values are:
  - de novo
  - mapped
- assembly software - this is a free text field where you should enter the name of the software used to generate the submitted sequence.

## 16.2.4 Paste in sequence(s)

Paste in the new variant sequences to the box. This can either be a stand- alone sequence or multiple sequences in FASTA format. The sequences must be trimmed to the start and end points of the loci - check existing allele definitions if in doubt. The submission is likely to be rejected if sequences are not trimmed. Click submit.

BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Submissions](#) > [New submission](#)

### Manage submissions

#### Submit new alleles

You need to make a separate submission for each locus for which you have new alleles - this is because different loci may have different curators. You can submit any number of new sequences for a single locus as one submission. Sequences should be trimmed to the correct start/end sites for the selected locus.

**Filter loci by scheme**

- All loci
- Strain typing
- Capsule
- Genetic Information Processing
- Genomic islands
- Lineage Schemes
- Metabolism
- N. gonorrhoeae AMR
- Plasmids
- Typing
  - MLST**
  - Finotyping antigens
  - rplF species
  - Antigen genes
  - Bexsero Antigen Sequence Typing (BAST)
  - Human-restricted Neisseria cgMLST v1.0
  - N. gonorrhoeae cgMLST v1.0
  - N. meningitidis cgMLST v1.0

**Select locus**
**Sequence details**

**Filter**

abcZ  
adk  
aroE  
fumC  
gdh  
pdhC  
pgm

technology: illumina  
 read length: 200-299  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Velvet

☐ Sequence length outside usual range ?

**FASTA or single sequence**
**Action**

```
>Nm322
TTTGATACCGTTGCCGAAGGTTTAGGCGAAATCCGCGATTATTGCGCCGTTATCATCAT
GTTAGCCATGAGTTGAAATGTTTCGAGTGAGGCTTTGTTGAAAGAGCTCAACGAATTG
CAACTTGAAATCGAAGCGAAGGACGGCTGGAACTGGATGCGGCAGTCAAGCAAACTTTG
GGGGAACCGGTTTGGCGGAAACGAAAAATCGGCAACCTCTCCGGCGGTGAGAAAAAG
CGCGTCGCTTTGGCGCAGGCTTGGGTGCAAAAGCCGACGATTGCTGCTAGACGAGCCG
ACCAACCATTTGGATATCGACGCGATTATTGGCTGGAATACTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCACGACGCCGCTTTTGGACAATATGCCACGCGGATT
```

SUBMIT

The system will perform some basic checks on the submitted sequences. If any of the sequences have been defined previously they must be removed from the submission before you can proceed. Curators do not want to waste their time dealing with previously defined sequences.

BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Submissions](#) > [New submission](#)

### Manage submissions

✗

**Error:**  
 Sequence 'Nm324' has already been defined as abcZ-3.

#### Submit new alleles

You need to make a separate submission for each locus for which you have new alleles - this is because different loci may have different curators. You can submit any number of new sequences for a single locus as one submission. Sequences should be trimmed to the correct start/end sites for the selected locus.

**Filter loci by scheme**

- All loci
- Strain typing
- Capsule
- Genetic Information Processing
- Genomic islands
- Lineage Schemes
- Metabolism
- N. gonorrhoeae AMR
- Plasmids
- Typing
  - Other schemes
  - Loc not in schemes

**Select locus**
**Sequence details**

**Filter**

'16S\_rDNA  
23S\_rRNA  
abcZ  
abcZ (NEIS1015)  
aceF (NEIS1279)  
ackA2 (NEIS1727)  
acnA (NEIS1729)  
acnB (NEIS1492)

technology: illumina  
 read length: 100-199  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Spades

☐ Sequence length outside usual range ?

**FASTA or single sequence**
**Action**

```
>Nm322
TTTGATACCGTTGCCGAAGGTTTAGGCGAAATCCGCGATTATTGCGCCGTTATCATCAT
GTTAGCCATGAGTTGAAATGTTTCGAGTGAGGCTTTGTTGAAAGAGCTCAACGAATTG
CAACTTGAAATCGAAGCGAAGGACGGCTGGAACTGGATGCGGCAGTCAAGCAAACTTTG
GGGGAACCGGTTTGGCGGAAACGAAAAATCGGCAACCTCTCCGGCGGTGAGAAAAAG
CGCGTCGCTTTGGCGCAGGCTTGGGTGCAAAAGCCGACGATTGCTGCTAGACGAGCCG
ACCAACCATTTGGATATCGACGCGATTATTGGCTGGAATACTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCACGACGCCGCTTTTGGACAATATGCCACGCGGATT
```

SUBMIT

Assuming the preliminary checks have passed you will then be able to add additional information to your submission.

16.2. Allele submission

395

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

Help

## Manage submissions

### Supporting files

Please note that if you are submitting alleles determined by Sanger sequencing that you must upload both forward and reverse trace files. Your submission will be rejected if you don't. Please do not pack or compress your files (zip, rar etc).

[Abort submission](#)

Submission: BIGSdb\_20200802122845\_002379\_40069

[Supporting files](#)

Please upload any supporting files required for curation. Ensure that these are named unambiguously or add an explanatory note so that they can be linked to the appropriate submission item. Individual filesize is limited to 64 MB. You can upload up to 64 MB in one go (the upload may fail if you try to do more than this - just try again with fewer files at a time if it does), although you can upload multiple times so that the total size of the submission can be larger.

Drop files here or click to upload.

### Sequences

You are submitting the following abcZ sequences: [Download](#)

Identifier	Length	Sequence	Status	Query	Assigned allele
Nm322	433	TTTGATACCGTTGCCGAAGG ... GCGGATTGTCGAACTCGATC	pending	<a href="#">Q</a>	
Nm323	433	TTTGATACTGTTGCCGAAGG ... GCGGATTGTCGAACTCGATC	pending	<a href="#">Q</a>	

### Sequence details

technology: Illumina  
 read length: 200-299  
 coverage: 20-49x  
 assembly: de novo  
 assembly software: Velvet

☐ Sequence length outside usual range ⓘ

[E-mail](#) [Action](#)

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

[Messages](#)

Message: [Append](#)

[FINALIZE SUBMISSION!](#)

### 16.2.5 Add message to curator

If you wish to enter a message to the curator, enter this in the messages box and click 'Append'. This is not normally necessary for routine submissions.

**E-mail**

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

**Messages**

Thanks !

Message: Append

The message will be attached. A curator may respond to the message and attach their own, with the full conversation becoming part of the submission record.

**E-mail**

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

**Messages**

Timestamp	User	Message
2020-08-02 11:30:58+00	Keith Jolley	Thanks!

Message: Append

### 16.2.6 Add supporting files

Some submissions will require the attachment of supporting files. This will depend on the policies of the individual databases. Sequences determined by Sanger sequencing should normally have forward and reverse trace files attached.


Files can be added to the submission by dragging and dropping in to the large dotted area in the ‘Supporting files’ section. Alternatively, you can click this area and select files from the local file system.



**Supporting files**

Please upload any supporting files required for curation. Ensure that these are named unambiguously or add an explanatory note so that they can be linked to the appropriate submission item. Individual filesize is limited to 64 MB. You can upload up to 64 MB in one go (the upload may fail if you try to do more than this - just try again with fewer files at a time if it does), although you can upload multiple times so that the total size of the submission can be larger.


Drop files here or click to upload.

**Sequences**

You are submitting the following abcZ sequences: [Download](#) 

Identifier	Length	Sequence	Status	Query	Assigned allele
Nm322	433	TTTGATACGGTTGCCGAAGG ... GCGGATTGTGCAACTCGATC	pending		
Nm323	433	TTTGATACTGTTGCCGAAGG ... GCGGATTGTGCAACTCGATC	pending		

**Sequence details**

technology:   
 read length:   
 coverage:   
 assembly:   
 assembly software:   
☐ Sequence length outside usual range 

The files will be uploaded and shown in a table.

**Supporting files**

Please upload any supporting files required for curation. Ensure that these are named unambiguously or add an explanatory note so that they can be linked to the appropriate submission item. Individual filesize is limited to 64 MB. You can upload up to 64 MB in one go (the upload may fail if you try to do more than this - just try again with fewer files at a time if it does), although you can upload multiple times so that the total size of the submission can be larger.

Drop files here or click to upload.

**Uploaded files**

Filename	Size	Delete
NM322_abcZ_R_ab1	252 KB	<input type="checkbox"/>
NM323_abcZ_F_ab1	269.6 KB	<input type="checkbox"/>
Nm322_abcZ_F_ab1	281.8 KB	<input type="checkbox"/>
NM323_abcZ_R_ab1	258.7 KB	<input type="checkbox"/>

[Delete selected files](#)


Files can be removed from the submission by checking the appropriate 'Delete' box and clicking 'Delete selected files'.



## 16.2.7 Finalize submission

Make sure the 'E-mail submission updates' box is checked if you wish to receive E-mail notification of the result of your submission. This setting is remembered between submissions.


Click 'Finalize submission!'.

**Sequences**

You are submitting the following abcZ sequences: [Download](#) 

Identifier	Length	Sequence	Status	Query	Assigned allele
Nm322	433	TTTGATACGGTTGCCGAAGG ... GCGGATTGTGCAACTCGATC	pending		
Nm323	433	TTTGATACTGTTGCCGAAGG ... GCGGATTGTGCAACTCGATC	pending		

**Sequence details**

technology:   
 read length:   
 coverage:   
 assembly:   
 assembly software:   
☐ Sequence length outside usual range 

**E-mail**

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

**Action**

**FINALIZE SUBMISSION!**

**Messages**

Timestamp	User	Message
2020-08-02 11:30:58+00	Keith Jolley	Thanks!

Message:  [Append](#)

Your submission will then be listed under ‘Pending submissions’ on your submission page.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- alleles
- MLST profiles
- Bexsero Antigen Sequence Typing (BAST) profiles
- Conjugative Plasmid profiles
- Cryptic Plasmid profiles
- NG MAST profiles
- beta lactamase plasmid profiles
- isolates (without assembly files) [Link to isolate database](#)
- genomes (isolate records with assembly files) [Link to isolate database](#)

### Pending submissions

You have submitted the following submissions that are pending curation:

Submission id	Submitted	Updated	Type	Details
BIGSdb_20200802122845_002379_40069	2020-08-02	2020-08-02	alleles	2 abcZ sequences

## 16.3 Profile submission

### 16.3.1 Start

**Note:** Most MLST databases on PubMLST.org require you to submit an isolate record for each new ST that you wish to be defined. In these cases, you should add the isolate name to the id field of your profile submission and make a corresponding *isolate submission* containing the allelic profile.

Click the appropriate profiles link under submission type on the submission management page.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- alleles
- MLST profiles**
- Bexsero Antigen Sequence Typing (BAST) profiles
- Conjugative Plasmid profiles
- Cryptic Plasmid profiles
- NG MAST profiles
- beta lactamase plasmid profiles
- isolates (without assembly files) [Link to isolate database](#)
- genomes (isolate records with assembly files) [Link to isolate database](#)

Download the Excel submission template.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

## Manage submissions

### Submit new MLST profiles

Paste in your profiles for assignment using the template available below.

#### Templates

Please paste in tab-delimited text (include a field header line)

Action

**SUBMIT**

### 16.3.2 Paste in profile(s)

Fill in the template. The first column 'id' can be used to enter an identifier that is meaningful to you - it is used to report back the results but is not uploaded to the database. It can be left blank, or the entire column can be removed - in which case individual profiles will be identified by row number.

