
BIGSdb Documentation

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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 454 or Illumina).

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 analogous 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 <http://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 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

1.7 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'.

Additional metadata fields can also be associated with each set so it is possible to have a database containing genomes from multiple species and a generic set of metadata, then have additional specific metadata fields for particular species or genera. These additional fields only become visible and searchable when the specific set that they belong to has been selected.

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
- Perl
- 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.

- **DBI** - Database independent interface - module used to interact with databases.
- **DBD-Pg** - PostgreSQL database driver for DBI.
- **XML::Parser::perlSAX** - part of libxml-perl - Used to parse XML configuration files.
- **Log::Log4perl** - Configurable status and error logging.
- **Log::Dispatch::File** - Object for logging to file.
- **Error** - Exception handling.

- `Config::Tiny` - Configuration file handling.
- `Bio::Biblio` - This used to be part of BioPerl but will need to be installed separately if using BioPerl 1.6.920 or later.
- `IO::String`
- `Data::UUID` - Globally unique identifier handling for preference storage.
- `List::MoreUtils` (version 0.28+).
- `Time::Duration` [optional] - Used by Job Viewer to display elapsed time in rounded units.
- `Excel::Writer::XLSX` - Used to export data in Excel format.
- `Parallel::ForkManager` - Required for multi-threading autotagger and autodefiner scripts.

2.1.3 Optional packages

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

- `ChartDirector` - library used for generating charts. Used by some plugins.
- `ImageMagick` - mogrify used by some plugins.
- `MAFFT` - 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](https://sourceforge.net) or [GitHub](https://github.com).

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 contents of the javascript directory to a javascript directory within the web root tree, i.e. accessible from http://your_website/javascript/.
5. Copy the `bigsdb.css` and `jquery-ui.css` stylesheets to the root directory of your website, i.e. accessible from http://your_website/bigsdb.css.
6. Copy the images directory to the root directory of your website, i.e. accessible from http://your_website/images.
7. 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.
8. 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';
```

9. 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
```

10. Create a writable temporary directory in the root of the web site called tmp, i.e. accessible from http://your_website/tmp.
11. 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/

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
```

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 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.

3.4 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. Note that CRON does not like '.' in executable filenames, so either rename the script to `'bigsjobs'` or create a symlink and call that from CRON, e.g.:

```
copy bigsjobs.pl to /usr/local/bin
sudo ln -s /usr/local/bin/bigsjobs.pl /usr/local/bin/bigsjobs
```

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 `splittree4` from the Genome Comparator plugin.

Add the following to `/etc/crontab`:

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

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

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
```

3.5 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
```

3.6 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'"
```

3.7 Log file rotation

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

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

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

3.8 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 (`bigsdbs_isolates`) from version 1.7 to 1.8, log in as the `postgres` user and type:

```
psql -f isolatedb_v1.8.sql bigsdbs_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. The version number is stored with the `bigsdbs.pl` script, so this should also be updated so that BIGSdb correctly reports its version.

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.

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 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 files (hyperlinks lead to the files used on the Neisseria database):

- 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.

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 and sample elements must match the physical structure of the database isolate and sample tables respectively. Required attributes are in **bold**:

<db>

Top level element. Contains child elements: system, field and sample.:

<system>

- **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’.
- **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.
- **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’.
- **curate_only**
 - Set to ‘yes’ to hide field on an isolate information page in the standard interface. The field will be visible if the page is accessed via the curator’s interface (version 1.10.0+).
- **curate_path_includes**
 - Partial path of the bigscurate.pl script used to curate the database. See user authentication.
- **default**
 - Default value. This will be entered automatically in the web form but can be overridden.
- **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_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’).

- 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.
- genome_comparator_limit
 - Overrides the isolate number limit for the Genome Comparator plugin. Default: '1000'.
- 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'.
- 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_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.
- 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'.
- 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'.
- 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’.
- script_path_includes
 - Partial path of the bigsdb.pl script used to access the database. See *user authentication*.
- seqbin_size_threshold
 - Sets the size values in Mbp to enable for the *seqbin filter*.
 - Example: seqbin_size_threshold=”0.5,1,2,4”.
- 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_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’.
- tblastx_tagging
 - Sets whether tagging can be performed using TBLASTX: either ‘yes’ or ‘no’, default ‘no’.
- user
 - Username for access to isolates database, default ‘apache’.
- use_temp_scheme_table
 - Sets whether entire schemes are imported in to the isolate database in to an indexed table rather than querying the seqdef scheme view for isolate results tables. Under some circumstances this can be considerably quicker than querying the seqdef scheme view (a few ms compared to >10s if the seqdef database contains multiple schemes with an uneven distribution of a large number of profiles so that the Postgres query planner picks a sequential rather than index scan). This scheme table can also be generated periodically using the update_scheme_cache.pl script to create a persistent cache. This is particularly useful for large schemes (>10000 profiles) but data will only be as fresh as the cache so ensure that the update script is run periodically.
- 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.
- webroot
 - URL of web root, which can be relative or absolute. The bigsdb.css stylesheet file should be located in this directory. Default ‘/’.

<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 or date.
- **comments** * optional
 - Comments about the field. These will be displayed in the field description plugin and as tooltips within the curation interface.
- **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.
- **length**
 - Length of field, default 12.
- **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 types. Special values such as CURRENT_YEAR can be used.
- **min**
 - Minimum value for integer types.
- **optlist**
 - Sets if this field has a list of allowed values, default ‘no’. Surround each option with an <option> tag.
- **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’ or ‘no’, default ‘yes’.
- **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_YEAR: the 4 digit value of the current year

<sample>

Element content: Sample field name + optional list <optlist> of allowed values. Attributes are essentially the same as isolate field attributes, but refer to the samples table rather than the isolates table.

The sample table, if defined, must include isolate_id and sample_id fields, which must also be described in the XML file. These must be set as integer fields.

4.3.2 Sequence definition database XML attributes

Required attributes are in **bold**.

<db>

Top level element. Contains child elements: system, field and sample.

<system>

- **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'.
- curate_path_includes
 - Partial path of the bigscure.pl script used to curate the database. See *user authentication*.

- `diploid`
 - Allow IUPAC 2-nucleotide ambiguity codes in allele definitions for use with diploid typing schemes: either ‘yes’ or ‘no’, default ‘no’ (Version 1.9.1+).
- `disable_seq_downloads`
 - Prevent users or curators from downloading all alleles for a locus (admins always can). ‘yes’ or ‘no’, 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.
- `materialized_views`
 - Enable materialized views: either ‘yes’ or ‘no’, default ‘no’.
- `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’.
- `script_path_includes`
 - Partial path of the `bigsdbs.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.
- `webroot`
 - URL of web root, which can be relative or absolute. The `bigsdbs.css` stylesheet file should be located in this directory. Default ‘/’.

4.4 User authentication

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

4.4.1 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 `bigsdbs.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'`.

4.4.2 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](#).

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

4.5 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,
datestamp, 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 encrypts the password to a hash 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 (or wherever you have located your `bigscurate.pl` script).

4.6 Updating PubMed citations

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 `getrefs.pl` and can be found in the `scripts/maintenance` directory. This script needs to know which BIGSdb databases and tables it needs to search for PubMed ids. These are listed in a configuration file (usually called `getrefs.conf`) which contains two columns - the first is the name of the database, the second is a comma-separated list of tables to search, e.g.

```
pubmlst_bigsdb_neisseria_isolates      refs
pubmlst_bigsdb_neisseria_seqdef        profile_refs,sequence_refs,locus_refs
```

The script can be called as follows:

```
getrefs.pl getrefs.conf
```

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

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.
- `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_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_experiments` - define new experiments that can be used to group contigs uploaded to the sequence bin.
- `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).

Permissions can be set by clicking the '?' button next to 'curator permissions' on the curator's interface:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
curator permissions			?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.

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

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Set curator permissions

Select curator(s)

Bratcher, Holly
Brehony, Carina
Exley, Rachel
Feavers, Ian
Hill, Dorothea
Hong, Eva
Maiden, Martin
Pannekoek, Yvonne

Action

Select

All None

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

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Set curator permissions

Select curator(s)

Bratcher, Holly
Brehony, Carina
Exley, Rachel
Feavers, Ian
Hill, Dorothea
Hong, Eva
Maiden, Martin
Pannekoek, Yvonne

Action

Select

All None

Update permissions

Permission	Curator		All/None
	Bratcher, Holly	Brehony, Carina	
disable access	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify users	<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 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 loci	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
modify schemes	<input type="checkbox"/>	<input 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 probes	<input type="checkbox"/>	<input 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"/>
All/None	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>


Action

Update

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’:


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	++	FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpIF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		




Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.

Select the curator from the list:


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)

Batch update locus curator access records

Select user

The user status must also be [set to curator](#) for permissions to work.

Users:

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:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Batch update locus curator access records

User: **Keith Jolley**
 Select values to enable or disable and then click the appropriate arrow button.

Select loci

Available		Selected
FHbp_segment_D		porA
FHbp_segment_E		NEIS1364
FetA_VR		PorA_VR1
NEIS0001	>	PorA_VR2
NEIS0004	<	abcZ
NEIS0005		adk
NEIS0006		aroE
NEIS0007		aspA
NEIS0008		carB
NEIS0009		dhpS
NEIS0010		fumC
NEIS0011		gdh

☒ Hide curator name from public view

[Back to main](#)

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.

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 link to 'set user passwords' at the bottom of the curator's index page. Click this.

allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.




Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- Set user passwords** - Set a user password to enable them to log on or change an existing password.
- Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Set user password

User: Jolley, Keith (keith)

New password: ●●●●●●

Retype password: ●●●●●●

Set 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.

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.

```
#Existing_host      Mapped_host
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 -d 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 tables 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.

Note that you will need to run this script periodically as a CRON job to refresh the cache.

If queries are taking longer than 5 seconds to perform and a cache is not in place, you will see a warning message in `bigsdb.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 materialized views for scheme definitions

Because of the way BIGSdb allows any number of profile schemes to be set up, the data are stored in a normalised manner in multiple tables. A database view, e.g. `scheme_1`, is created that joins these tables so that they can be queried as you would a single table. A view, however, is only a pre-selected query rather than a physical table and you can not index columns on it to optimise query performance.

A materialized view is a real table that is created from the view and refreshed every time the data in the underlying view changes. Because it is a real table, the database doesn't need to perform these joins every time it is queried and indexes can be set up on it, both of which greatly speeds up querying.

To use materialized views within a seqdef database set the following attribute in the system tag of the XML description file:

```
materialized_views="yes"
```

You will then need to run the 'configuration repair' function at the bottom of the administrator's main curation page for each scheme. This rebuilds the view and creates a materialized view called `mv_scheme_X`. This materialized view is updated automatically whenever profile data are added or altered via the web interface.

If you want an isolate database to benefit from this materialized view, make sure you put '`mv_scheme_X`' (where X is the scheme id) in the `dbase_table` field (rather than '`scheme_X`') when setting up the scheme in the isolate database configuration.

Please note that if you make changes to your profile data by means other than the web interface then the materialized view will not be updated. You can update it by running the following SQL command:

```
SELECT refresh_matview('mv_scheme_X');
```

The materialized view is used, for example, for looking up a ST from a profile and vice-versa. Significant speed improvements will only be realised if you have lots of profiles (>5000) and you are doing lots of lookups, e.g. displaying more than the default 25 records per page.

5.12 Dataset partitioning

5.12.1 Sets

Sets provide a means to partition the database into 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 and also include

additional metadata fields only applicable to that set.

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.

sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++		Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+			Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++		Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- [Set user passwords](#) - Set a user password to enable them to log on or change an existing password.
- [Configuration check](#) - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Neisseria PubMLST 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.

Datasets

This database contains multiple datasets. You can choose to display a single set or the whole database.

Please select: Whole database ▾ Choose

Query database

- [Search database](#) - advanced queries.
- [Browse database](#) - peruse all records.
- [Search by combinations of loci \(profiles\)](#) - including partial matching.
- [List query](#) - find isolates by matching a field to an entered list.

Option settings

- [Set general options](#) - including isolate table field handling
- Set display and query options for [locus](#), [schemes](#) or [scheme fields](#).

General information

- Isolates: 20854
- Last updated: 2014-07-01
- [Update history](#)
- [About BIGSdb](#)

Breakdown

- [Single field](#)
- [Two field](#)
- [Unique combinations](#)
- [Scheme and alleles](#)
- [Publications](#)
- [Sequence bin](#)

Export

- [Export dataset](#)
- [Contigs](#)
- [Sequences](#) - XMFA / concatenated FASTA formats

Analysis

- [Codon usage](#)
- [Presence/absence status of loci](#)
- [Genome comparator](#)
- [BLAST](#)

Miscellaneous

- [Description of database fields](#)

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 metadata

Additional metadata fields can be set within the XML configuration file. They are specified as belonging to a metaset by prefixing the field name with 'meta_NAME:' where NAME is the name of the metaset, e.g.

```
<field type="text" required="no" length="30" maindisplay="no"
  optlist="yes">meta_1:clinical_outcome
</optlist>
</option>
```

```

<option>hearing loss</option>
<option>amputation</option>
<option>death</option>
</optlist>
</field>

```

Metaset fields can be defined just like any other *provenance field* and their position in the output is determined by their position in the XML file.

Metaset fields can then be added to a set using the ‘Add set metadata’ link on the curator’s page.

user permissions	+	++	?	
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

A new database table needs to be added for each metaset. This should contain all the fields defined for a metaset. The table should also contain an `isolate_id` field to act as the foreign key linking to the isolate table, e.g. the SQL would look something like the following:

```

CREATE TABLE meta_1 (
  isolate_id integer NOT NULL,
  town text,
  clinical_outcome text,
  PRIMARY KEY (isolate_id),
  CONSTRAINT m1_isolate_id FOREIGN KEY (isolate_id) REFERENCES isolates
  ON DELETE CASCADE
  ON UPDATE CASCADE
);

```

```

GRANT SELECT,UPDATE,INSERT,DELETE ON meta_1 TO apache;

```

The above creates the database table for a metaset called '1', defining new text fields for 'town' and 'clinical_outcome'.

5.12.4 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.

5.12.5 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 Adding new loci

See also:

Loci (concept)

5.13.1 Sequence definition databases


Single locus

Click the add (+) loci link on the curator's interface contents page.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
schema members	+	++	?	Defines which loci belong to a scheme.

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 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).
- `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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.

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


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)
Toggle: [?](#)

Batch insert loci

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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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

Action

[Back](#)

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'.

5.13.2 Isolate databases

Single locus

Click the add (+) loci link on the curator's interface contents page.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Database curator's interface - Neisseria PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++		Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.

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

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

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

flag table: ☒ true ☐ false ! Seqdef database supports allele flags

isolate display: allele only !

main display: ☐ true ☒ false !

query field: ☒ true ☐ false !

analysis: ☒ true ☐ false !

curator: Keith Jolley (keith)

date entered: 2014-07-08

timestamp: 2014-07-08

formatted name: !

common name: !

formatted common name: !

allele id regex: !

length: !

orf: !

genome position: !

match longest: ☐ true ☐ false !

reference sequence: !

pcr filter: ☐ true ☐ false !

Action:

- `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.
- `flag_table` - Set to true to specify that the sequence definition database contains an allele flag table (which is the case for BIGSdb version 1.4 onwards).
 - 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.
- 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.
- 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_table` - Table in the sequence definition database that contains allele sequences for this locus. If the definition database uses BIGSdb this will be 'sequences'.
 - Allowed: any text (no spaces).
- `dbase_id_field` - Primary field in sequence database that defines allele. If the definition database uses BIGSdb this will be 'allele_id'.
 - Allowed: any text (no spaces).
- `dbase_id2_field` - Secondary field in sequence database that defines alleles. If `dbase_id_field` uniquely defines alleles for this locus then this should be left blank. If the definition database uses BIGSdb this will be 'locus'.
 - Allowed: any text (no spaces).
- `dbase_id2_value` - Secondary field value in sequence database that defines alleles. If `dbase_id_field` uniquely defines alleles for this locus then this should be left blank. If the definition database uses BIGSdb this will be the name of the locus used in the id field
 - Allowed: any text (no spaces).
- `dbase_seq_field` - Field in sequence database containing allele sequence. If the definition database uses BIGSdb this will be 'sequence'.
 - 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.

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 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Add new locus Show tools

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

Record	Action
id:!	?
data type:!	?
allele id format:!	?
length varies:!	?
coding sequence:!	?
flag table:!	?
isolate display:!	?
main display:!	?
query field:!	?
analysis:!	?
curator:!	?
date entered:!	?
timestamp:!	?
formatted name:!	?
common name:!	?
formatted common name:!	?
allele id regex:!	?
length:!	?
orf:!	?
genome position:!	?
match longest:!	?
reference sequence:!	?
pcr filter:!	?

Reset Submit

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Add new locus Hide tools

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

Record

id:

data type:

allele id format: [?](#)

length varies: ☐ true ☒ false [?](#)

coding sequence: ☒ true ☐ false

flag table: ☒ true ☐ false [?](#) Seqdef database supports allele flags

isolate display: [?](#)

main display: ☐ true ☒ false [?](#)

query field: ☒ true ☐ false [?](#)

analysis: ☒ true ☐ false [?](#)

curator: **Keith Jolley (keith)**

date entered: **2014-07-08**

timestamp: **2014-07-08**

formatted name: [?](#)

common name: [?](#)

formatted common name: [?](#)

allele id regex: [?](#)

length: [?](#)

orf: [?](#)

genome position: [?](#)

match longest: ☐ true ☐ false [?](#)

reference sequence: [?](#)

pcr filter: ☐ true ☐ false [?](#)

Copy configuration from: [Copy](#)

All parameters will be copied except id, common name, reference sequence, genome position and length. The copied locus id will be substituted for 'PUT_LOCUS_NAME_HERE' in fields that include it.

The configuration will be copied over to the web form, with the exception of name fields. Some fields will require you to change the value 'PUT_LOCUS_NAME_HERE' with the value you enter in the id field. These are usually the dbase_id2_value, description_url and url fields:

Curator: **Kevin Jolley (Kevin)**
 date entered: **2014-07-08**
 datestamp: **2014-07-08**
 formatted name:
 common name:
 formatted common name:
 allele id regex:
 length:
 orf:
 genome position:
 match longest: ☐ true ☐ false
 reference sequence:
 pcr filter: ☐ true ☐ false
 probe filter: ☐ true ☐ false
 dbase name: 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 table: Database table that holds sequence information for this locus
 dbase id field: Primary field in sequence database that defines allele, e.g. 'allele_id'
 dbase id2 field: Secondary field that defines allele, e.g. 'locus'
 dbase id2 value: Secondary field value, e.g. locus name
 dbase seq field: Field in sequence database containing allele sequence
 description url:
 url:

Complete the form and click 'Submit'.

Batch adding

Click the batch add (++) loci link on the curator's interface contents page.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Database curator's interface - Neisseria PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences		++	?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
schema members	+	++	?	Defines which loci belong to a scheme.

Click the link to download an Excel template:

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Batch insert loci

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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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

Action
 Reset Submit

Back

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 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.

user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
test profiles	+	++	query browse list batch update	
test2 profiles	+	++	query browse list batch update	
test2 profiles	+	++	query browse list batch update	
test3 profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++	?	



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.
- **Configuration repair** - Rebuild scheme tables

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#) Toggle: [?](#)

Add new locus extended attribute

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

Record	Action
locus: <input type="text"/> field: <input type="text"/> value format: <input type="text"/> text required: <input type="radio"/> true <input checked="" type="radio"/> false ? curator: Keith Jolley (keith) datestamp: 2014-07-09 value regex: <input type="text"/> ? description: <input type="text"/> option list: <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 but 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.

5.15 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)

5.15.1 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpIF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme	+	++	?	Defines which schemes belong to a group.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#) Toggle: [?](#)

Add new scheme

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

Record Action

id: 1 [Reset](#) [Submit](#)

description: MLST ?

curator: Keith Jolley (keith)

datestamp: 2014-07-04

date entered: 2014-07-04

display order: ?


allow missing loci: ☐ true ☐ false ?

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpiF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		


 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme	+	++	?	Defines which schemes belong to a group.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle: [?](#)

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: 2014-07-04 field order: 1	Reset Submit

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

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Loc: Add
 MLST profiles: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Database curator's interface - Neisseria locus/sequence definitions

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpiF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		


 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.

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

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Loc: Add
 MLST profiles: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password Toggle: [?]

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 (!).

<p>Record</p> <p>scheme id! <input type="text" value="MLST"/></p> <p>field! <input type="text" value="ST"/></p> <p>type! <input type="text" value="integer"/></p> <p>primary key! <input checked="" type="radio"/> true <input type="radio"/> false [?]</p> <p>dropdown! <input type="radio"/> true <input checked="" type="radio"/> false [?]</p> <p>curator! Keith Jolley (keith)</p> <p>timestamp! 2014-07-04</p> <p>description: <input type="text"/></p> <p>field order: <input type="text" value="1"/></p> <p>index: <input type="radio"/> true <input type="radio"/> false [?]</p> <p>value regex: <input type="text"/></p>	<p>Action</p> <p><input type="button" value="Reset"/> <input type="button" value="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

5.15.2 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.

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences	+	++	?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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

 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#) Toggle: [?](#)

Add new scheme

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

Record **Action**

id: 53 [?](#)

description: [?](#)

isolate display: ☒ true ☐ false [?](#)

main display: ☒ true ☐ false [?](#)

query field: ☒ true ☐ false [?](#)

query status: ☐ true ☒ false [?](#)

analysis: ☒ true ☐ false [?](#)

curator: **Keith Jolley (keith)**

datestamp: 2014-07-08

date entered: 2014-07-08

dbase name: [?](#)

dbase host: [?](#)

dbase port: [?](#)

dbase user: [?](#)

dbase password: [?](#)

dbase table: [?](#)

display order: [?](#)

allow missing loci: ☐ true ☐ false [?](#)

[Reset](#) [Submit](#)

- 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.
- `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_table` - Table in the sequence definition database that contains profiles for this scheme. If the definition database uses BIGSdb this will be 'scheme_X' where X is the scheme id number in the seqdef database.
 - Allowed: any text (no spaces).
- `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 '0' (locus missing) or 'N' (any allele).

5.16 Organizing schemes into hierarchical groups

Schemes can be organized in to 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.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [PoA](#) | [FeA](#) | [Options](#) | [Isolate Database](#)

Download allele sequences

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	Curator(s)
abcZ		DNA	687 Fixed: 433 bp	O. Harrison, K. Jolley	
adk		DNA	463 Fixed: 465 bp	O. Harrison, K. Jolley	
aroE		DNA	738 Fixed: 490 bp	O. Harrison, K. Jolley	
fumC		DNA	700 Fixed: 465 bp	O. Harrison, K. Jolley	
gdh		DNA	708 Fixed: 501 bp	O. Harrison, K. Jolley	
pdhC		DNA	713 Fixed: 480 bp	O. Harrison, K. Jolley	
pgm		DNA	724 Fixed: 450 bp	O. Harrison, K. Jolley	

[Download in tab-delimited text format](#)

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.

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- [Set user passwords](#) - Set a user password to enable them to log on or change an existing password.
- [Configuration check](#) - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#), [Log out](#) | [Change password](#) Toggle: [?](#)

Add new scheme group

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

<p>Record</p> <p>id: <input type="text" value="1"/></p> <p>name: <input type="text" value="Typing"/></p> <p>curator: Keith Jolley (keith)</p> <p>timestamp: 2014-07-10</p> <p>description: <input type="text"/></p> <p>display order: <input type="text"/></p> <p>seq query: <input type="radio"/> true <input type="radio"/> false</p>	<p>Action</p> <p>Reset Submit</p>
--	--

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 (+) scheme group scheme members link.

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

• [Set user passwords](#) - Set a user password to enable them to log on or change an existing password.
 • [Configuration check](#) - Checks database connectivity for loci and schemes and that required helper applications are properly installed.
 • [Configuration repair](#) - Rebuild scheme tables

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#) | [Toggle: i](#)

Add new scheme group scheme member

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

Record	Action
group id:! <input type="text" value="Typing"/> scheme id:! <input type="text" value="MLST"/> curator:! Keith Jolley (keith) datestamp:! 2014-07-10	<input type="button" value="Reset"/> <input type="button" value="Submit"/>

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

5.17 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpiF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#) Toggle: ?

Add new client database

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

Record

id: Action

name:

description:

dbase name: Name of the database holding isolate data

dbase config name: Name of the database configuration

curator:

datestamp:

dbase host: IP address of database host

dbase port: Network port accepting database connections

dbase user:

dbase password:

dbase view: View of isolates table to use

url: Web URL to database script

- 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.

5.17.1 Look up isolates with given allele

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpiF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loc: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle:

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: 2014-07-04

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.

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FeTA | Options | Isolate Database

Allele information - *abcZ*: 5

Provenance/meta data

locus: *abcZ*
 allele: 5

sequences: TTTGATACCG TTGCCGAAAG TTGGGCGAA ATTGCGGATT TATTGCGCCG TTATCAICAT GTACGCCATG ASITGGAAAA TGGTTCGAGT GAGGCITTGT TGAAGAGCT TAACGAATTG
 CAACTTGAAG TCGAAGCGAA GGACGGCTGG AAGCTGGATG CGGCAGTCAA GCAGACTTTG GGTGAACCTG GTTTCGCCAG AACGAAAAA ATCGSCAACG TCTCGGCGGG ACAGAAAAAG
 CGTGTTCGCC TAGCCGAGGC TTGGGTGCAG AAGCTGATG TATTGCTGCT GGACGAACCG ACCAACCATT TGGACATTGA CGCGATTATT TGGCTGGAAA ATCTGCTTAA AGCGTTTGAA
 GGCAGCCTGG TTGTGATTAC CCACGACCGC CGTTTTTTTG ACAATATGCG 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 (E-mail: man-suen.chan@paediatrics.ox.ac.uk)

Profiles containing this allele

MLST: 183 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.
 399 isolates

5.17.2 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.

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FeTA | Options | Isolate Database

Profile information for ST-11 (MLST)

ST	<i>abcZ</i>	<i>adk</i>	<i>aroE</i>	<i>fumC</i>	<i>gdh</i>	<i>pdhC</i>	<i>pgm</i>	clonal complex
11	2	3	4	3	8	4	6	ST-11 complex/ET-37 complex

sender: Paula Kriz, Paula Kriz and Keith Jolley
 curator: Keith Jolley, University of Oxford, UK (E-mail: keith.jolley@zoo.ox.ac.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.
 2288 isolates

5.17.3 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - Neisseria locus/sequence definitions

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group schema	+	++	?	Defines which schemes belong to a group.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle: [?]

Add new locus to client database isolate field definition

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

Record

client dbase id!: 1) PubMLST isolates **Action**

locus!: penA [Reset](#) [Submit](#)

isolate field!: penicillin_range


curator!: Keith Jolley (keith)

datestamp!: 2014-07-04

allele query: ☒ true ☐ false set to true to display field values when an allele query is done.

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.


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FeTA](#) | [Options](#) | [Isolate Database](#)

Allele information - penA: 9

Provenance/meta data

locus: penA
allele: 9

sequences: GACGGCGTTT TGCTGCCGGT CAGCTTTGAA AACAGGCGG TTGCGCCGCA AGGCAACGT ATATTAAAG CATCGACCGC ACGTCAGGTG CGTGAGTTGA TGGTTTCTGT AACCGAACCT
GGCGGTACGG GTACGGCGGG TGCGGTAGAT GGTTTCGACG TGGCGGCRAA AACCGGTACG GCGGTAACT TGGTTAACGG TCGTTACGTC GATTACAAAC ACGTTGCCAC TTTCATCGGT
TTTGGCCCGG CTAATAATCC GCGTGTGATT GTGGCGGTAA CCAATTGACGA GCCGACTGCA AACGGTTACT ACGCGCGCGT AGTGACAGGT CCGGCTTCA AACAAATTAT GGGCGGTAGC
CTGAACATCT TGGCGCTTTC 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 (E-mail: keith.jolley@zoo.ox.ac.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, Enríquez 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, Sagner 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.

141 isolates

Linked data

penicillin_range: >0.06 - 1 (intermediate) [n=86] [PubMLST isolates](#)

5.18 Rule-based sequence queries

The RuleQuery plugin has been designed to extract information from a pasted-in genome sequence, look up scheme fields and client database fields, and then format the output in a specified manner.

Rules are written in Perl, allowing the full power of this scripting language to be utilised. Helper functions that perform specific actions are available to the script (see example).

Please note that direct access to the database is prevented as are system calls.

5.18.1 Example rule code

An example can be found on the [Neisseria sequence database](#) that takes a genome sequence and determines a fine type and antibiotic resistance.

The code for this rule is as follows:

```
#Clinical identification rule

#Update job viewer status
update_status({stage=>'Scanning MLST loci'});

#Scan genome against all scheme 1 (MLST) loci
```

```
scan_scheme(1);

#Update job viewer status
update_status({percent_complete=>30, stage=>'Scanning PorA and FetA VRs'});

#Scan genome against the PorA VR and FetA VR loci
scan_locus($_) foreach qw(PorA_VR1 PorA_VR2 FetA_VR);

Add text to main output
append_html("<h1>Strain type</h1>");

#Set variables for the scanned results. These can be found in the
#$results->{'locus'} hashref
my %alleles;
$alleles{$_} = $results->{'locus'}->{$_} // 'ND' foreach qw(PorA_VR1 PorA_VR2);
$alleles{'FetA_VR'} = $results->{'locus'}->{'FetA_VR'} // 'F-ND';

#Scheme field values are automatically determined if a complete
#profile is available. These are stored in the $results->{'scheme'} hashref
my $st = $results->{'scheme'}->{1}->{'ST'} // 'ND';
append_html("<ul><li>P1.$alleles{'PorA_VR1'}, $alleles{'PorA_VR2'}; $alleles{'FetA_VR'}; ST-$st ");

#Reformat clonal complex using a regular expression, e.g.
# 'ST-11 clonal complex/ET-37 complex' gets rewritten to 'cc11'
my $cc = $results->{'scheme'}->{1}->{'clonal_complex'} // '-';
$cc =~ s/ST-(\S+) complex.*/cc$1/;

append_html("($cc)</li></ul>");
if ($st eq 'ND'){
    append_html("<p>ST not defined. If individual MLST loci have been found "
        . "they will be displayed below:</p>");

    #The get_scheme_html function automatically formats output for a scheme.
    #Select whether to display in a table rather than a list, list all loci, and/or list fields.
    append_html(get_scheme_html(1, {table=>1, loci=>1, fields=>0}));
}

#Antibiotic resistance
update_status({percent_complete=>80, stage=>'Scanning penA and rpoB'});
scan_locus($_) foreach qw(penA rpoB);
if (defined $results->{'locus'}->{'penA'} || defined $results->{'locus'}->{'rpoB'}) {
    append_html("<h1>Antibiotic resistance</h1><ul>");
    if (defined $results->{'locus'}->{'penA'}) {
        append_html("<li><i>penA</i> allele: $results->{'locus'}->{'penA'}");

        #If a client isolate database has been defined and values have been defined in
        #the client_dbase_loci_fields table, the values for a field in the isolate database can be
        #retrieved based on isolates that have a particular allele designated.
        #The min_percentage attribute states that only values that are represented by at least that
        #proportion of all isolates that had a value set are returned (null values are ignored).
        my $range = get_client_field(1, 'penA', 'penicillin_range', {min_percentage => 75});
        append_html(" (penicillin MIC: $range->[0]->{'penicillin_range'})" if @$range;
        append_html("</li>");
    }
    if (defined $results->{'locus'}->{'rpoB'}) {
        append_html("<li><i>rpoB</i> allele: $results->{'locus'}->{'rpoB'}");
        my $range = get_client_field(1, 'rpoB', 'rifampicin_range', {min_percentage => 75});
        append_html(" (rifampicin MIC: $range->[0]->{'rifampicin_range'})" if @$range;
    }
}
```

```

    append_html("</li>");
}
append_html("</ul>");
}

```

Rule files

The rule file is placed in a rules directory within the database configuration directory, e.g. `/etc/bigsdb/dbase/pubmlst_neisseria_seqdef/rules`. Rule files are suffixed with `.rule` and their name should be descriptive since it is used within the interface, i.e. the above rule file is named `Clinical_identification.rule` (underscores are converted to spaces in the web interface).

Linking to the rule query

Links to the rule query are not automatically placed within the web interface. The above rule query can be called using the following URL:

http://pubmlst.org/perl/bigsdb/bigsdb.pl?db=pubmlst_neisseria_seqdef&page=plugin&name=RuleQuery&ruleset=Clinical_identification

To place a link to this within the database contents page an HTML file called `job_query.html` can be placed in a contents directory within the database configuration directory, e.g. in `/etc/bigsdb/dbases/pubmlst_neisseria_seqdef/contents/job_query.html`. This file should contain a list entry (i.e. surrounded with `` and `` tags) that will appear in the ‘Query database’ section of the contents page.

Adding descriptive text

Descriptive text for the rule, which will appear on the rule query page, can be placed in a file called `description.html` in a directory with the same name as the rule within the rule directory, e.g. in `/etc/bigsdb/dbases/pubmlst_neisseria_seqdef/rules/Clinical_identification/description.html`.

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_table`: `sequences`
 - `dbase_id_field`: `allele_id`

- `dbase_id2_field`: locus
- `dbase_id_value`: atpD
- `dbase_seq_field`: sequence
- `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_table`: scheme_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 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’ on the curator’s contents pag.

The screenshot shows the BIGSdb interface. At the top, there is a table listing various database tables and their functions. Below this, the 'Database configuration' section is visible, featuring a table with columns for 'Table', 'Add', 'Batch Add', 'Update or delete', and 'Comments'. The 'loci' table is highlighted, and the 'database scan' button is visible in the 'Batch Add' column. Below the table, there are instructions for setting user passwords and checking database connectivity.

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

• **Set user passwords** - Set a user password to enable them to log on or change an existing password.

• **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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: [tab-delimited text](#) | [Excel format](#) (suitable for batch upload of loci).
 Download alleles: [tab-delimited text](#) | [Excel format](#) (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 [1]	1326
NMC0011		putative integral membrane protein	840
NMC0012		putative lipoprotein	1167
NMC0013		possible membrane protein	1266
NMC0014	phnA	putative phosphonoacetate hydrolase	330
NMC0015	glmU	bifunctional GlmU protein [includes: UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (N-acetylglucosamine-1-phosphate uridylyltransferase);	1371

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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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: [tab-delimited text](#) | [Excel format](#) (suitable for batch upload of loci).
Download alleles: [tab-delimited text](#) | [Excel format](#) (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 [1]	1326
NMC0011		putative integral membrane protein	840
NMC0012		putative lipoprotein	1167
NMC0013		possible membrane protein	1266
NMC0014	phnA	putative phosphonoacetate hydrolase	330
NMC0015	glmU	bifunctional GlmU protein [includes: UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (N-acetylglucosamine-1-phosphate uridylyltransferase);	1371

5.21 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.

5.21.1 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.