Copy and paste the entire contents of the submission worksheet. Click submit.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

## Manage submissions

### Submit new MLST profiles

Paste in your profiles for assignment using the template available below.

#### Templates

Please paste in tab-delimited text (include a field header line)

id	abcZ	adk	aroE	fumC	gdh	pdhC	pgm
8	5	32	2	6	43	32	
5	7	3	6	33	12	2	
3	6	4	3	8	4	6	
9	6	9	9	9	6	9	

Action

**SUBMIT**

Some basic checks will be performed. These include whether the profile has already been assigned and whether each allele identifier exists. The submission cannot proceed if the checks fail.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

## Manage submissions

**Error:**  
Row 4: Profile has already been defined as ST-44.

### Submit new MLST profiles

Paste in your profiles for assignment using the template available below.

#### Templates

Please paste in tab-delimited text (include a field header line)

id	abcZ	adk	aroE	fumC	gdh	pdhC	pgm
8	5	32	2	6	43	32	
5	7	3	6	33	12	2	
3	6	4	3	8	4	6	
9	6	9	9	9	6	9	

Action

**SUBMIT**

Provided the checks pass, you will then be able to add additional information to your submission. New profile submissions usually don't require supporting files directly in the submission. You generally will need to make a corresponding *submission to the isolate database* though.

### 16.3.3 Add message to curator

If you wish to enter a message to the curator, enter this in the messages box and click 'Append'.

BIGSdb

Home > Organisms > Organism > Neisseria typing > Submissions > New submission

## Manage submissions

Isolate submission required

Please note that you must make a corresponding submission *to the isolate database* - this is not the same as attaching an isolate template file to this submission. Please see the [submission guide](#) for details. Every newly defined ST should have a representative isolate record in the isolate database. Your submission will be rejected if you do not do this.

[Abort submission](#)

Submission: BIGSdb\_20200802163741\_003907\_56760

Supporting files

Please upload any supporting files required for curation. Ensure that these are named unambiguously or add an explanatory note so that they can be linked to the appropriate submission item. Individual filesize is limited to 64 MB. You can upload up to 64 MB in one go (the upload may fail if you try to do more than this - just try again with fewer files at a time if it does), although you can upload multiple times so that the total size of the submission can be larger.

Drop files here or click to upload.

Profiles

You are submitting the following MLST profiles: [Download](#)

Identifier	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	Status	Query	Assigned ST
Row 1	8	5	32	2	6	43	32	pending		
Row 2	5	7	3	6	33	12	2	pending		
Row 3	3	6	4	3	8	4	6	pending		

E-mail

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

Action

**FINALIZE SUBMISSION!**

Messages

Corresponding isolate submission has been made. [BIGSdb\\_20200802163741\\_003123\\_46421](#)

Message: [Append](#)

The message will be attached. A curator may respond to the message and attach their own, with the full conversation becoming part of the submission record.

Messages

Timestamp	User	Message
2020-08-02 15:40:36+00	Keith Jolley	Corresponding isolate submission has been made. <a href="#">BIGSdb_20200802163741_003123_46421</a>

Message: [Append](#)

### 16.3.4 Finalize submission

Make sure the ‘E-mail submission updates’ box is checked if you wish to receive E-mail notification of the result of your submission. This setting is remembered between sessions.

Click ‘Finalize submission!’.

E-mail	Action
Updates will be sent to keith.jolley@zoo.ox.ac.uk. <input checked="" type="checkbox"/> E-mail submission updates	<b>FINALIZE SUBMISSION!</b>

Your submission will then be listed under ‘Pending submissions’ on your submission page.

BIGSdb

[Home](#) > [Organisms](#) > [Organism](#) > [Neisseria typing](#) > [Submissions](#)

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- alleles
- MLST profiles
- Bexsero Antigen Sequence Typing (BAST) profiles
- Conjugative Plasmid profiles
- Cryptic Plasmid profiles
- NG MAST profiles
- beta lactamase plasmid profiles
- isolates (without assembly files) [Link to isolate database](#)
- genomes (isolate records with assembly files) [Link to isolate database](#)

### Pending submissions

You have submitted the following submissions that are pending curation:

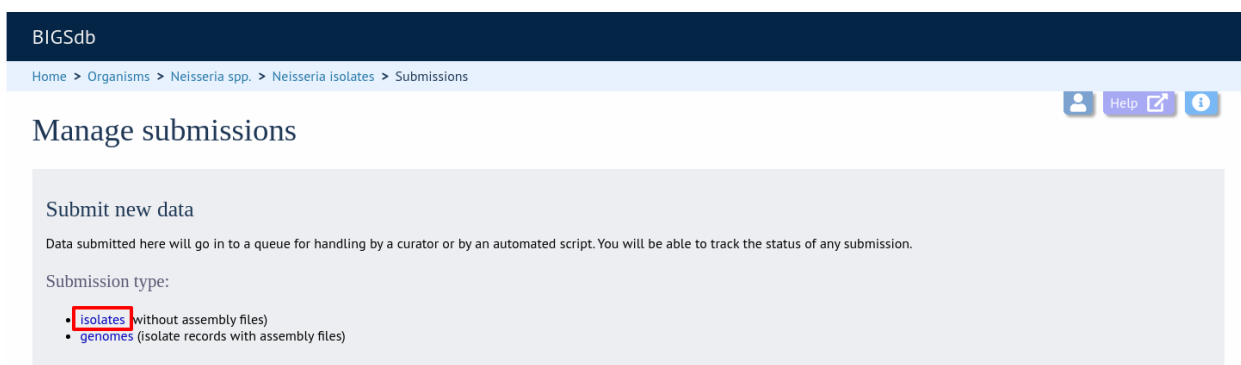
Submission Id	Submitted	Updated	Type	Details
BIGSdb_20200802163741_003907_56760	2020-08-02	2020-08-02	profiles	3 MLST profiles

## 16.4 Isolate submission

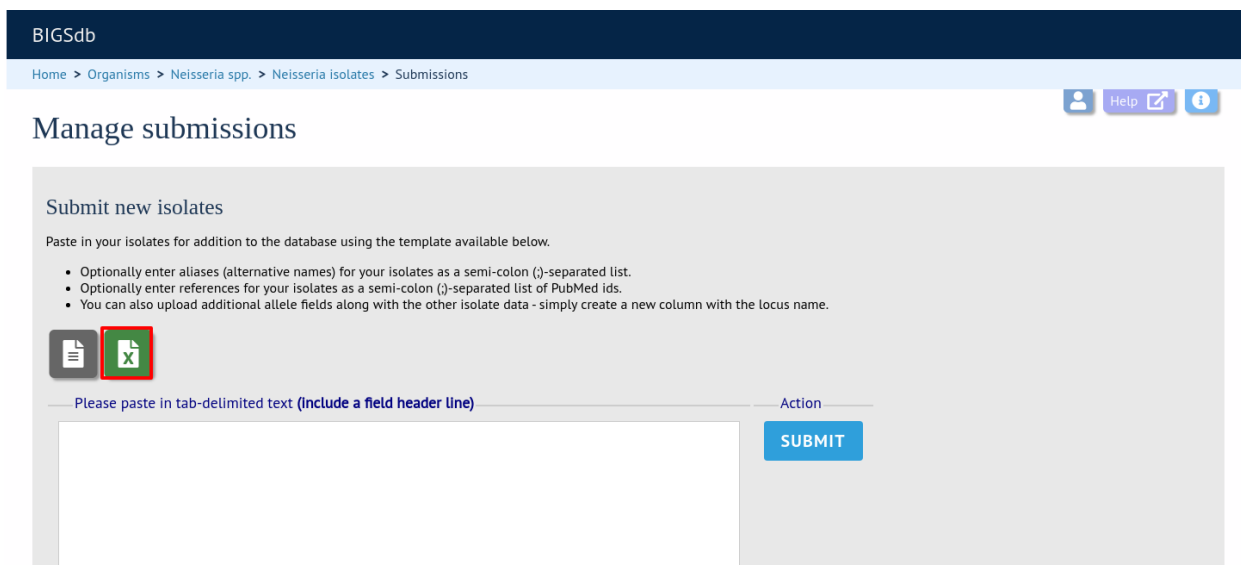
New isolate data can only be submitted from within the appropriate isolate database. You may be required to submit isolate data if you would like to get a new MLST sequence type defined, but this depends on individual database policy.

### 16.4.1 Start

Click the ‘isolates’ link under submission type on the submission management page.



Download the Excel submission template.



### 16.4.2 Paste in isolate data

Fill in the template. Some fields are required and cannot be left blank. Check the ‘Description of database fields’ link on the database contents page to see a description of the fields and allowed values where these have been defined. Where allowed values have been set, the template will have dropdown boxes (although these require newer versions of Excel to work).

Some databases may have hundreds of loci defined, and most will not have a column in the template. You can add new columns for any loci that have been defined and for which you would like to include allelic information for. These locus names must be the primary locus identifier. A list of loci can be found in the ‘allowed\_loci’ tab of the Excel submission template.



### 16.4.3 Add message to curator

If you wish to enter a message to the curator, enter this in the messages box and click 'Append'.

BIGSdb

Home > Organisms > *Neisseria* spp. > *Neisseria* isolates > Submissions

Manage submissions

New MLST profiles?

If your isolate record contains a new combination of MLST alleles, please also make a new profile submission to the sequence database. Please see the [submission guide](#) for details. This ensures that your STs will be assigned and that you get notified of these assignments.

Abort submission

Submission: BIGSdb\_20200802165311\_014297\_25699

Isolates

You are submitting the following isolates: [Download](#)

Isolate	country	year	disease	source	species	serogroup	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	PorA_VR1	PorA_VR2	FetA_VR1	ST (MLST)
UK325	UK	2020	meningitis and septicaemia	blood	<i>Neisseria meningitidis</i>	C	2	3	4	3	8	4	6	5	2	F1-5	11
UK326	UK	2020	septicaemia	blood	<i>Neisseria meningitidis</i>	W	2	3	4	3	18	4	6	5-1	2	F1-5	-

Messages

I think UK326 has a new MLST profile. I will also submit a new profile submission to the sequence definition database for this.

Message: [Append](#)

E-mail

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

Action

[FINALIZE SUBMISSION!](#)

The message will be attached. A curator may respond to the message and attach their own, with the full conversation becoming part of the submission record.

Messages

Timestamp	User	Message
2020-08-02 15:54:39+00	Keith Jolley	I think UK326 has a new MLST profile. I will also submit a new profile submission to the sequence definition database for this.

Message: [Append](#)

### 16.4.4 Finalize submission

Make sure the 'E-mail submission updates' box is checked if you wish to receive E-mail notification of the result of your submission. This setting is remembered between sessions.

Click 'Finalize submission!'.

E-mail

Updates will be sent to keith.jolley@zoo.ox.ac.uk.

☒ E-mail submission updates

Action

[FINALIZE SUBMISSION!](#)

Your submission will then be listed under 'Pending submissions' on your submission page.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions

Help

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- isolates (without assembly files)
- genomes (isolate records with assembly files)

### Pending submissions

You have submitted the following submissions that are pending curation:

Submission id	Submitted	Updated	Type	Details
BIGSdb_20200802165311_014297_25699	2020-08-02	2020-08-02	isolates	2 isolates

## 16.5 Genome submission

Submitting genomes uses the same process as standard *isolate submission*. The only difference is that there are a couple of extra required fields in the submission table:

- assembly\_filename - this is the name of the FASTA file containing the assembly contigs. This must be uploaded as a supporting file - you will not be able to finalize the submission until every isolate record has a matching contig file.
- sequence\_method - the sequencing technology used to generate the sequences. The allowed values are listed on the submission page.

Locus fields are not usually included in a genome submission as these can be readily extracted from the genome.

To start the submission, click the 'genomes' link under submission type on the submission management page.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions

Help

## Manage submissions

### Submit new data

Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- isolates (without assembly files)
- genomes (isolate records with assembly files)

Then follow the steps for *isolate submission*, uploading the contig files as supporting files.

**Note:** When including the filename for your FASTA file containing the genome assembly, please note that Windows will, by default, hide the file extension, e.g. .fas or .fasta. Even if it is hidden in the Windows interface, the file extension is part of the filename and must be included so that the uploaded file has exactly the same name as entered in the submission template. See <https://www.techadvisor.co.uk/how-to/windows/windows-10-file-extensions-3697651>

to see how to display hidden file extensions in Windows 10.

---

## 16.6 Removing submissions from your notification list

Once a submission has been closed by a curator, the results will be displayed in your ‘Manage submissions’ area. You can remove submissions once you have noted the result by clicking the ‘Remove’ link.

BIGSdb

Home > Organisms > Neisseria spp. > Neisseria isolates > Submissions

Help

### Manage submissions

#### Submit new data



Data submitted here will go in to a queue for handling by a curator or by an automated script. You will be able to track the status of any submission.

Submission type:

- isolates (without assembly files)
- genomes (isolate records with assembly files)

#### Recently closed submissions

You have submitted the following submissions which are now closed - they can be removed once you have recorded the results. Alternatively they will be removed automatically after 30 days.

Submission id	Submitted	Updated	Type	Details	Outcome	Remove
BIGSdb_20200802170054_019477_53719	2020-08-02	2020-08-02	isolates	2 isolates		

Alternatively, submissions will be removed automatically a specified period of time after closure. By default, this time is 90 days, but this can vary depending on the site configuration.

## RESTFUL APPLICATION PROGRAMMING INTERFACE (API)

The REST API allows third-party applications to retrieve data stored within BIGSdb databases or to send new submissions to database curators. To use the REST API, your application will make a HTTP request and parse the response. The response format is JSON (except for routes that request a FASTA or CSV file).

Access to protected resources, i.e. those requiring an account, can be accessed via the API using *OAuth authentication*.

### 17.1 Passing additional/optional parameters

If you are using a method called with GET, optional parameters can be passed as arguments to the query URL by adding a '?' followed by the first argument and its value (separated by a '='). Additional parameters are separated by a '&', e.g.

[https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates?page=2&page\\_size=100](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates?page=2&page_size=100)

Methods called with POST require their arguments to be sent as JSON within the post body.

### 17.2 Paging using request headers

Paging of results can be selected using query parameters as described above. In this case, methods that support paging will include a paging object in the JSON response. This will contain links to the next page, last page etc.

The API also supports paging using request headers. The following request headers are supported:

- X-OFFSET
- X-PER-PAGE

e.g.

```
curl -i -H "X-PER-PAGE:10" -H "X-OFFSET:0" https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates
```

If either of these headers are used, the paging object is no longer returned as part of the JSON response. The response will include the following headers:

- X-OFFSET
- X-PER-PAGE
- X-TOTAL-PAGES

## 17.3 Resources

- *GET /or/db* - List site resources
- *GET /db/{database}* - List database resources
- *GET /db/{database}/classification\_schemes* - List classification schemes
- *GET /db/{database}/classification\_schemes/{classification\_scheme\_id}* - Retrieve classification scheme information and groups
- *GET /db/{database}/classification\_schemes/{classification\_scheme\_id}/groups* - List groups defined for a classification scheme
- *GET /db/{database}/classification\_schemes/{classification\_scheme\_id}/groups/{group\_id}* - List isolates or profiles belonging to a classification scheme group
- *GET /db/{database}/loci* - List loci
- *GET /db/{database}/loci/{locus}* - Retrieve locus record
- *GET /db/{database}/loci/{locus}/alleles* - Retrieve list of alleles defined for a locus
- *GET /db/{database}/loci/{locus}/alleles\_fasta* - Download alleles in FASTA format
- *GET /db/{database}/loci/{locus}/alleles/{allele\_id}* - Retrieve full allele information
- *POST /db/{database}/loci/{locus}/sequence* - Query sequence to identify allele
- *POST /db/{database}/sequence* - Query sequence to identify allele without specifying locus
- *GET /db/{database}/sequences* - Get summary of defined sequences
- *GET /db/{database}/schemes* - List schemes
- *GET /db/{database}/schemes/{scheme\_id}* - Retrieve scheme information
- *GET /db/{database}/schemes/{scheme\_id}/loci* - Retrieve scheme loci
- *GET /db/{database}/schemes/{scheme\_id}/fields/{field}* - Retrieve information about scheme field
- *GET /db/{database}/schemes/{scheme\_id}/profiles* - List allelic profiles defined for scheme
- *GET /db/{database}/schemes/{scheme\_id}/profiles\_csv* - Download allelic profiles in CSV (tab-delimited) format
- *GET /db/{database}/schemes/{scheme\_id}/profiles/{profile\_id}* - Retrieve allelic profile record
- *POST /db/{database}/schemes/{scheme\_id}/sequence* - Query sequence to extract allele designations/fields for a scheme
- *POST /db/{database}/schemes/{scheme\_id}/designations* - Query allelic profile to extract fields for a scheme
- *GET /db/{database}/isolates* - Retrieve list of isolate records
- *GET /db/{database}/genomes* - Retrieve list of isolate records that have genome assemblies
- *POST /db/{database}/isolates/search* - Search isolate database
- *GET /db/{database}/isolates/{isolate\_id}* - Retrieve isolate record
- *GET /db/{database}/isolates/{isolate\_id}/allele\_designations* - Retrieve list of allele designations
- *GET /db/{database}/isolates/{isolate\_id}/allele\_designations/{locus}* - Retrieve full allele designation record
- *GET /db/{database}/isolates/{isolate\_id}/allele\_ids* - Retrieve allele identifiers

- *GET /db/{database}/isolates/{isolate\_id}/schemes/{scheme\_id}/allele\_designations* - Retrieve scheme allele designation records
- *GET /db/{database}/isolates/{isolate\_id}/schemes/{scheme\_id}/allele\_ids* - Retrieve list of scheme allele identifiers
- *GET /db/{database}/isolates/{isolate\_id}/contigs* - Retrieve list of contigs
- *GET /db/{database}/isolates/{isolate\_id}/contigs\_fasta* - Download contigs in FASTA format
- *GET /db/{database}/isolates/{isolate\_id}/history* - Retrieve isolate update history
- *GET /db/{database}/contigs/{contig\_id}* - Retrieve contig record
- *GET /db/{database}/fields* - Retrieve list of isolate provenance field descriptions
- *GET /db/{database}/fields/{field}* - Retrieve values set for a provenance field
- *GET /db/{database}/users/{user\_id}* - Retrieve user information
- *GET /db/{database}/curators* - Retrieve list of curators of the database
- *GET /db/{database}/projects* - Retrieve list of projects
- *GET /db/{database}/projects/{project\_id}* - Retrieve project information
- *GET /db/{database}/projects/{project\_id}/isolates* - Retrieve list of isolates belonging to a project
- *GET /db/{database}/submissions* - Retrieve list of submissions
- *POST /db/{database}/submissions* - Create new submission
- *GET /db/{database}/submissions/{submission\_id}* - Retrieve submission record
- *DELETE /db/{database}/submissions/{submission\_id}* - Delete submission record
- *GET /db/{database}/submissions/{submission\_id}/messages* - Retrieve submission correspondence
- *POST /db/{database}/submissions/{submission\_id}/messages* - Add submission correspondence
- *GET /db/{database}/submissions/{submission\_id}/files* - retrieve list of supporting files uploaded for submission
- *POST /db/{database}/submissions/{submission\_id}/files* - Upload submission supporting file
- *GET /db/{database}/submissions/{submission\_id}/files/{filename}* - Download submission supporting file
- *DELETE /db/{database}/submissions/{submission\_id}/files/{filename}* - Delete submission supporting file

### 17.3.1 GET / or /db - List site resources

**Required route parameters:** None

**Optional query parameters:** None

**Example request URI:** <https://rest.pubmlst.org/>

**Response:** List of resource groupings (ordered by name). Groups may consist of paired databases for sequence definitions and isolate data, or any set of related resources. Each group contains:

- name [string] - short name (usually a single word)
- description [string] - fuller description
- databases [array] - list of database objects, each consists of three key/value pairs:
  - name [string] - name of database config
  - description [string] - short description of resource

- href [string] - URI to access resource

### 17.3.2 GET /db/{database} - List database resources

These will vary depending on whether the resource is an isolate or a sequence definition database.

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates)

**Response:** Object containing a subset of the following key/value pairs:

- *fields* [string] - URI to isolate provenance field information
- *isolates* [string] - URI to isolate records
- *genomes* [string] - URI to genome records
- *schemes* [string] - URI to list of schemes
- *loci* [string] - URI to list of loci
- *projects* [string] - URI to list of projects

### 17.3.3 GET /db/{database}/classification\_schemes - List classification schemes

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/classification\\_schemes](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/classification_schemes)

**Response:** Object containing:

- records [integer] - Number of classification schemes.
- classification\_schemes [array] - List of *URIs to classification schemes*.

### 17.3.4 GET /db/{database}/classification\_schemes/{classification\_scheme\_id} - Retrieve classification scheme information and groups

**Required route parameters:**

- database [string] - Database configuration name
- classification\_scheme\_id [integer] - Classification scheme id number

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/classification\\_schemes/1](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/classification_schemes/1)

**Response:** Object containing some or all of:

- id [integer] - Classification scheme id
- name [text] - Name of classification scheme
- description [text] - Description of classification scheme
- relative\_threshold [boolean] - True if a *relative threshold* is used
- inclusion\_threshold [integer] - The threshold for number of loci difference used to group

- groups [string] (sequence definition databases only) - URI to list of groups
  - id [integer] - group id
  - profiles [array] - list of *URIs to profiles* belonging to the group

### 17.3.5 GET /db/{database}/classification\_schemes/{classification\_scheme\_id}/groups - List groups defined for a classification scheme

Sequence definition databases only.