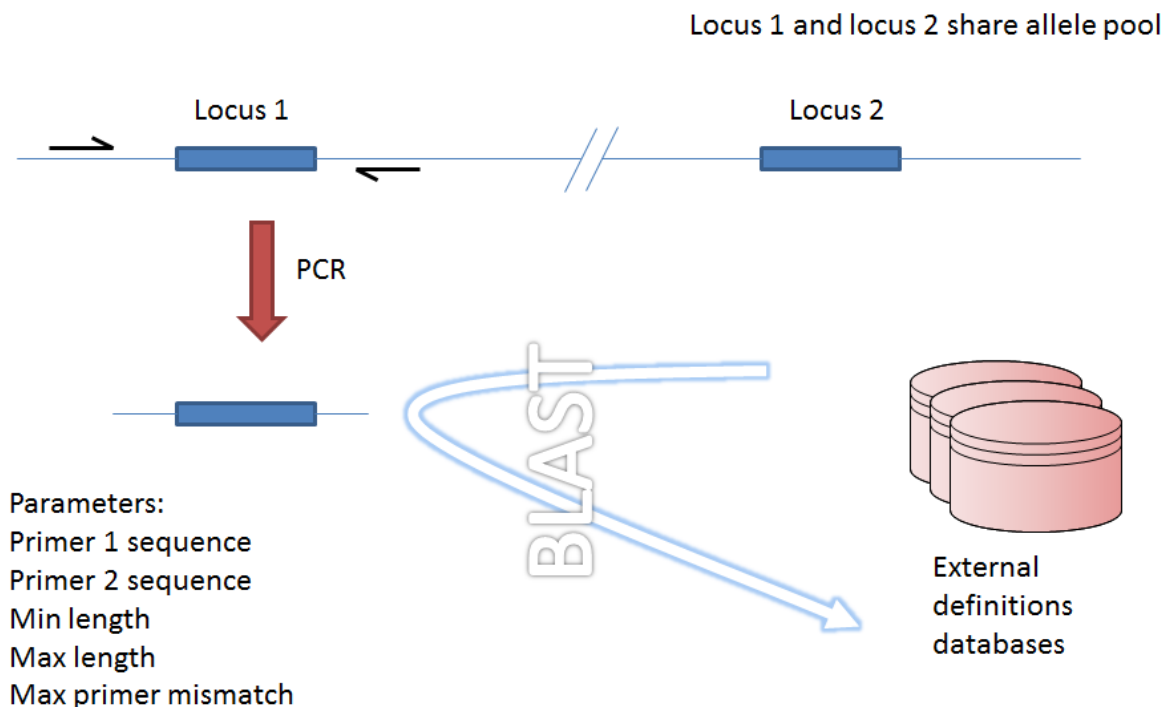


Figure 5.1: Genome filtering by in silico PCR.

users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences	+	++	?	Add links associating sequences to experiments.
sequence tags	+	scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration					
Table	Add	Batch Add	Update or delete	Comments	
loci	+	++	?		
	databank scan				
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.	
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.	
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.	
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.	
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.	
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.	
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.	
scheme members	+	++	?	Defines which loci belong to a scheme.	
scheme fields	+	++	?	Defines which fields belong to a scheme.	
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.	
scheme group scheme members	+	++	?	Defines which schemes belong to a group.	
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.	

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Add new PCR reaction

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

Record	Action
id: 1	Reset Submit
description:!	
primer1:!	
primer2:!	
curator:! Keith Jolley (keith)	
datestamp: 2014-07-08	
min length: <input type="text"/>	Minimum length of product to return
max length: <input type="text"/>	Maximum length of product to return
max primer mismatch: <input type="text"/> ?	Maximum sequence mismatch per primer

- 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.

experiment sequences		?	Add links associating sequences to experiments.
sequence tags	scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
PCR locus links	+	++		Link a locus to an <i>in silico</i> PCR reaction.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.

5.21.2 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.
- `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.

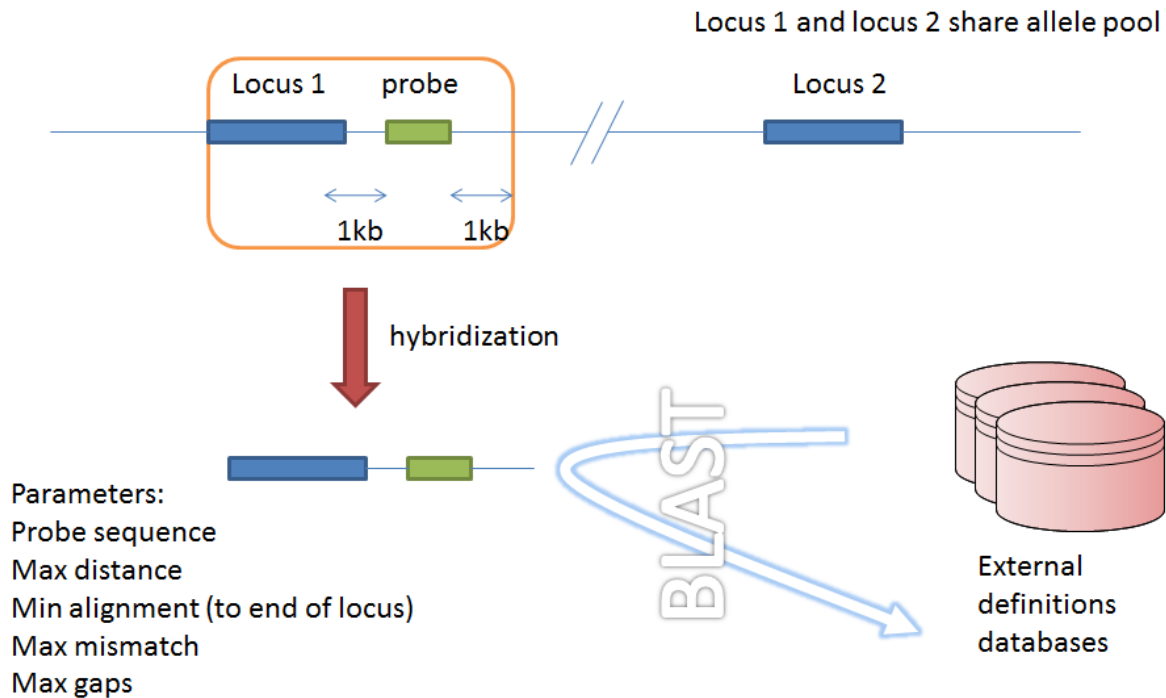


Figure 5.2: Filtering by in silico hybridization

experiment sequences		?	Add links associating sequences to experiments.
sequence tags	scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
PCR locus links	+	++		Link a locus to an <i>in silico</i> PCR reaction.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

sequence tags scan ? Tag regions of sequences within the sequence bin with locus information.


 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
PCR locus links	+	++	?	Link a locus to an <i>in silico</i> PCR reaction.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
probe locus links	+	++	?	Link a locus to an <i>in silico</i> hybridization reaction.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

– 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.

5.22 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.

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST

Datasets

This database contains multiple datasets. You can choose to display a single set or the whole database.

Please select: Whole database Choose

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	

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

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#) Field help: [id](#) Go

Isolate query/update

Isolate provenance/phenotype fields: isolate = MC58 + ?

Display/sort options: Order by: id ascending Display: 25 records per page ?

Action: Reset Submit

1 record returned. Click the hyperlink for detailed information.

Delete Tag scanning Projects

Delete ALL Scan Select project... Link

Delete	Update	Sequence bin	New version	Isolate fields ?					MLST		Finotyping antigens			test	test3		Loci			
				id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR	ST	PorA VR1	PorA VR2	'test9
delete	update	upload	create	240	MC58	Z7176	UK	1983		Neisseria meningitidis	B	74	ST-32 complex/ET-5 complex	7	16-2	F1-5		7	16-2	add

In the isolate record, click the sequence bin 'Display' button to bring up details of the isolate contigs.

species: *Neisseria meningitidis* update history: 137 updates [show details](#)

Publications (4)

- 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 [79 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](#)
- Stabler RA, Marsden GL, Witney AA, Li Y, Bentley SD, Tang CM, Hinds J (2005). Identification of pathogen-specific genes through microarray analysis of pathogenic and commensal *Neisseria* species. *Microbiology* **151**:2907-22 [3 isolates](#)
- Tettelin H, Saunders NJ, Heidelberg J, Jeffries AC, Nelson KE, Eisen JA, Ketchum KA, Hood DW, Peden JF, Dodson RJ, Nelson WC, Gwinn ML, DeBoy R, Peterson JD, Hickey EK, Haft DH, Salzberg SL, White O, Fleischmann RD, Dougherty BA, Mason T, Ciecko A, Parksey DS, Blair E, Clifton H, Clark EB, Cotton MD, Utterback TR, Khouri H, Qin H, Vamathevan J, Gill J, Scarlato V, Masignani V, Pizzi M, Grandi G, Sun L, Smith HO, Fraser CM, Moxon ER, Rappuoli R, Venter JC (2000). Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. *Science* **287**:1809-15 [1 isolate](#)

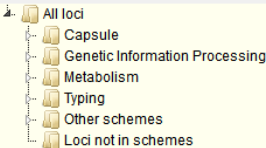
Sequence bin

contigs: 1 detailed breakdown: [Display](#)

length: 2272360 bp

loci tagged: 1283

Schemes and loci


 All loci
 Capsule
 Genetic Information Processing
 Metabolism
 Typing
 Other schemes
 Loci not in schemes

Navigate and select schemes within tree to display allele designations

Click the 'Renumber' button:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: *Keith Jolley (keith)*. [Log out](#) | [Change password](#) Toggle:


Sequence bin for MC58

Contig summary statistics

- Number of contigs: 1
- Length: 2272360
- [Download sequences \(FASTA format\)](#)
- [Download sequences with annotations \(EMBL format\)](#)

Sequence	Sequencing method	Original designation	Length	Comments	float test	SRA accession	test attribute	test date	test int	Locus	Start	End	Direction	EMBL format	Artemis	Renumber
1	Sanger		2272360	whole genome						NEIS2140	502	897	←	EMBL	Artemis	Renumber
										NEIS2141	918	2312	←			
										NEIS2142	2517	3161	←			
										NEIS2143	3158	3511	←			
										NEIS2144	3635	4117	→			
										NEIS2145	4311	4961	→			
										NEIS2146	4958	5875	→			
										NEIS2147	5936	6214	→			
										NEIS2148	6281	7492	←			
										(pgk)						
										NEIS2149	7573	8826	←			
										NEIS2150	9346	10317	←			
										NEIS2151	10350	10811	←			
										NEIS2152	10840	12177	←			
										(kdtA)						
										NEIS2153	12174	13622	←			
										NEIS0001	15221	16144	←			

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


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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
NEIS2140	2181973	502
NEIS2141	2182389	918
NEIS2142	2183899	2517
NEIS2143	2184552	3158
NEIS2144	2185029	3635
NEIS2145	2185705	4311
NEIS2146	2186352	4958
NEIS2147	2187330	5936
NEIS2148	2187675	6281
NEIS2149	2188934	7573
NEIS2150	2190551	9346
NEIS2151	2191558	10350
NEIS2152	2192048	10840
NEIS2153	2193382	12174
NEIS0001	1261	15221
NEIS0210	209923	17229
piIS	3271	18127
NEIS0004	4069	23904
NEIS0005	4476	24311
NEIS0007	5843	25679

5.23 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.

Table	Add	Batch Add	Update or delete	Comments
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.





Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
PCR locus links	+	++	?	Link a locus to an <i>in silico</i> PCR reaction.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
probe locus links	+	++	?	Link a locus to an <i>in silico</i> hybridization reaction.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.


 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)
Toggle: 

Add new composite field

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

Record

id:!

strain_designations

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)

datestamp:!

2014-07-08

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.



 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
PCR locus links	+	++		Link a locus to an <i>in silico</i> PCR reaction.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
probe locus links	+	++		Link a locus to an <i>in silico</i> hybridization reaction.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- [Set user passwords](#) - Set a user password to enable them to log on or change an existing password.
- [Configuration check](#) - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

Select the composite field from the list and click 'Update'.

 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)


Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Update or delete composite field

1 composite field defined.

Delete	Update	field name	position after	main display	definition	missing data
Delete	Update	strain_designation	isolate	false	[serogroup]: P1.[PorA_VR1],[PorA_VR2]: [FetA_VR]: ST-[scheme 1:ST] ([scheme 1:clonal_complex])	ND: P1.ND,ND: F-ND: ST-ND (-)

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.


 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Update composite field - strain designation

position after:
 main display:
 curator: Keith Jolley
 timestamp: 2014-04-09

field	empty value	regex	curator	timestamp	delete	edit	move
serogroup [isolate field]	ND		Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
: P1.			Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
PorA_VR1 [locus]	ND		Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
:			Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
PorA_VR2 [locus]	ND		Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
:			Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
FeiA_VR [locus]	F-ND		Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
: ST-			Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
ST [MLST field]	ND		Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
(Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
clonal_complex [MLST field]	-	s/ST-(\S+) complex.*/cc\$1/	Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>
)			Keith Jolley	2009-11-12	<input type="button" value="delete"/>	<input type="button" value="edit"/>	<input type="button" value="up"/> <input type="button" value="down"/>

Add new field:

curator: Keith Jolley
 timestamp: 2014-07-08

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'.

5.24 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.

users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++		Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- [Set user passwords](#) - Set a user password to enable them to log on or change an existing password.
- [Configuration check](#) - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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).

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences	+	++	?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
component fields	+	++	?	Used to restrict component fields available to fields from isolate, loci, sequence fields.

Download the Excel template:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [Z](#)

Batch insert isolate value extended attributes

This page allows you to upload isolate field extended attribute value 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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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

Action

[Back](#)

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'.

5.25 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.

PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.





Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++		Define attributes that can be set for contigs in the sequence bin.
sets	+	++	?	Sets describe a collection of loci and schemes that can be treated like a stand-alone database.
set loci	+	++	?	Add loci to sets.
set schemes	+	++	?	Add schemes to sets.
set metadata	+	++	?	Add metadata collection to sets.
set view	+	++	?	Set database views linked to sets.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- **Set user passwords** - Set a user password to enable them to log on or change an existing password.
- **Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Add new sequence attribute

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

Record

key: read_length
type: integer

Action

Reset Submit

curator: Keith Jolley (keith)
timestamp: 2014-07-15
description:

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Batch insert sequences

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

If an isolate id is chosen, then all sequences will be associated with that isolate. Alternatively, the isolate id, or any other isolate table field that uniquely defines the isolate, can be named in the identifier rows of the FASTA file. This allows data for multiple isolates to be uploaded.

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: !

identifier field:

sender: !

method:

run id:

assembly id:

read length:

Options

☐ Don't insert sequences shorter than bps.

Link to experiment:

Alternatively upload FASTA file

Select FASTA file: No file selected.


Action

[Back](#)

5.26 Checking external database configuration settings

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

user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
	databank scan			
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+		?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++		Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- Set user passwords - Set a user password to enable them to log on or change an existing password.
- Configuration check** - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Configuration check - Neisseria PubMLST

Helper applications

Program	Path	Installed	Executable
EMBOSS infoalign	/usr/bin/infoalign	ok	ok
EMBOSS sixpack	/usr/bin/sixpack	ok	ok
EMBOSS stretcher	/usr/bin/stretcher	ok	ok
blastn	/usr/local/ncbi-blast+/bin/blastn	ok	ok
blastp	/usr/local/ncbi-blast+/bin/blastp	ok	ok
blastx	/usr/local/ncbi-blast+/bin/blastx	ok	ok
ipress	/usr/bin/ipress	ok	ok
mafft	/usr/local/bin/mafft	ok	ok
makeblastdb	/usr/local/ncbi-blast+/bin/makeblastdb	ok	ok
mogrify	/usr/bin/mogrify	ok	ok
muscle	/usr/bin/muscle	ok	ok
tblastx	/usr/local/ncbi-blast+/bin/tblastx	ok	ok

Locus databases

Locus	Database	Host	Port	Table	Primary id field	Secondary id field	Secondary id field value	Sequence field	Database accessible	Sequence query	Sequences assigned
'16S rDNA	pubmlst_bigsdb_neisseria_seqdef	localhost	5432	sequences	allele_id	locus	'16S_rDNA	sequence	ok	ok	197
'porA	pubmlst_bigsdb_neisseria_seqdef	localhost	5432	sequences	allele_id	locus	'porA	sequence	ok	ok	164
'porB	pubmlst_bigsdb_neisseria_seqdef	localhost	5432	sequences	allele_id	locus	'porB	sequence	ok	ok	695
'tpiF	pubmlst_bigsdb_neisseria_seqdef	localhost	5432	sequences	allele_id	locus	'tpiF	sequence	ok	ok	109
BACT000001 (rpsA)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000001	sequence	ok	ok	8189
BACT000002 (rpsB)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000002	sequence	ok	ok	6567
BACT000003 (rpsC)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000003	sequence	ok	ok	5965
BACT000004 (rpsD)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000004	sequence	ok	ok	6195
BACT000005 (rpsE)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000005	sequence	ok	ok	5707
BACT000006 (rpsF)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000006	sequence	ok	ok	4918
BACT000007 (rpsG)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000007	sequence	ok	ok	5667
BACT000008 (rpsH)	bigsdb_multispecies_seqdef	localhost	5432	sequences	allele_id	locus	BACT000008	sequence	ok	ok	5260

Any problems will be highlighted with a red X.

5.27 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 '?' link (Update or delete) next to schemes in the curator's interface.

Project members

Table	Add	Batch Add	Update or delete	Comments
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.
composite fields	+	++	?	Used to construct composite fields consisting of fields from isolate, loci or scheme fields.
sequence attributes	+	++	?	Define attributes that can be set for contigs in the sequence bin.
schemes	+	++	?	Describes schemes consisting of collections of loci, e.g. MLST.
scheme members	+	++	?	Defines which loci belong to a scheme.
scheme fields	+	++	?	Defines which fields belong to a scheme.
scheme groups	+	++	?	Describes groups in to which schemes can belong - groups can also belong to other groups.
scheme group scheme members	+	++	?	Defines which schemes belong to a group.
scheme group group members	+	++	?	Defines which scheme groups belong to a parent group.

- Set user passwords - Set a user password to enable them to log on or change an existing password.
- Configuration check - Checks database connectivity for loci and schemes and that required helper applications are properly installed.

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

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Query schemes for *Neisseria* PubMLST database

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

Search criteria **Display**

id = Order by: id ascending

Display: 25 records per page [?](#)

Filter query by **Action**

isolate display: [?](#) Reset Submit

main display: [?](#)

query field: [?](#)

query status: [?](#)

analysis: [?](#)

allow missing loci: [?](#)

curator: [?](#)

scheme: MLST [?](#)

Click the button 'Export configuration/data'.

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Query schemes for *Neisseria* PubMLST database

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

Search criteria **Display**

id = Order by: id ascending

Display: 25 records per page [?](#)

Filter query by **Action**

isolate display: [?](#) Reset Submit

main display: [?](#)

query field: [?](#)

query status: [?](#)

analysis: [?](#)

allow missing loci: [?](#)

curator: [?](#)

scheme: MLST [?](#)

1 record returned.

Delete **Database configuration**

Delete ALL Export configuration/data

Delete	Update	id	description	dbase name	dbase host	dbase port	dbase table	isolate display*	main display*	query field*	query status*	analysis*	display order	allow missing loci	curator	d
Delete	Update	1	MLST	pubmlst_bigsdb_neisseria_seqdef			mv_scheme_1	true	true	true	true	true	1		Keith Jolley	2

* 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_di
1	MLST	pubmlst_bigsdb_neisseria_seqdef			mv_scheme_1	1 1 1 1 1 1	2	2012-03-22

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	q
1	ST	integer	1	1		/cgi-bin/bigsdb/bigsdb.pl?page=profileInfo&db=pubmlst_neisseria_seqdef&scheme			
1	clonal_complex	text	0	2	1 1 1 1 2	2009-11-16			


Curator's guide

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

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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
			databank scan	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.

Enter the user's details in to the form.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [Z](#)

Add new user

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


Record	Action
id: 286 user name: jbloggs surname: Bloggs first name: Joe email: joe.bloggs@ox.ac.uk affiliation: University of Oxford, UK status: user date entered: 2014-07-09 date stamp: 2014-07-09 curator: Keith Jolley (keith)	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.

6.2 Adding new allele sequence definitions


6.2.1 Single allele

To add a single new allele, click the sequences (all loci) add (+) link on the curator's main page - if only a few loci are defined with permission for the current user to curate then they will be listed individually and the specific locus allele addition links can also be used.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++	FASTA	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.

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 can either be:

- Sanger trace checked
- WGS: manual extract
- WGS: automated extract
- unchecked

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle:

Add new allele sequence

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

Record

locus:!

abcZ

allele id:!

688

sequence:!

TTTGATACCGTTGCCGAAGGTTTGGGTAAATTCGCGATTATTCGCCCGTTACCAACGC
GTCGGTCATGAGTTGGAAACGGTTCGGGTGAGGCTTTGTTGAAGAACTCAACGAATTA
CAACTTGAATCGAAGCGAAGGACGGCTGGAGCTGGATGCCGCAATCAAGCAGACTTTG
GCGGAATCGGTTTGGCGGAAACGAAAAATCGGCACCTTTCGGCGGTGAGAAAAAG
CGTGTCGCTTGGCGAGGCTTGGGTGCGAAGCCGACGTTATTCGCTGGACGAACCG
ACCAACCAATTCGATATGACCGATTATCTGTTGGAAACCTGCTCAAGGCGTTTGA
GGCAGCTTGGTCGTATTACCCACGACCCGCCGTTTTTTGGATAATAICGCTACGCGGATT

status:!

Sanger trace checked

sender:!

Jolley, Keith (keith)

curator:!

Keith Jolley (keith)

date entered:!

2014-07-09

datestamp:!

2014-07-09

comments:

Flags:

atypical
contains IS element
downstream fusion
frameshift
internal stop codon

PubMed ids:

ENA ids:

Genbank ids:

☐ Override sequence similarity check

Action

Reset Submit

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.

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 (all loci) link on the curator's main page.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		




 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Set extended attributes for loci.

Download a template Excel file from the following page.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)
Toggle: 

Batch insert sequences

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', 'WGS: automated extract', 'unchecked'
- Sequence flags can be added as a semi-colon (;) separated list
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)
- 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:

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. 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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Batch insert sequences

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', 'WGS: automated extract', 'unchecked'
- Sequence flags can be added as a semi-colon (;) separated list
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)
- 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

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).


locus	allele_id	sequence	status	comments	flags
abcZ		TTTGATACIGTGGCCGAAGCTTTGGGCGAAATTCGCGATTTATTGCAACGTTATCATCATGTCAGCCATGAGTTGGAAAAAT			
		GGITCGAGTGAGGCTTATGAAAGAGCTCAACGAATIGCAACTTGAGATCGAAGCGAAGGACGCGCTGGAAAGTGGATGCG			
		GCGGTGAAGCGAGACTTTGGGCGAATTCGCGTTTGGCGGAAACGAAAAATCGGCAACTCTCCGCGGTTCAGAAAAAGCGC			
		GTGCGCTTGGCCGAGGCTTGGGTGCGAAGCCGAGCTTTTCTGCTCGATGAAACGACCAACATTTGGACATCGACGCG			
		ATTATTTGGTTGGAAAACTTCTCAAAAGCGTTTGAAGGCGAGCTGGTTGIGATTACCCACGACCGCGTTTTTGGACAAAT			
		ATCGCCACGCGGATTGTGGAACCTCGATC	Sanger trace checked		
abcZ		TTTGATACIGTGGCCGAAGCTTTGGGCGAAATTCGCGATTTATTGCAACGTTATCATCATGTCAGCCATGAGTTGGAAAAAT			
		GGITCGAGTGAGGCTTATGAAAGAGCTCAACGAATIGCAACTTGAGATCGAAGCGAAGGACGCGCTGGAAAGTGGATGCG			
		GCGGTGAAGCGAGACTTTGGGCGAATTCGCGTTTGGCGGAAACGAAAAATCGGCAACTCTCCGCGGTTCAGAAAAAGCGC			
		GTGCGCTTGGCCGAGGCTTGGGTGCGAAGCCGAGCTTTTCTGCTCGATGAAACGACCAACATTTGGACATCGACGCG			
		ATTATTTGGTTGGAAAACTTCTCAAAAGCGTTTGAAGGCGAGCTGGTTGIGATTACCCACGACCGCGTTTTTGGACAAAT			
		ATCGCCACGCGGATTGTGGAACCTCGATC	Sanger trace checked		

[Back](#)

Action
Reset Submit

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)
Toggle: 


Batch insert sequences


Import status
Sender: Keith Jolley
No obvious problems identified so far.

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	sender	curator	date_entered	datestamp	comments	flags
abcZ	688	TTTGATACTGTTGCCGAAGG ... GCGGATTGTGCGAACTCGATC	Sanger trace checked	2	2	2014-07-09	2014-07-09		
abcZ	689	TTTGATACTGTTGCCGAAGC ... GCGGATTGTGCGAACTCGATC	Sanger trace checked	2	2	2014-07-09	2014-07-09		

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


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)
Toggle: 

Batch insert sequences

Import status

Primary key	Problem(s)
locus: abcZ; allele_id:	Sequence contains non nucleotide (G A T C) 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	sender	curator	date_entered	datestamp	comments	flags
abcZ	688	TTTGATACTGTTGCCGAAGG ... GCGGATTGTGCGAACTCGATC	Sanger trace checked	2	2	2014-07-09	2014-07-09		
abcZ	689	TTTGATACTGTTGCCGAAGC ... GCGGATTGTGCGAACTCGATC	Sanger trace checked	2	2	2014-07-09	2014-07-09		

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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rpIF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		





Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and

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


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)
Toggle: 

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
TTTGATACTGTTGCCGAAGCTTTGGGCGAAATTCGCGATTATTGCAACGTTATCATCAT
GTACGCCATGAGTIGSAAAAATGGTTCGAGTGAAGSCTTATTGAAAGAGCTCAACGAAATG
CAACTTGAGATCGAAGCGAAGGACGGCTGGAAGTIGGATGCGGCGGTGAAGCAGACTTTG
GGCGAACTCGGTTTCCGGAACGAAAAATCGGCAACCTCTCCGGCGGTGAGAAAAAG
CGCGTCGCTTGGCGCAGGCTTGGGTGCAGAAGCCGACGTATTGCTGCTCGATGAACCG
ACCAACCATTTGGACATCGACGCGATTATTGGTIGGAAACCTGCTCAAGCGTTTGAA
GGCAGCCTGGTGTGATTACCCACGACCCGCTTTTGGACAATATCACCACGCGGATT
GTGGAACCTCGATC
>isolate2
TTTGATACTGTTGCCGAAGCTTTGGGCGAAATTCGCGATTATTGCAACGTTATCATCAT

```

☐ 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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)


Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)
Toggle: 


Batch insert sequences

Sequence check

Original designation	Allele id	Status	Action
isolate1	688	OK	Upload valid sequences
isolate2	689	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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)
Toggle: 

Batch insert sequences

Sequence check


Original designation	Allele id	Status	Action
isolate1	688	OK	Upload valid sequences
isolate2	689	Sequence contains non nucleotide (G A T C) 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.


In order to update or delete an allele, first you must select it. Click the query (?) sequences (all loci) link - if only a

few loci are defined with permission for the current user to curate then they will be listed individually and the specific locus query links can also be used.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++	FASTA	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		




Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
databank scan				
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these

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 and enter the allele number in the allele_id field.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Toggle: [i](#)

Query sequences for *Neisseria* locus/sequence definitions database

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

Display

Order by: locus

Display: 25 records per page

Filter query by

Action

locus:

status:

sender:

curator:

allele flag:

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Query sequences for *Neisseria* locus/sequence definitions database

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 **Display**

allele id = 4 + [?](#) Order by: locus ascending Display: 25 records per page [?](#)

Filter query by **Action**

locus: abcZ [?](#) Reset Submit

status: [?](#)

sender: [?](#)

curator: [?](#)

allele flag: [?](#)

1 record returned.

[Delete](#) [Database configuration](#) [Flags](#)

[Delete ALL](#) [Export configuration/data](#) [Batch set](#)

Delete	Update	locus	allele id	sequence	sequence length	status	sender	curator	date entered	datestamp	comments	flags
Delete	Update	abcZ	4	TTTGATACCG TTGCGAAGG TTGGGGGAA ATTCTGATT TATTGGCGG TTAICATCAT GTACGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCTTTGT TGAAAGAACT CAACGAATTG CAACTTGAAA	433	Sanger trace checked	Keith Jolley	Man-Suen Chan	2001-02-07	2009-11-11		

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Delete allele sequence

You have chosen to delete the following record:

locus: abcZ

allele id: 4

sequence: TTTGATACCG TTGCGAAGG TTGGGGGAA ATTCTGATT TATTGGCGG TTAICATCAT GTACGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCTTTGT TGAAAGAACT CAACGAATTG CAACTTGAAA
 TCGAAGCGAA GGACGGCTGG AAACCTGGATG CGGCAGTCAA GCAGACTTTG GGGGAATCG GTTTCGCGGA AAATGAAAAA ATCGGCAACC TTTCGCGCGG TCAGAAAAAG CGCGTCGCTT TGGCTCAGGC
 TTGGGTGCAA AAGCCCGACG TATTGCTGCT GGACGAGCCG ACCAACCATT TGGATATCGA CGGATTATT TGGCTGGAAA ATCTGCTCAA AGCGTTTGAA GGCAGCTTGG TTGTGATTAC CCACGACCGC
 CGTTTTTTGG ACAATATCGC CACGCGGATT GTCGAACTCG ATC

status: Sanger trace checked

sender: Keith Jolley

curator: Man-Suen Chan

date entered: 2001-02-07


datestamp: 2009-11-11


comments:

[Delete!](#)

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](#).


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)
Toggle: 

Update allele sequence

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

Record

locus!: **abcZ**
allele id!: **4**
sequence!:

TTTGATACCG TTGCCGAAGG TTTGGGCGAA
AATCGTGATT TATTGCGCCG TTATCATCAT
GTCAGCCATG AGTTGGAAAA TGGTTCGAGT
GAGGCTTTGT TGAAAGAACT CAACGAATTG
CAACTTGAAA TCGAAGCGAA GGACGGCTGG
AAACTGGATG CGGCAGTCAA GCAGACTTTG
GGGGAACTCG GTTTGCCGGA AAATGAAAA

Action

Reset Submit

status!: Sanger trace checked
sender!: Jolley, Keith (keith)
curator!: Keith Jolley (keith)
date entered!: 2001-02-07
datestamp!: 2014-07-09
comments:

Flags:

atypical
contains IS element
downstream fusion
frameshift
internal stop codon

PubMed ids:

ENA ids:

Genbank ids:

6.4 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 next to 'locus descriptions'. 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 next to 'locus descriptions' 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).

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplIF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		



 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank		
		scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.

Either enter the name of the locus in the query box:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: 

Query locus descriptions for *Neisseria* locus/sequence definitions database

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

Search criteria: locus = NEIS0620 [+](#) [i](#) Display: Order by: locus ascending Display: 25 records per page [i](#)

Filter query by: Action

[Reset](#) [Submit](#)

or expand the filter list and select it from the dropdown box:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle: [i](#)

Query locus descriptions for *Neisseria* locus/sequence definitions database

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

Search criteria **Display**

locus: = Order by: locus ascending

☒ **Filter query by** Display: 25 records per page

locus: **Action**

curator: Reset Submit

common name:

Click 'Submit'.

If the locus description exists, click the 'Update' link (if it doesn't, see the note above).

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle: [i](#)

Query locus descriptions for *Neisseria* locus/sequence definitions database

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

Search criteria **Display**

locus: = Order by: locus ascending

☒ **Filter query by** Display: 25 records per page

locus: **Action**

curator: Reset Submit

common name:

1 record returned.

[Delete](#) [Database configuration](#)

[Delete ALL](#) [Export configuration/data](#)

Delete	Update	locus	full name	product	description	curator	timestamp
Delete	Update	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:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Update locus description

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

Record **Action**

locus: **NEIS0620** [Reset](#) [Submit](#)

curator: **Keith Jolley (keith)**

timestamp: **2014-11-04**

full name:

product: **malate oxidoreductase (EC 1.1.1.38)**

description: **Final step in TCA cycle producing oxaloacetate.**

aliases: **NMA0870
NMB0671
NMC0620**

PubMed ids: **14917678**

links: **[http://www.enzyme-database.org](http://www.enzyme-database.org/query.php?ec=1.1.1.38)
/query.php?ec=1.1.1.38|EC 1.1.1.38**

(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.

6.5 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 next to the scheme name (e.g. MLST):


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* locus/sequence definitions


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank		
		scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
locus extended attributes	+	++	?	Define additional fields to associate with sequences of a particular locus.
client databases	+	++	?	Add isolate databases that use locus allele or scheme profile definitions defined in this database - this enables backlinks and searches of these databases when you query sequences or profiles in this database.
client database loci	+	++	?	Define loci that are used in client databases.
client database schemes	+	++	?	Define schemes that are used in client databases. You will need to add the appropriate loci to the client database loci table.
client database fields linked to loci	+	++	?	Define fields in client database whose value can be displayed when isolate has matching allele.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: ?

Add new MLST profile

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

Record

ST: ! 10880
 abcZ: ! 2
 adk: ! 3
 aroE: ! 4
 fumC: ! 122
 gdh: ! 8
 pdhC: ! 4
 pgm: ! 6
 sender: !
 clonal_complex:
 curator: ! Keith Jolley (keith)
 date_entered: ! 2014-07-10
 datestamp: ! 2014-07-10
 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:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria locus/sequence definitions*

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	+	++ FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.

Click the 'Download submission template (xlsx format)' link to download an Excel submission template.

 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: 


Batch insert MLST profiles


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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

Please paste in tab-delimited text (include a field header line)

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loci: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Batch insert MLST profiles

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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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
Sender: Jolley, Keith (keith)
Value will be overridden if you include a sender field in your pasted data.
☐ Ignore duplicate profiles

Action
Reset Submit

[Back](#)

You will be given a final confirmation page stating what will be uploaded. If you wish to proceed with the submission, click 'Import data'.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: ?

Batch insert MLST profiles

Import status
 Sender: Keith Jolley
 No obvious problems identified so far.

[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	timestamp
10880	2	3	4	122	8	4	6		2	2	2014-07-10	2014-07-10


6.6 Updating and deleting scheme profile definitions

In order to update or delete a scheme profile, first you must select it. Click the query (?) profiles link next to the scheme name (e.g. MLST):

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria locus/sequence definitions

 **Add, update or delete records**

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
locus descriptions	+	++	?	
scheme curator control list	+	++	query batch	Define which curators can add or update profiles for particular schemes.
locus curator control list	+	++	query batch	Define which curators can add or update sequences for particular loci.
sequences (all loci)	++	FASTA	?	
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
PubMed links (to sequences)	+	++	?	
MLST profiles	+	++	query browse list batch update	
rplF species profiles	+	++	query browse list batch update	
PubMed links (to profiles)	+	++		


 **Database configuration**

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		

Search for your profile by entering search criteria (alternatively you can use the browse or list query functions).

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle:

Query/update profiles - *Neisseria* locus/sequence definitions

Schemes
 Please select the scheme you would like to query:

MLST

Locus/scheme fields **Display/sort options**

ST Order by: ST
 Display: 25 records per page

Filter query by **Action**

clonal complex:

1 record returned.

[Delete](#)

Delete	Update	ST	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	clonal complex
Delete	Update	4563	2	7	6	13	9	18	8	ST-167 complex

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!'.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Loci: [Add](#)
 MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)


Delete profile


You have chosen to delete the following record:

```

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
  
```

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Loc: [Add](#)
MLST profiles: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Update profile

Record


Action

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: ! 2014-07-10
PubMed ids:

6.7 Adding isolate records

To add a single record, click the add (+) isolates link on the curator's index page.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.

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.

[Database: Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
[Users: Add](#) | [Query/update](#)
[Isolates: Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle:

Add new isolate

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

Isolate fields

id: 30457

isolate: J323_2

country: UK

species: *Neisseria meningitidis*

sender: Jolley, Keith (keith)

curator: **Keith Jolley (keith)**

date entered: 2014-07-10

datestamp: 2014-07-10

region:

year: 2014

epidemiological year:

age yr:

age mth:

sex:

disease: meningitis

source: CSF

epidemiology:

serogroup: B

MLEE designation:

serotype:

sero subtype:

ET no:

penicillin:

penicillin range:

amoxicillin:

sulphonamide:

ceftriaxone:

Allele designations

MLST

abcZ	adk	aroE	fumC
gdh	pdhC	pgm	

Finotyping antigens


PorA VR1	PorA VR2	FetA VR

Action

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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.





Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.

Download a submission template in Excel format from the link.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)
Toggle: 

Batch insert isolates

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.
- Enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- 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. 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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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).


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Batch insert isolates

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.
- Enter aliases (alternative names) for your isolates as a semi-colon (;) separated list.
- 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. 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.

- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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).

isolate aliases references country region year epidemiological_year

age_yr age_mth sex disease source epidemiology species serogroup

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 pending_assembly assembly_status ENA_accession

private_project comments abcZ adk aroF fumC qdh pdhC

pgm


J392_1 UK 2014 12 male


meningitis and septicaemia CSF Neisseria meningitidis

B

Action
Reset Submit

Press submit. Data are checked for consistency and if there are no problems you can then confirm the submission.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)
Toggle: 

Batch insert isolates

Import status
Sender: Keith Jolley
No obvious problems identified so far.

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	epidemiological_year	age_yr	age_mth	sex	disease	source	epidemiology	species	serogroup	MLEE_desig
30457	J392_1			UK		2014		12		male	meningitis and septicaemia	CSF		Neisseria meningitidis	B	

Any problems with the data will be listed and highlighted within the table. Fix the data and resubmit if this happens.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#) Toggle: [Z](#)

Batch insert isolates

Import status

Primary key	Problem(s)
id: 30457	species 'Neisseria meningitidis' 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.

id	isolate	aliases	references	country	region	year	epidemiological_year	age_yr	age_mth	sex	disease	source	epidemiology	species	serogroup	MLEE_desig
30457	J392_1			UK		2014		12		male	meningitis and septicaemia	CSF		Neisseria meningitidis	B	


6.8 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST

 **Add, update or delete records**

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.


 **Database configuration**

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridisation reactions to filter genomes for tagging to specific repetitive loci.

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Toggle: [?](#) Field help: [id](#) [Go](#)

Isolate query/update

Isolate provenance/phenotype fields

Combine with: **AND**

country = USA + [?](#)

year = 2009

Display/sort options

Order by: **id** ascending

Display: 25 records per page [?](#)

Action

[Reset](#) [Submit](#)

19 records returned. Click the hyperlinks for detailed information.

[Delete](#) [Tag scanning](#) [Projects](#)

[Delete ALL](#) [Scan](#) [Select project...](#) [Link](#)

Delete	Update	Sequence bin	New version	Isolate fields ?								Seqbin size (bp)	MLST		Finely	
				id	isolate	aliases	country	year	disease	species	serogroup		ST	clonal complex	PorA VR1	PorA VR2
delete	update	upload	create	12674	M18700		USA	2009		Neisseria meningitidis	B	0	7301	ST-32 complex/ET-5 complex	add	ac
delete	update	upload	create	12675	M18701		USA	2009		Neisseria meningitidis	B	0	7302		add	ac
delete	update	upload	create	12676	M18725		USA	2009		Neisseria meningitidis	B	0	7303		add	ac
delete	update	upload	create	13090	M19024	PA09015	USA	2009	meningitis	Neisseria meningitidis	B	0	7575		add	ac
delete	update	upload	create	14627	M20918		USA	2009		Neisseria meningitidis	A	1718070	4789, 7980	ST-5 complex/subgroup III	update	upd
delete	update	upload	create	14998	M21319		USA	2009	invasive	Neisseria	B	0	8250	ST-60 complex	add	ac

Clicking the 'Delete' link takes you to a page displaying the full isolate record.

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Delete isolate

You have selected to delete the following record:

Provenance/meta data

id: 14627	source: CSF	update history: 26 updates show details
isolate: M20918	species: <i>Neisseria meningitidis</i>	date entered: 2010-01-26
strain designation: A: P1.20.9: F3-1: ST- 4789.7980 (cc5)	serogroup: A	datestamp: 2014-06-17
country: USA	sender: Xin Zhao, Novartis (formerly at US CDC)	
continent: North America	curator: Carina Brehony, University of Oxford, UK (E-mail: carina.brehony@zoo.ox.ac.uk)	
region: IA		
year: 2009		

Publication (1)

- Kislyuk 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 [18 isolates](#)

Sequence bin


contigs: 2049	N90: 456
total length: 1718070 bp	N95: 324
max length: 5436 bp	loci tagged: 979
mean length: 839 bp	detailed breakdown: Display
N50: 1155	

Action

[Delete](#)

Pressing 'Delete' from this record page confirms the deletion.































Clicking the 'Update' link for an isolate takes you to an update form. Make the required changes and click 'Update'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Update isolate


Isolate fields

id: **14627** 
isolate: M20918 
country: USA 
species: **Neisseria meningitidis** 
sender: Zhao, Xin (xinzha) 
curator: **Keith Jolley (keith)** 
date entered: **2010-01-26** 
datestamp: **2014-07-10** 
region: IA 
year: 2009 
epidemiological year: 
age yr: 
age mth: 
sex: 
disease: 
source: CSF 
epidemiology: 
serogroup: A 
MLEE designation: 
serotype: 
sero subtype: 
ET no: 
penicillin: 
penicillin range: 
amoxicillin: 
sulphonamide: 
ceftriaxone: 
ceftriaxone range: 
chloramphenicol: 
chloramphenicol range: 


Loci

- All loci
 - Genetic Information Processing
 - Metabolism
 - Pilin
 - Typing
 - Other schemes
 - Loci not in schemes

Navigate and select schemes within tree to display allele designations

Locus: '16S_rDNA'  [Add/update](#)

Allele designations can also be updated by clicking within the scheme tree and selecting the 'Add' or 'Update' link next to a displayed locus.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Update isolate

Isolate fields

id: **14627**

isolate: M20918

country: USA

species: *Neisseria meningitidis*

sender: Zhao, Xin (xinzha)

curator: **Keith Jolley (keith)**

date entered: 2010-01-26

datestamp: 2014-07-10

region: IA

year: 2009

epidemiological year:

age yr:

age mth:

sex:

disease:

source: CSF

epidemiology:

serogroup: A

MLEE designation:

serotype:

sero subtype:

ET no:

penicillin:

penicillin range:

amoxicillin:

sulphonamide:

ceftriaxone:

ceftriaxone range:

chloramphenicol:

chloramphenicol range:

Loci

- All loci
 - Genetic Information Processing
 - Metabolism
 - Pilin
 - Typing**
 - Other schemes
 - Loci not in schemes

Navigate and select schemes within tree to display allele designations

Locus: '16S_rDNA' [Add/update](#)

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Update isolate

Isolate fields

id: 14627 [i](#)

isolate: M20918 [i](#)

country: USA [i](#)

species: *Neisseria meningitidis* [i](#)

sender: Zhao, Xin (xinzha) [i](#)

curator: Keith Jolley (keith) [i](#)

date entered: 2010-01-26 [i](#)

datestamp: 2014-07-10 [i](#)

region: IA [i](#)

year: 2009 [i](#)

epidemiological year: [i](#)

age yr: [i](#)

age mth: [i](#)

sex: [i](#)

disease: [i](#)

source: CSF [i](#)

epidemiology: [i](#)

serogroup: A [i](#)

MLEE designation: [i](#)

serotype: [i](#)

sero subtype: [i](#)

ET no: [i](#)

penicillin: [i](#)

penicillin range: [i](#)

amoxicillin: [i](#)

sulphonamide: [i](#)

ceftriaxone: [i](#)

ceftriaxone range: [i](#)

chloramphenicol: [i](#)

chloramphenicol range: [i](#)

Loci


- All loci
- Genetic Information Processing
- Metabolism
- Pilin
- Typing
 - MLST**
 - Finetyping antigens
 - Antigen genes
 - Ribosomal MLST

MLST

abcZ	adk	aroE	fumC	gdh
1 S update	1 S update	2 S update	1 S update	3 S update
pdhC	pgm	ST	clonal complex	
6, 334 S update	19 S update	4789, 7980	ST-5 complex/subgroup III	

Locus: '16S_rDNA' [Add/update](#)

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)** | [Log out](#) | [Change password](#)

Update isolate

Isolate fields

id: **14627**

isolate: M20918

country: USA

species: **Neisseria meningitidis**

sender: Zhao, Xin (xinzhao)

curator: **Keith Jolley (keith)**

date entered: **2010-01-26**

datestamp: **2014-07-10**

region: IA

year: 2009

epidemiological year:

age yr:

age mth:

sex:

disease:

source: CSF

epidemiology:

serogroup: A

MLEE designation:

serotype:

sero subtype:

ET no:

penicillin:

penicillin range:

amoxicillin:

sulphonamide:

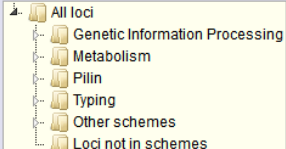
ceftriaxone:

ceftriaxone range:

chloramphenicol:

chloramphenicol range:

Loci



Navigate and select schemes within tree to display allele designations

Locus: **abcZ**

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Update *abcZ* allele for isolate 14627

Provenance/meta data

id: 14627
 isolate: M20918
 strain designation: A: P1.20.9: F3-1: ST-4789,7980 (cc5)
 country: USA
 region: IA
 year: 2009
 source: CSF
 species: *Neisseria meningitidis*
 serogroup: A
 sender: Xin Zhao
 curator: Carina Brehony
 update history: [26 updates](#) [show details](#)
 date entered: 2010-01-26
 datestamp: 2014-06-17

Update other loci:
 Locus: *abcZ*

Locus: *abcZ*

Add new allele designation

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

Record

isolate id: 14627
 locus: *abcZ*
 allele id: 5
 sender: Jolley, Keith (keith)
 status: confirmed
 method: manual
 curator: Keith Jolley (keith)
 datestamp: 2014-07-10
 date entered: 2014-07-10
 comments:

Action

Existing designations

Update	Delete	allele id	sender	status	method	comments
<input type="button" value="Update"/>	<input type="button" value="Delete"/>	1	Xin Zhao	confirmed	manual	


6.9 Batch updating multiple isolate records

Select 'batch update' isolates link on the curator's index page.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Database curator's interface - Neisseria PubMLST

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.


 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		database scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.

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'.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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/focus 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.
- The script is compatible with STARS output files.

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

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Batch isolate update

The following changes will be made to the database. Please check that this is what you intend and then press 'Upload'. 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

[Back to main page](#)

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

6.10 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 Query isolates link:


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.

Enter search criteria that specifically return the isolates you wish to delete. Click 'Delete ALL'.

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#) Toggle: [?](#) Field help: [id](#) [Go](#)

Isolate query/update

Isolate provenance/phenotype fields — Display/sort options

Combine with: **AND**
 date entered = 2014-03-17 + [?](#)
 curator (surname) = Jolley

Order by: **id** ascending
 Display: 25 records per page [?](#)

Action
[Reset](#) [Submit](#)

3 records returned. Click the hyperlinks for detailed information.

[Delete](#) [Tag scanning](#) [Projects](#)
[Delete ALL](#) [Scan](#) [Select project...](#) [Link](#)

Delete	Update	Sequence bin	New version	Isolate fields ?								Seqbin size (bp)	MLST		Finotyping antigens			
				id	isolate	aliases	country	year	disease	species	serogroup		ST	clonal complex	PorA VR1	PorA VR2	FetA VR	
delete	update	upload	create	28783	0012/14		Czech Republic	2014	carrier	Neisseria meningitidis	W	0	10733			5-2	10-1	F5-8
delete	update	upload	create	28784	0014/14		Czech Republic	2014	carrier	Neisseria meningitidis	B	0	35	ST-35 complex		22-1	14	F4-1
delete	update	upload	create	28785	0015/14		Czech Republic	2014	invasive (unspecified/other)	Neisseria meningitidis	B	0	10734	ST-41/44 complex/Lineage 3		22-1	14	F5-2

You will have a final chance to change your mind:

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Delete multiple isolate records

If you proceed, you will delete 3 isolate records. Please confirm that this is your intention.

[Confirm deletion!](#)




Click 'Confirm deletion!'.

6.11 Uploading sequence contigs linked to isolate records


6.11.1 Select isolate from drop-down list

To upload sequence data, click the sequences batch add (++) link on the curator's main page.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.



Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.

Select the isolate that you wish to link the sequence to from the dropdown list 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Batch insert sequences

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

If an isolate id is chosen, then all sequences will be associated with that isolate. Alternatively, the isolate id, or any other isolate table field that uniquely defines the isolate, can be named in the identifier rows of the FASTA file. This allows data for multiple isolates to be uploaded.

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:

```
TTTAATCTAAAAATATATTTTTCAAAGTACTCATATTTAGTTAGTTTCCTTTTACT
GGGTATGTAGTAATCAAATTCCTGACTATCTGTAAATACCTTAATGTAGTTGTGGGT
TGTCACCTCTTTTAATAGAGTAGTACCAATAACCTTTCTACATCGACAGTCCGCATA
TATTGGCCATCAGGAGTCATGATACGGAGAAAGAACTCTTTATTACTTTGAAGTATA
ACCTTCAATTCATTGGGGAGATGTAAGAACTGAACGGTTATCGCAATAGGCCTATGG
AAGTGGCCCTCAAGAACATGCTCAAGCCAGCAGATACGGTTGTCCGGTTTGTCTCAT
GGTGTATATCGAGTAGTACTATTGCTATATTAATTCGTGTATTACAGCACCTATATT
TTTGATTCTGTAGTAGCCATCAAGTCTTTTAACTGTCTGGGTGGTATAGCTGTCTG
SCCGCTTCGCTTTCGACAACGCCCCACAGCGCTTCCCAAGCGTTGCCTACCGTTACC
SCACCCGTGGCGATTCCCGCGCCCTTCGGAGCGCTGAGTGACCATGACAGTACAACCA
GAAGGATTAGCCATGCAGGTGCTGATAGCTAATTTACCGCTGTACCGATCAGCGAGCT
GTCCAACTCGACGATAAACCCTAGCTGTGTAATCAATCGGGCTGTGATGCCAATTA
CGGATATTGCTTATCCAAATGGCAGCATCCTTATCTGCGGATTAGTCATCGCACTGCC
SCATGTGCGGCAATAACTTTGGATGATTTTTCAGTGGCGTTTGTCTGGGCTTCTGC
GGTTGATGCTTTTTCGCAATGGTAGGGGTACTGTCAAAATCAAGCAITATTCACTACC
SCCACTCGCCGCGCTTCGCCAGTATTACATCGCCCGCTTGAGTGCCGCCACGCTG
CCGGCAATAATCTTCGAGTAAGTATAACCTTATGCTTTCCGCACTGCTGAGTGTAGCA
GGGTTCTGCGGCCAAGTAGGATTGAGTACGATTTCCCAACTGCTGCGCAATTGGC
CGCTCTTACATTTCTGTACCAATCGGTAAACACACCCAGCCAAAGCGTGGGCGAAC
TGTTTGGCAACATA
```

Attributes

isolate id: 2) 120M
 identifier field: id
 sender: Jolley, Keith (keith)
 method:
 run id:
 assembly id:

Options

☐ Don't insert sequences shorter than 250 bps.
 Link to experiment:

Alternatively upload FASTA file

Select FASTA file: No file selected.

[Back](#)

Click 'Submit'. A summary of the number of isolates and their lengths will be displayed. To confirm upload, click 'Upload'.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Batch insert sequences

The following sequences will be entered.

Original designation	Sequence length	Comments
180426 NODE_1211_length_26135_cov_16.536217	26167	
180427 NODE_619_length_1208_cov_9.455298	1240	
180428 NODE_655_length_1534_cov_15.418513	1566	
180429 NODE_675_length_1548_cov_17.753876	1580	
180430 NODE_31_length_8390_cov_14.525030	8422	
180431 NODE_254_length_2721_cov_18.400587	2753	
180432 NODE_262_length_1955_cov_8.388747	1987	
180433 NODE_252_length_30791_cov_15.767627	30823	
180434 NODE_189_length_536_cov_31.078358	568	
180435 NODE_716_length_511_cov_12.113503	543	
180436 NODE_465_length_13739_cov_15.131669	13771	
180437 NODE_38_length_15888_cov_17.174660	15920	
180438 NODE_778_length_2398_cov_8.673060	2430	
180439 NODE_1765_length_657_cov_8.754947	689	
180440 NODE_729_length_255_cov_13.007843	287	
180441 NODE_52_length_16337_cov_17.192997	16369	
180442 NODE_190_length_652_cov_116.434052	684	
180443 NODE_95_length_3094_cov_14.927279	3126	
180444 NODE_770_length_5072_cov_12.878943	5104	
180445 NODE_263_length_1223_cov_10.451349	1255	
180446 NODE_181_length_4496_cov_14.635231	4528	
180447 NODE_558_length_4436_cov_14.670198	4468	
180448 NODE_1179_length_917_cov_13.504908	949	
180449 NODE_527_length_4033_cov_15.608480	4065	
180450 NODE_212_length_2435_cov_12.223409	2467	
180451 NODE_54_length_790_cov_9.398734	822	
180452 NODE_146_length_12761_cov_14.578794	12793	
180453 NODE_11_length_16414_cov_13.733703	16446	
180454 NODE_386_length_3699_cov_13.323060	3731	
180455 NODE_215_length_395_cov_4.250633	427	

- Number of contigs: 359
- Minimum length: 265
- Maximum length: 33563
- Total length: 2059411
- Mean length: 5736
- N50: 10581
- N90: 3126
- N95: 1863

It is also possible to upload data for multiple isolates at the same time, but these must exist as single contigs for each isolate. To do this, select 'Read identifier from FASTA' in the isolate id field and select the field that you wish to use as the identifier in the 'identifier field', e.g. to use isolate names select 'isolate' here.

PubMLST Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password Toggle: [i]

Batch insert sequences

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

If an isolate id is chosen, then all sequences will be associated with that isolate. Alternatively, the isolate id, or any other isolate table field that uniquely defines the isolate, can be named in the identifier rows of the FASTA file. This allows data for multiple isolates to be uploaded.

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:

```
>0021/93
GAAGCGAAAAAATCATTGACGAAGGCGGCTTGGTGGCGGACGACATCATTCGSCATG
GTCAAGAAACGCAATCGCGCAAGACGACTGCAAAAACGGTTTCCTGTTGACGGTTTCGG
CGCACATTGGCACAAGCGGAAGCGATGGTGAAGCAGGCGTGGATTGGATGCGATCGT
GAAATCGACGTGCTTACACGCTGATTGTGACCGGTATGACGGGCCCGCGCGTGCATTG
SCITCCGSCGCTTACACGCTTACCTACACCGCCCGCCAAAGTGAAGGCAAGACGAC
GTAAACGSCGAAGATTGATTGACGCGGACGACGACAAAGAGAACCGTGAAAAACGC
CTTGGCGTTTACACGAGCAACCGAAGTTTGGTGGATTGTTTACAGCAAACTGGAAAGC
GAACACGCGGCTAAATATATCAAGTTGACGCGGCTGACCGGTA
>0030/93
GAAGCGAAAAAATCATTGACGAAGGCGGCTTGGTGGCGGACGACATCATTCGSCATG
GTCAAGAAACGCAATCGCGCAAGACGACTGCAAAAACGGTTTCCTGTTGACGGTTTCGG
CGCACATTGGCACAAGCGGAAGCGATGGTGAAGCAGGCGTGGATTGGATGCGATCGT
GAAATCGACGTGCTTACACGCTGATTGTGACCGGTATGACGGGCCCGCGCGTGCATTG
SCITCCGSCGCTTACACGCTTACCTACACCGCCCGCCAAAGTGAAGGCAAGACGAC
GTAAACGSCGAAGATTGATTGACGCGGACGACGACAAAGAGAACCGTGAAAAACGC
CTTGGCGTTTACACGAGCAACCGAAGTTTGGTGGATTGTTTACAGCAAACTGGAAAGC
GAACACGCGGCTAAATATATCAAGTTGACGCGGCTGACCGGTA
>0033/93
GAAGCGAAAAAATCATTGACGAAGGCGGCTTGGTGGCGGACGACATCATTCGSCATG
GTCAAGAAACGCAATCGCGCAAGACGACTGCAAAAACGGTTTCCTGTTGACGGTTTCGG
```

Attributes

isolate id: ! Read identifier from FASTA

identifier field: isolate

sender: ! Jolley, Keith (keith)

method: [v]

run id: []

assembly id: []

Options

☐ Don't insert sequences shorter than 250 bps.

Link to experiment: [v]

Alternatively upload FASTA file

Select FASTA file: [Browse...] No file selected.

Action

[Reset] [Submit]

Back

Provided the identifier used uniquely identifies the isolate you will get a confirmation screen. If the isolate name does not do this you'll probably have to use the database id number instead. Click 'Upload' to confirm.

PubMLST Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password Toggle: [i]

Batch insert sequences

The following sequences will be entered. Any problems are highlighted.

BIGSdb id	Identifier field (isolate)	Sequence length	Comments	Status
938	0021/93	465		Will upload
944	0030/93	465		Will upload
946	0033/93	465		Will upload

[Upload]

6.11.2 Select from isolate query

As an alternative to selecting the isolate from a dropdown list (which can become unwieldy for large databases), it is also possible to upload sequence data following an isolate query.

Click the isolate query link from the curator's main page.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++		Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++		Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.

Enter your search criteria. From the list of isolates displayed, click the 'Upload' link in the sequence bin column of the appropriate isolate record.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Toggle: [?](#) Field help: [id](#) [Go](#)

Isolate query/update

Isolate provenance/phenotype fields: isolate = FAM18 [+](#) [?](#)

Display/sort options: Order by: id ascending Display: 25 records per page [?](#)

Action: [Reset](#) [Submit](#)

1 record returned. Click the hyperlink for detailed information.

[Delete](#) [Tag scanning](#) [Projects](#)

[Delete ALL](#) [Scan](#) [Select project...](#) [Link](#)

Delete	Update	Sequence bin	New version	Isolate fields ?							Seqbin size (bp)	MLST		Finotyping antigens			
				id	isolate	aliases	country	year	disease	species	serogroup		ST	clonal complex	PorA VR1	PorA VR2	FetA VR
delete	update	upload	create	698	FAM18	Z4259	USA	1983	invasive (unspecified/other)	Neisseria meningitidis	C	2194961	11	ST-11 complex/ET-37 complex	5 update	2 update	F1-30 update

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.

PubMLST Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) Log out | [Change password](#) Toggle: ?

Batch insert sequences

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

If an isolate id is chosen, then all sequences will be associated with that isolate. Alternatively, the isolate id, or any other isolate table field that uniquely defines the isolate, can be named in the identifier rows of the FASTA file. This allows data for multiple isolates to be uploaded.

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: ! 698) FAM18

sender: !

method:

run id:

assembly id:

Options

☐ Don't insert sequences shorter than 250 bps.

Link to experiment:

Alternatively upload FASTA file

Select FASTA file:

No file selected.

Action

[Back](#)

6.11.3 Upload options

On the upload form, you can select to filter out short sequences from your contig list.

If your database has experiments defined (experiments are used for grouping sequences and can be used to filter the sequences used in [tag scanning](#)), you can also choose to upload your contigs as part of an experiment. To do this, select the experiment from the dropdown list box.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Batch insert sequences

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

If an isolate id is chosen, then all sequences will be associated with that isolate. Alternatively, the isolate id, or any other isolate table field that uniquely defines the isolate, can be named in the identifier rows of the FASTA file. This allows data for multiple isolates to be uploaded.

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: ! Read identifier from FASTA

identifier field: id

sender: !

method:

run id:

assembly id:

Options

☐ Don't insert sequences shorter than 250 bps.

Link to experiment:

Alternatively upload FASTA file

Select FASTA file:

Browse... No file selected. Reset Submit

[Back](#)

6.12 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.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

Database curator's interface - Neisseria PubMLST

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences	+	++	?	Add links associating sequences to experiments.
sequence tags			scan	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.

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.

Select either individual loci or schemes (collections of loci) to scan against. Again, multiple selections can be made.

Database: Species home | Curator's page (species) | Curator's page (database)
 Users: Add | Query/update
 Isolates: Add | Query/update | Batch insert

Logged in: Keith Jolley (keith). Log out | Change password

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

- 19) S3131
- 24) S4355
- 30) 14
- 31) 10
- 34) 20
- 35) 26
- 46) 255
- 52) 243
- 61) 393
- 64) 254
- 67) S5611

All None

Loci

- a2 (pgm)
- abcZ (NEIS1015)
- abcZ (test)
- aceF (NEIS1279)
- acnA (NEIS1729)
- acnB (NEIS1492)
- adk
- adk (NEIS0767)
- aroE
- aroE (NEIS1810)
- aspA

All None

Schemes

- All loci
- Capsule
- Genetic Information Process
- Metabolism
- Typing
- MLST
- Finotyping antigens
- Antigen genes
- eMLST (20 locus parti

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)

☐ Use TBLASTX

☐ Hunt for nearby start and stop codons

☐ Return partial matches even when exact matches are found

☐ Rescan even if allele designations are already set

☐ Rescan even if allele sequences are tagged

☐ 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

Options can be returned to their default setting by clicking the 'Defaults' button.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

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

- 19) S3131
- 24) S4355
- 30) 14
- 31) 10
- 34) 20
- 35) 26
- 46) 255
- 52) 243
- 61) 393
- 64) 254
- 67) S5611

[All](#) [None](#)

Loci

- a2 (pgm)
- abcZ (NEIS1015)
- abcZ (test)
- aceF (NEIS1279)
- acnA (NEIS1729)
- acnB (NEIS1492)
- adk
- adk (NEIS0767)
- aroE
- aroE (NEIS1810)
- aspA

[All](#) [None](#)

Schemes

- All loci
- Capsule
- Genetic Information Process
- Metabolism
- Typing
- MLST
- Finotyping antigens
- Antigen genes
- eMLST (20 locus parti

Parameters [Defaults](#)

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)

☒ Use TBLASTX [?](#)

☐ Hunt for nearby start and stop codons [?](#)

☐ Return partial matches even when exact matches are found

☐ Rescan even if allele designations are already set

☐ Rescan even if allele sequences are tagged

☐ Mark missing sequences as provisional allele '0'

Restrict included sequences by

Sequence method: [?](#)

Project: [?](#)

Experiment: [?](#)

Action

[Reset](#) [Scan](#)

Press 'Scan'. The system takes approximately 1-2 seconds to identify each sequence (depending on machine speed and size of definitions databases). Any identified sequences will be listed in a table, with checkboxes indicating whether allele sequences or sequence regions are to be tagged.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

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"/>
												extract →				
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"/>
												extract →				
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"/>
												extract →				
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"/>
												extract →				
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"/>
												extract →				
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"/>
												extract →				
34) 20	exact	pgm ^(a2)	3	100.00	450	450	0.0	182831	24559	25008	24559	25008	→	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="text"/>
												extract →				

Action

Started: Thu Jul 10 11:26:16 2014
 Finished: Thu Jul 10 11:26:30 2014
 Elapsed time: 14 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

6.13 Projects

6.13.1 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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.


 Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.
isolate field extended attributes	+	++	?	Define additional attributes to associate with values of a particular isolate record field.

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.

New in version 1.10.0: 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.

Click 'Submit'.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#). [Log out](#) | [Change password](#) Toggle: [?](#)

Add new project description

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

Record

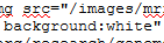
id:

short description:

curator:

timestamp:

full description:




The [MRF Meningococcus Genome Library](http://www.meningitis.org/research/genome) is a collaboration between Public Health England, The Wellcome Trust, Sanger Institute and the University of Oxford, funded by the Meningitis Research Foundation.

Use of the MRF Genome Library data [cgi-bin/bigadb](#)

Action


6.13.2 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.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Database curator's interface - Neisseria PubMLST


Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations		++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences			?	Add links associating sequences to experiments.
sequence tags		scan	?	Tag regions of sequences within the sequence bin with locus information.




Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
		databank scan		
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.

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'.


Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
Users: [Add](#) | [Query/update](#)
Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: **Keith Jolley (keith)**. [Log out](#) | [Change password](#)

Toggle: [?](#)

Add new project member

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

Record

Action

project id: MRF Meningococcus Genome Library

isolate id: 18968

curator: Keith Jolley (keith)

timestamp: 2014-07-10

Reset

Submit

To add isolates in batch mode. Click the batch add (++) project members link on the curator's main page.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

Database curator's interface - *Neisseria* PubMLST

 Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.

Download an Excel submission template:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#)

Batch insert project members

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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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

Action

[Back](#)

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 Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [\[i\]](#)

Batch insert project members

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.
- [Download tab-delimited header for your spreadsheet](#) - use Paste special → text to paste the data.
- [Download submission template \(xlsx format\)](#)

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

project_id	isolate_id
3	18968
3	18969
3	19023
3	19024
3	19025
3	19026
3	19027
3	19028
3	19029
3	19030
3	19031
3	19032
3	19958
3	19959
3	19960
3	19961
3	19962
3	19963
3	19964
3	19965

Back

Action:

6.14 Isolate record versioning

New in version 1.9.0.

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:

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Full information on isolate 5

Provenance/meta data

id: 21	source: throat swab	update history: 1 update show details
isolate: 5	epidemiology: endemic	date entered: 2014-06-30
strain designation: NG: P1.ND.ND: F-ND: ST-ND (-)	species: <i>Neisseria meningitidis</i>	datestamp: 2014-06-30
country: Germany	serogroup: NG	
continent: Europe	comments: Bavarian carriage study	
region: Volkach	sender: Ulrich Vogel, University of Wuerzburg, Wuerzburg, Germany	
year: 1999	curator: Keith Jolley, University of Oxford, UK (E-mail: keith.jolley@zoo.ox.ac.uk)	
age yr: 18		
disease: carrier		

Versions
More than one version of this isolate record exist.
Older versions: [20](#)

Publication (1)

- Claus H. Maiden MC, Wilson DJ, McCarthy ND, Jolley KA, Urwin R, Hessler F, Frosch M, Vogel U (2005). Genetic analysis of meningococci carried by children and young adults. *J Infect Dis* **191**:1263-71

[822 isolates](#)

Schemes and loci
No loci available for analysis.

The different versions will also be listed in analysis plugins, with old versions identified with an [old version] designation after their name.

To create a new version of an isolate record, query or browse for the isolate:

PubMLST Database: Species home | Curator's page (species) | Curator's page (database)
Users: Add | Query/update
Isolates: Add | Query/update | Batch insert

Logged in: [Keith Jolley \(keith\)](#). Log out | Change password

Database curator's interface - *Neisseria* PubMLST

Datasets
This database contains multiple datasets. You can choose to display a single set or the whole database.
Please select: [Whole database](#) [Choose](#)

Add, update or delete records

Record type	Add	Batch Add	Update or delete	Comments
users	+	++	?	
user groups	+	++	?	Users can be members of these groups - use for setting access permissions.
user group members	+	++	?	Add users to groups for setting access permissions.
user permissions	+	++	?	Set curator permissions for individual users - these are only active for users with a status of 'curator' in the users table.
isolates	+	++	query browse list batch update	
isolate field extended attribute values	+	++	?	Add values for additional isolate field attributes.
projects	+	++	?	Set up projects to which isolates can belong.
project members	+	++	?	Add isolates to projects.
isolate aliases	+	++	?	Add alternative names for isolates.
PubMed links	+	++	?	
allele designations	+	++	?	Allele designations can be set within the isolate table functions.
sequences	+	++	?	The sequence bin holds sequence contigs from any source.
accession number links	+	++	?	Associate sequences with Genbank/EMBL accession number.
experiments	+	++	?	Set up experiments to which sequences in the bin can belong.
experiment sequences	+	++	?	Add links associating sequences to experiments.
sequence tags	+	++	?	Tag regions of sequences within the sequence bin with locus information.

Database configuration

Table	Add	Batch Add	Update or delete	Comments
loci	+	++	?	
locus aliases	+	++	?	Add alternative names for loci. These can also be set when you batch add loci.
PCR reactions	+	++	?	Set up <i>in silico</i> PCR reactions. These can be used to filter genomes for tagging to specific repetitive loci.
nucleotide probes	+	++	?	Define nucleotide probes for <i>in silico</i> hybridization reaction to filter genomes for tagging to specific repetitive loci.

Click the 'create' new version link next to the isolate record:

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#) Toggle: [?](#) Field help: [id](#) [Go](#)

Browse *Neisseria* PubMLST database

Browse criteria **Action**

Order by: [id](#) [Browse all records](#)

Direction: [ascending](#)

Display: 25 records per page [?](#)

☐ Include old record versions

30456 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Delete **Tag scanning** **Projects**

[Delete ALL](#) [Scan](#) [Select project...](#) [Link](#)

Page: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [>](#) [Last](#)

Delete		Update		Sequence bin		New version		Isolate fields ?										Seqbin size (bp)		MLST		Finotyping antigens		
delete	update	upload	create	id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR								
delete	update	upload	create	1	A4/M1027	B1; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	2069108	4	ST-4 complex/subgroup IV	5-2	10	F1-5							
delete	update	upload	create	2	120M	B35; Z1035	Pakistan	1967	meningitis and septicemia	<i>Neisseria meningitidis</i>	A	2059411	1	ST-1 complex/subgroup III	5-2	10	F5-1							
delete	update	upload	create	3	M00242905		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	0	1099		19	15	add							
delete	update	upload	create	4	M1027	B43; Z1043	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	0	4	ST-4 complex/subgroup IV	add	add	add							
delete	update	upload	create	5	M00240227		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	0	1100	ST-32 complex/ET-5 complex	7	16	add							
delete	update	upload	create	6	M00282207		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	0	1101	ST-22 complex	add	add	add							
delete	update	upload	create	7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	2057385	5	ST-5 complex/subgroup III	20	9	F3-1							
delete	update	upload	create	8	M00242007		UK	2000	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	0	1102	ST-18 complex	add	14	add							
delete	update	upload	create	9	0021/84		Czech Republic	1984	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	W	0	114	ST-22 complex	add	add	add							

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.

Database: [Species home](#) | [Curator's page \(species\)](#) | [Curator's page \(database\)](#)
 Users: [Add](#) | [Query/update](#)
 Isolates: [Add](#) | [Query/update](#) | [Batch insert](#)

Logged in: [Keith Jolley \(keith\)](#) | [Log out](#) | [Change password](#)

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: 30457 [+](#) ☒ Add new version to projects [Create](#)

Provenance/meta data

id: 7	source: CSF	comments: Pili I/Lia
isolate: 7891	epidemiology: epidemic	sender: Wendell Zollinger, Dept Bacterial Diseases, Walter Reed Army Institute of Research, Washington DC, USA
aliases: B54; Z1054	species: <i>Neisseria meningitidis</i>	curator: Carina Brehony, University of Oxford, UK (E-mail: carina.brehony@zoo.ox.ac.uk)
strain designation: A: P1.20.9; F3-1; ST-5 (cc5)	serogroup: A	update history: 35 updates show details
country: Finland	MLEE designation: Subgroup III	date entered: 2001-02-07
continent: Europe	serotype: 4,21	datestamp: 2014-06-17
year: 1975	sero subtype: P1.9	
disease: invasive (unspecified/other)	ET no: 48	

Publications (7) [show/hide](#)

Sequence bin

contigs: 199	N50: 23361	detailed breakdown: Display
total length: 2057385 bp	N90: 6218	
max length: 112831 bp	N95: 3616	
mean length: 10339 bp	loci tagged: 1673	

Offline curation tools

7.1 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.
```

```
-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).

-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).

-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.

-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
    Maximum isolate id.

```

7.2 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.

-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).

-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.

-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
    Maximum isolate id.
```

7.3 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
```

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.

8.1 Allele sequence definitions

Click the ‘Allele sequences’ link in the ‘Downloads’ section. 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.