#### Required route parameters:

- database [string] - Database configuration name
- classification\_scheme\_id [integer] - Classification scheme id number

#### Optional parameters:

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/classification\\_schemes/1/groups](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/classification_schemes/1/groups)

**Response:** Object containing of:

- records [integer] - Number of groups
- groups [array] - List of *URIs to classification group records*.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.6 GET /db/{database}/classification\_schemes/{classification\_scheme\_id}/groups/{group\_id} - List isolates or profiles belonging to a classification scheme group

#### Required route parameters:

- database [string] - Database configuration name
- classification\_scheme\_id [integer] - Classification scheme id number
- group\_id [integer] - Group id number

#### Optional parameters:

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/classification\\_schemes/4/groups/65](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/classification_schemes/4/groups/65)

**Response:** Object containing some of:

- records [integer] - Number of isolates or profiles
- isolates (isolate database only) [array] - List of *URIs to isolate records*. Pages are 100 records by default. Page size can be modified using the `page_size` parameter.
- profiles (sequence definition databases only) [array] - List of *URIs to profile records*. Pages are 100 records by default. Page size can be modified using the `page_size` parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.7 GET /db/{database}/loci - List loci

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.
- alleles\_added\_after [date] - Include only loci with alleles added after (but not on) specified date (ISO 8601 format). Only recognized in sequence definition databases.
- alleles\_updated\_after [date] - Include only loci with alleles last modified after (but not on) specified date (ISO 8601 format). Only recognized in sequence definition databases.
- alleles\_added\_reldate [integer] - Include only loci with alleles added within the number of days specified. Only recognized in sequence definition databases.
- alleles\_updated\_reldate [integer] - Include only loci with alleles last modified within the number of days specified. Only recognized in sequence definition databases.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/loci](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/loci)

**Response:** Object containing:

- records [integer] - Number of loci
- loci [array] - List of *URIs to defined locus records*. Pages are 100 records by default. Page size can be modified using the `page_size` parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results

- return\_all - URI to page containing all results (paging disabled)

---

**Note:** See also the *scheme specific version*, allowing filtering by date of last allele update for just the loci that are members of a scheme.

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### 17.3.8 GET /db/{database}/loci/{locus} - Retrieve locus record

Provides information about a locus, including links to allele sequences (in seqdef databases).

**Required route parameters:**

- database [string] - Database configuration name
- locus [string] - Locus name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/loci/abcZ](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/loci/abcZ)

**Response:** Object containing a subset of the following key/value pairs:

- id [string] - locus name
- data\_type [string] - 'DNA' or 'peptide'
- allele\_id\_format [string] - 'integer' or 'text'
- allele\_id\_regex [string] - regular expression constraining allele ids
- common\_name [string]
- aliases [array] - list of alternative names of the locus
- length\_varies [boolean]
- length [integer] - length if alleles are of a fixed length
- coding\_sequence [boolean]
- orf [integer] - 1-6
- schemes [array] - list of scheme objects, each consisting of:
  - scheme [string] - URI to scheme information
  - description [string]
- min\_length [integer] (seqdef databases) - minimum length for variable length loci
- max\_length [integer] (seqdef databases) - maximum length for variable length loci
- alleles [string] (seqdef databases) - *URI to list of allele records*
- alleles\_fasta [string] (seqdef databases) - *URI to FASTA file of all alleles of locus*
- curators [array] (seqdef databases) - list of *URIs to user records* of curators of the locus
- publications [array] (seqdef databases) - list of PubMed id numbers of papers describing the locus
- full\_name [string] (seqdef databases)
- product [string] (seqdef databases)
- description [string] (seqdef databases)

- `extended_attributes` [array] (seqdef databases) - list of extended attribute objects. Each consists of a subset of the following fields:
  - `field` [string] - field name
  - `value_format` [string] - 'integer', 'text', or 'boolean'
  - `value_regex` [string] - regular expression constraining value
  - `description` [string] - description of field
  - `length` [integer] - maximum length of field
  - `required` [boolean]
  - `allowed_values` [array] - list of allowed values
- `genome_position` [integer] (isolate databases)

### 17.3.9 GET /db/{database}/loci/{locus}/alleles - Retrieve list of alleles defined for a locus

#### Required route parameters:

- `database` [string] - Database configuration name
- `locus` [string] - Locus name

#### Optional parameters:

- `page` [integer]
- `page_size` [integer]
- `return_all` [integer] - Set to non-zero value to disable paging.
- `added_after` [date] - Include only alleles added after (but not on) specified date (ISO 8601 format).
- `added_reldate` [integer] - Include only alleles added within the specified number of days.
- `added_on` [date] - Include only alleles added on specified date (ISO 8601 format).
- `updated_after` [date] - Include only alleles last modified after (but not on) specified date (ISO 8601 format).
- `updated_reldate` [integer] - Include only alleles updated within the specified number of days.
- `updated_on` [date] - Include only alleles last modified on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/loci/abcZ/alleles](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/loci/abcZ/alleles)

**Response:** Object containing:

- `records` [integer] - Number of alleles.
- `last_updated` [date] - Latest allele addition/modification date (ISO 8601 format).
- `alleles` [array] - List of *URIs to defined allele records*. Pages are 100 records by default. Page size can be modified using the `page_size` parameter.
- `paging` [object] - Some or all of the following:
  - `previous` - URI to previous page of results
  - `next` - URI to next page of results
  - `first` - URI to first page of results
  - `last` - URI to last page of results

- return\_all - URI to page containing all results (paging disabled)

### 17.3.10 GET /db/{database}/loci/{locus}/alleles\_fasta - Download alleles in FASTA format

**Required route parameters:**

- database [string] - Database configuration name
- locus [string] - Locus name

**Optional parameters:**

- added\_after [date] - Include only alleles added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Include only alleles added within the specified number of days.
- added\_on [date] - Include only alleles added on specified date (ISO 8601 format).
- updated\_after [date] - Include only alleles last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Include only alleles last modified within the specified number of days.
- updated\_on [date] - Include only alleles last modified on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/loci/abcZ/alleles\\_fasta](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/loci/abcZ/alleles_fasta)

**Response:** FASTA format file of allele sequences

### 17.3.11 GET /db/{database}/loci/{locus}/alleles/{allele\_id} - Retrieve full allele information

**Required route parameters:**

- database [string] - Database configuration name
- locus [string] - Locus name
- allele\_id [string] - Allele identifier

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/loci/abcZ/alleles/5](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/loci/abcZ/alleles/5)

**Response:** Object containing the following key/value pairs:

- locus [string] - *URI to locus description*
- allele\_id [string] - allele identifier
- sequence [string] - sequence
- status [string] - either 'Sanger trace checked', 'WGS: manual extract', 'WGS: automated extract', or 'unchecked'
- sender [string] - *URI to user details* of sender
- curator [string] - *URI to user details* of curator
- date\_entered [string] - record creation date (ISO 8601 format)
- timestamp [string] - last updated date (ISO 8601 format)

### 17.3.12 POST /db/{database}/loci/{locus}/sequence - Query sequence to identify allele

**Required route parameters:**

- database [string] - Database configuration name
- locus [string] - Locus name

**Required additional parameters (JSON-encoded in POST body):**

- sequence [string] - Sequence string or base64-encoded FASTA file

**Optional parameters (JSON-encoded in POST body):**

- details [true/false] - Return detailed exact match parameters
- base64 [true/false] - Sequence is a base64-encoded FASTA file

**Response:** Object containing the following key/value pairs:

- exact\_matches [array] - list of match objects, each consisting of:
  - allele\_id
  - href - *URI to allele record.*

additionally if 'details' parameter passed:

- start - start position on query
- end - end position on query
- orientation - forward/reverse
- length - length of matched allele
- contig - contig name if FASTA file is uploaded

If the locus is linked to field data in client isolate databases, there may also be an object called 'linked\_data' containing values and frequencies of the field for the returned allele.

- best\_match [object] - consisting of key/value pairs (if no exact matches)
  - allele\_id
  - href - *URI to allele record.*
  - start - start position on query (predicted taking account of allele length)
  - end - end position on query (predicted taking account of allele length)
  - orientation - forward/reverse
  - length - length of matched allele
  - alignment - length of BLAST alignment
  - mismatches - number of mismatches
  - identity - %identity of match
  - gaps - number of gaps in alignment

### 17.3.13 POST /db/{database}/sequence - Query sequence to identify allele without specifying locus

**Required route parameters:**

- database [string] - Database configuration name

**Required additional parameters (JSON-encoded in POST body):**

- sequence [string] - Sequence string or base64-encoded FASTA file

**Optional parameters (JSON-encoded in POST body):**

- details [true/false] - Return detailed exact match parameters
- base64 [true/false] - Sequence is a base64-encoded FASTA file

**Response:**

- exact\_matches [object] consisting of locus keys, each consisting of array of match objects consisting of:
  - allele\_id
  - href - *URI to allele record.*

additionally if 'details' parameter passed:

- start - start position on query
- end - end position on query
- orientation - forward/reverse
- length - length of matched allele
- contig - contig name if FASTA file is uploaded

If the locus is linked to field data in client isolate databases, there may also be an object called 'linked\_data' containing values and frequencies of the field for the returned allele.

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**Note:** This method only supports exact matches. If no match is indicated for a specific locus, use the *locus-specific call* to identify the closest match.

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### 17.3.14 GET /db/{database}/sequences - Get summary of defined sequences

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- added\_after [date] - Count only alleles added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Count only alleles added within the specified number of days.
- added\_on [date] - Count only alleles added on specified date (ISO 8601 format).
- updated\_after [date] - Count only alleles last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Count only alleles last modified within the specified number of days.
- updated\_on [date] - Count only allele updated on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/sequences](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/sequences)

**Response:** Object containing a subset of the following key/value pairs:

- *loci* [string] - URI to list of loci
- records [integer] - Number of alleles defined
- last\_updated [date] - Latest allele addition/modification date (ISO 8601 format).

### 17.3.15 GET /db/{database}/schemes - List schemes

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- with\_pk [integer] - Set to non-zero value to only show indexed schemes, i.e. those with a primary key field that defines each unique combination of alleles, e.g. MLST.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes)

**Response:**

- records [integer] - Number of schemes
- schemes [array] - list of scheme objects, each containing:
  - scheme [string] - *URI to scheme information*
  - description [string]

### 17.3.16 GET /db/{database}/schemes/{scheme\_id} - Retrieve scheme information

Includes links to allelic profiles (in seqdef databases, if appropriate). **Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id number

**Optional parameters:**

- added\_after [date] - Count only profiles added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Count only profiles added within the specified number of days.
- added\_on [date] - Count only profiles added on specified date (ISO 8601 format).
- updated\_after [date] - Count only profiles last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Count only profiles last modified within the specified number of days.
- updated\_on [date] - Count only profiles updated on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1)

**Response:** Object containing a subset of the following key/value pairs:

- id [integer]
- description [string]
- locus\_count [integer] - number of loci belonging to scheme
- loci [array] - list of *URIs to locus descriptions*
- has\_primary\_key\_field [boolean]
- fields [array] - list of *URIs to scheme field descriptions*
- primary\_key\_field [string] - *URI to primary key field description*

- profiles [string] - URI to list of profile definitions (only seqdef databases)
- profiles\_csv [string] - URI to tab-delimited file of all scheme profiles
- curators [array] (seqdef databases) - list of *URIs to user records* of curators of the scheme
- records [integer] - Number of profiles
- last\_added [date] - Latest profile addition/modification date (ISO 8601 format).
- last\_updated [date] - Latest profile addition/modification date (ISO 8601 format).

### 17.3.17 GET /db/{database}/schemes/{scheme\_id}/loci - Retrieve scheme loci

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id number

**Optional parameters:**

- alleles\_added\_after [date] - Include only loci with alleles added after (but not on) specified date (ISO 8601 format). Only recognized in sequence definition databases.
- alleles\_added\_reldate [integer] - Include only loci with alleles added within the specified number of days. Only recognized in sequence definition databases.
- alleles\_updated\_after [date] - Include only loci with alleles last modified after specified date (ISO 8601 format). Only recognized in sequence definition databases.
- alleles\_updated\_reldate [integer] - Include only loci with alleles last modified within the specified number of days. Only recognized in sequence definition databases.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1/loci](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/loci)

**Response:** Object containing:

- records [integer] - Number of loci
- loci [array] - List of *URIs to defined locus records*.

### 17.3.18 GET /db/{database}/schemes/{scheme\_id}/fields/{field} - Retrieve information about scheme field

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id number
- field [string] - Field name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1/fields/ST](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/fields/ST)

**Response:** Object containing the following key/value pairs:

- field [string] - field name
- type [string] - data type of field (integer or text)
- primary\_key [boolean] - true if field is the scheme primary key

### 17.3.19 GET /db/{database}/schemes/{scheme\_id}/profiles - List allelic profiles defined for scheme

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.
- added\_after [date] - Include only profiles added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Include only profiles added within the specified number of days.
- added\_on [date] - Include only profiles added on specified date (ISO 8601 format).
- updated\_after [date] - Include only profiles last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Include only profiles last modified within the specified number of days.
- updated\_on [date] - Include only profiles last modified on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1/profiles](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/profiles)

**Response:** Object containing:

- records [integer] - Number of profiles
- last\_updated [date] - Latest profile addition/modification date (ISO 8601 format).
- profiles [array] - List of *URIs to defined profile records*. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

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**Note:** This method also supports content negotiation. If the request accepts header includes TSV or CSV, then the call is redirected to `/db/{database}/schemes/{scheme_id}/profiles_csv`.

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### 17.3.20 GET /db/{database}/schemes/{scheme\_id}/profiles\_csv - Download allelic profiles in CSV (tab-delimited) format

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id

**Optional parameters:**

- added\_after [date] - Include only profiles added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Include only profiles added within the specified number of days.
- added\_on [date] - Include only profiles added on specified date (ISO 8601 format).
- updated\_after [date] - Include only profiles last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Include only profiles last modified within the specified number of days.
- updated\_on [date] - Include only profiles last modified on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1/profiles\\_csv](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/profiles_csv)

**Response:** Tab-delimited text file of allelic profiles

### 17.3.21 GET /db/{database}/schemes/{scheme\_id}/profiles/{profile\_id} - Retrieve allelic profile record

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id
- profile\_id [string/integer] - Profile id

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/schemes/1/profiles/11](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/profiles/11)

**Response:** Object containing the following key/value pairs:

- *primary\_key\_term* [string/integer] - The field name is the primary key, e.g. ST. The value is the primary key value (primary\_id used as an argument).
- *alleles* [object] - *list of URIs to allele descriptions*
- *other\_scheme\_fields* [string/integer] - Each scheme field will have its own value if defined. The field name is the name of the field.
- *sender* [string] - *URI to user details* of sender
- *curator* [string] - *URI to user details* of curator
- *date\_entered* [string] - record creation date (ISO 8601 format)
- *timestamp* [string] - last updated date (ISO 8601 format)

### 17.3.22 POST /db/{database}/schemes/{scheme\_id}/sequence - Query sequence to extract allele designations/fields for a scheme

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id

**Required additional parameters (JSON-encoded in POST body):**

- sequence [string] - Sequence string or base64-encoded FASTA file

**Optional parameters (JSON-encoded in POST body):**

- details [true/false] - Return detailed exact match parameters
- base64 [true/false] - Sequence is a base64-encoded FASTA file

**Response:** Object containing the following key/value pairs:

- exact\_matches [array] - list of match objects, each consisting of:
  - allele\_id
  - href - *URI to allele record*.

additionally if ‘details’ parameter passed:

- start - start position on query
- end - end position on query
- orientation - forward/reverse
- length - length of matched allele
- contig - contig name if FASTA file is uploaded

If the locus is linked to field data in client isolate databases, there may also be an object called ‘linked\_data’ containing values and frequencies of the field for the returned allele.

Example curl call to upload a FASTA file ‘contigs.fasta’ and extract MLST results from Neisseria database:

```
(echo -n '{"base64":true,"sequence": ""; base64 contigs.fasta; echo "{}"}' |  
curl -s -H "Content-Type: application/json" -X POST "https://rest.pubmlst.org/db/pubmlst_  
↪neisseria_seqdef/schemes/1/sequence" -d @-
```

---

**Note:** This method only supports exact matches. If no match is indicated for a specific locus, use the *locus-specific call* to identify the closest match.

---

### 17.3.23 POST /db/{database}/schemes/{scheme\_id}/designations - Query allelic profile to extract fields for a scheme

**Required route parameters:**

- database [string] - Database configuration name
- scheme\_id [integer] - Scheme id

**Required additional parameters (JSON-encoded in POST body):**

- designations [object] - consisting of
  - locus objects each containing an array of alleles (see example)

**Response:** Object containing the following key/value pairs:

- exact\_matches [object] - consisting of locus values, each consisting of an array of allele values:
  - allele\_id [string]

If the locus is linked to field data in client isolate databases, there may also be an object called 'linked\_data' containing values and frequencies of the field for the returned allele.

- fields [object] - consisting of key/value pairs of scheme fields (if defined)

Example curl call to query an allelic profile and extract MLST results from Neisseria database:

```
curl -s -H "Content-Type: application/json" -X POST "https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/schemes/1/designations" -d '{"designations":{"abcZ":[{"allele":"2"}], "adk":[{"allele":"3"}], "aroE":[{"allele":"4"}], "fumC":[{"allele":"3"}], "gdh":[{"allele":"8"}], "pdhC":[{"allele":"4"}], "pgm":[{"allele":"6"}]}}'
```

### 17.3.24 GET /db/{database}/isolates - Retrieve list of isolate records

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.
- added\_after [date] - Include only isolates added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Include only isolates added within the specified number of days.
- added\_on [date] - Include only isolates added on specified date (ISO 8601 format).
- include\_old\_versions [integer] - Set to 1 to include old record versions (the default is to only include new versions)
- updated\_after [date] - Include only isolates last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Include only isolates last modified within the specified number of days.
- updated\_on [date] - Include only isolates updated on specified date (ISO 8601 format).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates)

**Response:** Object containing:

- records [integer] - Number of isolates

- isolates [array] - List of *URIs to isolate records*. Pages are 100 records by default. Page size can be modified using the `page_size` parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.25 GET /db/{database}/isolates/{isolate\_id} - Retrieve isolate record

#### Required route parameters:

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

#### Optional parameter:

- provenance\_only [integer] - Set to non-zero value to only return provenance metadata

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1)

**Response:** Object containing some or all of the following key/value pairs:

- provenance [object] - set of key/value pairs. Keys are defined by calling the */fields route*. The fields will vary by database but will always contain the following:
  - id [integer]
  - sender [string] - *URI to user details* of sender
  - curator [string] - *URI to user details* of curator
  - date\_entered [string] - record creation date (ISO 8601 format)
  - timestamp [string] - last updated date (ISO 8601 format)
- publications [array] (seqdef databases) - list of PubMed id numbers of papers that refer to the isolate
- sequence\_bin [object] - consists of the following key/value pairs:
  - contigs\_fasta [string] - *URI to FASTA file containing all the contigs belonging to this isolate*
  - contigs [string] - *URI to list of contig records*
  - contig\_count [integer] - number of contigs
  - total\_length [integer] - total length of contigs
- allele\_designations [object] - consists of the following key/value pairs:
  - allele\_ids - *URI to list of all allele\_id values* defined for the isolate
  - designation\_count - number of allele designations defined for the isolate
  - full\_designations - *URI to list of full allele designation records*
- schemes [array] - list of scheme objects, each containing some of the following:
  - description [string] - description of scheme

- loci\_designated\_count [integer] - number of loci within scheme that have an allele designated for this isolate.
- allele\_ids [string] - *URI to list of all allele\_id values defined for this scheme* for this isolate
- full\_designations [string] - *URI to list of full allele designation records* for this isolate
- fields [object] - consisting of key/value pairs where the key is the name of each scheme field
- classification\_schemes [object] - consisting of key/value pairs, where each key is the name of the classification scheme and the value is an object consisting of:
  - \* href [string] - *URI to classification scheme description*
  - \* groups [array] - list of group objects consisting of:
    - group [integer] - group id
    - records [integer] - number of isolates in group
    - isolates [string] - URI to classification group record containing URIs to member isolate records
- projects [array] - list of project objects, each containing the following:
  - id [string] - *URI to project information*
  - description [string] - description of project
- history [string] - *URI to isolate history record*
- new\_version [string] - URI to newer version of record
- old\_version [string] - URI to older version of record

### 17.3.26 GET /db/{database}/isolates/{isolate\_id}/allele\_designations - Retrieve list of allele designation records

#### Required route parameters:

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

#### Optional parameters:

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/allele\\_designations](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/allele_designations)

#### Response: Object containing:

- records [integer] - Number of allele designations
- allele\_designations [array] - List of *URIs to allele designation records*. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results

- last - URI to last page of results
- return\_all - URI to page containing all results (paging disabled)

### 17.3.27 GET /db/{database}/isolates/{isolate\_id}/allele\_designations/{locus} - Retrieve full allele designation record

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier
- locus [string] - Locus name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/allele\\_designations/BACT000065](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/allele_designations/BACT000065)

**Response:** List of allele\_designation objects (there may be multiple designations for the same locus), each containing:

- locus [string] - *URI to locus description*
- allele\_id [string]
- method [string] - either 'manual' or 'automatic'
- status [string] - either 'confirmed' or 'provisional'
- comments [string]
- sender [string] - *URI to user details* of sender
- curator [string] - *URI to user details* of curator
- timestamp [string] - last updated date (ISO 8601 format)

### 17.3.28 GET /db/{database}/isolates/{isolate\_id}/allele\_ids - Retrieve allele identifiers

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/allele\\_ids](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/allele_ids)

**Response:** Object containing:

- records [integer] - Number of allele id objects
- allele\_ids [array] - List of allele id objects, each consisting of a key/value pair where the key is the locus name. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:

- previous - URI to previous page of results
- next - URI to next page of results
- first - URI to first page of results
- last - URI to last page of results
- return\_all - URI to page containing all results (paging disabled)

### 17.3.29 GET /db/{database}/isolates/{isolate\_id}/schemes/{scheme\_id}/allele\_designations - Retrieve scheme allele designation records

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier
- scheme\_id [integer] - Scheme identifier

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/schemes/1/allele\\_designations](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/schemes/1/allele_designations)

**Response:**

- records [integer] - Number of allele designation objects
- allele\_designations [array] - List of *allele designation objects* for each locus in the specified scheme that has been designated.

### 17.3.30 GET /db/{database}/isolates/{isolate\_id}/schemes/{scheme\_id}/allele\_ids - Retrieve list of scheme allele identifiers

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier
- scheme\_id [integer] - Scheme identifier

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/schemes/1/allele\\_ids](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/schemes/1/allele_ids)

**Response:**

- records [integer] - Number of allele id objects
- allele\_ids [array] - List containing allele id objects for each locus in the specified scheme that has been designated. Each allele\_id object contains a key which is the name of the locus with a value that may be either a string, integer or array of strings or integers (required where there are multiple designations for a locus). The data type depends on the allele\_id\_format set for the specific locus.