8.1.1 Scheme tree

The screenshot shows the 'Download allele sequences' page on the PubMLST website. At the top, there is a navigation bar with links: Query, Sequences, Batch sequences, Compare alleles, Profile/ST, Batch profiles, List, Browse, and Query. Below this, there are links for Download: Alleles, MLST profiles, and Links: Contents, Home, PorA, Feta, Options, and Isolate Database. The main heading is 'Download allele sequences'. Below the heading, there are three tabs: 'Loci by scheme' (which is highlighted with a red box), 'Alphabetical list', and 'All loci by scheme'. A text box below the tabs states: '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.' Below this text is a hierarchical tree structure. The root node is 'All loci', which is expanded to show several subgroups: 'Capsule', 'Genetic Information Processing', 'Metabolism', 'Typing', 'Other schemes', and 'Loci not in schemes'. Each subgroup is represented by a folder icon and a list of its members.

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.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FeTA | Options | Isolate Database

Download allele sequences

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
 - Capsule
 - Genetic Information Processing
 - Metabolism
 - Typing
 - MLST**
 - Finelytyping antigens
 - rpiF species
 - Antigen genes
 - eMLST (20 locus partial genes)
 - eMLST (20 locus whole genes)
 - Other schemes
 - Loci not in schemes

MLST

Locus	Download	Type	Alleles	Length	Curator(s)
abcZ		DNA	687	Fixed: 433 bp	O. Harrison, K. Jolley
adk		DNA	463	Fixed: 465 bp	O. Harrison, K. Jolley
aroE		DNA	738	Fixed: 490 bp	O. Harrison, K. Jolley
fumC		DNA	700	Fixed: 465 bp	O. Harrison, K. Jolley
gdh		DNA	708	Fixed: 501 bp	O. Harrison, K. Jolley
pdhC		DNA	713	Fixed: 480 bp	O. Harrison, K. Jolley
pgm		DNA	724	Fixed: 450 bp	O. Harrison, K. Jolley

Download table: [tab-delimited text](#) | [Excel format](#)

Click the green download link for the required locus

MLST

Locus	Download	Type	Alleles	Length	Curator(s)
abcZ		DNA	687	Fixed: 433 bp	O. Harrison, K. Jolley
adk		DNA	463	Fixed: 465 bp	O. Harrison, K. Jolley
aroE		DNA	738	Fixed: 490 bp	O. Harrison, K. Jolley
fumC		DNA	700	Fixed: 465 bp	O. Harrison, K. Jolley
gdh		DNA	708	Fixed: 501 bp	O. Harrison, K. Jolley
pdhC		DNA	713	Fixed: 480 bp	O. Harrison, K. Jolley
pgm		DNA	724	Fixed: 450 bp	O. Harrison, K. Jolley

Download table: [tab-delimited text](#) | [Excel format](#)

Alleles will be downloaded in FASTA format, e.g.

```
>fumC_1
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCTGCGGT
TTGGGCGAAATCAAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTCGGCAACGACGTT
ACCATCGGTATGGCGGGCGCGTCGGGCAATTTTCGAGCTGAACGTCTATATGCCCGTCATC
GCCTACAACCTCTTGCAATCCATCCGCCTGTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCGTCGGCATTGAACCCGTACCGGAAAAAATCGACTATTTCTGCACCATTCC
CTGATGCTCGTTACCGCGTTAAACCGCAAAATCGGTTACGAAAAC

>fumC_2
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCTGCGGT
TTGGGCGAAATCAAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTCGGCAACGACGTT
ACCATCGCATGGCGGGCGCGTCGGGCAATTTTCGAGCTGAACGTCTATATGCCCGTTATC
GCCTACAACCTCTTGCAATCCATCCGCCTCTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCATCGGCATCGAACCCGTACCGGAAAAAATCGACTATTTCTGCACCATTCC
```


```

CTGATGCTCGTTACCGCGTTAAACCGCAAAATCGGTTACGAAAAC
>fumC_3
GAAGCCTTGGGCGGACGCGATGCCGCCGTTGCCGCTTCGGGCGCATTGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAACGACATCCGCTGGCTGGCAAGCGGCCCGCTGCGGT
TTGGGCGAAATCAAAATCCCCGAAAACGAGCCGGGTTTCGTCCATCATGCCGGGCAAAGTC
AACCCGACCCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTCGGCAACGACGTT
ACCATCGGCATGGCGGGCGCGTCGGGCAATTTTCGAGCTGAACGTCTATATGCCCGTTATC
GCCTACAACCTCTTGAATCCATCCGCCTGTTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCCGTCGGCATCGAACCCTACCGGAAAAAATCGACTATTTCTGCACCATTCC
CTGATGCTGGTTACTGCGTTAAACCGTAAATCGGCTACGAAAAC

```

8.1.2 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.


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FeTA](#) | [Options](#) | [Isolate Database](#)

Download allele sequences

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

A

Locus	Download	Type	Alleles	Length	Full name/product	Curator(s)
ArsR [NEIS1769] i	Download	DNA	54	Variable: No limits set	ArsR family transcriptional regulator	
AsnC [NEIS1566] i	Download	DNA	121	Variable: No limits set	transcription regulator AsnC	
abcZ i	Download	DNA	687	Fixed: 433 bp		O. Harrison, K. Jolley
abcZ [NEIS1015] i	Download	DNA	330	Variable: No limits set	ABC transporter ATP-binding protein	
aceF [NEIS1279] i	Download	DNA	333	Variable: (1563 min; 1641 max)	dihydrolipoamide acetyltransferase (EC 2.3.1.12)	
ackA2 [NEIS1727] i	Download	DNA	260	Variable: No limits set	acetate kinase	
acnA [NEIS1729] i	Download	DNA	396	Variable: No limits set	aconitate hydratase 1 (EC 4.2.1.3)	
acnB [NEIS1492] i	Download	DNA	349	Variable: No limits set	aconitate hydratase 2 (EC 4.2.1.3)	
adhA [NEIS0486] i	Download	DNA	415	Variable: No limits set	alcohol dehydrogenase	
adhC [NEIS1241] i	Download	DNA	169	Variable: No limits set	alcohol dehydrogenase	
adk i	Download	DNA	463	Fixed: 465 bp		O. Harrison, K. Jolley
adk [NEIS0767] i	Download	DNA	169	Variable: No limits set	adenylate kinase	
aldA [NEIS1942] i	Download	DNA	306	Variable: No limits set	aldehyde dehydrogenase	
apaH [NEIS0610] i	Download	DNA	92	Variable: No limits set	diadenosine tetraphosphatase	
argH [NEIS0580] i	Download	DNA	288	Variable: No limits set	argininosuccinate lyase	
aroE i	Download	DNA	738	Fixed: 490 bp		O. Harrison, K. Jolley
aroE [NEIS1810] i	Download	DNA	223	Variable: No limits set	shikimate dehydrogenase	
aspA i	Download	DNA	97	Fixed: 432 bp		K. Jolley
aspA [NEIS1185] i	Download	DNA	326	Variable: No limits set	aspartate ammonia-lyase	
atlA [NEIS2274] i	Download	DNA	4	Variable: No limits set	atlA / peptidoglycan transglycosylase	
autA [NEIS1859] i	Download	DNA	178	Variable: No limits set	autotransporter A	

B

Click the green download links for the required locus.

8.1.3 All loci by scheme

Loci can also be displayed by scheme with all schemes displayed.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Download allele sequences

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

MLST

Locus	Download	Type	Alleles	Length	Curator(s)
abcZ		DNA	687	Fixed: 433 bp	O. Harrison, K. Jolley
adk		DNA	463	Fixed: 465 bp	O. Harrison, K. Jolley
aroE		DNA	738	Fixed: 490 bp	O. Harrison, K. Jolley
fumC		DNA	700	Fixed: 465 bp	O. Harrison, K. Jolley
gdh		DNA	708	Fixed: 501 bp	O. Harrison, K. Jolley
pdhC		DNA	713	Fixed: 480 bp	O. Harrison, K. Jolley
pgm		DNA	724	Fixed: 450 bp	O. Harrison, K. Jolley

Finotyping antigens

Locus	Download	Type	Alleles	Length	Full name/product	Curator(s)
PorA VR1		peptide	253	Variable: No limits set	PorA variable region 1	K. Jolley
PorA VR2		peptide	713	Variable: No limits set	PorA variable region 2	K. Jolley
FetA VR		peptide	426	Variable: No limits set		I. Feavers

rplF species

Locus	Download	Type	Alleles	Length	Full name/product	Curator(s)
rplF		DNA	109	Fixed: 413 bp	50S ribosomal protein L6 (partial)	E. Watkins

ADP-heptose biosynthesis

Locus	Download	Type	Alleles	Length	Full name/product	Aliases	Curator(s)
NEIS0769 (hldA)		DNA	187	Variable: No limits set	D-beta-D-heptose-7-phosphate kinase	NMB0825; NMC0769; rfaE	C. Kahler
NEIS0773 (hldD)		DNA	241	Variable: No limits set	ADP-D-beta-D heptose epimerase	NMB0828; NMC0773	C. Kahler
NEIS2014 (gmhB)		DNA	166	Variable: No limits set	D-alpha,beta,D-Heptose 1,7 bisphosphate phosphatase	NMB2033; NMC2014	C. Kahler
NEIS2055 (hldC)		DNA	156	Variable: No limits set	D-beta-D-heptose-1-phosphate adenylyltransferase	NMB2076; NMC2055	C. Kahler
NEIS2070 (gmhA)		DNA	158	Variable: No limits set	sedoheptulose-7-phosphate isomerase	NMB2090; NMC2070	C. Kahler

Click the green download links for the required locus.

8.1.4 Download locus table

The locus table can be downloaded in tab-delimited text or Excel formats by clicking the links following table display.

Capsule
 Genetic Information Processing
 Metabolism
 Typing
 MLST
 Finotyping antigens
 rplF species
 Antigen genes
 eMLST (20 locus partial genes)
 eMLST (20 locus whole genes)
 Other schemes
 Loci not in schemes

MLST

Locus	Download	Type	Alleles	Length	Curator(s)
abcZ		DNA	687	Fixed: 433 bp	O. Harrison, K. Jolley
adk		DNA	463	Fixed: 465 bp	O. Harrison, K. Jolley
aroE		DNA	738	Fixed: 490 bp	O. Harrison, K. Jolley
fumC		DNA	700	Fixed: 465 bp	O. Harrison, K. Jolley
gdh		DNA	708	Fixed: 501 bp	O. Harrison, K. Jolley
pdhC		DNA	713	Fixed: 480 bp	O. Harrison, K. Jolley
pgm		DNA	724	Fixed: 450 bp	O. Harrison, K. Jolley

Download table: [tab-delimited text](#) | [Excel format](#)

8.2 Scheme profile definitions

Scheme profiles, e.g. those for MLST, can be downloaded by clicking the appropriate link on the contents page.

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | Options | PubMLST.org | Isolate Database

Campylobacter locus/sequence definitions database

The Campylobacter PubMLST sequence definition database contains allele and profile data representing the total known diversity of *C. jejuni* and *C. coli*. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse MLST profiles
- Search MLST profiles
- List - find MLST profiles matched to entered list.
- Search by combinations of MLST alleles - including partial matching.
- Batch profile query - lookup MLST profiles copied from a spreadsheet.

Downloads

- Allele sequences
- MLST profiles**

Option settings

- Set general options

General information

- Number of sequences: 364203
- Number of profiles (MLST): 7281
- Last updated: 2014-07-10
- Profile update history
- About BIGSdb

Export

- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

If multiple schemes are available, you will need to select the scheme in the dropdown box and click 'Download profiles'

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | Feta | Options | Isolate Database

Neisseria locus/sequence definitions database

The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of Neisseria species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse profiles
- Search profiles
- List - find profiles matched to entered list.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.
- Extract finetype from whole genome data

Downloads

- Allele sequences
- MLST

Option settings

- Set general options

General information

- Number of sequences: 339729
- Number of profiles: Show
- Last updated: 2014-07-10
- Profile update history
- About BIGSdb

Export

- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

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.

9.1 Isolate records

An Isolate record page displays everything known about an isolate.



[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Full information on isolate M10 240474

Projects

This isolate is a member of the following projects:

MRF Meningococcus Genome Library

The [MRF Meningococcus Genome Library](#) is a collaboration between Public Health England, 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.



899_MRF

MRF-MGL isolates epi years 2010/2011 to 2011/2012 excluding Northern Ireland

E&W_genogroup_B_MRF

All MRF Meningococcus Genome Library genogroup B isolates from England and Wales in 2010/11 and 2011/12

MRF_no_NI

All MRF genomes excluding Northern Ireland

Provenance/meta data

id: 18968	species: <i>Neisseria meningitidis</i>
isolate: M10 240474	serogroup: B
strain designation: B: P1.19-1,15-11: F3-9: ST-269 (cc269)	ENA accession: ERR086224 → www.ebi.ac.uk
country: UK	sender: Dorothea Hill
continent: Europe	curator: Dorothea Hill, University of Oxford, UK (E-mail: dorothea.hill@zoo.ox.ac.uk)
region: South East	update history: 103 updates show details
year: 2010	date entered: 2012-02-15
epidemiological year: 07/2010-06/2011	timestamp: 2014-06-23
disease: invasive (unspecified/other)	

Sequence bin

contigs: 275	N90: 6405
total length: 2195045 bp	N95: 3513
max length: 109859 bp	loci tagged: 1611
mean length: 7982 bp	detailed breakdown: Display
N50: 34308	

Schemes and loci



Navigate and select schemes within tree to display allele designations

Each record will have some or all of the following sections:

9.1.1 Projects

Projects

This isolate is a member of the following projects:

MRF Meningococcus Genome Library

The [MRF Meningococcus Genome Library](#) is a collaboration between Public Health England, 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 will be displayed.

9.1.2 Provenance metadata

Provenance/meta data

id:	18968	species:	Neisseria meningitidis
isolate:	M10 240474	serogroup:	B
strain designation:	B: P1.19-1,15-11: F3-9: ST-269 (cc269)	ENA accession:	ERR086224 → www.ebi.ac.uk
country:	UK	sender:	Dorothea Hill
continent:	Europe	curator:	Dorothea Hill, University of Oxford, UK (E-mail: dorothea.hill@zoo.ox.ac.uk)
region:	South East	update history:	103 updates show details
year:	2010	date entered:	2012-02-15
epidemiological year:	07/2010-06/2011	timestamp:	2014-06-23
disease:	invasive (unspecified/other)		

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.

PubMLST

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Full information on isolate M10 240474

Update history

[Back to isolate information](#)

Timestamp	Curator	Action
2014-06-23 09:44	Dorothea Hill	NEIS2363: new designation '28' (sequence bin scan) NEIS2363: sequence tagged. Seqbin id: 4836; 3070-5108 (sequence bin scan)
2014-06-17 10:55	Carina Brehony	gyrA: designation '1000' deleted
2014-06-16 16:17	Carina Brehony	gyrA: sequence tagged. Seqbin id: 4885; 23385-23909 (sequence bin scan)
2014-06-16 14:48	Carina Brehony	gyrA: new designation '12' (sequence bin scan)
2014-06-05 15:55	Carina Brehony	gyrA: new designation '1000'
2014-06-05 15:55	Carina Brehony	gyrA: designations '12,30' deleted
2014-05-30 13:26	Eloise Orton	gyrA: new designation '30' (sequence bin scan) gyrA: sequence tagged. Seqbin id: 4989; 25611-26135 (sequence bin scan)
2014-05-17 09:26	Auto Tagger	NEIS2155: new designation '244' (sequence bin scan) NEIS2155: sequence tagged. Seqbin id: 5030; 977-1984 (sequence bin scan) pip: new designation '127' (sequence bin scan) pip: sequence tagged. Seqbin id: 4818; 35321-35736 (sequence bin scan) serC: new designation '123' (sequence bin scan) serC: sequence tagged. Seqbin id: 4765; 3629-4078 (sequence bin scan)
2014-03-16 11:15	Auto Tagger	NEIS0020: new designation '3' (sequence bin scan) NEIS0020: sequence tagged. Seqbin id: 4845; 4412-5980 (sequence bin scan) NEIS0036: new designation '8' (sequence bin scan) NEIS0036: sequence tagged. Seqbin id: 4977; 2774-3817 (sequence bin scan) NEIS0408: new designation '70' (sequence bin scan) NEIS0408: sequence tagged. Seqbin id: 4850; 28381-30666 (sequence bin scan) NEIS0409: new designation '25' (sequence bin scan) NEIS0409: sequence tagged. Seqbin id: 4850; 30685-31230 (sequence bin scan) NEIS0410: new designation '7' (sequence bin scan) NEIS0410: sequence tagged. Seqbin id: 4850; 31248-31895 (sequence bin scan) NEIS0411: new designation '2' (sequence bin scan) NEIS0411: sequence tagged. Seqbin id: 4850; 31896-32495 (sequence bin scan) NEIS0412: new designation '3' (sequence bin scan) NEIS0412: sequence tagged. Seqbin id: 4850; 32498-33613 (sequence bin scan) NEIS0721: new designation '14' (sequence bin scan) NEIS0721: sequence tagged. Seqbin id: 4950; 33102-34214 (sequence bin scan) NEIS1838: new designation '12' (sequence bin scan)

9.1.3 Publications

Publications (8)

showhide

Bennett JS, Jolley KA, Sparling PF, Saunders NJ, Hart CA, Feavers IM, Maiden MC (2007). Species status of Neisseria gonorrhoeae: evolutionary and epidemiological inferences from multilocus sequence typing. *BMC Biol* 5:35

576 isolates

Didelot X, Urwin R, Maiden MC, Falush D (2009). Genealogical typing of Neisseria meningitidis. *Microbiology* 155:3176-86

93 isolates

Jolley KA, Sun L, Moxon ER, Maiden MC (2004). Dam inactivation in Neisseria meningitidis: prevalence among diverse hyperinvasive lineages. *BMC Microbiol* 4:34

84 isolates

Jolley KA, Wilson DJ, Kriz P, McVean G, Maiden MC (2005). The influence of mutation, recombination, population history, and selection on patterns of genetic diversity in Neisseria meningitidis. *Mol Biol Evol* 22:562-9

376 isolates

Maiden MC, Bygraves JA, Feil E, Morelli G, Russell JE, Urwin R, Zhang Q, Zhou J, Zurth K, Caugant DA, Feavers IM, Achtman M, Spratt BG (1998). Multilocus sequence typing: a portable approach to the identification of clones within populations of pathogenic microorganisms. *Proc Natl Acad Sci U S A* 95:3140-5

107 isolates

Thompson EA, Feavers IM, Maiden MC (2003). Antigenic diversity of meningococcal enterobactin receptor FetA, a vaccine component. *Microbiology* 149:1849-58

107 isolates

Urwin R, Russell JE, Thompson EA, Holmes EC, Feavers IM, Maiden MC (2004). Distribution of surface protein variants among hyperinvasive meningococci: implications for vaccine design. *Infect Immun* 72:5955-62

78 isolates

Wang JF, Caugant DA, Li X, Hu X, Poolman JT, Crowe BA, Achtman M (1992). Clonal and antigenic analysis of serogroup A Neisseria meningitidis with particular reference to epidemiological features of epidemic meningitis in the People's Republic of China. *Infect Immun* 60:5267-82

47 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.

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Chapter 9. Data records

9.1.4 Sequence bin summary

Sequence bin

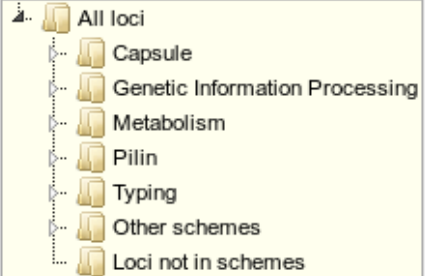
contigs:	275	N90:	6405
total length:	2195045 bp	N95:	3513
max length:	109859 bp	loci tagged:	1611
mean length:	7982 bp	detailed breakdown:	<input type="button" value="Display"/>
N50:	34308		

This section contains basic statistics describing the sequence bin. Clicking the ‘Display’ button navigates to the *sequence bin record*.

9.1.5 Scheme and locus data

A hierarchical tree displays available schemes. Click within internal nodes to expand them.

Schemes and loci



Navigate and select schemes within tree to display allele designations

Clicking any terminal node will display data available for a scheme or group of schemes.

Schemes and loci



MLST

abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST	clonal complex
4 S	10 S	15 S	9 S	8 S	11 S	9 S	269	ST-269 complex

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*.

9.2 Allele definition records

An allele definition record displays information about a defined allele in a sequence definition database.

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.

9.3 Sequence tag records

[illegible]

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.

9.4 Profile records

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

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/ET-37 complex

sender: Paula Kriz, Paula Kriz and Keith Jolley
curator: Keith Jolley, University of Oxford, UK (E-mail: keith.jolley@zoo.ox.ac.uk)
date entered: 2001-02-07
datestamp: 2009-11-11

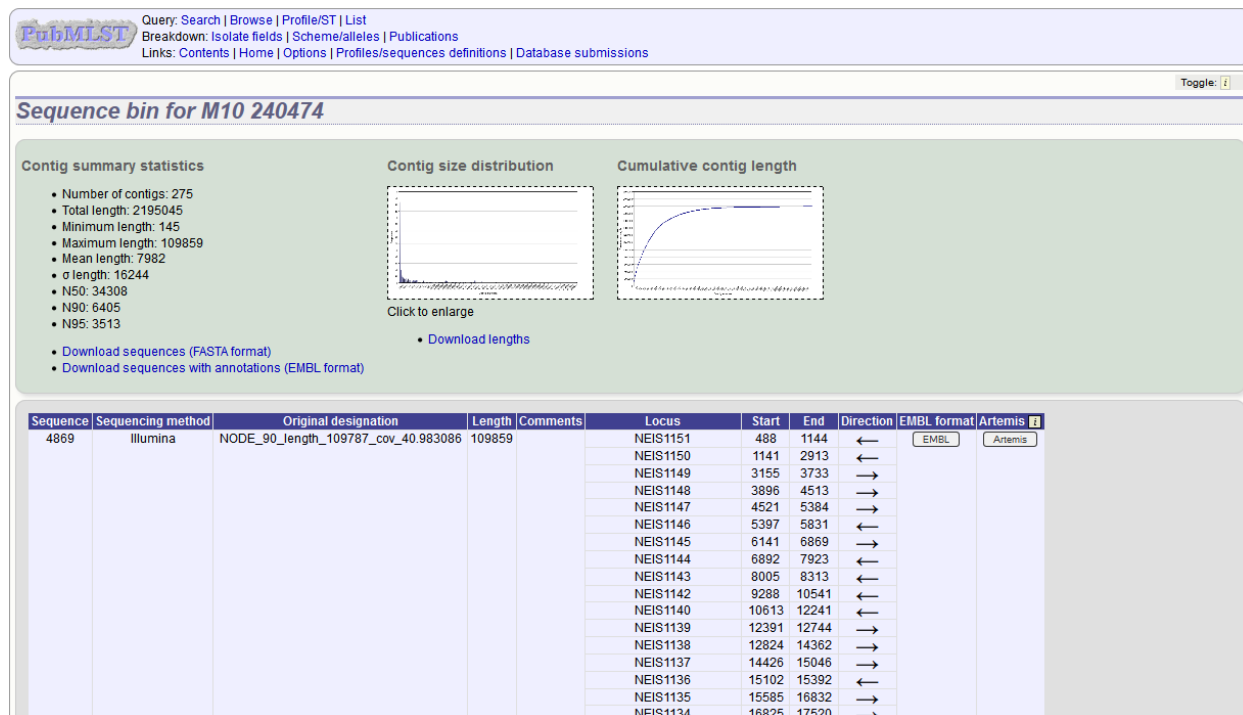
Client database

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. [2699 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.

9.5 Sequence bin records



A sequence bin record contains information about that 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

There are also links to download the contigs in FASTA or EMBL format.

Finally there is a table that shows the loci that are tagged on each contig. Individual contigs can also be downloaded in EMBL format.

Querying data

10.1 Querying sequences to determine allele identity

Sequence queries are performed in the sequence definition database. Click 'Sequence query' from the contents page.

The screenshot shows the Neisseria locus/sequence definitions database interface. At the top, there is a navigation bar with links: Query, Sequences, Batch sequences, Compare alleles, Profile/ST, Batch profiles, List, Browse, Query, Download: Alleles, MLST profiles, and Links: Contents, Home, PorA, FetA, Options, Isolate Database. Below this is a header for the 'Neisseria locus/sequence definitions database' with a 'Toggle' button. A descriptive paragraph states: 'The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of Neisseria species. Every new ST deposited in this database should have a corresponding record in the isolate database.' The main content area is divided into three columns: 'Query database', 'Downloads', and 'Option settings'. The 'Query database' column contains a list of links: 'Sequence query' (highlighted with a red box), 'Batch sequence query', 'Sequence attribute search', 'Browse profiles', 'Search profiles', 'List', 'Search by combinations of alleles', 'Batch profile query', and 'Extract finetype from whole genome data'. The 'Downloads' column has a 'Downloads' section with a dropdown menu set to 'MLST' and a 'Download profiles' button. The 'Option settings' column has a 'Set general options' link. Below these columns is a 'General information' section with details: 'Number of sequences: 341811', 'Number of profiles: Show', 'Last updated: 2014-07-11', 'Profile update history', and 'About BIGSdb'. At the bottom, there are two sections: 'Export' with a link to 'Sequences - XMF / concatenated FASTA formats' and 'Analysis' with links to 'Sequence similarity', 'Sequence comparison', and 'Locus Explorer'.

Paste your sequence in to the box - there is no need to trim. Normally, you can leave the locus setting on 'All loci' - the software should identify the correct locus based on your sequence. Sometimes, 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'.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Sequence query - *Neisseria* locus/sequence definitions

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: All loci Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

```
GACGCGGTGCGCGATGAAAAAGTCAAAGTCATCAAGTCATTGAAGCCGCTGACCGTCGAA
TCTGTCAATGAAAAATGTCGTGCGCGGACAAATATACCGCCGCAAGGSCATGAACGSCAT
CTTGAAGAAATCAACTATCGGTTTGGCCAAACGACATCACGCGAGGTCAAAAACATTGCCAT
TGAGGGCAAAACCAATTTTGTCTTTGGGCGCGGGCGGCGGTTGCGCGGCGTAAATTCGGT
TTTGAAGGACACCGCCCTGCCGATATCGTGTTCGCAACCGCACCCACGCCAAAGCCGA
AGAATTGCGCGGGCTTTTCGGCATTGAAGCCGTCCCGATGGCGGATGTGAACGGCGTTT
TGATATCATCATCAA
```

Alternatively upload FASTA file

Select FASTA file: No file selected.

Action:

If an exact match is found, this will be indicated along with the start position of the locus within your sequence.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Sequence query - *Neisseria* locus/sequence definitions

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: MLST Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

```
GACGCGGTGCGCGATGAAAAAGTCAAAGTCATCAAGTCATTGAAGCCGCTGACCGTCGAA
TCTGTCAATGAAAAATGTCGTGCGCGGACAAATATACCGCCGCAAGGSCATGAACGSCAT
CTTGAAGAAATCAACTATCGGTTTGGCCAAACGACATCACGCGAGGTCAAAAACATTGCCAT
TGAGGGCAAAACCAATTTTGTCTTTGGGCGCGGGCGGCGGTTGCGCGGCGTAAATTCGGT
TTTGAAGGACACCGCCCTGCCGATATCGTGTTCGCAACCGCACCCACGCCAAAGCCGA
AGAATTGCGCGGGCTTTTCGGCATTGAAGCCGTCCCGATGGCGGATGTGAACGGCGTTT
TGATATCATCATCAAACGGCACGCTCTGGCGGCTTGAGCGGTGAGCTTCCTGCCGTCAGTCC
```

Alternatively upload FASTA file

Select FASTA file: No file selected.

Action:

1 exact match found.

Allele	Length	Start position	End position	Flags	Comments
aroE: 8	490	136	625		

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.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Sequence query - *Neisseria* locus/sequence definitions

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: MLST Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

```
GACGCGGTSCGCGATGAAAAAGTCAAAGTCATCAAGTCATTGAAGCCGCTGACCGTCAAA
TCTGTCAATGAAAAATGTCGTGCGCGGACAATATACCGCCGCAAGGSCATGAACGSCAT
CTTGAGAAATCAACTATCAGTTTGGCCAAACGACATCACGCGAGGTCAAAAACATTSCCAT
TGAGGGCAAAACCAATTTTGCTTTTGGGCGCGGGCGCGGTCGCGCGCGTAAATTCGGT
TTTGAAGGACACCGCCCTGCGCGTATCGTTCGTTGCCAACCGCACCCACGCCAAAGCCGA
AGAATTGCGCGGCTTTTCGGCATTGAAGCCGTCCCGATGGCGGATGTGAACGGCGGTTT
TGATATCATCATCAACGGCAGCTCTGGCGGCTAGAGCGGTGAGCTTCTGCGGTCAATCC
```

Alternatively upload FASTA file

Select FASTA file: [Browse...](#) No file selected.

Action: [Reset](#) [Submit](#)

[Translate query](#)

Closest match: *aroE*: 8

[Show alignment](#)

Differences

2 differences found. [?](#)

258 T → 393 A
333 A → 406 G

The locus start point is at position 136 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.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Sequence query - *Neisseria* locus/sequence definitions

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: All loci Order results by: locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file: [Browse...](#) No file selected.

Action: [Reset](#) [Submit](#)

10.1.1 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.

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FetA | Options | Isolate Database

Sequence query - *Neisseria* locus/sequence definitions

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: **MLST** Order results by: **locus**

Enter query sequence (single or multiple contigs up to whole genome in size)

```
>4758|NODE_192_length_1326_cov_47.828808
TAGAACACAGCAATATTCAGAGATTATCTGAAGTCCGAGATTCTAGATTCCCGCTTTC
GCGGGAATGACGAAAAGCAAGCCGTAGGTTCGGATACCTTGTATCCGACAAAAGCCTGCCAT
CTCAAAATAGCGCTCGGATTCCGAGATCCGACCTGCCAAACCGGGCGCGGACGCTCCGGCC
GGCAGTTAGTACGCAATTCGACAGAACATCACAATAAGCCGATTCCGATTTCGCAAT
CGGGCTTTTTCGCCCGCTTTTGTATCCCGTGAATATCCGCATGACAAAAATATAGTG
AATTACAAAAATCAGGACAAAGCGACGAAGCCGACAGTACAGATAGTACGGTAAGG
```

Alternatively upload FASTA file: **Action**
 Select FASTA file: **Browse...** No file selected. **Reset** **Submit**

7 exact matches found.

Allele	Length	Start position	End position	Flags	Comments
abcZ: 4	433	203051	203483		
adk: 10	465	938327	938791		
aroE: 15	490	1775325	1775814		
fumC: 9	465	1134240	1134704		
gdh: 8	501	961439	961939		
pdhC: 11	480	1341678	1342157		
pgm: 9	450	1416246	1416695		

MLST

ST **269**
 clonal complex ST-269 complex

10.2 Searching for specific allele definitions

To retrieve specific allele designations, click ‘Sequence attribute search’ on a sequence definition database contents page.

Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FetA | Options | Isolate Database

Neisseria locus/sequence definitions database

The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of *Neisseria* species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search** - find alleles by matching attributes.
- Browse profiles
- Search profiles
- List - find profiles matched to entered list.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.
- Extract finetype from whole genome data

Downloads

- Allele sequences
- MLST

Option settings

- Set general options

General information

- Number of sequences: 342126
- Number of profiles: [Show](#)
- Last updated: 2014-07-14
- [Profile update history](#)
- [About BIGSdb](#)

Export


- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

Enter your query using the dropdown search box - additional terms can be added by clicking the ‘+’ button.

Designations can be queried using *standard operators*.


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Toggle: [?](#)

Query sequences for *Neisseria* locus/sequence definitions database

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

Filter query by

Display


Order by: locus ascending

Display: 25 records per page

Action

Reset Submit

Click submit.


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Toggle: [?](#)

Query sequences for *Neisseria* locus/sequence definitions database

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

Display

Order by: locus ascending


Display: 25 records per page

Action

Reset Submit

1 record returned. Click the hyperlink for detailed information.

Click the hyperlinked results to display allele records.


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Toggle: [?](#)

Query sequences for *Neisseria* locus/sequence definitions database

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


Display
Order by: locus ascending
Display: 25 records per page

Filter query by:

Action
Reset Submit

1 record returned. Click the hyperlink for detailed information.

locus	allele id	sequence	sequence length	comments	flags
abcZ	5	TTTGATACCGTTGCC ... TCGTGAACCTGATC	433		


[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Allele information - abcZ: 5

Provenance/meta data

locus: [abcZ](#)
allele: 5

sequences: TTTGATACCG TTGCCGAAGG TTGGGGCGAA ATTGCGGATT TATTGGGCGG TTATCAICAT GTCAGCCATG AGTTGGAAAA TGGTTCGAGT GAGGCTTTGT TGAAAGAGCT TAACGAATTG
CAACTTGAAA TCGAAGCGAA GGACGGCTGG AAGCTGGATG CGGCAGTCAA GCAGACTTTG GGTGAACCTTG GTTTGCCAGA AAACGAAAAA ATCGGCAACC TCTCCGCGG ACAGAAAAAG
CGTGTGCCC TAGCGCAGGC TTGGGTGCAG AAGCCTGATG TATTGCTGCT GGACGAACCG ACCAACCATT TGGACATTGA CCGGATTATT TGGCTGGAAA ATCTGCTTAA ASCGTTTGAA
GGCAGCCTGG TTGTGATTAC CCACGACCGC CGTTTTTTGG ACAATATCGC CACGCGCATC GTCGAACCTG 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 (E-mail: man-suen.chan@paediatrics.ox.ac.uk)

Profiles containing this allele

MLST: [183 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.
[399 isolates](#)

Various search criteria can also be selected by combining with filters. Click the filter heading to display these.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | Feta | Options | Isolate Database

Toggle: [?]

Query sequences for *Neisseria* locus/sequence definitions database

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 < 10 [?] [?]

Display: Order by: locus ascending [?]
Display: 25 records per page [?]

Filter query by:

locus: abcZ [?]
status: [?]
sender: [?]
curator: [?]
allele flag: [?]

Action: Reset Submit

9 records returned. Click the hyperlinks for detailed information.

locus	allele id	sequence	sequence length	comments	flags
abcZ	1	TTTGATACTGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	2	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	3	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	4	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	5	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	6	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	7	TTTGATACTGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	8	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		
abcZ	9	TTTGATACCGTTGCC ... TTGTGGAACCTCGATC	433		

10.2.1 Locus-specific attributes

Some loci have *extended attribute fields*. To query these, you need to navigate to a locus-specific query page, by clicking the 'locus-specific query' link on the sequence attribute search page.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | Feta | Options | Isolate Database

Toggle: [?]

Query sequences for *Neisseria* locus/sequence definitions database

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 = [?] [?]

Display: Order by: locus ascending [?]
Display: 25 records per page [?]

Filter query by:

Action: Reset Submit

Pick the required locus from the dropdown box.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Toggle: [?]

Query PorA VR2 sequences - Neisseria locus/sequence definitions database

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).

Locus fields: allele id = [] + [?]

Display: Order by: allele id ascending Filter query by: status: []
Display: 25 records per page [?] allele flag: []

Action: Reset Submit

The fields specific for that locus will be added to the dropdown query boxes.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Toggle: [?]

Query PorA VR2 sequences - Neisseria locus/sequence definitions database

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).

Locus fields: family = 2 + [?]

Display: Order by: allele id ascending Filter query by: status: []
Display: 25 records per page [?] allele flag: []

Action: Reset Submit

83 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page: [1] [2] [3] [4] [>] [Last]

locus	allele id	sequence	sequence length	comments	family	variant	old name	mAb1	mAb1 reactivity	mAb2	mAb2 reactivity	flags
PorA VR2	2	HFVQQIPKSPILVP	15		2			MN16C13F4	+	AF202	-	
PorA VR2	2-1	HFVQQPKSPILVP	15		2	1	2b	MN16C13F4	-	AF202	+	
PorA VR2	2-10	HFVQQAPKSPILVP	15		2	10						
PorA VR2	2-11	HFVQIPKSPILVP	15		2	11						
PorA VR2	2-12	HFVQQIPKSPILVP	15		2	12						
PorA VR2	2-13	YFVQQIPKSPILVP	15		2	13		MN16C13F4	+			
PorA VR2	2-14	HFVQQKLSKSPILVP	15		2	14	33					
PorA VR2	2-15	HFVQQKLSKSPILVP	15		2	15	33a (33-1)					
PorA VR2	2-16	HFVQQKLSKSPILVP	15		2	16	33b (33-2)					
PorA VR2	2-17	HFVQQKLSKSPILVP	15		2	17	33c (33-3)					
PorA VR2	2-18	HFVQQIPKSPILVP	15		2	18						
PorA VR2	2-19	HFVQQIPKSPILVP	15		2	19						

10.3 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, click the link to 'Browse profiles'.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Campylobacter locus/sequence definitions database

The Campylobacter PubMLST sequence definition database contains allele and profile data representing the total known diversity of *C. jejuni* and *C. coli*. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse MLST profiles**
- Search MLST profiles
- List - find MLST profiles matched to entered list.
- Search by combinations of MLST alleles - including partial matching.
- Batch profile query - lookup MLST profiles copied from a spreadsheet.

Downloads

- Allele sequences
- MLST profiles

Option settings

- Set general options

General information

- Number of sequences: 364232
- Number of profiles (MLST): 7281
- Last updated: 2014-07-11
- Profile update history
- About BIGSdb

Export

- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

Choose the field to order the results by, the number of results per page to display, and click 'Browse all records'.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Browse profiles - Campylobacter locus/sequence definitions

Toggle: [?](#)

Browse criteria
Order by:
Direction:
Display: records per page [?](#)

Action

7281 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [>](#) [Last](#)

ST	aspA	glnA	gltA	glyA	pgm	tkf	uncA	clonal complex
1	2	1	54	3	4	1	5	ST-21 complex
2	4	7	51	4	1	7	1	ST-45 complex
3	3	2	5	10	11	11	6	ST-49 complex
4	10	11	16	7	10	5	7	ST-403 complex
5	7	2	5	2	10	3	6	ST-353 complex
6	63	34	27	33	45	5	7	
7	8	10	2	2	14	12	6	ST-354 complex
8	2	1	1	3	2	1	6	ST-21 complex
9	1	6	22	24	12	7	1	ST-508 complex
10	2	59	4	38	17	12	5	ST-433 complex
11	48	7	10	4	1	7	1	ST-45 complex
12	7	1	5	2	11	3	6	ST-353 complex
13	2	1	1	9	2	1	5	ST-21 complex

Clicking the hyperlink for any profile will display full information about the profile.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Profile information for ST-8 (MLST)

ST	aspA	glnA	gltA	glyA	pgm	tki	uncA	clonal complex
8	2	1	1	3	2	1	6	ST-21 complex

sender: Frances Colles
curator: Frances Colles, University of Oxford, UK (E-mail: frances.colles@medawar.ox.ac.uk)
date entered: 2001-05-02
datestamp: 2001-05-02

Client database

PubMLST isolates: Contains data for a collection of isolates that represent the total known diversity of *C. jejuni* and *C. coli*. 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.

[49 isolates](#)

10.4 Querying scheme profile definitions

click the link to ‘Search profiles’ for the appropriate scheme on the main contents page.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Campylobacter locus/sequence definitions database

The Campylobacter PubMLST sequence definition database contains allele and profile data representing the total known diversity of *C. jejuni* and *C. coli*. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse MLST profiles**
- Search MLST profiles**
- List - find MLST profiles matched to entered list.
- Search by combinations of MLST alleles - including partial matching.
- Batch profile query - lookup MLST profiles copied from a spreadsheet.

Downloads

- Allele sequences
- MLST profiles

Option settings

- Set general options

General information

- Number of sequences: 364232
- Number of profiles (MLST): 7281
- Last updated: 2014-07-11
- Profile update history
- About BIGSdb

Export

- Sequences - XMTA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

Enter the search criteria you wish to search on. You may also see some drop-down list boxes that allow further filtering of results. You can add search criteria by clicking the ‘+’ button in the ‘Locus/scheme fields’ section. These can be combined using ‘AND’ or ‘OR’.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
 Download: [Alleles](#) | [MLST profiles](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Toggle: [?]

Search profiles - *Campylobacter* locus/sequence definitions

Locus/scheme fields

Combine searches with: AND

date entered > 2014-02-01 + [?]

sender (surname) = Cody

Display/sort options

Order by: ST ascending

Display: 25 records per page [?]

Filter query by

clonal complex: [?] [?]

Action: [Reset] [Submit]

17 records returned. Click the hyperlinks for detailed information.

ST	aspA	glnA	gltA	glyA	pgm	tkf	uncA	clonal complex
7117	33	66	65	192	189	44	17	
7162	1	2	3	539	5	9	3	ST-42 complex
7172	8	1	6	3	2	1	384	ST-21 complex
7176	7	448	5	2	10	3	6	ST-353 complex
7177	55	21	2	566	11	37	3	
7178	7	17	5	2	705	3	6	ST-353 complex
7179	3	495	5	10	11	68	6	ST-49 complex
7180	79	496	420	372	20	1	17	
7181	121	497	421	567	706	560	94	
7182	7	2	5	72	22	561	6	

Each field can be queried using *standard operators*.

Clicking the hyperlink for any profile will display full information about the profile.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
 Download: [Alleles](#) | [MLST profiles](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [PubMLST.org](#) | [Isolate Database](#)

Toggle: [?]

Search profiles - *Campylobacter* locus/sequence definitions

Locus/scheme fields

Combine searches with: AND

date entered > 2014-02-01 + [?]

sender (surname) = Cody

Display/sort options

Order by: ST ascending

Display: 25 records per page [?]

Filter query by

clonal complex: [?] [?]

Action: [Reset] [Submit]

17 records returned. Click the hyperlinks for detailed information.

ST	aspA	glnA	gltA	glyA	pgm	tkf	uncA	clonal complex
7117	33	66	65	192	189	44	17	
7162	1	2	3	539	5	9	3	ST-42 complex
7172	8	1	6	3	2	1	384	ST-21 complex
7176	7	448	5	2	10	3	6	ST-353 complex
7177	55	21	2	566	11	37	3	
7178	7	17	5	2	705	3	6	ST-353 complex
7179	3	495	5	10	11	68	6	ST-49 complex
7180	79	496	420	372	20	1	17	
7181	121	497	421	567	706	560	94	
7182	7	2	5	72	22	561	6	

10.5 Investigating allele differences

10.5.1 Sequence similarity

To find sequences most similar to a selected allele within a sequence definition database, click 'Sequence similarity' on the contents page.

Toggle: [?]

Neisseria locus/sequence definitions database

The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of Neisseria species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse profiles
- Search profiles
- List - find profiles matched to entered list.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.
- Extract finetype from whole genome data

Downloads

- Allele sequences
- MLST

Option settings

- Set general options

General information

- Number of sequences: 341811
- Number of profiles: [Show](#)
- Last updated: 2014-07-11
- Profile update history
- About BIGSdb

Export

- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity** - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

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.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Find most similar alleles - Neisseria locus/sequence definitions

This page allows you to find the most similar sequences to a selected allele using BLAST.

Select parameters

Locus:

Allele:

Number of results:

Action

A list of nearest alleles will be displayed, along with the percentage identity and number of gaps between the sequences.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Find most similar alleles - *Neisseria* locus/sequence definitions

This page allows you to find the most similar sequences to a selected allele using BLAST.

— **Select parameters** — **Action** —

Locus:

Allele:

Number of results:

abcZ-5

Allele	% Identity	Mismatches	Gaps	Alignment	Compare
abcZ: 657	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 657"/>
abcZ: 453	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 453"/>
abcZ: 405	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 405"/>
abcZ: 404	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 404"/>
abcZ: 213	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 213"/>
abcZ: 166	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 166"/>
abcZ: 114	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 114"/>
abcZ: 103	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 103"/>
abcZ: 646	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 646"/>
abcZ: 671	99.77	1	0	433/433	<input type="button" value="Compare abcZ: 671"/>

Click the appropriate ‘Compare’ button to display a list of nucleotide differences and/or a sequence alignment.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Allele sequence comparison - *Neisseria* locus/sequence definitions

This tool allows you to select two alleles and highlight the nucleotide differences between them.

— **Select parameters** — **Action** —

Locus:

Allele #1:

Allele #2:

Nucleotide differences between abcZ: 5 and abcZ: 453

Identity: 99.77 %

[Show alignment](#)

Differences: 1
300: G → A

10.5.2 Sequence comparison

To directly compare two sequences click ‘Sequence comparison’ from the contents page of a sequence definition database.

Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
 Download: [Alleles](#) | [MLST profiles](#)
 Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Toggle: [?](#)

Neisseria locus/sequence definitions database

The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of Neisseria species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse profiles
- Search profiles
- List - find profiles matched to entered list.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.
- Extract finetype from whole genome data

Downloads

- Allele sequences
- MLST

Option settings

- Set general options

General information

- Number of sequences: 341811
- Number of profiles: [Show](#)
- Last updated: 2014-07-11
- Profile update history
- About BIGSdb

Export

- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer - tool for analysing allele sequences stored for particular locus.

Enter the locus and two allele identifiers to compare. Press submit.

Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
 Download: [Alleles](#) | [MLST profiles](#)
 Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Allele sequence comparison - Neisseria locus/sequence definitions

This tool allows you to select two alleles and highlight the nucleotide differences between them.

Select parameters

Locus:

Allele #1:

Allele #2:

Action

A list of nucleotide differences and/or an alignment will be displayed.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
 Download: [Alleles](#) | [MLST profiles](#)
 Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Allele sequence comparison - *Neisseria* locus/sequence definitions

This tool allows you to select two alleles and highlight the nucleotide differences between them.

— **Select parameters** — **Action** —

Locus:

Allele #1:

Allele #2:

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
 95: C → T
 99: G → A
 102: G → A

See also:

Locus explorer plugin.

10.6 Querying isolate data

The ‘Search database’ page of an isolate database allows you to search by combinations of provenance criteria, scheme and locus data, and more.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Neisseria PubMLST 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** - advanced queries.
- Browse database** - peruse all records.
- Search by combinations of loci (profiles)** - including partial matching.
- List query** - find isolates by matching a field to an entered list.

Option settings

- Set general options** - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.**

General information

- Isolates: 29172
- Last updated: 2014-07-11
- [Update history](#)
- [About BIGSdb](#)

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMF / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

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’.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#) Field help: [id](#) [Go](#)

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields

Combine with: **AND**

country **=** **USA** [+](#) [?](#)

year **>** **1999**

Display/sort options

Order by: **id** **ascending**

Display: **25** records per page [?](#)

Action

[Reset](#) [Submit](#)

300 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [>](#) [Last](#)

Isolate fields ?							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
341	M7085		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex			
499	MDL01A0601		USA	2001	meningitis	Neisseria meningitidis	Y	1378	ST-23 complex/Cluster A3			
500	MDL01A2447		USA	2001	invasive (unspecified/other)	Neisseria meningitidis	Y	1379	ST-23 complex/Cluster A3			
866	MDO1227		USA	2001		Neisseria meningitidis		1624	ST-167 complex			
867	MDO1056		USA	2001		Neisseria meningitidis		1625	ST-23 complex/Cluster A3			
868	MDO1066		USA	2001		Neisseria meningitidis		1626	ST-269 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2299	M7257		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2316	M7086		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2317	M7084		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2322	M7092		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1065	ST-22 complex	6	3	
2323	M7100		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1286	ST-22 complex	6	3	
2324	M7259		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1066	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:

- 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.
- Filters
 - Various filters may be available, including
 - * Publications
 - * Projects
 - * MLST profile completion status
 - * Clonal complex
 - * Sequence bin size
 - * Inclusion/exclusion of *old versions*

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: Field help:

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields

Combine with: **AND**

country = USA +

year > 1999

Action

Display/sort options

Order by: id

Display: 25 records per page

300 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page:

Modify form parameters

Click to add or remove additional query terms:

- Allele designations/scheme field values
- Allele designation status
- Tagged sequence status
- Filters

Isolate fields							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
341	M7085		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex			
499	MDL01A0601		USA	2001	meningitis	Neisseria meningitidis	Y	1378	ST-23 complex/Cluster A3			
500	MDL01A2447		USA	2001	invasive (unspecified/other)	Neisseria meningitidis	Y	1379	ST-23 complex/Cluster A3			
866	MDO1227		USA	2001		Neisseria meningitidis		1624	ST-167 complex			
867	MDO1056		USA	2001		Neisseria meningitidis		1625	ST-23 complex/Cluster A3			
868	MDO1066		USA	2001		Neisseria meningitidis		1626	ST-269 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2299	M7257		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2316	M7086		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2317	M7084		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2322	M7092		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1065	ST-22 complex	6	3	
2323	M7100		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1286	ST-22 complex	6	3	
2324	M7259		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1066	ST-22 complex	6	3	

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.

10.6.1 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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: ☐ Field help: id

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields

Combine with: AND

country = USA +

year > 1999

Allele designations/scheme fields

Enter value... +

Display/sort options

Order by: id

Display: 25 records per page

Action

Reset Submit

300 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page:

Modify form options

Click to add or remove additional query terms:

- ☒ Hide Allele designations/scheme field values
- ☐ Show Allele designation status
- ☐ Show Tagged sequence status
- ☐ Show Filters

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
341	M7085		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex			
499	MDL01A0601		USA	2001	meningitis	Neisseria meningitidis	Y	1378	ST-23 complex/Cluster A3			
500	MDL01A2447		USA	2001	invasive (unspecified/other)	Neisseria meningitidis	Y	1379	ST-23 complex/Cluster A3			
866	MDO1227		USA	2001		Neisseria meningitidis		1624	ST-167 complex			
867	MDO1056		USA	2001		Neisseria meningitidis		1625	ST-23 complex/Cluster A3			
868	MDO1066		USA	2001		Neisseria meningitidis		1626	ST-269 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2299	M7257		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2316	M7086		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2317	M7084		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	22	ST-22 complex	6	3	
2322	M7092		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1065	ST-22 complex	6	3	
2323	M7100		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1286	ST-22 complex	6	3	
2324	M7259		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1066	ST-22 complex	6	3	

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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: ☐ Field help: id

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields

Combine with: AND

country = USA +

year > 1999

Allele designations/scheme fields

ST (MLST) = 11 +

Display/sort options

Order by: id

Display: 25 records per page

Action

Reset Submit

8 records returned. Click the hyperlinks for detailed information.

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
341	M7085		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex			
2281	M7089		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
2299	M7257		USA	2000	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	
19369	M13519		USA	2005	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5-1	10-8	F3-6
19371	M15141		USA	2006	invasive (unspecified/other)	Neisseria meningitidis	C	11	ST-11 complex/ET-37 complex	5-1	10-8	
19374	M16917		USA	2007	invasive (unspecified/other)	Neisseria meningitidis	NG	11	ST-11 complex/ET-37 complex	5-1	10-8	
19377	M17661		USA	2008	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5-1	10-8	
19379	M18774		USA	2009	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	F1-94

Analysis tools:

Breakdown:

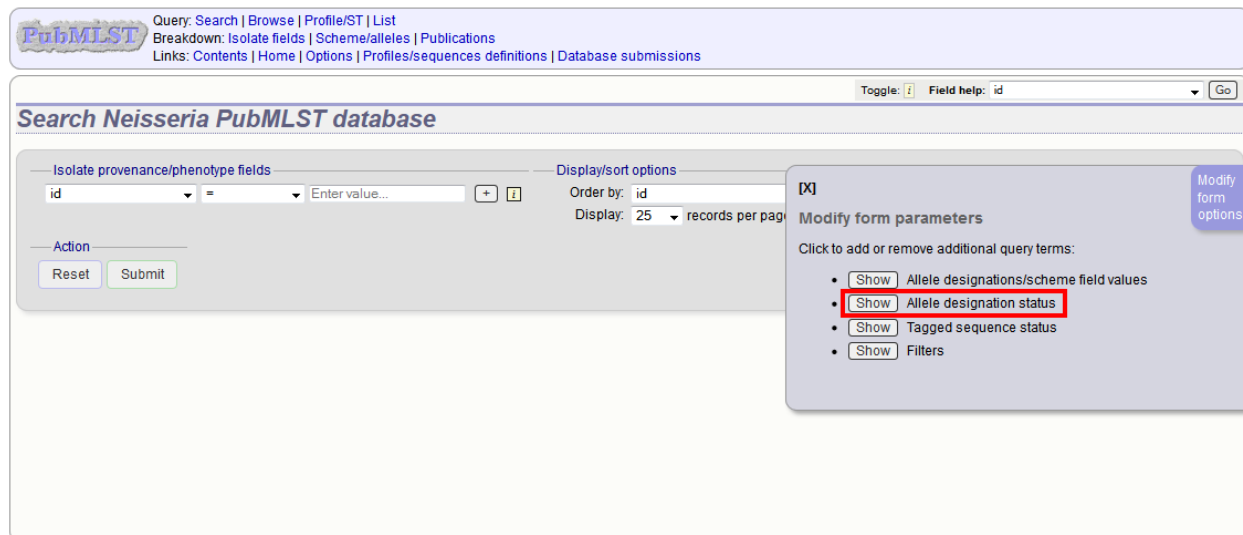
Analysis:

Export:

10.6.2 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.



Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Search Neisseria PubMLST database

Isolate provenance/phenotype fields: id = Enter value... + ?

Display/sort options: Order by: id, Display: 25 records per page

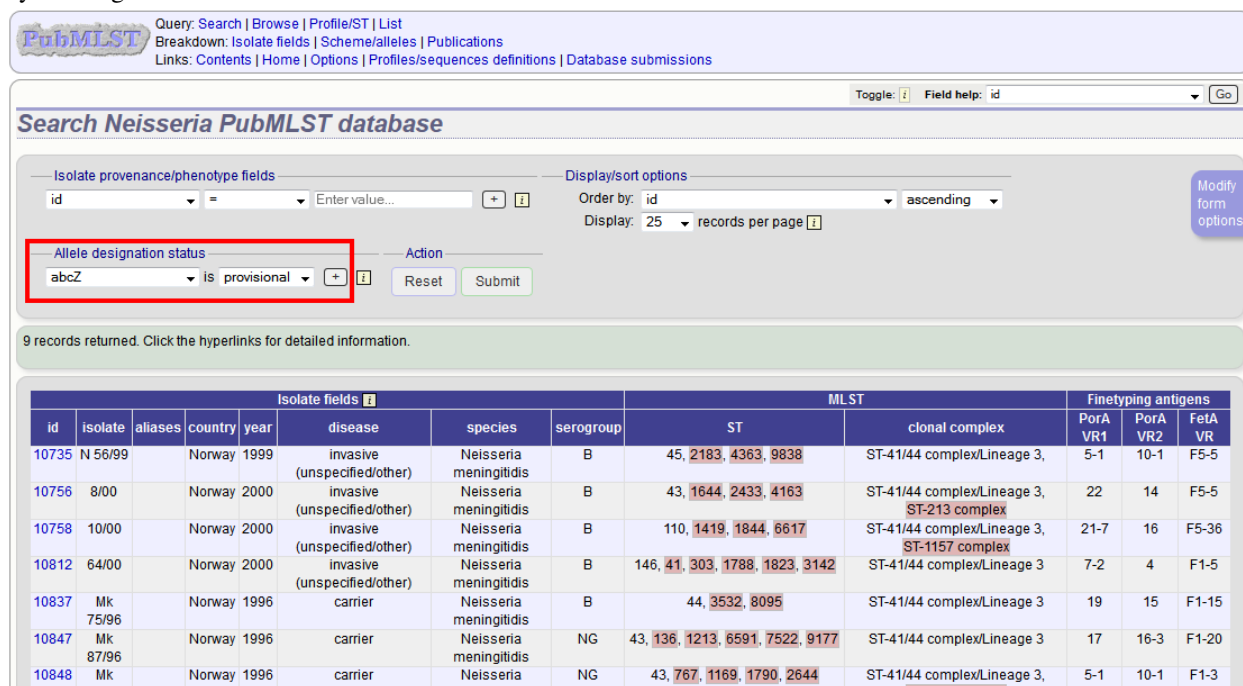
Action: Reset Submit

Modify form options

Click to add or remove additional query terms:

- Show Allele designations/scheme field values
- Show **Allele designation status**
- Show Tagged sequence status
- Show 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’.



Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Search Neisseria PubMLST database

Isolate provenance/phenotype fields: id = Enter value... + ?

Display/sort options: Order by: id ascending, Display: 25 records per page

Action: Reset Submit

Allele designation status: abcZ is provisional + ?

9 records returned. Click the hyperlinks for detailed information.

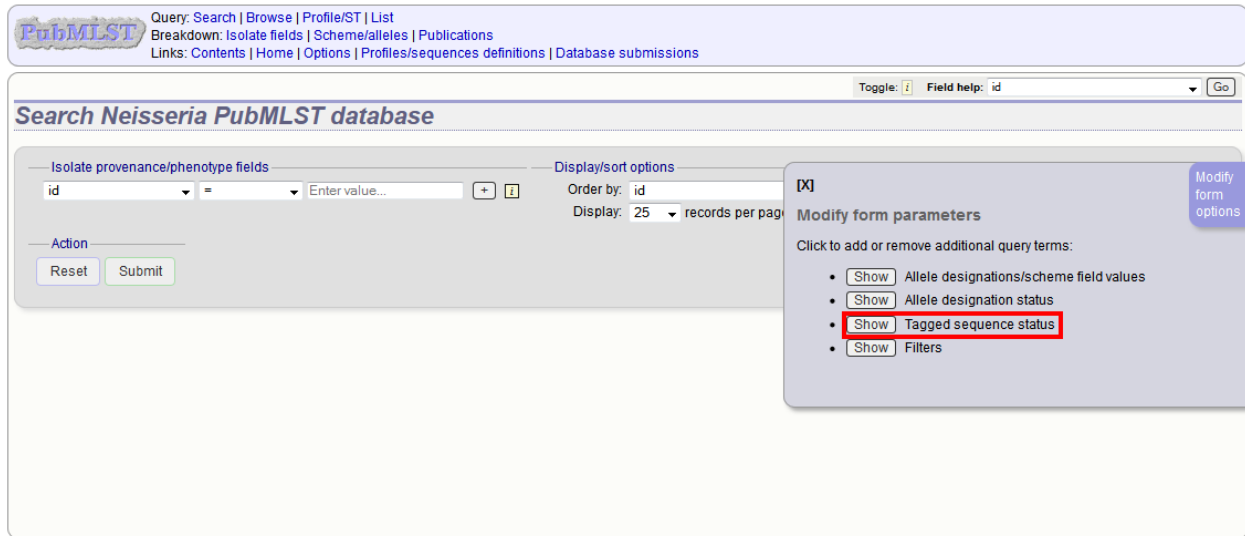
Isolate fields							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
10735	N 56/99		Norway	1999	invasive (unspecified/other)	Neisseria meningitidis	B	45, 2183, 4363, 9838	ST-41/44 complex/Lineage 3,	5-1	10-1	F5-5
10756	8/00		Norway	2000	invasive (unspecified/other)	Neisseria meningitidis	B	43, 1644, 2433, 4163	ST-41/44 complex/Lineage 3, ST-213 complex	22	14	F5-5
10758	10/00		Norway	2000	invasive (unspecified/other)	Neisseria meningitidis	B	110, 1419, 1844, 6617	ST-41/44 complex/Lineage 3, ST-1157 complex	21-7	16	F5-36
10812	64/00		Norway	2000	invasive (unspecified/other)	Neisseria meningitidis	B	146, 41, 303, 1788, 1823, 3142	ST-41/44 complex/Lineage 3	7-2	4	F1-5
10837	Mk 75/96		Norway	1996	carrier	Neisseria meningitidis	B	44, 3532, 8095	ST-41/44 complex/Lineage 3	19	15	F1-15
10847	Mk 87/96		Norway	1996	carrier	Neisseria meningitidis	NG	43, 136, 1213, 6591, 7522, 9177	ST-41/44 complex/Lineage 3	17	16-3	F1-20
10848	Mk 00/96		Norway	1996	carrier	Neisseria meningitidis	NG	43, 767, 1169, 1790, 2644	ST-41/44 complex/Lineage 3, ST-427 complex	5-1	10-1	F1-3

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.

10.6.3 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.



The screenshot shows the 'Search Neisseria PubMLST database' interface. At the top, there are navigation links: Query: Search | Browse | Profile/ST | List; Breakdown: Isolate fields | Scheme/alleles | Publications; Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions. Below this is a search bar with a 'Toggle' dropdown set to 'id' and a 'Field help' link. The main search area has a dropdown for 'Isolate provenance/phenotype fields' set to 'id', an 'Enter value...' input, and a 'Display/sort options' section with 'Order by: id' and 'Display: 25 records per page'. A 'Modify form parameters' dialog box is open on the right, showing a list of query terms: 'Allele designations/scheme field values', 'Allele designation status', 'Tagged sequence status' (highlighted with a red box), and 'Filters'. The 'Tagged sequence status' option is selected.

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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [i](#) Field help: [id](#) [Go](#)

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields: [id](#) = Enter value... [+](#) [i](#)

Display/sort options: Order by: [id](#) ascending Display: 25 records per page [i](#)

Tagged sequence status: NEIS0001 (lpxC) is flagged: internal stop codon [+](#) [i](#) Action: [Reset](#) [Submit](#)

1 record returned. Click the hyperlink for detailed information.

Isolate fields i						MLST		Finotyping antigens				
id	isolate	aliases	country	year	disease	species	serogroup	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](#) [Codons](#) [Polymorphic sites](#) [Combinations](#) [Schemes/alleles](#) [Publications](#) [Sequence bin](#) [Tag status](#)

Analysis: [Presence/Absence](#) [Genome Comparator](#) [BLAST](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

[Modify form options](#)

See also:

Sequence tag flags

10.6.4 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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [i](#) Field help: [id](#) [Go](#)

Search *Neisseria* PubMLST database

Isolate provenance/phenotype fields: [id](#) = Enter value... [+](#) [i](#)

Display/sort options: Order by: [id](#) Display: 25 records per page

Action: [Reset](#) [Submit](#)

[Modify form options](#)

Modify form parameters

Click to add or remove additional query terms:

- [Show](#) Allele designations/scheme field values
- [Show](#) Allele designation status
- [Show](#) Tagged sequence status
- [Show](#) **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.
- Sequence bin - Specify whether any sequence data has been associated with a record. Specific threshold values may be selected if these have been *set up for the database*.
 - 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*.

10.7 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. This can also be done in sequence definition databases if the scheme has a primary key field defined.

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.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29174
- Last updated: 2014-07-14
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XIMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

If multiple schemes are defined, you may have to select the scheme you wish to query in the ‘Schemes’ dropdown box and click ‘Select’.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

Search *Neisseria* PubMLST database by combinations of loci

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:

Filters **Options** **Display/sort options**
 Project: Search: Order by:
☐ Include old record versions Display: records per page

Action

Enter the combination of alleles that you want to query for. Fields can be left blank.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

Search *Neisseria* PubMLST database by combinations of loci

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
2	3	4	3	8	4	

 ST:

Filters **Options** **Display/sort options**
 Project: Search: Order by:
☐ Include old record versions 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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Search *Neisseria* PubMLST database by combinations of loci

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
9	6	9	9	9	6	9

Autofill profile by searching remote database
ST: 44

Filters
Project: ☐ Include old record versions

Options
Search:

Display/sort options
Order by:
Display: 25

Action

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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Search *Neisseria* PubMLST database by combinations of loci

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
9	6	9	9	9	6	9

Autofill profile by searching remote database
ST: 44

Filters
Project: ☐ Include old record versions

Options
Search:

Display/sort options
Order by:
Display: 25

Action

Click 'Submit'.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?]

Search *Neisseria* PubMLST database by combinations of loci

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
9	6	9	9	9	6	9	44 <input type="button" value="Autofill"/>

Filters Options Display/sort options

Project: Search: Order by:

☐ Include old record versions Display: 25 records per page

Action

Exact matches found (7 loci).

119 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page:

Isolate fields							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
41	19		Germany	1999	carrier	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3			
70	38		Germany	1999	carrier	<i>Neisseria meningitidis</i>	NG	44	ST-41/44 complex/Lineage 3			
427	NG E30	Z4692	Norway	1988	carrier	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3	21	16	F1-7
774	99 182		Canada	1999	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3			
792	99-132		Canada	1999	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3			
975	0069/93		Czech Republic	1993	carrier	<i>Neisseria meningitidis</i>	NG	44	ST-41/44 complex/Lineage 3	22	14-4	F1-7
1097	3532	Z7184	The Netherlands	1975		<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3		4	
1603	0213/93		Czech Republic	1993	carrier	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3	22	14-4	F1-19
1604	0214/93		Czech Republic	1993	carrier	<i>Neisseria meningitidis</i>	NG	44	ST-41/44 complex/Lineage 3	22	14-4	F1-7
1633	0244/93		Czech Republic	1993	carrier	<i>Neisseria meningitidis</i>	B	44	ST-41/44 complex/Lineage 3	22	14-4	F1-7

10.8 Retrieving list of isolates or profiles

Both isolate and sequence definition databases can be queried against a list of values matching any criteria (isolate provenance fields, alleles, or scheme fields).

Click 'List query' on the main contents page.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Neisseria PubMLST 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](#) - advanced queries.
- [Browse database](#) - peruse all records.
- [Search by combinations of loci \(profiles\)](#) - including partial matching.
- List query** - find isolates by matching a field to an entered list.

Option settings

- [Set general options](#) - including isolate table field handling
- Set display and query options for [locus](#), [schemes](#) or [scheme fields](#).

General information

- Isolates: 29174
- Last updated: 2014-07-14
- [Update history](#)
- [About BIGSdb](#)

Breakdown

- [Single field](#)
- [Two field](#)
- [Unique combinations](#)
- [Scheme and alleles](#)
- [Publications](#)
- [Sequence bin](#)

Export

- [Export dataset](#)
- [Configs](#)
- [Sequences](#) - XMFA / concatenated FASTA formats

Analysis

- [Codon usage](#)
- [Presence/absence status of loci](#)
- [Genome comparator](#)
- [BLAST](#)

Miscellaneous

- [Description of database fields](#)

Select the attribute you wish to search against in the drop-down list box and enter the list of attributes in the box (one per line). Click 'Submit'.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: Field help: id Go

Query *Neisseria* PubMLST database matching a field against a list

Please select attribute
isolate
Enter your list of attribute values below (one per line)
H44/76
MC58
alpha14

Filters
☐ Include old record versions

Display/sort options
Order by: id ascending
Display: 25 records per page

Action
Reset Submit

4 records returned. Click the hyperlinks for detailed information.

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
30	14	alpha14	Germany	1999	carrier	<i>Neisseria meningitidis</i>	NG	53	ST-53 complex	7	30-3	F5-5
237	H44/76	44/76-3; Z3842	Norway	1976	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	32	ST-32 complex/ET-5 complex	7	16	F3-3
240	MC58	Z7176	UK	1983		<i>Neisseria meningitidis</i>	B	74	ST-32 complex/ET-5 complex	7	16-2	F1-5
20477	H44/76	44/76-3; Z3842	Norway	1976	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	B	32	ST-32 complex/ET-5 complex	7	16	F3-3

Analysis tools:

Breakdown: Fields Two Field Codons Polymorphic sites Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST Presence/Absence Genome Comparator BLAST

Export: Dataset Contigs Sequences

10.9 Retrieving isolates by linked publication

Click 'Publications' in the Breakdown section of the contents page.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29174
- Last updated: 2014-07-14
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications**
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

A list of publications linked by isolates within the database will be displayed.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Publication breakdown of dataset

Filter query by: Author: Year: Display: Order by: Display: records per page Action:

73 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page:

PubMed id	Year	Citation	Title	Isolates in database
17517841	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, Lambertsen L, Levenet I, Musilek M, Paragi M, Sagner A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zaronelli ML (2007) Antimicrob Agents Chemother 51: 2784-92	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> .	1670 isolates
18815379	2008	Buckee CO, Jolley KA, Recker M, Penman B, Kriz P, Gupta S, Maiden MC (2008) Proc Natl Acad Sci U S A 105: 15082-7	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> .	1054 isolates
15776372	2005	Claus H, Maiden MC, Wilson DJ, McCarthy ND, Jolley KA, Urwin R, Hessler F, Frosch M, Vogel U (2005) J Infect Dis 191: 1263-71	Genetic analysis of meningococci carried by children and young adults.	822 isolates
15528708	2004	Yazdankhah SP, Kriz P, Tzanakaki G, Kremastinou J, Kalmusova J, Musilek M, Alvestad T, Jolley KA, Wilson DJ, McCarthy ND, Caugant DA, Maiden MC (2004) J Clin Microbiol 42: 5146-53	Distribution of serogroups and genotypes among disease-associated and carried isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway.	667 isolates
17825091	2007	Bennett JS, Jolley KA, Sparling PF, Saunders NJ, Hart CA, Feavers IM, Maiden MC (2007) BMC Biol 5: 35	Species status of <i>Neisseria gonorrhoeae</i> : evolutionary and epidemiological inferences from multilocus sequence typing.	576 isolates
15537808	2005	Jolley KA, Wilson DJ, Kriz P, McVean G, Maiden MC (2005) Mol Biol Evol 22: 562-9	The influence of mutation, recombination, population history, and selection on patterns of genetic diversity in <i>Neisseria meningitidis</i> .	378 isolates
18375809	2008	Russell JE, Urwin R, Grav SJ, Fox AJ, Feavers IM, Maiden MC (2008) Microbiol Rev 72: 1542-51	Molecular epidemiology of meningococcal disease in England and Wales.	323 isolates

These can be filtered by author and/or year, and the sort order changed.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Publication breakdown of dataset

Filter query by: Author: Year: Display: Order by: Display: records per page Action:

13 records returned. Click the hyperlinks for detailed information.

PubMed id	Year	Citation	Title	Isolates in database
17517841	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, Lambertsen L, Levenet I, Musilek M, Paragi M, Sagner A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zaronelli ML (2007) Antimicrob Agents Chemother 51: 2784-92	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> .	1670 isolates
18815379	2008	Buckee CO, Jolley KA, Recker M, Penman B, Kriz P, Gupta S, Maiden MC (2008) Proc Natl Acad Sci U S A 105: 15082-7	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> .	1054 isolates
15776372	2005	Claus H, Maiden MC, Wilson DJ, McCarthy ND, Jolley KA, Urwin R, Hessler F, Frosch M, Vogel U (2005) J Infect Dis 191: 1263-71	Genetic analysis of meningococci carried by children and young adults.	822 isolates
15528708	2004	Yazdankhah SP, Kriz P, Tzanakaki G, Kremastinou J, Kalmusova J, Musilek M, Alvestad T, Jolley KA, Wilson DJ, McCarthy ND, Caugant DA, Maiden MC (2004) J Clin Microbiol 42: 5146-53	Distribution of serogroups and genotypes among disease-associated and carried isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway.	667 isolates
17825091	2007	Bennett JS, Jolley KA, Sparling PF, Saunders NJ, Hart CA, Feavers IM, Maiden MC (2007) BMC Biol 5: 35	Species status of <i>Neisseria gonorrhoeae</i> : evolutionary and epidemiological inferences from multilocus sequence typing.	576 isolates
15537808	2005	Jolley KA, Wilson DJ, Kriz P, McVean G, Maiden MC (2005) Mol Biol Evol 22: 562-9	The influence of mutation, recombination,	378 isolates

To display the isolate records for any of the displayed publications, click the button to the right of the citation.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Publication breakdown of dataset

Filter query by: Author: Year: Display: Order by: Action: Display: 25 records per page

13 records returned. Click the hyperlinks for detailed information.