### 17.3.31 GET /db/{database}/isolates/{isolate\_id}/contigs - Retrieve list of contigs

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/contigs](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/contigs)

**Response:** Object containing:

- records [integer] - Number of contigs
- contigs [array] - List of *URIs to contig records* Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.32 GET /db/{database}/isolates/{isolate\_id}/contigs\_fasta - Download contigs in FASTA format

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

**Optional parameter:**

- header [string] - either 'original\_designation' or 'id' (default is 'id'). This selects whether the FASTA header lines contain the originally uploaded FASTA headers or the sequence bin id numbers.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/contigs\\_fasta?header=original\\_designation](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/contigs_fasta?header=original_designation)

**Response:** FASTA format file of isolate contig sequences

### 17.3.33 GET /db/{database}/isolates/{isolate\_id}/history - Retrieve isolate update history

**Required route parameters:**

- database [string] - Database configuration name
- isolate\_id [integer] - Isolate identifier

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/isolates/1/history](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/1/history)

**Response:** Object containing:

- records [integer] - Number of updates
- contigs [array] - List of update objects each consisting of the following key/value pairs:
  - curator [string] - *URI to user details* of curator
  - timestamp [string] - Time of update
  - actions [array] - List of update descriptions [strings]

### 17.3.34 GET /db/{database}/genomes - Retrieve list of isolate records that have genome assemblies

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.
- added\_after [date] - Include only isolates added after (but not on) specified date (ISO 8601 format).
- added\_reldate [integer] - Include only isolates added within the specified number of days.
- added\_on [date] - Include only isolates added on specified date (ISO 8601 format).
- include\_old\_versions [integer] - Set to 1 to include old record versions (the default is to only include new versions)
- updated\_after [date] - Include only isolates last modified after (but not on) specified date (ISO 8601 format).
- updated\_reldate [integer] - Include only isolates last modified within the specified number of days.
- updated\_on [date] - Include only isolates updated on specified date (ISO 8601 format).
- genome\_size [integer] - Filter to only include records with a sequence bin of at least the specified size (default is 500,000bp).

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/genomes](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/genomes)

**Response:** Object containing:

- records [integer] - Number of isolates
- isolates [array] - List of *URIs to isolate records*. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results

- next - URI to next page of results
- first - URI to first page of results
- last - URI to last page of results
- return\_all - URI to page containing all results (paging disabled)

### 17.3.35 POST /db/{database}/isolates/search - Search isolate database

#### Required route parameters:

- database [string] - Database configuration name

#### Optional parameters (appended to URI):

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

#### Query parameters (JSON-encoded in POST body):

You must include at least one query parameter.

Parameter names in the following forms are supported:

- field.{field} - key/value pairs for provenance fields. Supported field names can be found by calling the [/fields route](#). The fields will vary by database.
- locus.{locus} - key/value pairs of locus and its allele designation. Supported locus names can be found by calling the [/loci route](#).
- scheme.{scheme\_id}.{scheme\_field} - key/value pairs of scheme fields and their values. Supported field names can be determined by following routes from the [/schemes route](#).

**Example method call using curl:** The following searches for *Neisseria* ST-11 isolates from Europe in 2015 (MLST is scheme#1 in this database).

```
curl -s -H "Content-Type: application/json" -X POST \
"https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/isolates/search" \
-d '{"field.continent":"europe","field.year":2015,"scheme.1.ST":11}'
```

#### Response: Object containing:

- records [integer] - Number of isolates
- isolates [array] - List of [URIs to isolate records](#). Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.36 GET /db/{database}/contigs/{contig\_id} - Retrieve contig record

**Required route parameters:**

- database [string] - Database configuration name
- contig\_id [integer] - Contig identifier

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/contigs/180062](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/contigs/180062)

**Response:** Contig object consisting of the following key/value pairs:

- id [integer] - contig identifier
- isolate\_id [integer] - isolate identifier
- sequence [string] - contig sequence
- length [integer] - length of contig sequence
- method [string] - sequencing method
- sender [string] - *URI to user details* of sender
- curator [string] - *URI to user details* of curator
- date\_entered [string] - record creation date (ISO 8601 format)
- datestamp [string] - last updated date (ISO 8601 format)
- loci [array] - list of sequence tag objects consisting of:
  - locus [string] - *URI to locus description*
  - locus\_name [string]
  - start [integer]
  - end [integer]
  - direction [string] - forward/reverse
  - complete [boolean] - true/false

### 17.3.37 GET /db/{database}/fields - Retrieve list of isolate provenance field descriptions

**Required route parameters:**

- database [string] - Database configuration name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/fields](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/fields)

**Response:** Array of field objects, each consisting of some or all of the following key/value pairs:

- name [string] - name of field
- type [string] - data type (int, text, date, float)
- length [integer] - maximum length of field
- required [boolean] - true if field value is required
- min [integer] - minimum value for integer values

- max [integer] - maximum value for integer values
- regex [string] - regular expression that constrains the allowed value of the field
- comments [string]
- allowed values [array] - list of allowed values for the field
- values [string] - URI to list of used field values

### 17.3.38 GET /db/{database}/fields/{field} - Retrieve values set for a provenance field

**Required route parameters:**

- database [string] - Database configuration name
- field [string] - Provenance metadata field name

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/fields/country](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/fields/country)

**Response:** Object containing:

- records [integer] - Number of values
- values [array] - List of values used in isolate records. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.39 GET /db/{database}/users/{user\_id} - Retrieve user information

Users may be data submitters or curators.

**Required route parameters:**

- database [string] - Database configuration name
- user\_id [integer] - User id number

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/users/2](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/users/2)

**Response:** Object containing the following key/value pairs:

- id [integer] - user id number
- first\_name [string]

- surname [string]
- affiliation [string] - institutional affiliation
- email [string] - E-mail address (may be hidden depending on server configuration)

#### 17.3.40 GET /db/{database}/curators - Retrieve list of curators

**Required route parameters:**

- database [string] - Database configuration name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/curators](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/curators)

**Response:** Object containing:

- records [integer] - Number of curators
- curators [array] - List of *URIs to user records*.

#### 17.3.41 GET /db/{database}/projects - Retrieve list of projects

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/projects](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/projects)

**Response:**

- projects [array] - List of project objects, each containing:
  - project [string] - *URI to project information*
  - description [string]
  - isolate\_count [integer] - number of isolates in project

#### 17.3.42 GET /db/{database}/projects/{project\_id} - Retrieve project information

**Required route parameters:**

- database [string] - Database configuration name
- project\_id [integer] - Project id number

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/projects/3](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/projects/3)

**Response:** Object containing a subset of the following key/value pairs:

- id [integer]
- description [string]
- isolates [string] - *URI to list of URIs of member isolate records*.

### 17.3.43 GET /db/{database}/projects/{project\_id}/isolates - Retrieve list of isolates belonging to a project

**Required route parameter:**

- database [string] - Database configuration name
- project\_id [integer] - Project id number

**Optional parameters:**

- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/projects/3/isolates](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/projects/3/isolates)

**Response:** Object containing:

- records [integer] - Number of isolates in the project
- isolates [array] - List of URIs to isolate records. Pages are 100 records by default. Page size can be modified using the page\_size parameter.
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results
  - first - URI to first page of results
  - last - URI to last page of results
  - return\_all - URI to page containing all results (paging disabled)

### 17.3.44 GET /db/{database}/submissions - retrieve list of submissions

**Required route parameter:** database [string] - Database configuration name

**Optional parameters:**

- type [string] - either 'alleles', 'profiles' or 'isolates'
- status [string] - either 'closed' or 'pending'
- page [integer]
- page\_size [integer]
- return\_all [integer] - Set to non-zero value to disable paging.

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_isolates/submissions](https://rest.pubmlst.org/db/pubmlst_neisseria_isolates/submissions)

**Response:** Object containing:

- records [integer] - Number of submissions
- submissions [array] - List of *URIs to submission records*
- paging [object] - Some or all of the following:
  - previous - URI to previous page of results
  - next - URI to next page of results

- first - URI to first page of results
- last - URI to last page of results
- return\_all - URI to page containing all results (paging disabled)

### 17.3.45 POST /db/{database}/submissions - create new submission

**Required route parameter:** database [string] - Database configuration name

**Required additional parameters (JSON-encoded in POST body):**

- type [string] - either:
  - alleles (sequence definition databases only)
  - profiles (sequence definition databases only)
  - isolates (isolate databases only)
  - genomes (isolate databases only)

The following are required with the specified database type:

#### Allele submissions

- locus [string] - name of locus
- technology [string] - name of sequencing technology: either '454', 'Illumina', 'Ion Torrent', 'PacBio', 'Oxford Nanopore', 'Sanger', 'Solexa', 'SOLiD', or 'other'
- read\_length [string] - read length of sequencing: either '<100', '100-199', '200-299', '300-499', '>500', or any positive integer (only required for Illumina)
- coverage [string] - mean coverage of sequencing: either '<20x', '20-49x', '50-99x', '>100x', or any positive integer (only required for Illumina)
- assembly [string] - assembly method: either 'de novo' or 'mapped'
- software [string] - name of assembly software
- sequences [string] - either single raw sequence or multiple sequences in FASTA format

#### Profile submissions

- scheme\_id [integer] - scheme id number
- profiles [string] - tab-delimited profile data - this should include a header line containing the name of each locus

#### Isolate submissions

- isolates [string] - tab-delimited isolate data - this should include a header line containing each field or locus included

#### Genome submissions

- isolates [string] - tab-delimited isolate data - this should include a header line containing each field or locus included as well as for 'assembly\_filename' and 'sequence\_method'. The 'sequence\_method' should be either '454', 'Illumina', 'Ion Torrent', 'PacBio', 'Oxford Nanopore', 'Sanger', 'Solexa', 'SOLiD', or 'other'. Following submission, contig files should be uploaded with the same names as set for 'assembly\_filename'. This can be done using the [file upload route](#).

**Optional parameters:**

- message [string] - correspondence to the curator
- email [integer] - set to 1 to enable E-mail updates (E-mails will be sent to the registered user account address).

**Response:** Object containing:

- submission - *URI to submission record*

For genome submissions, the response object will also contain:

- missing\_files [array] - List of filenames that need to be uploaded to complete the submission. These filenames are defined in the 'assembly\_filename' field of the isolate record upload. The files should contain the contig assemblies.
- message [string] - 'Please upload missing contig files to complete submission.'