PubMed id	Year	Citation	Title	Isolates in database
17517841	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, Kadubowski M, Kechrid A, Kesanopoulos K, Kriz P, Lamberts L, Levenet I, Musilek M, Paragi M, Sauer A, Skoczynska A, Stefanelli P, Thulin S, Tzanakaki G, Unemo M, Vogel U, Zorantonelli ML (2007) <i>Antimicrob Agents Chemother</i> 51: 2784-92	Target gene sequencing to characterize the penicillin G susceptibility of <i>Neisseria meningitidis</i> .	1670 isolates
18815379	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> 105: 15082-7	Role of selection in the emergence of lineages and the evolution of virulence in <i>Neisseria meningitidis</i> .	1054 isolates
15776372	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> 191: 1263-71	Genetic analysis of meningococci carried by children and young adults.	822 isolates
15528708	2004	Yazdankhah SP, Kriz P, Tzanakaki G, Kremastinou J, Kalmusova J, Musilek M, Alvestad T, Jolley KA, Wilson DJ, McCarthy ND, Caugant DA, Maiden MC (2004) <i>J Clin Microbiol</i> 42: 5146-53	Distribution of serogroups and genotypes among disease-associated and carried isolates of <i>Neisseria meningitidis</i> from the Czech Republic, Greece, and Norway.	667 isolates
17825091	2007	Bennett JS, Jolley KA, Sparling PF, Saunders NJ, Hart CA, Feavers IM, Maiden MC (2007) <i>BMC Biol</i> 5: 35	Species status of <i>Neisseria gonorrhoeae</i> : evolutionary and epidemiological inferences from multilocus sequence typing.	576 isolates
15537808	2005	Jolley KA, Wilson DJ, Kriz P, McVean G, Maiden MC (2005) <i>Mol Biol Evol</i> 22: 562-9	The influence of mutation, recombination, population history, and selection on patterns of genetic diversity in <i>Neisseria meningitidis</i> .	378 isolates
15784588	2005	Bennett JS, Griffiths DT, McCarthy ND, Sleeman KL, Jolley KA, Crook DW, Maiden MC (2005) <i>Infect Immun</i> 73: 2424-32	Genetic diversity and carriage dynamics of <i>Neisseria lactamica</i> in infants.	271 isolates
11101585	2000	Jolley KA, Kalmusova J, Fiala E, Gupta S, Musilek M, Kriz P, Maiden MC (2000) <i>J Clin Microbiol</i> 38: 4492-8	Carried meningococci in the Czech Republic.	217 isolates

The abstract of the paper will be displayed (if available), along with all isolates linked to it.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Publications cited in the *Neisseria* PubMLST database

Citation query (PubMed id: 17825091)

Bennett JS, Jolley KA, Sparling PF, Saunders NJ, Hart CA, Feavers IM, Maiden MC (2007) *BMC Biol* 5:35
Species status of *Neisseria gonorrhoeae*: evolutionary and epidemiological inferences from multilocus sequence typing.
 The seven loci *Neisseria* MLST scheme was readily adapted to *N. gonorrhoeae* isolates, providing a highly discriminatory typing method. In addition, these data permitted phylogenetic and population genetic inferences to be made, including direct comparisons with *N. meningitidis* and *N. lactamica*. Examination of these data demonstrated that alleles were rarely shared among the three species. Analysis of variation at a single locus, *gdh*, provided a rapid means of identifying misclassified isolates and determining whether mixed cultures were present.

576 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page:

Isolate fields							MLST		Finotyping antigens			
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4M1027	B1; Z1001	USA	1937	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	5-2	10	F1-5
2	120M	B35; Z1035	Pakistan	1967	meningitis and septicaemia	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex/subgroup III	20	9	F3-1
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
13	139M	B99; Z1099	Philippines	1968		<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
19	S3131	B213; Z1213	Ghana	1973	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	7	13-1	F1-5
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
31	10	B269; Z1269	Burkina Faso	1963	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	7	13-1	F1-5
34	20	B275; Z1275	Niger	1963	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F1-7
35	26	B278; Z1278	Niger	1963	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	7	13	F1-5
46	255	B318; Z1318	Burkina Faso	1966	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	7-2	13-1	F1-5
52	243	B362; Z1362	Cameroon	1966		<i>Neisseria meningitidis</i>	A	4	ST-4 complex/subgroup IV	7	13	F1-5
61	393	B392; Z1392	Greece	1968	carrier	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
64	254	B439; Z1439	Djibouti	1966	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F1-7
67	S5611	B466; Z1466	Australia	1977	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
82	11-004	B503; Z1503	China	1984	invasive (unspecified/other)	<i>Neisseria meningitidis</i>	A	5	ST-5 complex/subgroup III	20	9	F3-8

10.10 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 'Set general options' link on the database contents page. Most of the available options are visible for isolate databases, whereas sequence definition databases have fewer available.

The screenshot shows the Neisseria PubMLST database interface. At the top, there is a navigation bar with links for Query, Breakdown, and Links. Below this, the main content area is titled 'Neisseria PubMLST database'. A descriptive paragraph explains that the database contains data for a collection of isolates representing the total known diversity of Neisseria species. The interface is divided into several sections: 'Query database' with links for Search, Browse, and List; 'Option settings' with a red box highlighting 'Set general options'; 'General information' with details about the number of isolates and last update; 'Breakdown' with links for Single field, Two field, Unique combinations, Scheme and alleles, Publications, and Sequence bin; 'Export' with links for Export dataset, Contigs, and Sequences; 'Analysis' with links for Codon usage, Presence/absence status of loci, Genome comparator, and BLAST; and 'Miscellaneous' with a link for Description of database fields.

10.10.1 General options

The general options tab is displayed by default. If another tab is being shown, click the 'General options' header.


[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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 records per page.
Page bar position:
Display nucleotides per line in sequence alignments.
Display nucleotides of flanking sequence (where available).
☒ Display locus aliases if set.
☒ Enable tooltips (beginner's mode).

► Main results table

► Isolate record display

► Provenance field display

► Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

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.

10.10.2 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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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 records per page.
 Page bar position:
 Display nucleotides per line in sequence alignments.
 Display nucleotides of flanking sequence (where available).
☒ Display locus aliases if set.
☒ Enable tooltips (beginner's mode).

Main results table

Isolate record display

Provenance field display

Query filters

Reset
 Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

The 'main results table' tab will scroll up.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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

Isolate record display

Provenance field display

Query filters

☐ 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.

Reset
 Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

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.

10.10.3 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.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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 records per page.
 Page bar position:
 Display nucleotides per line in sequence alignments.
 Display nucleotides of flanking sequence (where available).
☒ Display locus aliases if set.
☒ Enable tooltips (beginner's mode).

► Main results table

► Isolate record display

► Provenance field display

► Query filters

Reset
 Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

The ‘Isolate record display’ tab will scroll up.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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
- 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).
 - ☒ Display full information about sample records (tooltip).
 - [Set options](#)
- Provenance field 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:

- 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.
- Display full information about sample records - Used when the database is used as part of a basic laboratory information management system (LIMS). This option will display records of samples available for the displayed isolate.

10.10.4 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.


[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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 records per page.
Page bar position:
Display nucleotides per line in sequence alignments.
Display nucleotides of flanking sequence (where available).
☒ Display locus aliases if set.
☒ Enable tooltips (beginner's mode).

Main results table

Isolate record display


Provenance field display

Query filters

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

The 'Provenance field display' tab will scroll up.


[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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

Isolate record display

Provenance field display

Query filters

Provenance field display

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 checked="" type="checkbox"/> disease	<input type="checkbox"/> amoxicillin	<input type="checkbox"/> ciprofloxacin_range
<input checked="" type="checkbox"/> aliases	<input type="checkbox"/> source	<input type="checkbox"/> sulphonamide	<input type="checkbox"/> pending_assembly
<input type="checkbox"/> strain_designation	<input type="checkbox"/> epidemiology	<input type="checkbox"/> ceftriaxone	<input type="checkbox"/> assembly_status
<input checked="" type="checkbox"/> country	<input checked="" type="checkbox"/> species	<input type="checkbox"/> ceftriaxone_range	<input type="checkbox"/> ENA_accession
<input type="checkbox"/> continent	<input checked="" type="checkbox"/> serogroup	<input type="checkbox"/> chloramphenicol	<input type="checkbox"/> private_project
<input type="checkbox"/> region	<input type="checkbox"/> MLEE_designation	<input type="checkbox"/> chloramphenicol_range	<input type="checkbox"/> comments
<input checked="" type="checkbox"/> year	<input type="checkbox"/> serotype	<input type="checkbox"/> cefotaxime	<input type="checkbox"/> sender
<input type="checkbox"/> epidemiological_year	<input type="checkbox"/> sero_subtype	<input type="checkbox"/> cefotaxime_range	<input type="checkbox"/> curator
<input type="checkbox"/> age_yr	<input type="checkbox"/> ET_no	<input type="checkbox"/> rifampicin	<input type="checkbox"/> date_entered
<input type="checkbox"/> age_mth	<input type="checkbox"/> penicillin	<input type="checkbox"/> rifampicin_range	<input type="checkbox"/> datestamp
<input type="checkbox"/> sex	<input type="checkbox"/> penicillin_range	<input type="checkbox"/> ciprofloxacin	

Reset

Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

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’.

10.10.5 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.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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 PubMLST) 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 records per page.
Page bar position:
Display nucleotides per line in sequence alignments.
Display nucleotides of flanking sequence (where available).
☒ Display locus aliases if set.
☒ Enable tooltips (beginner's mode).

► Main results table
► Isolate record display
► Provenance field display
► **Query filters**

Reset
Click the reset button to remove all user settings for this database - this includes locus and scheme field preferences.

The ‘Query filters’ tab will scroll up.

▶ Main results table
 ▶ Isolate record display
 ▶ Provenance field display

▼ 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"/> ENA_accession	<input type="checkbox"/> LOS alpha chain transferases profile completion
<input type="checkbox"/> country	<input type="checkbox"/> private_project	<input type="checkbox"/> LOS inner core transferases profile completion
<input type="checkbox"/> continent	<input type="checkbox"/> comments	<input type="checkbox"/> LOS transport/export profile completion
<input type="checkbox"/> region	<input type="checkbox"/> sender	<input type="checkbox"/> Lipid A biosynthesis: acyltransferases profile completion
<input type="checkbox"/> year	<input type="checkbox"/> curator	<input type="checkbox"/> Lipid A biosynthesis: other profile completion
<input type="checkbox"/> epidemiological_year	<input type="checkbox"/> date_entered	<input type="checkbox"/> N. meningitidis profile completion
<input type="checkbox"/> age_yr	<input type="checkbox"/> datestamp	<input type="checkbox"/> Neisseria genus core genes profile completion
<input type="checkbox"/> age_mth	<input checked="" type="checkbox"/> MLST profile completion	<input type="checkbox"/> Nucleotide excision repair profile completion
<input type="checkbox"/> sex	<input type="checkbox"/> Finelytyping antigens profile completion	<input type="checkbox"/> Pilus genes profile completion
<input type="checkbox"/> disease	<input type="checkbox"/> 16S profile completion	<input type="checkbox"/> Protein glycosylation profile completion
<input type="checkbox"/> source	<input type="checkbox"/> ADP-heptose biosynthesis profile completion	<input type="checkbox"/> Purine metabolism profile completion
<input type="checkbox"/> epidemiology	<input type="checkbox"/> Aminoacyl-tRNA biosynthesis profile completion	<input type="checkbox"/> Pyrimidine metabolism profile completion
<input type="checkbox"/> species	<input type="checkbox"/> Antibiotic resistance profile completion	<input type="checkbox"/> Pyruvate dehydrogenase complex profile completion
<input type="checkbox"/> serogroup	<input type="checkbox"/> Antigen genes profile completion	<input type="checkbox"/> RNA polymerase profile completion
<input type="checkbox"/> MLEE_designation	<input type="checkbox"/> Capsule Region A - Serogroup A profile completion	<input checked="" type="checkbox"/> Ribosomal MLST profile completion
<input type="checkbox"/> serotype	<input type="checkbox"/> Capsule Region A - Serogroup B profile completion	<input type="checkbox"/> Small regulatory RNAs profile completion
<input type="checkbox"/> sero_subtype	<input type="checkbox"/> Capsule Region A - Serogroup C profile completion	<input type="checkbox"/> TCA cycle profile completion
<input type="checkbox"/> ET_no	<input type="checkbox"/> Capsule Region A - Serogroup E profile completion	<input type="checkbox"/> UDP-GlcNAc synthesis profile completion
<input type="checkbox"/> penicillin	<input type="checkbox"/> Capsule Region A - Serogroup H profile completion	<input type="checkbox"/> UDP-glucose and UDP-galactose biosynthesis profile completion
<input type="checkbox"/> penicillin_range	<input type="checkbox"/> Capsule Region A - Serogroup L profile completion	<input type="checkbox"/> completion
<input type="checkbox"/> amoxicillin	<input type="checkbox"/> Capsule Region A - Serogroup W profile completion	<input type="checkbox"/> VirB T4SS profile completion
<input type="checkbox"/> sulphonamide	<input type="checkbox"/> Capsule Region A - Serogroup X profile completion	<input type="checkbox"/> beta lactamase plasmid profile completion
<input type="checkbox"/> ceftriaxone	<input type="checkbox"/> Capsule Region A - Serogroup Y profile completion	<input type="checkbox"/> eMLST (20 locus partial genes) profile completion
<input type="checkbox"/> ceftriaxone_range	<input type="checkbox"/> Capsule Region A - Serogroup Z profile completion	<input type="checkbox"/> eMLST (20 locus whole genes) profile completion
<input type="checkbox"/> chloramphenicol	<input type="checkbox"/> Capsule Region B profile completion	<input type="checkbox"/> rplF species profile completion
<input type="checkbox"/> chloramphenicol_range	<input type="checkbox"/> Capsule Region C profile completion	<input checked="" type="checkbox"/> Publications
<input type="checkbox"/> cefotaxime	<input type="checkbox"/> Capsule Region D and D' profile completion	
<input type="checkbox"/> cefotaxime_range	<input type="checkbox"/> Conjugative Plasmid profile completion	
<input type="checkbox"/> rifampicin	<input type="checkbox"/> DNA replication profile completion	
<input type="checkbox"/> rifampicin_range	<input type="checkbox"/> Factor H-binding protein profile completion	
<input type="checkbox"/> ciprofloxacin	<input type="checkbox"/> Glycolysis profile completion	
<input type="checkbox"/> ciprofloxacin_range	<input type="checkbox"/> Gonococcal Genetic Island profile completion	
<input type="checkbox"/> pending_assembly	<input type="checkbox"/> Iron acquisition profile completion	
<input type="checkbox"/> assembly_status	<input type="checkbox"/> Kdo addition profile completion	

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’.

10.10.6 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 on the isolate contents page.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling.
- Set display and query options for **locus, schemes or scheme fields.**

General information

- Isolates: 29174
- Last updated: 2014-07-14
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

Either select the locus id by querying for it directly.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Query loci for Neisseria PubMLST database

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 Submit

1 record returned. Click the hyperlink for detailed information.

Customize
 locus options

id	data type	allele id	format	length	length varies	coding sequence	orf	genome position	isolate display*	main display*	query field*	analysis*
abcZ	DNA	integer	433	false	true	1	1176340	allele only	false	true	true	true

* 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.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

Query loci for *Neisseria* PubMLST database

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 = + [?](#) Display: Order by: id ascending Display: 25 records per page [?](#)

Filter query by:

data type:
 allele id format:
 length varies: [?](#)
 coding sequence:
 orf:
 match longest: [?](#)
 pcr filter: [?](#)
 probe filter: [?](#)
 flag table: [?](#)
 isolate display:
 main display: [?](#)
 query field: [?](#)
 analysis: [?](#)
 curator: [?](#)
 scheme: MLST [?](#)

Action:

7 records returned. Click the hyperlinks for detailed information.

Customize

id	data type	allele id format	length	length varies	coding sequence	orf	genome position	isolate display*	main display*	query field*	analysis*
abcZ	DNA	integer	433	false	true	1	1176340	allele only	false	true	true
adk	DNA	integer	465	false	true	1	991951	allele only	false	true	true
aroE	DNA	integer	490	false	true	2	2079469	allele only	false	true	true
fumC	DNA	integer	465	false	true	1	1592943	allele only	false	true	true
gdh	DNA	integer	501	false	true	1	1514394	allele only	false	true	true
pdhC	DNA	integer	480	false	true	1	1453970	allele only	false	true	true
pgm	DNA	integer	450	false	true	1	965481	allele only	false	true	true

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

Once loci have been selected, click Customize 'locus options'.

7 records returned. Click the hyperlinks for detailed information.

Customize

id	data type	allele id format	length	length varies	coding sequence	orf	genome position	isolate display*	main display*	query field*	analysis*
abcZ	DNA	integer	433	false	true	1	1176340	allele only	false	true	true
adk	DNA	integer	465	false	true	1	991951	allele only	false	true	true
aroE	DNA	integer	490	false	true	2	2079469	allele only	false	true	true
fumC	DNA	integer	465	false	true	1	1592943	allele only	false	true	true
gdh	DNA	integer	501	false	true	1	1514394	allele only	false	true	true
pdhC	DNA	integer	480	false	true	1	1453970	allele only	false	true	true
pgm	DNA	integer	450	false	true	1	965481	allele only	false	true	true

* 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).

Data analysis plugins

11.1 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.

Click 'Locus Explorer' from the sequence definition database contents page.

PubMLST Query: [Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
Download: [Alleles](#) | [MLST profiles](#)
Links: [Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

Neisseria locus/sequence definitions database Toggle: [z]

The Neisseria PubMLST sequence definition database contains allele and profile data representing the total known diversity of Neisseria species. Every new ST deposited in this database should have a corresponding record in the isolate database.

Query database

- Sequence query - query an allele sequence.
- Batch sequence query - query multiple sequences in FASTA format.
- Sequence attribute search - find alleles by matching attributes.
- Browse profiles
- Search profiles
- List - find profiles matched to entered list.
- Search by combinations of alleles - including partial matching.
- Batch profile query - lookup profiles copied from a spreadsheet.
- Extract finetype from whole genome data

Downloads

- Allele sequences
- MLST

Option settings

- Set general options

General information

- Number of sequences: 342758
- Number of profiles: [Show](#)
- Last updated: 2014-07-16
- [Profile update history](#)
- [About BIGSdb](#)

Export

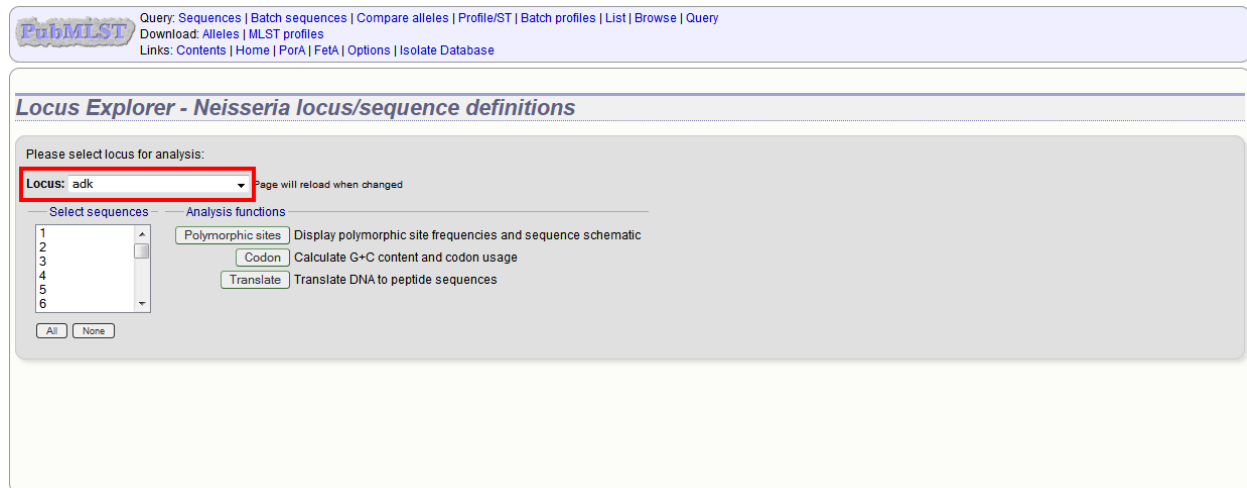
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Sequence similarity - find sequences most similar to selected allele.
- Sequence comparison - display a comparison between two sequences.
- Locus Explorer** - tool for analysing allele sequences stored for particular locus.

11.1.1 Polymorphic site analysis

Select the locus you would like to analyse in the Locus dropdown box. The page will reload.



PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Locus Explorer - *Neisseria* locus/sequence definitions

Please select locus for analysis:
Locus: adk Page will reload when changed

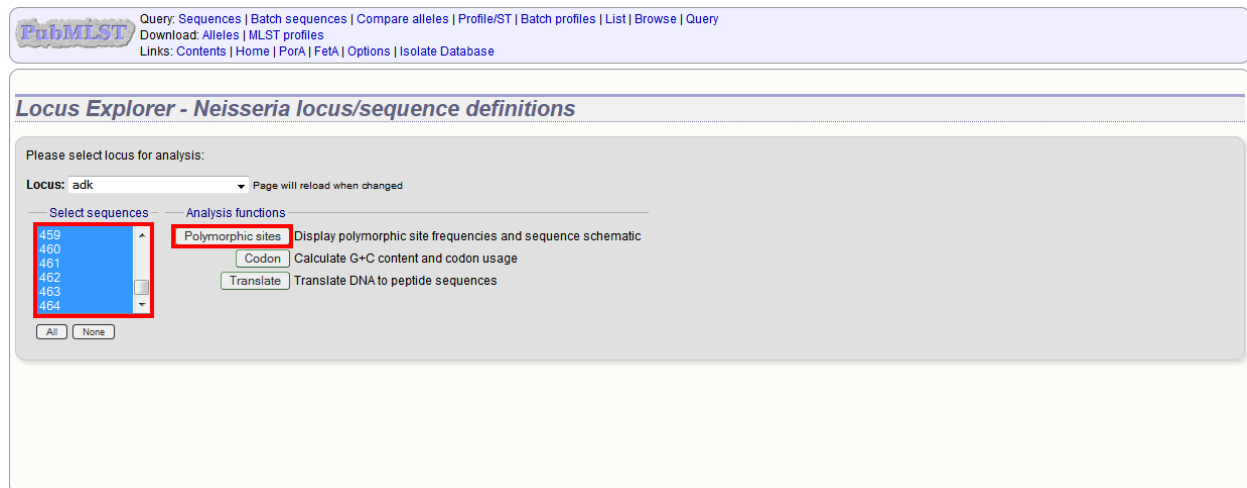
Select sequences Analysis functions

1
2
3
4
5
6

Polymorphic sites Display polymorphic site frequencies and sequence schematic
Codon Calculate G+C content and codon usage
Translate Translate DNA to peptide sequences

All None

Select the alleles that you would like to include in the analysis. Variable length loci are limited to 200 sequences or fewer since these need to be aligned. Click 'Polymorphic sites'.



PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Locus Explorer - *Neisseria* locus/sequence definitions

Please select locus for analysis:
Locus: adk Page will reload when changed

Select sequences Analysis functions

459
460
461
462
463
464

Polymorphic sites Display polymorphic site frequencies and sequence schematic
Codon Calculate G+C content and codon usage
Translate Translate DNA to peptide sequences

All None

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.

adk

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.

464 alleles included in analysis. 265 polymorphic sites found.

Key: 0 - 10% | 10 - 20% | 20 - 30% | 30 - 40% | 40 - 50% | 50 - 60% | 60 - 70% | 70 - 80% | 80 - 90% | 90 - 100%

1 10 20 30 40 50 60 70 80 90 100

GAAGCGAAAAATCATTCGAAGGCGCTTGGTGCGGACGACATCATTTATGCGCATGCTCAAGAAGCGCATCGGCAAGAGACTGCAAAAAAGCGTT

GGAG C AT G TA TAA TC C T T T T S TAA T CC T TA S GACTA T ATGCC T CC

AC A A T A A G T A T A A CG T A

G T G

101 110 120 130 140 150 160 170 180 190 200

TCCTGTTTGAAGGTTTCGCGGACATTTGGCACAAGCGGAGCGATGGTTGAAGCAGGCGTGCGATTTGGATGCA GTGTTTGAATGCA GTTCCGACAG

T T A C T T T T A A T C AATG A C A C ACAGC G T C A A AATGGC CTGATG A C G T C C T S GTGC

T A C A A A AGC G A CTC A T A G G

C T A T

201 210 220 230 240 250 260 270 280 290 300

CGTGAATTGCGACGACATGAGCGGGCGCGGTCGATTTGGCTTCGCGCCGCTAC TTACCAAGTTACCTACAA CCGCGCCAAAGT GAAGGCAAGACGAC

T CA CA TA T ATA T TT T C ACTC G TA S GT TACGGTTCTT GTT A S GAC GATT G T T

G T T A G A T T A AA C T A A C AA A T G

C G A A A A T GG A

301 310 320 330 340 350 360 370 380 390 400

GTAACGGCGGAAGATTGATTTCAGCGGAGACGACAAGAAGAAACCGTGAAAAACGGCTTGCCGCTTACCAAGAGCAACCGAAGTTTGGTGCATT

T T TAAA G GGC AG C A T GT T G G C GTG C TT CTAT GTTGT GA GG TT CCA C AA A G C

T C TT G GC G A C A T A T A A A G

C G T

401 410 420 430 440 450 460

TTTACAGCAAACTGGAAGCGGAACAGCGGCCATAATCATCAAAGTTGACGGCACTCAGCGGTGA

AC GTC TCG TACACCA TAGGTCT TAT CG T T GA C T T S CACTC G

C G G CACA GG CAG C C G A G TTAC T

T A A T C

40 - 50% | >50 - 60% | >60 - 70% | >70 - 80%

40 50 60

GGTGC GCGACGACATCATTATCGGCATGGTCAAA

C A T T T T C TAATT CG

A T A A T

T G G A A

[Query: Sequences](#) | [Batch sequences](#) | [Compare alleles](#) | [Profile/ST](#) | [Batch profiles](#) | [List](#) | [Browse](#) | [Query](#)
[Download: Alleles](#) | [MLST profiles](#)
[Links: Contents](#) | [Home](#) | [PorA](#) | [FetA](#) | [Options](#) | [Isolate Database](#)

adk position 51			
464 alleles included in analysis.			
Base	Number of alleles	Percentage of alleles	MLST profiles
T	370	79.74	10619 / 10883 (97.57%)
C	92	19.83	262 / 10883 (2.41%)
A	1 (adk-351)	0.22	1 / 10883 (0.01%)
G	1 (adk-413)	0.22	1 / 10883 (0.01%)

11.1. Locus explorer

401 410 420 430 440 450 460

TTTACGCAACTGGGAAGGCGACACGGCGCTAATACATCAAGTTGACGGCAGTCAGCGCTA

AC GTC TCG TACACCA TAGGTCT TAT CG T T GA T T G GACTAC G

C G G CACA GG CAG C C G A G TTAC T

T A A A T C

Nucleotide frequencies

Position	Nucleotide									
	A	C	G	T	%A	%C	%G	%T	%-	%N
2	463	0	1	0	99.78	0.22				
3	462	0	2	0	99.57	0.43				
4	1	0	463	0	0.22	99.78				
5	0	463	1	0		99.78	0.22			
6	52	7	405	0	11.21	1.51	87.28			
9	463	0	1	0	99.78	0.22				
14	1	0	0	463	0.22		99.78			
15	0	452	0	12		97.41	2.59			
18	0	76	7	381		16.38	1.51	82.11		
21	0	295	0	169		63.58	36.42			
22	8	0	456	0	1.72	98.28				
27	3	451	0	10	0.65	97.20	2.16			
28	2	1	461	0	0.43	0.22	99.35			
29	1	0	463	0	0.22	99.78				
30	3	341	1	119	0.65	73.49	0.22	25.65		
31	0	10	0	454		2.16	97.84			
33	2	5	455	2	0.43	1.08	98.06	0.43		
36	51	0	410	3	10.99	88.36	0.65			
37	0	463	0	1		99.78	0.22			

See also:

- *Investigating allele differences.*
- *Polymorphism analysis following isolate query.*

11.1.2 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’.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
Download: Alleles | MLST profiles
Links: Contents | Home | PorA | FetA | Options | Isolate Database

Locus Explorer - Neisseria locus/sequence definitions

Please select locus for analysis:

Locus: adk Page will reload when changed

Select sequences Analysis functions

459 460 461 462 463 464

Polymorphic sites Display polymorphic site frequencies and sequence schematic

Codon Calculate G+C content and codon usage

Translate Translate DNA to peptide sequences

All None

The GC content of the alleles will be determined and a table of the codon frequencies displayed.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FetA | Options | Isolate Database

Codon Usage

adk

ORF used: 1

464 alleles included in analysis.

GC content

Coding: GC 52.47%
 1st letter: GC 65.31%
 2nd letter: GC 31.73%
 3rd letter: GC 60.37%

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	0.262	17.353	1248
GCC	A	0.246	16.254	1169
GCG	A	0.389	25.751	1852
GCT	A	0.103	6.813	490
TGC	C	0.987	6.452	464
TGT	C	0.013	0.083	6
GAC	D	0.747	91.073	6550
GAT	D	0.253	30.812	2216
GAA	E	0.916	82.397	5926
GAG	E	0.084	7.564	544
TTC	F	0.594	15.295	1100
TTT	F	0.406	10.470	753
GGA	G	0.007	0.542	39
GGC	G	0.765	59.497	4279
GGG	G	0.001	0.042	3
GGT	G	0.227	17.659	1270
CAC	H	0.749	19.258	1385
CAT	H	0.251	6.438	463
ATA	I	0.001	0.083	6
ATC	I	0.698	40.788	2932

11.1.3 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'.

PubMLST Query: Sequences | Batch sequences | Compare alleles | Profile/ST | Batch profiles | List | Browse | Query
 Download: Alleles | MLST profiles
 Links: Contents | Home | PorA | FetA | Options | Isolate Database

Locus Explorer - *Neisseria* locus/sequence definitions

Please select locus for analysis:

Locus: adk ▼ Page will reload when changed

Select sequences: 459 460 461 462 463 464 ▼

Analysis functions:

Polymorphic sites Display polymorphic site frequencies and sequence schematic

Codon Calculate G+C content and codon usage

Translate Translate DNA to peptide sequences

All None

An aligned amino acid sequence will be displayed.


434_1S.....L.....T.....
435_1
436_1
437_1
438_1
439_1
440_1K.....
441_1
442_1L.....
443_1
444_1
445_1
446_1
447_1
448_1
449_1
450_1
451_1
452_1K.....T.....
453_1
454_1IA.....T.....
455_1
456_1
457_1G.....A.....N.....P.....IAF.....T.....
458_1
459_1
460_1S.....
461_1
462_1
463_1
464_1I.....
Consensus	EAKKIIDEGGLVDDIIIGMVKERIAQDDCRNGFLFDGFPRTLAQAEAMVEAGVDLDAVVEIDVPDSVIVDRMSGRRVHLASGRTHVITYNPPKVEGKDD		
	110	120	130 140 150
1_1
2_1
3_1
4_1
5_1
6_1
7_1
8_1

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.

11.2 Field breakdown


The field breakdown plugin for isolate databases displays the frequency of each value for fields stored in the isolates table. *Allele and scheme field breakdowns* are handled by a different plugin.

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.



[Query: Search | Browse | Profile/ST | List](#)
[Breakdown: Isolate fields | Scheme/alleles | Publications](#)
[Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions](#)

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.


Option settings


- Set general options - including isolate table field handling.
- Set display and query options for locus, schemes or scheme fields.


General information


- Isolates: 29177
- Last updated: 2014-07-16
- Update history
- About BIGSdb


Breakdown


- Single field**
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin


Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats


Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST


Miscellaneous

- Description of database fields

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.

5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	20	9	F3-1
8	M00242007		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex		14	
9	002184		Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex			
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

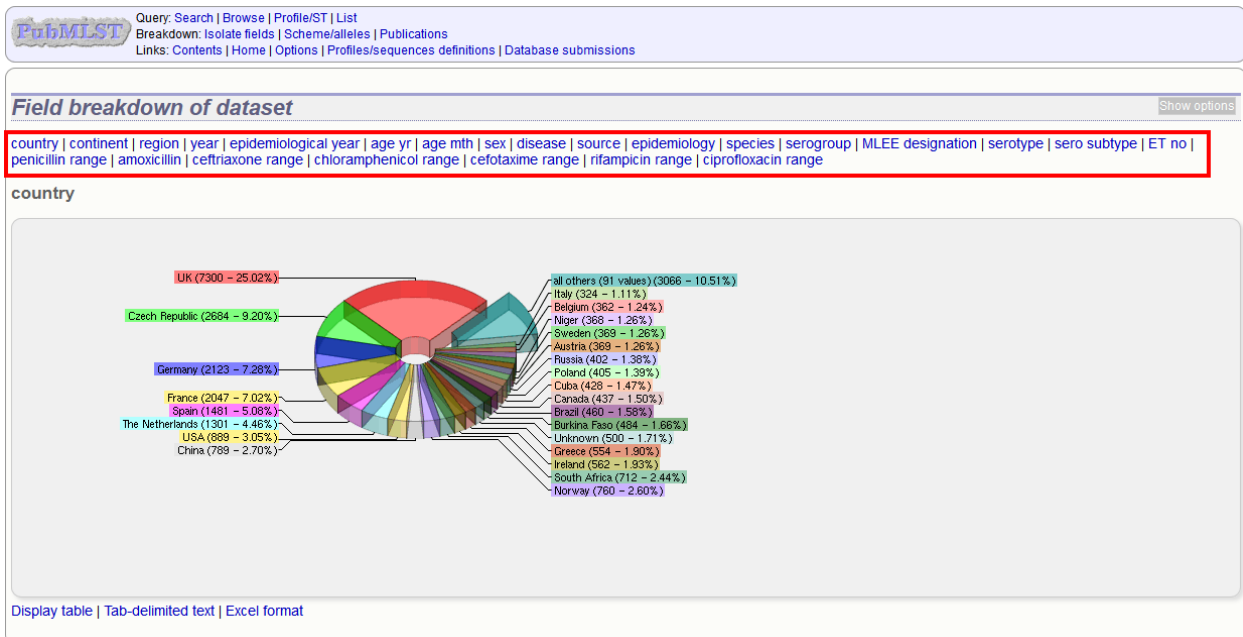
Breakdown: **Fields** Two Field Codons Polymorphic sites Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST Presence/Absence Genome Comparator BLAST

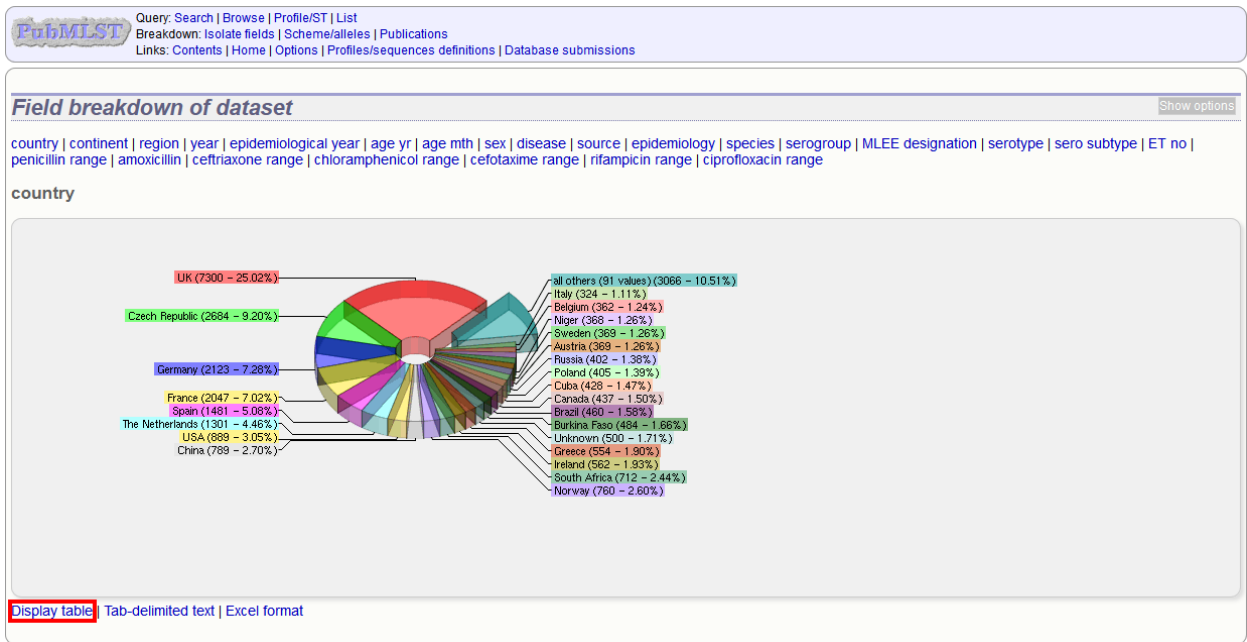
Export: Dataset Contigs Sequences

Page: 1 2 3 4 5 6 7 8 9 > Last

A series of charts will be displayed. Pick the field to display from the list at the top.



The values used to generate the chart can be displayed or extracted by clicking the 'Display table' link at the bottom of the page.



This displays a table that can be ordered by clicking the appropriate header.

PubMLST

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

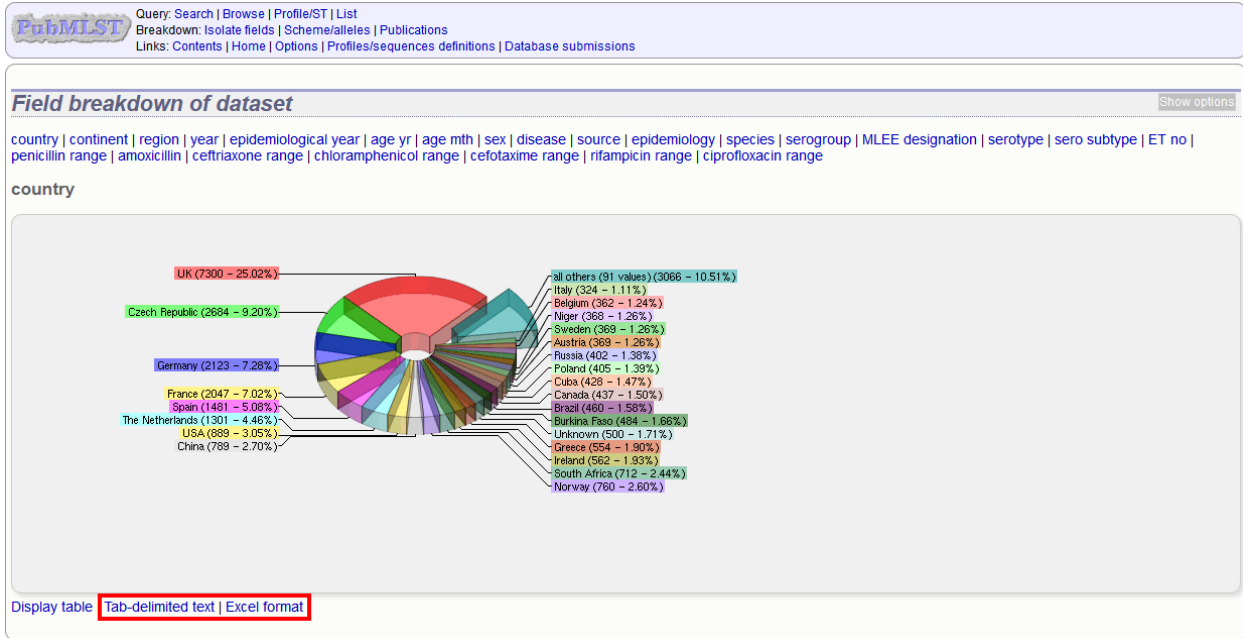
Breakdown by country

Show options

115 values.

country	Frequency	Percentage
UK	7300	25.02%
Czech Republic	2684	9.20%
Germany	2123	7.28%
France	2047	7.02%
Spain	1481	5.08%
The Netherlands	1301	4.46%
USA	889	3.05%
China	789	2.70%
Norway	760	2.60%
South Africa	712	2.44%
Ireland	562	1.93%
Greece	554	1.90%
Unknown	500	1.71%
Burkina Faso	484	1.66%
Brazil	460	1.58%
Canada	437	1.50%
Cuba	428	1.47%
Poland	405	1.39%
Russia	402	1.38%
Austria	369	1.26%
Sweden	369	1.26%
Niger	368	1.26%
Belgium	362	1.24%
Italy	324	1.11%
Finland	312	1.07%
Denmark	307	1.05%
Japan	238	0.82%

The data can also be downloaded in tab-delimited text or Excel formats by clicking the appropriate links.



11.3 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 selected for the whole database by clicking the ‘Two field breakdown’ link on the main contents page.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29177
- Last updated: 2014-07-16
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field**
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

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.

6	M0028220/		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex				
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	20	9	F3-1	
8	M00242007		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex		14		
9	002184		Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex				
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1	
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6	
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16		
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex				
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1	
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex				

Analysis tools:

Breakdown:

Analysis:

Export:

Page:

Select the two fields you wish to breakdown and how you would like the values displayed (percentage/absolute values and totaling options).

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Two field breakdown of dataset Show options

Here you can create a table breaking down one field by another, e.g. breakdown of serogroup by year.

Select fields

Field 1:

Field 2:

Display

☒ values only

☐ values and percentages

☐ percentages only

Calculate percentages by

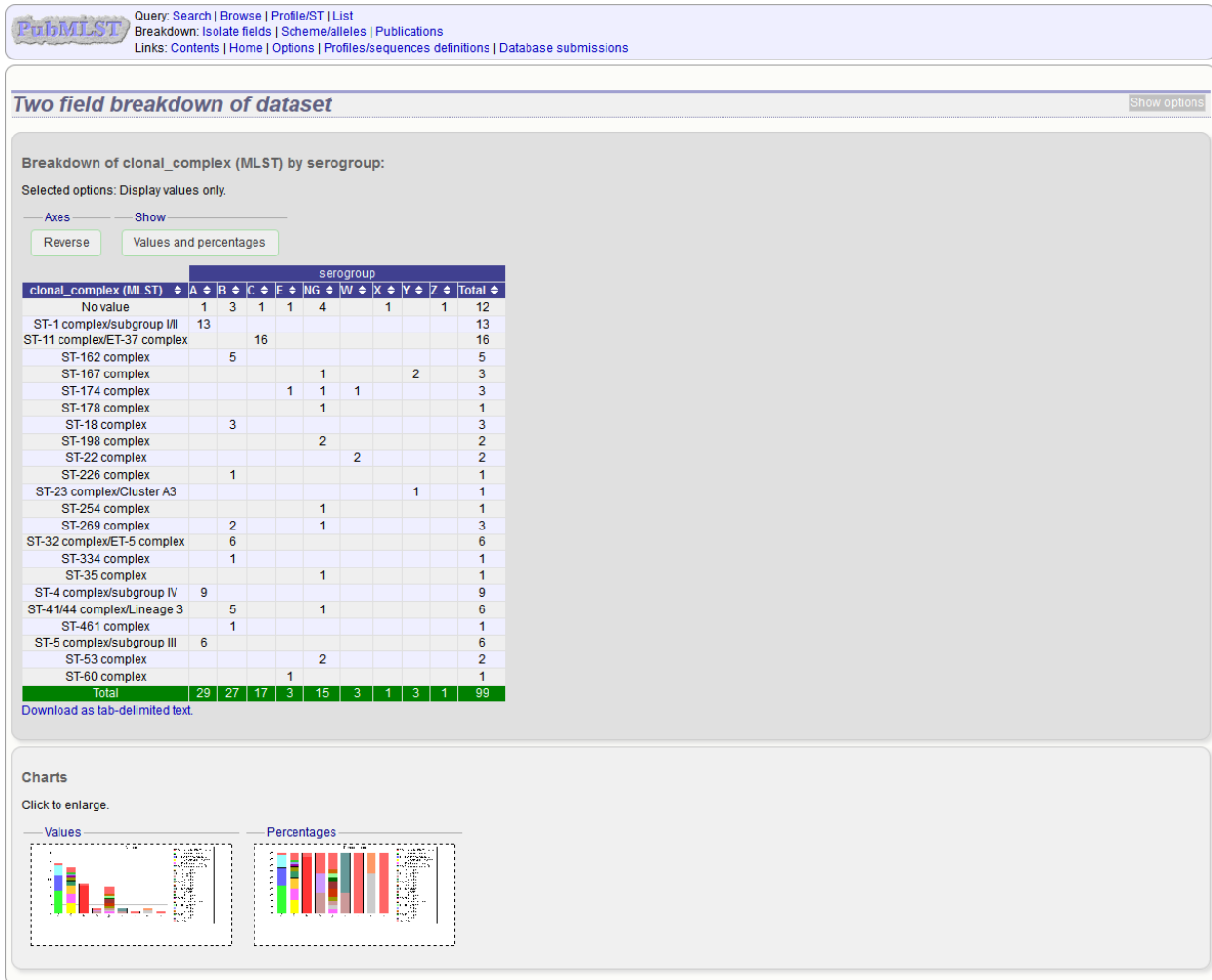
☒ dataset

☐ row

☐ column

Action

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 less than 30.



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.

11.4 Scheme and allele breakdown

The scheme and allele breakdown plugin displays the frequency of each allele and scheme field (e.g. ST or clonal complex).

The function can be selected for the whole database by clicking the ‘Scheme and allele breakdown’ link on the main contents page.

[Query](#) | [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown](#) | [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links](#) | [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling.
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29177
- Last updated: 2014-07-16
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles**
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

Alternatively, a breakdown can be displayed of the dataset returned from a query by clicking the ‘Schemes/alleles’ 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.

1	A4M1027	B1; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	5-2	10	F1-5
2	120M	B35; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1099		19	15	
4	M1027	B43; Z1043	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV			
5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:
Breakdown:
Analysis:
Export:


Page:

A scheme tree is shown. Select any combination of schemes to analyse.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Scheme field and allele breakdown of dataset Show options

Select schemes or groups of schemes within the tree. A breakdown of the individual fields and loci belonging to these schemes will then be performed.



Select

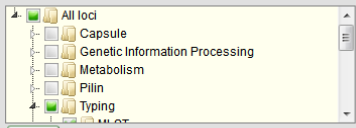
Click 'Select'.

A table showing the number of unique values for each locus and scheme field will be displayed.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Scheme field and allele breakdown of dataset Show options

Select schemes or groups of schemes within the tree. A breakdown of the individual fields and loci belonging to these schemes will then be performed.



Select

MLST

Fields			Alleles			
Field name	Unique values	Analyse	Locus	Unique alleles	Analyse	Download
ST	554	Breakdown	abcZ	64	Breakdown	Download
clonal complex	43	Breakdown	adk	57	Breakdown	Download
			aroE	80	Breakdown	Download
			fumC	85	Breakdown	Download
			gdh	79	Breakdown	Download
			pdhC	83	Breakdown	Download
			pgm	68	Breakdown	Download

A detailed display of allele or field frequencies can be displayed by clicking the appropriate 'Breakdown' button.

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Scheme field and allele breakdown of dataset

Select schemes or groups of schemes within the tree. A breakdown of the individual fields and loci belonging to these schemes will then be performed.

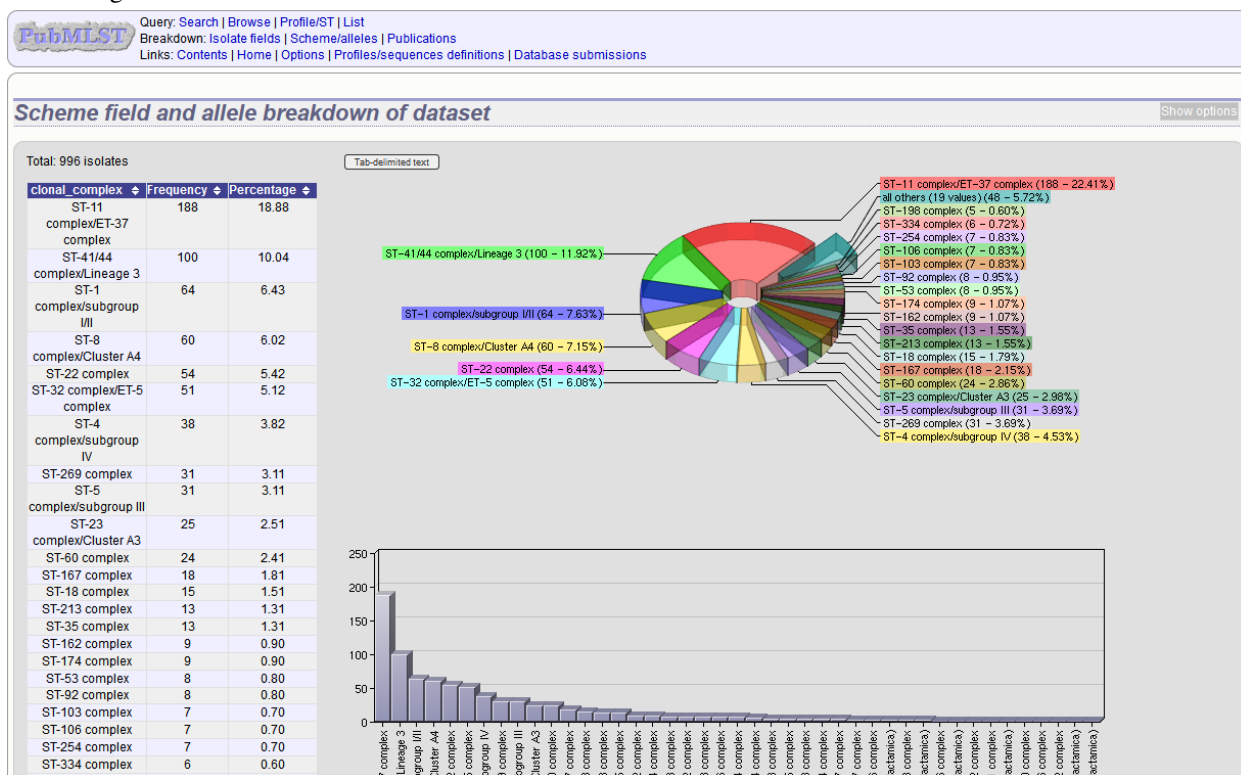
☐ All loci
☐ Capsule
☐ Genetic Information Processing
☐ Metabolism
☐ Pilin
☒ Typing

Select

MLST

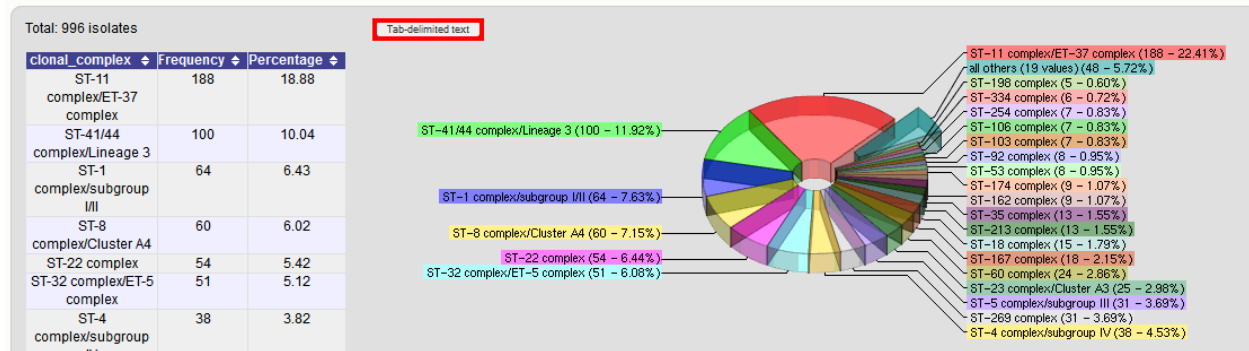
Fields			Alleles			
Field name	Unique values	Analyse	Locus	Unique alleles	Analyse	Download
ST	554	Breakdown	abcZ	64	Breakdown	Download
clonal complex	43	Breakdown	adk	57	Breakdown	Download
			aroE	80	Breakdown	Download
			fumC	85	Breakdown	Download
			gdh	79	Breakdown	Download
			pdhC	83	Breakdown	Download
			pgm	68	Breakdown	Download

The sorting of the table can be changed by clicking the appropriate header - this toggles between ascending and descending order.



The table values can be exported in a format suitable for copying in to a spreadsheet by clicking the 'Tab-delimited text' button.

Scheme field and allele breakdown of dataset



You can also download the sequences for alleles designated in the dataset for the loci belonging to the scheme by clicking the appropriate 'Download' button in the first results table.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Scheme field and allele breakdown of dataset

Select schemes or groups of schemes within the tree. A breakdown of the individual fields and loci belonging to these schemes will then be performed.

All loci
Capsule
Genetic Information Processing
Metabolism
Pilin
Typing
MLST

Select

Fields			Alleles			
Field name	Unique values	Analyse	Locus	Unique alleles	Analyse	Download
ST	554	Breakdown	abcZ	64	Breakdown	Download
clonal complex	43	Breakdown	adk	57	Breakdown	Download
			aroE	80	Breakdown	Download
			fumC	85	Breakdown	Download
			gdh	79	Breakdown	Download
			pdhC	83	Breakdown	Download
			pgm	68	Breakdown	Download

Sequences will be served in FASTA format in order of frequency.

>2

```
TTTGATACCGTTGCCGAAGGTTTGGGTGAAATTCGCGATTTATTGCGCCGTTACCAACCGC
GTCGCCATGAGTTGGAACCGTTTCGGGTGAGGCTTTGTTGAAAGAACTCAACGAATTA
CAACTTGAAATCGAAGCGAAGGACGGCTGGAAGCTGGATGCGGCAGTCAAGCAGACTTTG
GGGGAATCGGTTTCCCGGAAAACGAAAAATCGGCAACCTTTCCGGCGGTCAGAAAAAG
CGTGTCGCCTTGGCGCAGGCTTGGGTGCAGAAGCCCGACGTATTGCTGCTGGACGAACCG
ACCAACCATTGATATCGACGCGATTATTTGGCTGGAAAATCTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCACGACCGCGCTTTTGGACAATATCGCCACGCGGATT
GTCGAACTCGATC
```

>1

```
TTTGATACTGTTGCCGAAGGTTTGGGCGAAAATTCGCGATTTATTGCGCCGTTATCATCAT
GTCAGCCATGAGTTGGAACATGGTTTCGAGTGAGGCTTTATTGAAAGAGCTCAACGAATTG
CAACTTGAGATCGAAGCGAAGGACGGCTGGAAGTTGGATGCGGCGGTGAAGCAGACTTTG
GGCGAATCGGTTTCCCGGAAAACGAAAAATCGGCAACCTCTCCGGCGGTCAGAAAAAG
CGCGTCGCCTTGGCGCAGGCTTGGGTGCAGAAGCCCGACGTATTGCTGCTGATGAACCG
ACCAACCATTGATATCGACGCGATTATTTGGTTGGAAAACCTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCACGACCGCGCTTTTGGACAATATCGCCACGCGGATT
GTCGAACTCGATC
```

>4

```

TTTGATACCGTTGCCGAAGGTTTGGGCGAAATTCGTGATTATTGCGCCGTTATCATCAT
GTCAGCCATGAGTTGGAAAATGGTTCGAGTGAGGCTTTGTTGAAAGAACTCAACGAATTG
CAACTTGAAATCGAAGCGAAGGACGGCTGAAACTGGATGCGGCAGTCAAGCAGACTTTG
GGGGAACTCGTTTCCGGAATAAATAATCGGCAACCTTTCCGGCGGTCAGAAAAAG
CGCGTCGCCTTGGCTCAGGCTTGGGTGCAAAAGCCGACGTATTGCTGCTGGACGAGCCG
ACCAACCATTGGATATCGACGCGATTATTTGGCTGGAAAATCTGCTCAAAGCGTTTGAA
GGCAGCTTGGTTGTGATTACCCACGACCGCCGTTTTTTGGACAATATCGCCACGCGGATT
GTCGAACTCGATC

```

11.5 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 selected by clicking the ‘Sequence bin’ link on the Breakdown section of the main contents page.

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29177
- Last updated: 2014-07-16
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin**

Export

- Export dataset
- Contigs
- Sequences - XMF / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

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.

2	12UM	B43; Z1035	Pakistan	1997	meningitis and septicemia	Neisseria meningitidis	A	1	ST-1 complex/subgroup III	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1099		19	15	
4	M1027	B43; Z1043	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV			
5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup III	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup III	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup III	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

Breakdown: Fields Two Field Codons Polymorphic sites Combinations Schemes/alleles Publications **Sequence bin** Tag status

Analysis: BURST Presence/Absence Genome Comparator BLAST

Export: Dataset Contigs Sequences

Page: 1 2 3 4 > Last

Select the isolate records to analyse - these will be pre-selected if you accessed the plugin following a query. Click submit.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Breakdown of sequence bin contig properties

Please select the required isolate ids for comparison - use Ctrl or Shift to make multiple selections.

Isolates
64) 254
67) S5611
82) 11-004
84) AL2229
89) CN100
120) F4698
128) F6124
160) 1014

Filter by
Sequence method:
Project:
Experiment:

Action
Reset Submit

All None Paste list

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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Breakdown of sequence bin contig properties

Please select the required isolate ids for comparison - use Ctrl or Shift to make multiple selections.

Isolates
1) A4/M1027
2) 120M
7) 7891
10) 6748
11) 129
13) 139M
19) S3131
24) S4355

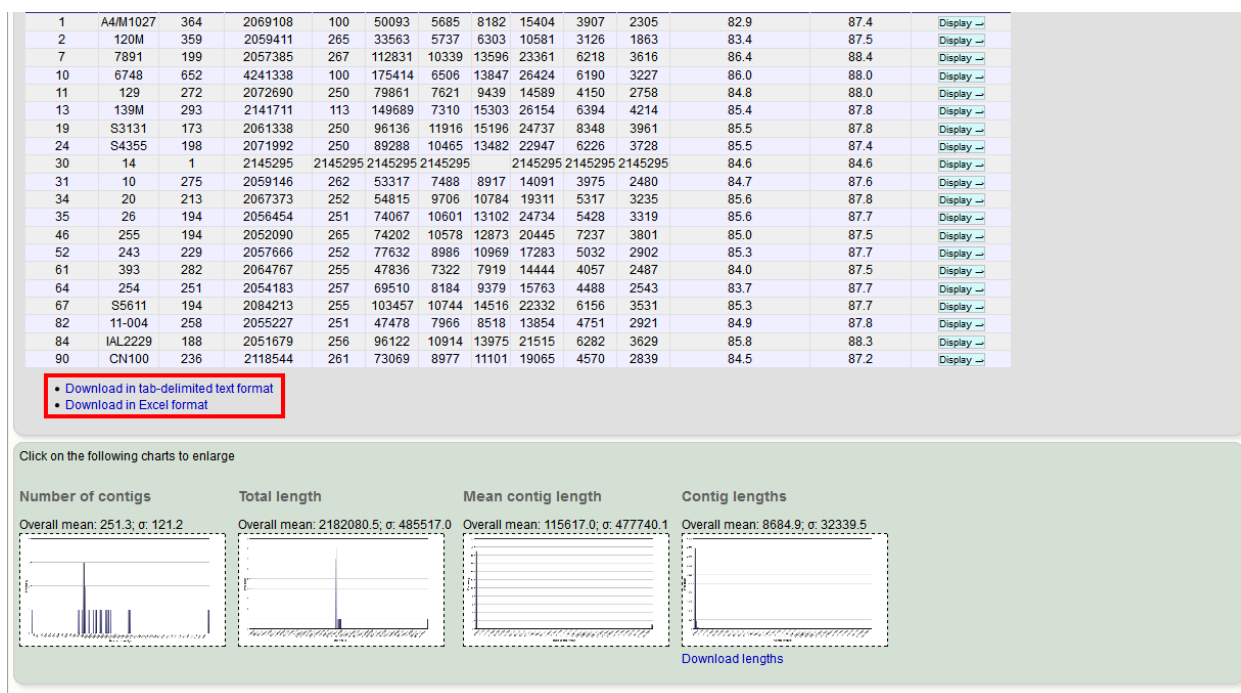
Filter by
Sequence method:
Project:
Experiment:

Action
Reset Submit

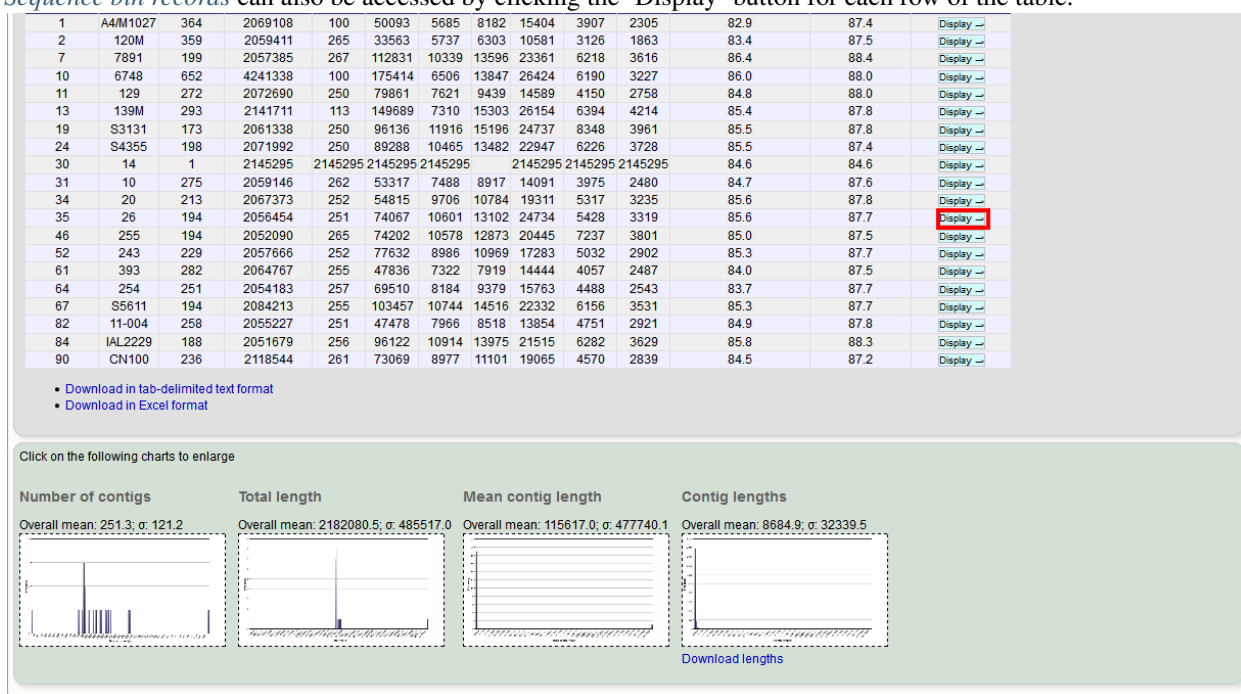
All None Paste list

Isolate id	Isolate	Contigs	Total length	Min	Max	Mean	σ	N50	N90	N95	% Alleles designated	% Loci tagged	Sequence bin
1	A4/M1027	364	2069108	100	50093	5685	8182	15404	3907	2305	82.9	87.4	Display
2	120M	359	2059411	265	33563	5737	6303	10581	3126	1863	83.4	87.5	Display
7	7891	199	2057385	267	112831	10339	13596	23361	6218	3616	86.4	88.4	Display
10	6748	652	4241338	100	175414	6506	13847	26424	6190	3227	86.0	88.0	Display
11	129	272	2072690	250	79861	7621	9439	14589	4150	2758	84.8	88.0	Display
13	139M	293	2141711	113	149689	7310	15303	26154	6394	4214	85.4	87.8	Display
19	S3131	173	2061338	250	96136	11916	15196	24737	8348	3961	85.5	87.8	Display
24	S4355	198	2071992	250	89288	10465	13482	22947	6226	3728	85.5	87.4	Display
30	14	1	2145295	2145295	2145295	2145295	2145295	2145295	2145295	2145295	84.6	84.6	Display
31	10	275	2059146	262	53317	7488	8917	14091	3975	2480	84.7	87.6	Display
34	20	213	2067373	252	54815	9706	10784	19311	5317	3235	85.6	87.8	Display
35	26	194	2056454	251	74067	10601	13102	24734	5428	3319	85.6	87.7	Display
46	255	194	2052090	265	74202	10578	12873	20445	7237	3801	85.0	87.5	Display
52	243	229	2057666	252	77632	8986	10969	17283	5032	2902	85.3	87.7	Display
61	393	282	2064767	255	47836	7322	7919	14444	4057	2487	84.0	87.5	Display
64	254	251	2054183	257	69510	8184	9379	15763	4488	2543	83.7	87.7	Display
67	S5611	194	2084713	255	103457	10744	14516	22332	6156	3531	85.3	87.7	Display

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.



11.6 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 on databases where it is enabled from the contents page by clicking the ‘Genome Comparator’ link.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for **locus**, **schemes** or **scheme fields**.

General information

- Isolates: 29177
- Last updated: 2014-07-15
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator**
- BLAST

Miscellaneous

- Description of database fields

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.

19025	M10 240481	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1831		22	9	F3-3
19026	M10 240482	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	3754	ST-41/44 complex/Lineage 3	7-2	4	F5-1
19027	M10 240484	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1097	ST-41/44 complex/Lineage 3	17-1	23	F1-5
19028	M10 240485	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	275	ST-269 complex	22	9	F5-12
19029	M10 240487	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1049	ST-269 complex	19-1	15-11	F5-1
19030	M10 240489	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	461	ST-461 complex	19-2	13-1	F3-9
19031	M10 240490	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1161	ST-269 complex	22	9	F5-12
19032	M10 240498	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	41	ST-41/44 complex/Lineage 3	7-2	4	F1-5
19958	M10 240476	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	9812	ST-213 complex	22	14	F5-5
19959	M10 240499	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	275	ST-269 complex	22	9	F5-12
19960	M10 240500	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	41	ST-41/44 complex/Lineage 3	7-2	4	F1-5
19961	M10 240502	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	340	ST-41/44 complex/Lineage 3	7-2	4	F1-5
19962	M10 240503	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	23	ST-23 complex/Cluster A3	5-1	2-2	F1-96
19963	M10 240505	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	1655	ST-23 complex/Cluster A3	5-1	10-10	F4-1
19964	M10 240507	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	183	ST-23 complex/Cluster A3	21	16-5	deleted
19965	M10 240508	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	1575		7-2	13-1	F1-7
19966	M10 240511	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	4713		22	9	F5-12
19967	M10 240512	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	41	ST-41/44 complex/Lineage 3	7-1	1	F1-5
19968	M10 240514	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	W	11	ST-11 complex/ET-37 complex	5	2	F1-1
19969	M10 240515	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	B	269	ST-269 complex	5-1	2-2	F5-1
19970	M10 240520	UK	2010	invasive (unspecified/other)	Neisseria meningitidis	Y	1655	ST-23 complex/Cluster A3	5-1	10-1	F4-1

Analysis tools:

Breakdown: Fields Two Field Codons Polymorphic sites Combinations Schemes/alleles Publications Sequence bin

Analysis: Presence/Absence **Genome Comparator** BLAST

Export: Dataset Contigs Sequences

Page: 1 2 3 4 5 6 7 8 9 > Last

11.6.1 Analysis using defined loci

Select the isolate genomes that you wish to analyse and then either the loci from the list or a set of schemes. Press submit.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator - Neisseria PubMLST

Please select the required isolate ids and loci for comparison - 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. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates	Loci	Include in identifiers	Schemes
658) 890326 659) A22 660) 71894 661) 860800 662) 2837 663) 2839 664) 2838 665) 2845	16S_rDNA 16S_rRNA (SSU_rRNA) 23S_rRNA abcZ abcZ (NEIS1015) aceF (NEIS1279) ackA2 (NEIS1727) acnA (NEIS1729)	isolate country region year epidemiological year age yr age mth sex disease source	Genomic islands Lineage Schemes Metabolism Pilin MLST Typing Finotyping antigens

Reference genome
 Enter accession number:
 or choose annotated genome:
 or upload Genbank/EMBL/FASTA file: No file selected.

Parameters / options
 Min % identity: 70
 Min % alignment: 50
 BLASTN word size: 15
☒ Use TBLASTX
☒ Use tagged designations if available
☐ Disable HTML output

Distance matrix calculation
 With incomplete loci:
☒ Completely exclude from analysis
☐ Treat as distinct allele
☐ Ignore in pairwise comparison
☒ Exclude paralogous loci
☐ paralogous in all isolates
☐ paralogous in any isolate

Alignments
☐ Produce alignments
☒ Include ref sequences in alignment
☐ Align all loci (not only variable)
 Aligner: MAFFT

Core genome analysis
 Core threshold (%): 90
☐ Calculate mean distances

Filter by:
 Sequence method:
 Project:
 Experiment:

Action:

The job will be submitted to the job queue and will start running shortly. Click the link to follow the job progress and view the output.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator - Neisseria PubMLST

This analysis has been submitted to the job queue.

Please be aware that this job may take a long time depending on the number of comparisons and how busy the server is.

[Follow the progress of this job and view the output.](#)

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.



Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Job status viewer

Status

Job id:	BIGSdb_27748_1405410063_94241
Submit time:	2014-07-15 08:41:03
Status:	finished
Start time:	2014-07-15 08:41:05
Progress:	100%
Stop time:	2014-07-15 08:41:22
Total time:	17 seconds

Output

Analysis against defined 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'. Truncated alleles (located at end of contig) are marked as 'T'.

Locus	644 (L93/4286)	662 (2837)	663 (2839)	664 (2838)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)
abcZ	2	2	2	2	2	2	2	7	2	2	2	2
adk	3	3	3	3	3	3	3	3	3	3	3	3
aroE	4	19	4	4	4	4	4	4	19	19	19	4
fumC	3	3	3	3	24	23	23	3	3	3	3	3
gdh	8	8	8	8	8	8	8	8	8	8	8	8
pdhC	4	4	4	4	4	6	6	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	644 (L93/4286)	662 (2837)	663 (2839)	664 (2838)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)
abcZ	2	2	2	2	2	2	2	7	2	2	2	2
aroE	4	19	4	4	4	4	4	4	19	19	19	4
fumC	3	3	3	3	24	23	23	3	3	3	3	3
pdhC	4	4	4	4	4	6	6	4	4	4	4	4

Exactly matching loci

These loci are identical in all isolates.