### 17.3.46 GET /db/{database}/submissions/{submission\_id} - Retrieve submission record

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/submissions/BIGSdb\\_20151013081836\\_14559\\_14740](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/submissions/BIGSdb_20151013081836_14559_14740)

**Response:** Object containing some of the following:

- id [string] - Submission id
- type [string] - Either 'alleles', 'profiles', 'isolates'
- date\_submitted [string] - Submission date (ISO 8601 format)
- timestamp [string] - Last updated date (ISO 8601 format)
- submitter [string] - *URI to user details* of submitter
- curator [string] - *URI to user details* of curator
- status [string] - either 'started', 'pending', or 'closed'
- outcome [string] - either 'good' (data uploaded), 'bad' (data rejected), or 'mixed' (parts of submission accepted)
- correspondence [array] - List of correspondence objects in time order. Each contains:
  - user [string] *URI to user details* of user
  - timestamp [string]
  - message [string]

#### Allele submissions

- locus [string] - name of locus
- technology [string] - name of sequencing technology: either '454', 'Illumina', 'Ion Torrent', 'PacBio', 'Oxford Nanopore', 'Sanger', 'Solexa', 'SOLiD', or 'other'
- read\_length [string] - read length of sequencing: either '<100', '100-199', '200-299', '300-499', '>500', or any positive integer (only required for Illumina)
- coverage [string] - mean coverage of sequencing: either '<20x', '20-49x', '50-99x', '>100x', or any positive integer (only required for Illumina)
- assembly [string] - assembly method: either 'de novo' or 'mapped'

- software [string] - name of assembly software
- seqs [array] - List of sequence objects each containing:
  - seq\_id [string] - Sequence identifier
  - assigned\_id [string] - Allele identifier if uploaded to the database (otherwise undefined)
  - status [string] - Either 'pending', 'assigned', or 'rejected'
  - sequence [string]

#### Profile submissions

- scheme [string] - *URI to scheme information*
- profiles [array] - List of profile record objects. Each contains:
  - profile\_id [string] - Record identifier
  - assigned\_id [string] - Profile identifier if uploaded to the database (otherwise undefined)
  - status [string] - Either 'pending', 'assigned', or 'rejected'
  - designations [object] containing key/value pairs for each locus containing the allele identifier

#### Isolate submissions

- isolates [array] - List of isolate record objects. Each contains key/value pairs for included fields.

### 17.3.47 DELETE /db/{database}/submissions/{submission\_id} - Delete submission record

You must be the owner and the record must be closed.

#### Required route parameters:

- database [string] - Database configuration name
- submission\_id [string] - Submission id

Optional parameters: None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/submissions/BIGSdb\\_20151013081836\\_14559\\_14740](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/submissions/BIGSdb_20151013081836_14559_14740)

**Response:** message [string] - 'Submission deleted.'

### 17.3.48 GET /db/{database}/submissions/{submission\_id}/messages - Retrieve submission correspondence

#### Required route parameters:

- database [string] - Database configuration name
- submission\_id [string] - Submission id

Optional parameters: None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/submissions/BIGSdb\\_20151013081836\\_14559\\_14740/messages](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/submissions/BIGSdb_20151013081836_14559_14740/messages)

**Response:** Array of correspondence objects in time order. Each contains:

- user [string] *URI to user details* of user

- timestamp [string]
- message [string]

### 17.3.49 POST /db/{database}/submissions/{submission\_id}/messages - Add submission correspondence

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id

**Required additional parameter (JSON-encoded in POST body):**

- message [string] - Message text

**Optional parameters:** None

**Response:** message [string] - 'Message added.'

### 17.3.50 GET /db/{database}/submissions/{submission\_id}/files - Retrieve list of supporting files uploaded for submission

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id

**Optional parameters:** None

**Example request URI:** [https://rest.pubmlst.org/db/pubmlst\\_neisseria\\_seqdef/submissions/BIGSdb\\_20151013081836\\_14559\\_14740/files](https://rest.pubmlst.org/db/pubmlst_neisseria_seqdef/submissions/BIGSdb_20151013081836_14559_14740/files)

**Response:** Array of URIs to files

### 17.3.51 POST /db/{database}/submissions/{submission\_id}/files - Upload submission supporting file

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id

**Required additional parameters (JSON-encoded in POST body):**

- filename [string] - Name of file to store within submission
- upload [base64 encoded data] - Raw file data

**Optional parameters:** None

**Response:** message [string] - 'File uploaded.'

### 17.3.52 GET /db/{database}/submissions/{submission\_id}/files/{filename} - Download submission supporting file

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id
- filename [string] - Name of file

**Optional parameters:** None

**Response:** File download

### 17.3.53 DELETE /db/{database}/submissions/{submission\_id}/files/{filename} - Delete submission supporting file

**Required route parameters:**

- database [string] - Database configuration name
- submission\_id [string] - Submission id
- filename [string] - Name of file

**Optional parameters:** None

**Response:** message [string] - 'File deleted.'

## 17.4 Authentication

Protected resources, i.e. those requiring a user to log in, can be accessed via the API using OAuth (1.0A) authentication (see [IETF RFC5849](#) for details). Third-party client software has to be registered with the BIGSdb site before they can access authenticated resources. The overall three-legged flow works as follows:

1. *Developer signs up* and gets a consumer key and consumer secret specific to their application.
2. Application *gets a request token* and directs user to authorization page on BIGSdb.
3. BIGSdb *asks user for authorization* for application to access specific resource using their credentials. A verifier code is provided.
4. The application exchanges the request token and OAuth verifier code for an *access token and secret* (these do not expire but may be revoked by the user or site admin).
5. Application uses access token/secret to *request session token* (this is valid for 12 hours).
6. All calls to *access protected resources* are signed using the session token/secret and consumer key/secret.

It is recommended that application developers use an OAuth library to generate and sign requests.

---

**Note:** There are Python and Perl example scripts available at [https://github.com/kjolley/BIGSdb/tree/develop/scripts/rest\\_examples](https://github.com/kjolley/BIGSdb/tree/develop/scripts/rest_examples) to demonstrate and test OAuth authentication.

---

### 17.4.1 Developer sign up to get a consumer key

Application developers should apply to the site administrator of the site running BIGSdb. The administrator can *generate a key and secret* using a script - both of these will need to be used by the application to sign requests.

The client id is usually a 24 character alphanumeric string. The secret is usually a 42 character alphanumeric (including punctuation) string, e.g.

- **client\_id:** efKXmqp2D0EB1MBkZaGC2lPf
- **client\_secret:** F\$M+fQ2AFFB2YBDfF9fpHF^qSWJdmmN%L4Fxf5Gur3

### 17.4.2 Getting a request token

- **Relative URL:** /db/{database}/oauth/get\_request\_token
- **Supported method:** GET

The application uses the consumer key to obtain a request token. The request token is a temporary token used to initiate user authorization for the application and will expire in 60 minutes. The request needs to contain the following parameters and to be signed using the consumer secret:

- `oauth_consumer_key`
- `oauth_request_method` ('GET')
- `oauth_request_url` (request URL)
- `oauth_signature_method` ('HMAC-SHA1')
- `oauth_signature`
- `oauth_timestamp` (UNIX timestamp - seconds since Jan 1 1970) - this must be within 600 seconds of the current time.
- `oauth_callback` ('oob' for desktop applications)
- `oauth_nonce` (random string)
- `oauth_version` ('1.0')

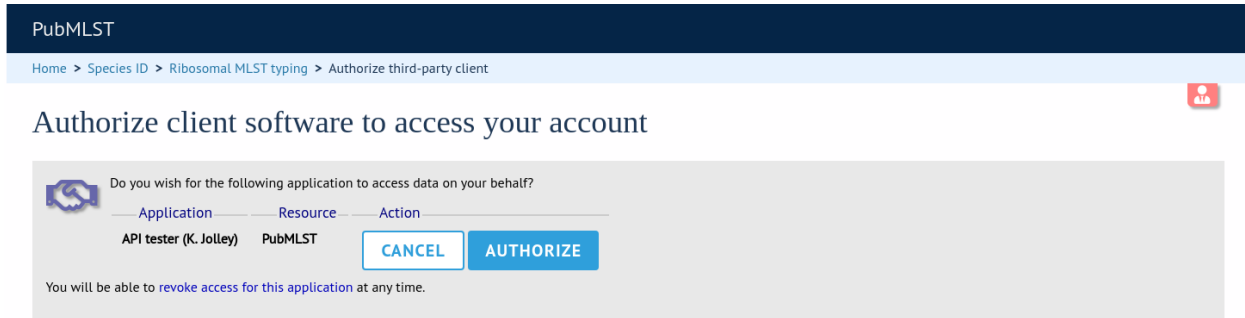
If the application has been registered and has been granted permission to access the specific resource, a JSON response will be returned containing the following parameters:

- **oauth\_token**
  - This is the request token. It is usually a 32 character alphanumeric string.
  - e.g. fKFm0WNhCfbEX8zQm6qhDA8K23FOWDGE
- **oauth\_token\_secret**
  - This is the secret associated with the request token. It is usually a 32 character alphanumeric string.
  - e.g. aZ0fncP7i5w5jlebdK5zyQ4vrRRVcdnv
- **oauth\_callback\_confirmed**
  - This parameter is always set to true.

### 17.4.3 Getting user authorization

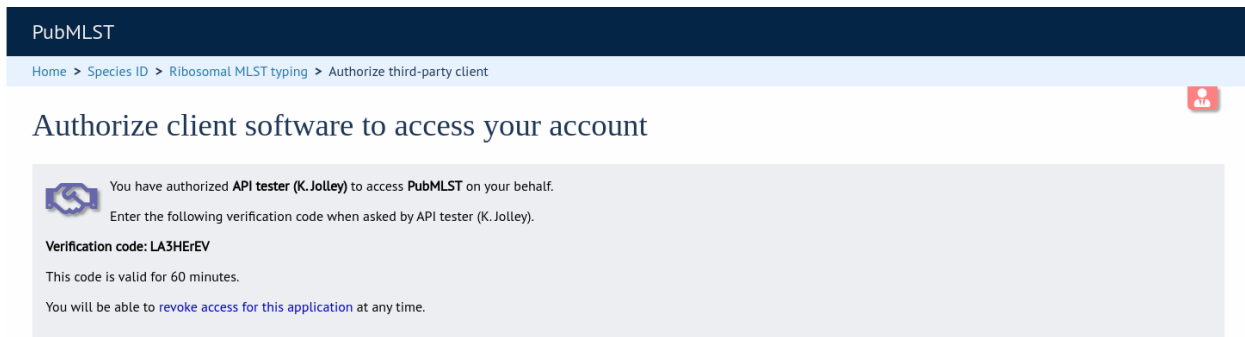
Once a request token has been obtained, this can be used by the end user to grant permission to access a specific resource to the application. The application should direct the user to the client authorization page (`authorizeClient`) specific to a database within BIGSdb, e.g. [http://pubmlst.org/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst\\_neisseria\\_seqdef&page=authorizeClient&oauth\\_token=fKFm0WNhCfbEX8zQm6qhDA8K23FOWDGE](http://pubmlst.org/cgi-bin/bigsdb/bigsdb.pl?db=pubmlst_neisseria_seqdef&page=authorizeClient&oauth_token=fKFm0WNhCfbEX8zQm6qhDA8K23FOWDGE)

The user will be asked if they wish to grant access to the application on their behalf:



The screenshot shows the PubMLST website header with the title 'PubMLST' and a breadcrumb trail: 'Home > Species ID > Ribosomal MLST typing > Authorize third-party client'. The main heading is 'Authorize client software to access your account'. Below this is a form asking 'Do you wish for the following application to access data on your behalf?'. The form contains a table with columns 'Application', 'Resource', and 'Action'. The 'Application' column lists 'API tester (K. Jolley)', the 'Resource' column lists 'PubMLST', and the 'Action' column has two buttons: 'CANCEL' and 'AUTHORIZE'. Below the table, it states 'You will be able to revoke access for this application at any time.'

If they authorize the access, they will be presented with a verifier code. This should be entered in to the client application which will use this together with the request token to request an access token.



The screenshot shows the PubMLST website header with the title 'PubMLST' and a breadcrumb trail: 'Home > Species ID > Ribosomal MLST typing > Authorize third-party client'. The main heading is 'Authorize client software to access your account'. Below this is a form stating 'You have authorized API tester (K. Jolley) to access PubMLST on your behalf.' and 'Enter the following verification code when asked by API tester (K. Jolley)'. The 'Verification code' is 'LA3HErEV'. Below the code, it states 'This code is valid for 60 minutes.' and 'You will be able to revoke access for this application at any time.'

The verifier code is valid for 60 minutes.

### 17.4.4 Getting an access token

- **Relative URL:** `/db/{database}/oauth/get_access_token`
- **Supported method:** GET

The application uses the request token, verifier code and its consumer key to obtain an access token. The access token does not expire but can be revoked by either the end user or the site administrator. The request needs to contain the following parameters and to be signed using the consumer secret and request token secret:

- `oauth_consumer_key`
- `oauth_request_method` ('GET')
- `oauth_request_url` (request URL)
- `oauth_signature_method` ('HMAC-SHA1')
- `oauth_signature`
- `oauth_token` (request token)

- `oauth_timestamp` (UNIX timestamp - seconds since Jan 1 1970) - this must be within 600 seconds of the current time.
- `oauth_nonce` (random string)
- `oauth_version` ('1.0')

If the application has been registered and has been granted permission to access the specific resource, a JSON response will be returned containing the following parameters:

- **`oauth_token`**
  - This is the access token. It is usually a 32 character alphanumeric string.
  - e.g. `SDrC74ZVl5SYSqY8lWZqrRxnyDnNGVFO`
- **`oauth_token_secret`**
  - This is the secret associated with the access token. It is usually a 32 character alphanumeric string.
  - e.g. `tYl2SPzgiO02lRVzW4JR1ez6Vvm4gVyy`

### 17.4.5 Getting a session token

- **Relative URL:** `/db/{database}/oauth/get_session_token`
- **Supported method:** GET

The application uses the access token and its consumer key to obtain a session token. The session token is valid for 12 hours before it expires. The request needs to contain the following parameters and to be signed using the consumer secret and access token secret:

- `oauth_consumer_key`
- `oauth_request_method` ('GET')
- `oauth_request_url` (request URL)
- `oauth_signature_method` ('HMAC-SHA1')
- `oauth_signature`
- `oauth_token` (access token)
- `oauth_timestamp` (UNIX timestamp - seconds since Jan 1 1970) - this must be within 600 seconds of the current time.
- `oauth_nonce` (random string)
- `oauth_version` ('1.0')

If the application has been registered and has been granted permission to access the specific resource, a JSON response will be returned containing the following parameters:

- **`oauth_token`**
  - This is the session token. It is usually a 32 character alphanumeric string.
  - e.g. `H8CjIS8Ikq6hwCUqUfF1l4pTaCYl8Ljw`
- **`oauth_token_secret`**
  - This is the secret associated with the session token. It is usually a 32 character alphanumeric string.
  - e.g. `RfponbaNPO7tkZ2miHFISk0pMndePNfJ`

### 17.4.6 Accessing protected resources

The application uses the session token and its consumer key to access a protected resource. The request needs to contain the following parameters and to be signed using the consumer secret and session token secret:

- `oauth_consumer_key`
- `oauth_request_method` ('GET')
- `oauth_request_url` (request URL)
- `oauth_signature_method` ('HMAC-SHA1')
- `oauth_signature`
- `oauth_token` (session token)
- `oauth_timestamp` (UNIX timestamp - seconds since Jan 1 1970) - this must be within 600 seconds of the current time.
- `oauth_nonce` (random string)
- `oauth_version` ('1.0')



## FREQUENTLY ASKED QUESTIONS (FAQS)

### 18.1 General

#### 1. What is the minimum specification of hardware required to run BIGSdb?

The software will run on fairly modest hardware. For an installation with only local users, the following minimum is recommended:

- 4 processor cores
- 16 GB RAM
- 50 GB partition for temporary files
- 100 GB partition for databases

As usual, the more RAM that is available the better. Ideally you would want enough RAM that the whole database(s) can reside in memory (an approximation is roughly twice the total size of your contigs), although this is not absolutely required.

Offline jobs, such as *Genome Comparator* will use multiple cores (depending on the settings in `bigsdb.conf`), so if you want to run multiple jobs in parallel then you may want more cores (and memory). Tagging of new genomes using the offline *autotagger* is usually run in multi-threaded mode so the more cores available the faster this will be.

As a comparison, the PubMLST site is run on two machines - separate web and database servers. All offline jobs and tagging of genomes is performed on the database server. These have the following specification:

- web server: 40 cores, 128GB RAM
- database server: 80 cores, 1TB RAM, 7TB ZFS RAID-Z2 NVMe local storage

#### 2. Why might icons be missing when using Internet Explorer?

This can occur if you have Compatibility Mode enabled. BIGSdb generates valid HTML5 and Compatibility Mode should not be used. Please ensure this is not enabled in the Internet Explorer tools section.

## 18.2 Installation

### 1. BIGSdb is accumulating files in various temp directories - is this normal and how do I clean them out?

See: *Periodically delete temporary files.*

### 2. BIGSdb is complaining of an invalid script path - what does this mean?

In your database config.xml file system tag are two attributes - script\_path\_includes and curate\_path\_includes. These contain regexes that the web url to your script (bigsdbs.pl and bigscurate.pl respectively) must match. This prevents somebody from accessing a private database using an instance of bigsdbs.pl that is not in a protected directory if you're using apache authentication.

So, if you access the script from <http://localhost/cgi-bin/bigsdbs/bigsdbs.pl> then you can set script\_path\_includes to something like "/bigsdbs/" (which is the default), or "/cgi-bin/" or just "/" if you don't care about this check.

## 18.3 Administration

### 1. How can I make some isolates public but not others?

The easiest way to do this is to set up two or more separate configuration directories that refer to the database. The URLs to access these will differ by the value of the 'db' attribute, which refers to the name of the configuration directory (in /etc/bigsdbs/dbases/). The database view accessed by each of these configurations can be different as can the access restrictions.

*Example:*

We have a database 'bigsdbs\_test' that contains data, only some of which we wish to make publicly available. The isolates to make public are all members of a project. First we can make a view of the isolates table that contains only isolates within this project.

For isolates in project id 3, create a database view by logging in to psql as the postgres user. We will name this view 'public':

```
sudo su postgres
psql bigsdbs_test

CREATE VIEW public AS SELECT * FROM isolates WHERE id IN (SELECT isolate_id
  FROM project_members WHERE project_id=3);
GRANT SELECT ON public TO apache;
```

Create a private configuration that can access everything in the database in /etc/bigsdbs/dbases/test\_private. This will be accessible from [http://IP\\_ADDRESS/cgi-bin/bigsdbs/bigsdbs.pl?db=test\\_private](http://IP_ADDRESS/cgi-bin/bigsdbs/bigsdbs.pl?db=test_private).

The important attributes to set in the system tag of the config.xml file in this directory are::

```
view="isolates"
read_access="authenticated_users"
```

This means that anyone with an account can log in and view all the isolates (because the view is set to the isolates table).

Now create a public configuration in /etc/bigsdbs/dbases/test\_public. This will be accessible from [http://IP\\_ADDRESS/cgi-bin/bigsdbs/bigsdbs.pl?db=test\\_public](http://IP_ADDRESS/cgi-bin/bigsdbs/bigsdbs.pl?db=test_public). It is better to create a symlink to the private config.xml and then override the attributes that are different. So create a symlink to the private config file:

```
cd /etc/bigsdb/dbases/test_public  
sudo ln -s ../test_private/config.xml .
```

You can now override the view and access settings. Within `/etc/bigsdb/dbases/test_public`, create a file called `system.overrides` and add the following:

```
view="public"  
read_access="public"
```

See also *Restricting particular configurations to specific user accounts* and *private records*.



## 19.1 Query operators

Various query forms have operators for use with field values. Available operators are:

- =
  - Exact match (case-insensitive).
- contains
  - Match to a partial string (case-insensitive), e.g. searching for clonal complex 'contains' st-11 would return all STs belonging to the ST-11 complex.
- starts with
  - Match to values that start with the search term (case-insensitive).
- ends with
  - Match to values that end with the search term (case-sensitive).
- >
  - Greater than the search term.
- >=
  - Greater than or equal the search term.
- <
  - Less than the search term.
- <=
  - Less than or equal the search term.
- NOT
  - Match to values that do not equal the search term (case-insensitive).
- NOT contain
  - Match to values that do not contain the search term (case-insensitive).

## 19.2 Sequence tag flags

Sequences tagged in the sequence bin can have features indicated by specific flags. The presence of these flags can be queried. These are a superset of *flags available for allele sequences*. Available flags are:

- alternative start codon
  - A start codon other than ATG, GTG, or TTG is used. This can be the case with some yeasts.
- ambiguous read
  - Genome sequence contains ambiguous nucleotides in coding sequence.
- apparent misassembly
  - Sequence has a region of very high identity to existing allele in one region but looks completely different in another.
- atypical
  - Catch-all term for a sequence that is unusual compared to other alleles of locus.
- contains IS element
  - Coding sequence is interrupted by insertion sequence.
- downstream fusion
  - No stop codon present resulting in translation continuing.
- frameshift
  - Frameshift in sequence relative to other alleles, not resulting in internal stop codon.
- indel
  - Insertion/deletion in sequence that is uncommon compared to other alleles.
- internal stop codon
  - Frameshift in sequence relative to other alleles, resulting in internal stop codon.
- no start codon
  - No apparent start codon in immediate vicinity of usual start.
- no stop codon
  - No stop codon in immediate vicinity of usual stop.
- phase variable: off
  - Coding sequence has a homopolymeric run with a frameshift resulting in a stop codon preventing complete translation.
- truncated
  - Coding sequence is unusually short resulting in a truncated protein (not the same as running off the end of a contig).
- upstream fusion
  - No apparent start codon in immediate vicinity of usual start, likely due to a gene fusion (sequence is transcribed together with upstream coding sequence).

## 19.3 Allele sequence flags

Sequences can be flagged with specific attributes - these are searchable when doing a sequence attribute query. These are a subset of *flags available for tagged sequences*. These are mainly for use with whole genome MLST type data. Multiple flags can be selected by Ctrl-clicking the list. Available flags are:

- alternative start codon
  - A start codon other than ATG, GTG, or TTG is used. This can be the case with some yeasts.
- atypical
  - Catch-all term for a sequence that is unusual compared to other alleles of locus.
- contains IS element
  - Coding sequence is interrupted by insertion sequence.
- downstream fusion
  - No stop codon present resulting in translation continuing.
- frameshift
  - Frameshift in sequence relative to other alleles, not resulting in internal stop codon.
- indel
  - Insertion/deletion in sequence that is uncommon compared to other alleles.
- internal stop codon
  - Frameshift in sequence relative to other alleles, resulting in internal stop codon.
- no start codon
  - No apparent start codon in immediate vicinity of usual start.
- no stop codon
  - No stop codon in immediate vicinity of usual stop.
- phase variable: off
  - Coding sequence has a homopolymeric run with a frameshift resulting in a stop codon preventing complete translation.
- truncated
  - Coding sequence is unusually short resulting in a truncated protein (not the same as running off the end of a contig).
- upstream fusion
  - No apparent start codon in immediate vicinity of usual start, likely due to a gene fusion (sequence is transcribed together with upstream coding sequence).



## **DATABASE SCHEMA**

- Sequence definition database
- Isolate database



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