Matches: 3

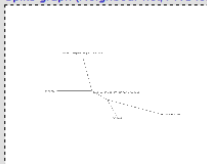
Locus	644 (L93/4286)	662 (2837)	663 (2839)	664 (2838)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)
adk	3	3	3	3	3	3	3	3	3	3	3	3
gdh	8	8	8	8	8	8	8	8	8	8	8	8
pgm	6	6	6	6	6	6	6	6	6	6	6	6

Unique strains

Unique strains: 5

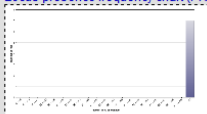
Strain 1	Strain 2	Strain 3	Strain 4	Strain 5
644 (L93/4286)	662 (2837)	666 (2843)	665 (2845)	669 (2846)
663 (2839)	670 (2840)	667 (2842)		
664 (2838)	671 (2844)			
698 (FAM18)	672 (2847)			

- [Text output file](#)
- [Excel format](#)
- [Distance matrix \(Nexus format\)](#) - Suitable for loading in to [SplitsTree](#). Distances between taxa are calculated as the number of loci with different allele sequences
- [Splits graph \(Neighbour-net, PNG format\)](#)



(click to enlarge)

- [Splits graph \(Neighbour-net, SVG format\)](#) - This can be edited in [Inkscape](#) or other vector graphics editors
- [Locus presence frequency](#)
- [Locus presence frequency chart \(PNG format\)](#)



(click to enlarge)

- [Tar file containing output files](#)

Please note that job results will remain on the server for 7 days.

11.6.2 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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Genome Comparator - Neisseria PubMLST

Please select the required isolate ids and loci for comparison - 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. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates

658) 890326
659) A22
660) 71/94
661) 860800
662) 2837
663) 2839
664) 2838
665) 2845

Include in identifiers

isolate
country
region
year
epidemiological year
age yr
age mth
sex
disease
source

Reference genome

Enter accession number:
or choose annotated genome:
FAM18 (Nm)
or upload Genbank/EMBL/FASTA file:
Browse... No file selected.

Parameters / options

Min % identity: 70
Min % alignment: 50
BLASTN word size: 15
☒ Use TBLASTX
☒ Use tagged designations if available
☐ Disable HTML output

Distance matrix calculation

With incomplete loci:
☒ Completely exclude from analysis
☐ Treat as distinct allele
☐ Ignore in pairwise comparison
☒ Exclude paralogous loci
☐ paralogous in all isolates
☐ paralogous in any isolate

Alignments

☐ Produce alignments
☒ Include ref sequences in alignment
☐ Align all loci (not only variable)
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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Job status viewer

Status

Job id: BIGSdb_21911_1405410488_8452
Submit time: 2014-07-15 08:48:08
Status: finished
Start time: 2014-07-15 08:48:34
Progress: 100%
Stop time: 2014-07-15 09:12:58
Total time: 24 minutes and 24 seconds

Output

Analysis by reference genome

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

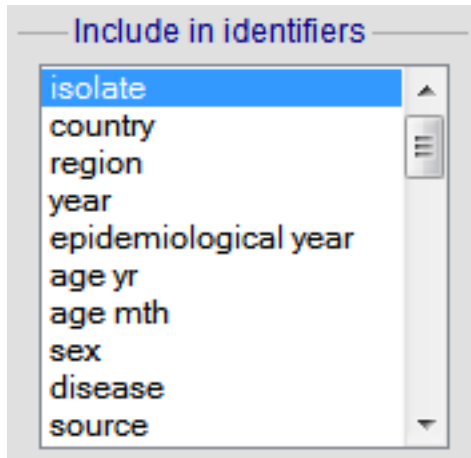
All loci

Each unique allele is defined a number starting at 1. Missing alleles are marked as 'X'. Truncated alleles (located at end of contig) are marked as 'T'.

Locus	Product	Sequence length	Genome position	Reference genome	644 (L93/4286)	662 (2837)	663 (2839)	664 (2838)	665 (2845)	666 (2843)	667 (2842)	669 (2846)	670 (2840)	671 (2844)	672 (2847)	698 (FAM18)
lpxC envA NMC0001	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	924	1261	1	1	1	1	1	1	1	1	1	1	1	1	1
pilS1 NMC0002	pilin (fragment)	291	3341	1	1	1	1	1	1	1	1	1	1	1	1	1
pilS2 NMC0003	truncated pilin	366	3675	1	2	2	2	2	2	2	2	2	2	2	2	1
tpb NMC0004	peptidyl-prolyl cis-trans isomerase	330	4069	1	2	2	2	2	2	2	2	T	2	2	2	1
NMC0005	putative membrane protein	219	4476	1	2	3	3	3	3	3	3	4	3	5	3	1
NMC0006	putative glycerate dehydrogenase	954	4816	1	2	2	2	2	2	2	2	2	2	2	2	1
metG NMC0007	methionyl-tRNA synthetase	2058	5843	1	2	2	3	3	2	2	2	2	2	2	2	1
glmS NMC0008	glucosamine-fructose-6-phosphate aminotransferase [isomerizing]	1839	8016	1	2	2	2	2	2	2	2	2	2	2	2	1

11.6.3 Include in identifiers fieldset

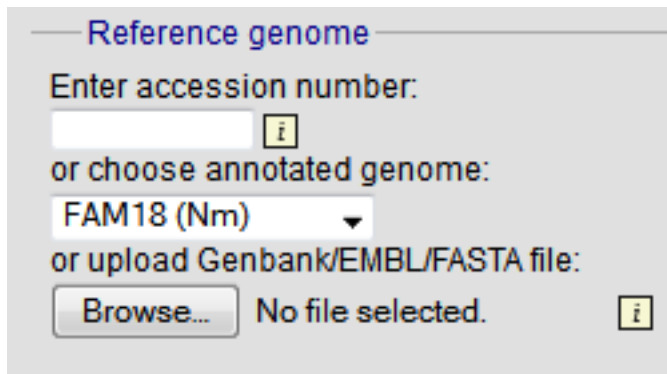
This selection box allows you to choose which isolate provenance fields will be included in the results table and sequence exports.



Multiple values can be selected by clicking while holding down Ctrl.

11.6.4 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.

11.6.5 Parameters/options fieldset

This section allows you to modify BLAST parameters. This affects sensitivity and speed.

Parameters / options

Min % identity: 70

Min % alignment: 50

BLASTN word size: 15

☐ Use TBLASTX

☒ Use tagged designations if available

☐ Disable HTML output

- **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: 15). Increasing this value improves speed at the expense of sensitivity. The default value gives good results in most cases, but increasing this to 20 is almost as good (there was 1 difference among 2000 loci in a test run) and will speed up the analysis approximately two-fold.
- **Use TBLASTX** - This compares the six-frame translation of your nucleotide query sequence against the six-frame translation of the contig sequences. Sequences will be classed as identical if they result in the same translated sequence even if the nucleotide sequence is different. This is significantly slower than using BLASTN.

Additionally, two other options are available in this fieldset:

- **Use tagged designations** - When analysing using defined loci, Genome Comparator can use the designations stored within the database (this is the default). This is much quicker since it doesn't need to run BLAST against these sequences. If a designation is missing, BLAST will be run for that locus anyway.
- **Disable HTML output** - If running Genome Comparator against a large number of genomes, the resulting table may get so large that your web browser struggles to render it properly and may use up too much memory on your computer. Clicking this button prevents this output - this output is not required for further analysis since everything present in it is also generated in Excel format at the end. HTML output is automatically disabled when more than 150 genomes are analysed.

11.6.6 Distance matrix calculation fieldset

This section provides options for the treatment of incomplete and paralogous loci when generating the distance matrix.

Distance matrix calculation

With incomplete loci:

☒ Completely exclude from analysis

☐ Treat as distinct allele

☐ Ignore in pairwise comparison

☒ Exclude paralogous loci

☒ paralogous in all isolates

☐ paralogous in any isolate

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.

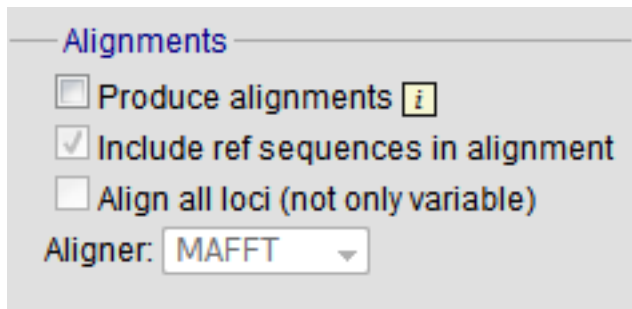
Paralogous loci, i.e. those with multiple good matches, can be excluded from the analysis (default). This is the safest option since there is no guarantee that differences seen between isolates at paralogous loci are real if the alternative matches are equally good. NB: Loci are also only classed as paralogous when the alternative matches identify different sequences, otherwise multiple contigs of the same sequence region would result in false positives.

When paralogous loci are excluded, there are two further options:


- Exclude when paralogous in all isolates (default). Loci are only classed as paralogous when there are multiple hits in every genome (except if a genome is missing the locus entirely, in which case that genome is ignored in the calculation). This is generally the option that you will want to use with the default BLAST parameters since you can often expect multiple hits even when loci are not paralogous if you have used relaxed thresholds.
- Exclude when paralogous in any isolate. Unless you use stringent BLAST thresholds, this is likely to overestimate the number of paralogous loci, but may be useful if you are specifically looking for them.

11.6.7 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)

Aligner: MAFFT

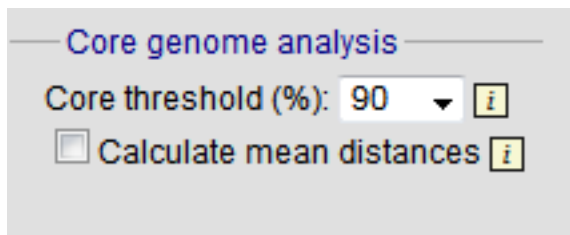
Available options are:

- 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 approximately twice as long 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.

11.6.8 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).

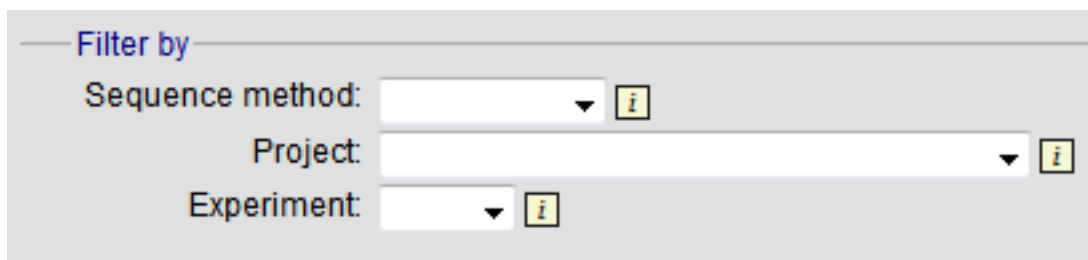


The default setting of 90% means that a locus is counted as core if it appears within 90% or more of the genomes in the dataset.

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.

11.6.9 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.
- Experiment - Contig files can belong to an experiment. How this is used can vary between databases, but this enables you to only include contigs from a particular experiment.

11.6.10 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.

11.7 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 'BLAST' link on the Analysis section of the main contents page.

The screenshot shows the Neisseria PubMLST database interface. At the top, there are navigation links: Query, Search, Browse, Profile/ST, List, Breakdown, Isolate fields, Scheme/alleles, Publications, Links, Contents, Home, Options, Profiles/sequences definitions, and Database submissions. The main heading is "Neisseria PubMLST database". Below this, a description 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 interface is divided into several sections: Query database (with links to Search database, Browse database, Search by combinations of loci, and List query), Option settings (with links to Set general options and Set display and query options), General information (with links to Isolates, Last updated, Update history, and About BIGSdb), Breakdown (with links to Single field, Two field, Unique combinations, Scheme and alleles, Publications, and Sequence bin), Export (with links to Export dataset, Contigs, and Sequences), Analysis (with links to Codon usage, Presence/absence status of loci, Genome comparator, and BLAST, which is highlighted with a red box), and Miscellaneous (with a link to Description of database fields).

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.

The screenshot shows a table of isolate records with columns for ID, Accession, Country, Year, Invasiveness, Disease, Locus, Allele, ST, and F3-1. The table contains 25 rows of data. Below the table, there is an "Analysis tools:" section with buttons for Breakdown (Fields, Two Field, Codons, Polymorphic sites, Combinations, Schemes/alleles, Publications, Sequence bin, Tag status), Analysis (BURST, Presence/Absence, Genome Comparator, and BLAST, which is highlighted with a red box), and Export (Dataset, Contigs, Sequences). At the bottom, there is a "Page:" section with buttons for 1, 2, 3, 4, and Last.

ID	Accession	Country	Year	Invasiveness	Disease	Locus	Allele	ST	F3-1
5	M00240227	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	
6	M00282207	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex	
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III
8	M00242007	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex	
9	002184	Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex	
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup III
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup III
12	0090/89	Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	
13	139M	B99; Z1099	Philippines	1968	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup III
14	0120/95	Czech Republic	1995	invasive (unspecified/other)	Neisseria meningitidis	X	117		
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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV
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/ET-5 complex	
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III
25	9	Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex	

Select the isolate records to analyse - 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.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

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

64) 254
67) S5611
82) 11-004
84) IAL2229
90) CN100
120) F4698
128) F6124
160) 1014

Paste sequence

GAAGCCTTGGGCGGACGGATGCCGCCGTTGCCGCTTCGGGCGCATGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAAACGACATCCGCTGGCTGGCAAGCGGCCGCGCTGCGGT
TTGGGCGAAATCAAAATCCCGAAACGAGCGGGTTCGTCATCATGCCGGGCAAGTC
AACCCGACCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTCGGCAACGACGTT
ACCATCGGCAATGGCGGGCGCTGGGCAATTCGAGCTGAACGCTTATATGCCGTTATC
GCCACAACTCTTGCAATCCATCCGCTGTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCGCTCGGCATCGAACCCTACCGGAAAAATCGACTATTCTCTGCACCATTC
CTGATGCTGGTTACTGCGTTAAACCGTAAATCGGCTACGAAAC

Include in results table

country
region
year
epidemiological year
age yr
age mth
sex
disease
source
epidemiology

Parameters
Options
Restrict included sequences by
Action

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

☐ Show 0% matches in table
Sequence method:
Project:
Experiment:

Reset Submit

Click submit.

A table of BLAST results will be displayed.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

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) A4M1027
2) 120M
7) 7891
10) 6748
11) 129
13) 139M
19) S3131
24) S4355

Paste sequence

GAAGCCTTGGGCGGACGGATGCCGCCGTTGCCGCTTCGGGCGCATGAAAACGCTGGCG
GCAAGCCTGAATAAAATCGCCAAACGACATCCGCTGGCTGGCAAGCGGCCGCGCTGCGGT
TTGGGCGAAATCAAAATCCCGAAACGAGCGGGTTCGTCATCATGCCGGGCAAGTC
AACCCGACCAATGCGAAGCGATGACCATGGTGTGCTGCCAAGTGTTCGGCAACGACGTT
ACCATCGGCAATGGCGGGCGCTCGGCAATTCGAGCTGAACGCTTATATGCCGTTATC
GCCACAACTCTTGCAATCCATCCGCTGTGGGCGACGCGTGCAACAGCTTCAACGAA
CACTGCGCGCTCGGCATCGAACCCTACCGGAAAAATCGACTATTCTCTGCACCATTC
CTGATGCTGGTTACTGCGTTAAACCGTAAATCGGCTACGAAAC

Include in results table

country
region
year
epidemiological year
age yr
age mth
sex
disease
source
epidemiology

Parameters
Options
Restrict included sequences by
Action

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

☐ Show 0% matches in table
Sequence method:
Project:
Experiment:

Reset Submit

Isolate id	Isolate	% identity	Alignment length	Mismatches	Gaps	Seqbin id	Start	End	Orientation	E-value	Bit score
1	A4M1027	98.49	465	7	0	180177	19444	19908	extract	0.0	807
2	120M	98.49	465	7	0	180583	4782	5246	extract	0.0	807
7	7891	98.49	465	7	0	180965	19869	20333	extract	0.0	807
10	6748	98.49	465	7	0	181186	19181	19645	extract	0.0	807
11	129	98.49	465	7	0	181867	35889	36353	extract	0.0	807
13	139M	98.49	465	7	0	182004	36775	37239	extract	0.0	807
19	S3131	98.49	465	7	0	182318	19090	19554	extract	0.0	807
24	S4355	98.49	465	7	0	215673	4534	4998	extract	0.0	807
30	14	97.42	465	12	0	8	1363524	1363988	extract	0.0	785
31	10	98.49	465	7	0	182380	5559	6023	extract	0.0	807
34	20	98.49	465	7	0	182815	19783	20247	extract	0.0	807
35	26	98.49	465	7	0	182880	18879	19343	extract	0.0	807
46	255	98.49	465	7	0	183179	4982	5446	extract	0.0	807
52	243	98.49	465	7	0	183381	4532	4996	extract	0.0	807
61	393	98.49	465	7	0	183648	7217	7681	extract	0.0	807
64	254	98.49	465	7	0	183818	4716	5180	extract	0.0	807
67	S5611	98.49	465	7	0	184143	4804	5268	extract	0.0	807
82	11-004	98.49	465	7	0	184297	19518	19982	extract	0.0	807
84	IAL2229	98.49	465	7	0	184635	4530	4994	extract	0.0	807
90	CN100	98.49	465	7	0	184814	5350	5814	extract	0.0	807

Download FASTA | FASTA with flanking | Table (tab-delimited text) | Excel format

Clicking any of the ‘extract’ buttons will display the matched sequence along with a translated sequence and flanking sequences.

181867	35889	36353	extract	→	0.0	807
182004	36775	37239	extract	→	0.0	807
182318	19090	19554	extract	→	0.0	807
215673	4534	4998	extract	←	0.0	807
8	1363524	1363988	extract	→	0.0	785
182380	5559	6023	extract	→	0.0	807
182815	19783	20247	extract	→	0.0	807

[PubMLST](#)
[Query](#) | [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown](#): [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links](#): [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Extracted sequence: Seqbin id#:182318 (19090-19554)

sequence bin id#182318

sequence	method	start	end	length	orientation	translation
Solexa	CGGACGGGT TGAACAGC ATCCGAATA CGCCGAAARA GCGCGGCCA AACTCGCCGA ATGTCCGGG TTGCGGTTTG TCAGCGGCC GAACAAATTT GAAGCCTTGG GCGGACGCGA TGCCGCCGTT GCGGCTTCGG	19090	19554	465	→	
	GCGCATTTGAA AACGCTGGCG GCAAGCCTGA ATAAATCGC CAACGACATC CGCTGGCTGG CAAGCGGCC GCGCTGCGGT TTGGGCGAAA TCAAATCCC CAAAACGAG CGGGTTTGT CCATCATGCC GGGCAAGTC					
	CATCGGCTG TTGGGCGAG CGTGCAACAG CTTCAACGAA CACTGCGCG TGCGCATTTGA ACCGCTACG GAAAAATCG ACTATTTCCT GCACCATTC CTGATGCTG TTACGCGGTT AAACGCGAAA ATCGGTTACG					
	AAAAACCGCG CAAAGTGGC AAAACCGCCT ACAAAACAA CAATCGTTG CGGAAACCG CGGTGAGTT GGGCTTGTCT ACGGGCGAAG AATTGACGA ACTGG					
	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 Q 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 CGGACGGGTTTGAACAGCATTCCGGAATACGCGAAAAAGCGCCGCGCAACTCGCCGAATTGTCCGGCTTTCGCGTTTGTTCAGCGCGCGCAACAAATTT 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 Q A * I K S P T T S A G W F3					
	101 GAAGCCTTGGGCGGACGCGATCCGCGCTTGGCGCTTGGGCGCGATTGAAAACGCTGGCGCAAGCTGAAATAAAATGCGCAACGACATCCGCTGGCTGG 200					
	K R P A L R F G R N Q N P R K R A G F V H H A G Q S Q P D P M R S F1					
	S G P R C G L G E I K I P E N E P G S S I M P G K V N P T Q C E A F2					
	Q A A A R A A V W A K S K S P K T S R V R P S C R A K S T R P N A K R F3					
	201 CAAGCGCCGCGCGCTGGGTTTGGGCGAAATCAAAATCCCGAAAAACGAGCGCGGTTTCGTCATCATGCGGCGCAAGTCAACCGGCAACCCCAATTCGGAAG 300					
	D D H G V L P S V R Q R R Y H R Y G G R V G Q F R A E R L Y A R H R F1					
	M T M V C C Q V F G N D V T I G M A G A S G N F E L N V Y M P V I F2					
	P W C A A K C S A T T L P S V W R A R R A I S S * T S I C P S S F3					
	301 GATGACCATGGTGTGTCGCAAGTGTTCGCGACGCGTTACCATCGGTATGGCGGCGCGCTCGGCGCAATTTGCAAGTGAACGCTATATATGCGCGTCATC 400					
	L Q P L A I H P P V G R R V Q Q L Q R T L R R R H * T R T G K N R F1					
	A Y N L L Q S I R L L G D A C N S F N E H C A V G I E P V P E K I D F2					
	P T T S C N P S A C W A T R A T A S T N T A P S A L N P Y R K K S F3					
	401 GCTTACACCTCTTTGCAATCCATCCGCTGTTGGGCGACGCGTGCACGAGCTTCAACGACACTGCGCGCTCGGCATTGAACCGGTACCGGAAAAATCG 500					

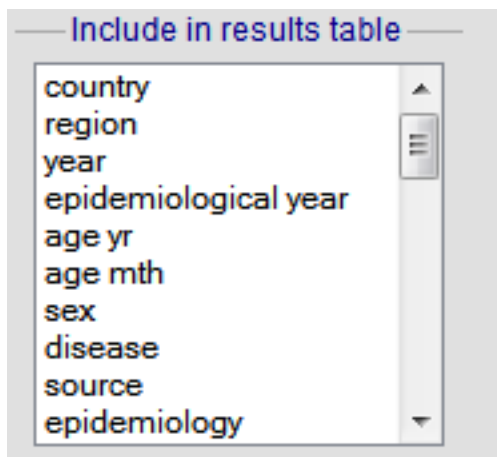
At the bottom of the results table are links to export the matching sequences in FASTA format, (optionall) including flanking sequences. You can also export the table in tab-delimited text or Excel formats.

82	11-004	98.49	465	7	0	184297	19518	19982	extract	→	0.0	807
84	IAL2229	98.49	465	7	0	184635	4530	4994	extract	→	0.0	807
90	CN100	98.49	465	7	0	184814	5350	5814	extract	→	0.0	807

[Download FASTA](#) | [FASTA with flanking](#) | [Table \(tab-delimited text\)](#) | [Excel format](#)

11.7.1 Include in results table fieldset

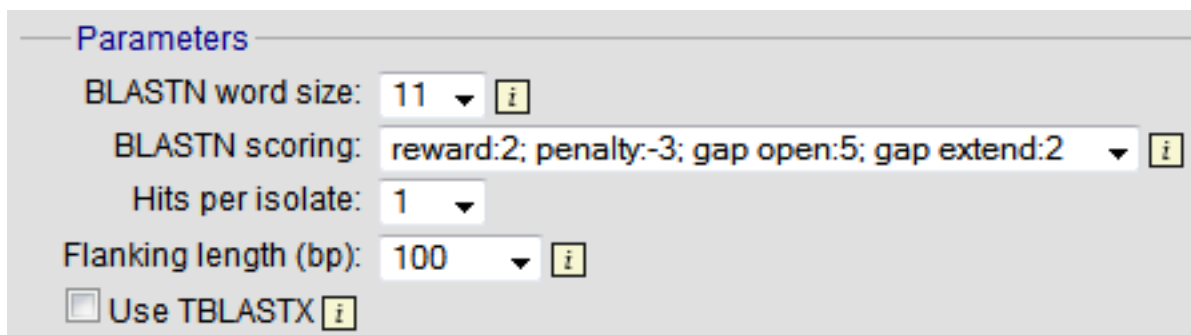
This selection box allows you to choose which isolate provenance fields will be included in the results table.



Multiple values can be selected by clicking while holding down Ctrl.

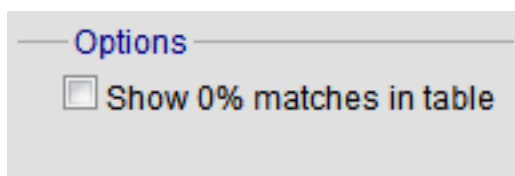
11.7.2 Parameters fieldset

This section allows you to modify BLAST parameters. This affects sensitivity and speed.



- 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.

11.7.3 No matches



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.

11.7.4 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: ⓘ

Experiment: ⓘ

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.
- Experiment - Contig files can belong to an experiment. How this is used can vary between databases, but this enables you to only include contigs from a particular experiment.

11.8 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.

6	M00282207	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex				
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:


Breakdown:

Analysis:

Export:

Page:

If there multiple schemes that can be analysed, these can then be selected along with the group definition.


[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

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)

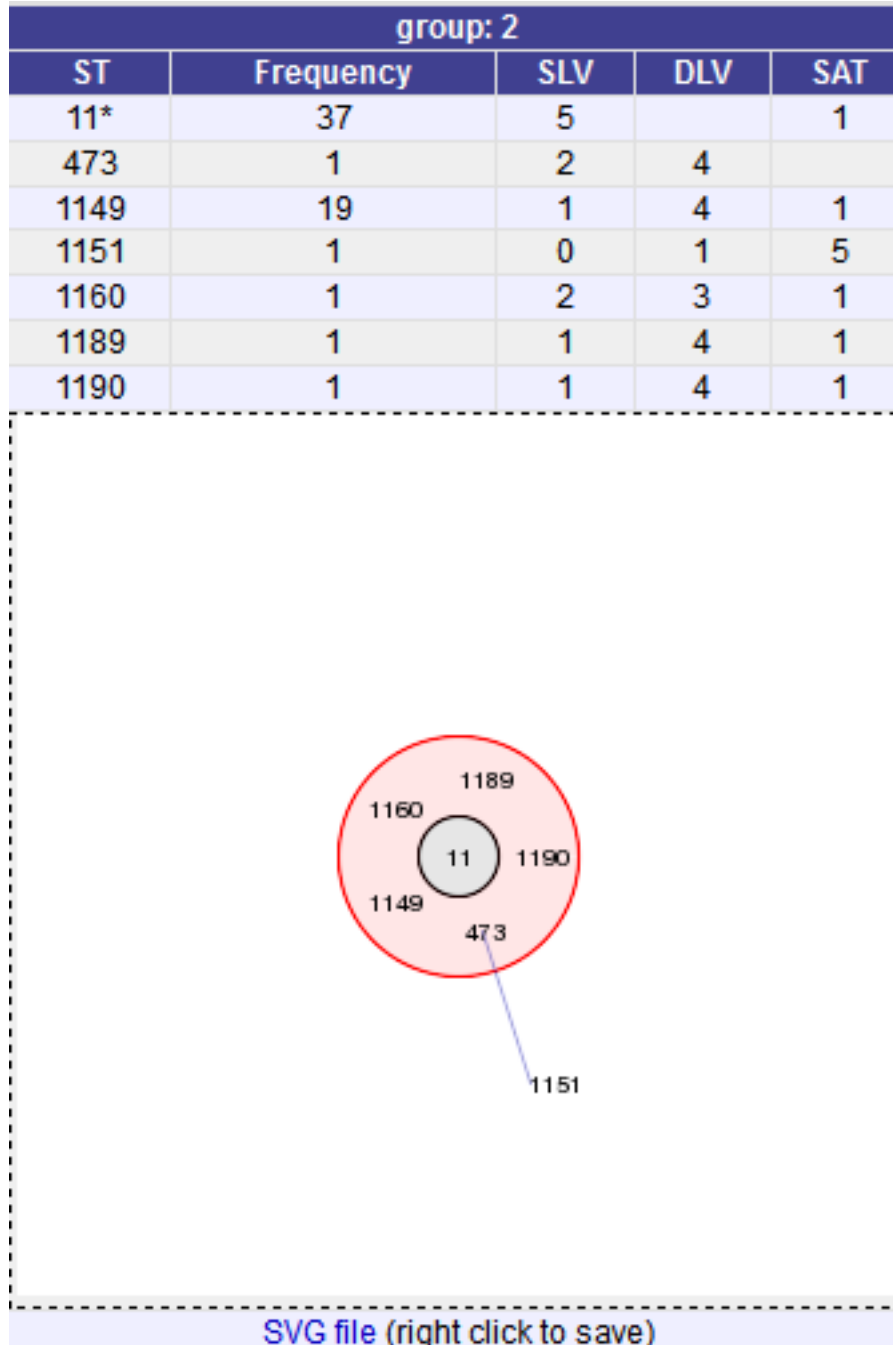
Action

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.

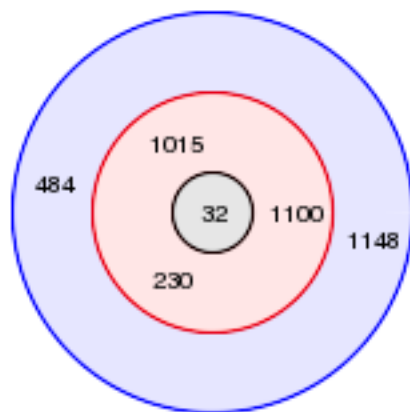
Click Submit.

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.

group: 6				
ST	Frequency	SLV	DLV	SAT
32*	2	3	2	
230	1	1	3	1
484	1	0	3	2
1015	1	1	4	
1100	1	1	2	2
1148	1	0	4	1



[SVG file \(right click to save\)](#)

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.

11.9. Codon usage

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29178
- Last updated: 2014-07-17
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMF / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

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.

5	M00240227	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16		
6	M00282207	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex				
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89	Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16		
13	139M	B99; Z1099	Philippines	1968	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex				
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9	Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex				

Analysis tools:

Breakdown: Fields Two Field Polymorphic sites Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST **Codons** Presence/Absence Genome Comparator BLAST

Export: Dataset Contigs Sequences

Page: 1 2 3 4 > Last

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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Codon usage analysis Toggle: [i]

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
Paste in list of ids to include, start a new line for each. Leave blank to include all ids.

1
2
3
4
5
6

Include in identifier

isolate
country
region
year
epidemiological year
age yr
age mth
sex
disease
source

Loci

16S_rDNA
16S_rRNA (SSU_rRNA)
_23S_rRNA
abcZ
abcZ (NEIS1015)
aceF (NEIS1279)
ackA2 (NEIS1727)
ackA (NEIS1729)

All None Paste list

Schemes

Genetic Information Process
Metabolism
Pilin
Typing
MLST
Finetyping antigens
16S
Antigen genes

Sequence retrieval
If both allele designations and tagged sequences exist for a locus, choose how you want these handled: [i]

☒ 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. Click the link to follow the job progress and view the output.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Codon usage analysis Toggle: [i]

This analysis has been submitted to the job queue.
Please be aware that this job may take some time depending on the number of sequences to analyse and how busy the server is.

[Follow the progress of this job and view the output.](#)

Four tab-delimited text files will be created.

- 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

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Job status viewer

Status

Job id:	BIGSdb_13269_1405586315_76138
Submit time:	2014-07-17 09:38:35
Status:	finished
Start time:	2014-07-17 09:38:39
Progress:	100%
Stop time:	2014-07-17 09:39:05
Total time:	26 seconds

Output

- Absolute frequency of codon usage by isolate
- Absolute frequency of codon usage by locus
- Relative synonymous codon usage (RSCU) by isolate
- Relative synonymous codon usage (RSCU) by locus
- Tar file containing output files

Please note that job results will remain on the server for 7 days.

11.10 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 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.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29178
- Last updated: 2014-07-17
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations**
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMF / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

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.

5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

Breakdown:

Analysis:

Export:

Page:

Select the combination of fields to analyse, e.g. serogroup and finotyping antigens.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [\[i\]](#)

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.

Isolate fields

☐ id ☒ serogroup ☐ rifampicin ☐ strain designation

☐ isolate ☐ MLEE designation ☐ rifampicin range ☐ All

☐ aliases ☐ serotype ☐ ciprofloxacin ☐ None

☐ country ☐ sero subtype ☐ ciprofloxacin range

☐ continent ☐ ET no ☐ pending assembly

☐ region ☐ penicillin ☐ assembly status

☐ year ☐ penicillin range ☐ ENA accession

☐ epidemiological year ☐ amoxicillin ☐ private project

☐ age yr ☐ sulphonamide ☐ comments

☐ age mth ☐ ceftriaxone ☐ sender

☐ sex ☐ ceftriaxone range ☐ curator

☐ disease ☐ chloramphenicol ☐ date entered

☐ source ☐ chloramphenicol range ☐ datestamp

☐ epidemiology ☐ cefotaxime

☐ species ☐ cefotaxime range

Composite fields ☐ strain designation

Loci


16S_rDNA
16S_rRNA (SSU_rRNA)
23S_rRNA
abcZ
abcZ (NEIS1015)
aceF (NEIS1279)
ackA2 (NEIS1727)
acnA (NEIS1729)

Schemes

Metabolism
Pilin
Typing
MLST
Finotyping antigens
16S
Antigen genes

☒ Include all fields from selected schemes
☒ Include all loci from selected schemes

Click submit. When the analysis has completed you will see a table showing the unique combinations of the selected fields along with the frequency and percentage of the combination.


[Query: Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
[Breakdown: isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
[Links: Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?]

Frequencies of field combinations

Number of unique combinations: 2939

The percentages may add up to more than 100% if you have selected loci or scheme fields with multiple values for an isolate.

serogroup	PorA VR1	PorA VR2	FetA VR	Frequency	Percentage
B	7-2	4	F1-5	625	5.65
W	5	2	F1-1	513	4.64
B	19	15	F5-1	385	3.48
C	5	2	F3-6	283	2.56
-	18-10	43	F3-14	281	2.54
B	7	16	F3-3	252	2.28
C	5-1	10-8	F3-6	222	2.01
B	22	9	F5-12	171	1.55
B	22	14	F5-5	167	1.51
A	5-2	10	F3-5	135	1.22
B	19-1	15-11	F5-1	107	0.97
Y	5-1	10-1	F4-1	96	0.87
-	5	2	F1-1	93	0.84
Y	5-2	10-1	F4-1	79	0.71
C	5	2	F5-8	79	0.71
W	18-1	3	F4-1	77	0.70
B	22-1	14	F4-1	77	0.70
C	5	2	F3-3	76	0.69
B	18-1	3	F1-5	72	0.65
Y	5-1	2-2	F5-8	69	0.62
B	19	15	F1-14	61	0.55
B	7-2	13-2	F1-5	61	0.55
B	7-2	16	F3-3	56	0.51

The table can be downloaded in tab-delimited text or Excel formats by clicking the links at the bottom of the page.

C	22	14-6	F1-7	1	0.01
B	19	13-2	F5-1	1	0.01
B	12-1	13-1	F3-29	1	0.01
NG	7-2	16-126	F3-3	1	0.01
B	7-2	30	F5-1	1	0.01
B	7	30-3	F1-14	1	0.01
B	5-1	10-10	F3-16	1	0.01
-	7-2	30-3	F1-7	1	0.01
C	5-2	10	F1-7	1	0.01
NG	18-1	3	F1-34	1	0.01
NG	22	14-6	F4-2	1	0.01
B	7-2	4	F1-88	1	0.01
NG	5-1	10-62	F1-3	1	0.01
Y	12-3	4	F4-1	1	0.01
NG	7-2	16	F1-104	1	0.01
X	12-1	16-52	F3-9	1	0.01
NG	18-4	35-34	F4-1	1	0.01

[Download as tab-delimited text](#)
[Download in Excel format](#)

11.11 Polymorphisms

The Polymorphisms plugin generates a *Locus Explorer* polymorphic site analysis on the alleles designated in an isolate dataset following a query.

The analysis is accessed by clicking the ‘Polymorphic sites’ button in the Breakdown list at the bottom of a results table following a query.

10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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-19 complex			
19	S3131	B213; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

Breakdown: Fields Two Field **Polymorphic sites** Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST Codons Presence/Absence Genome Comparator BLAST

Export: Dataset Contigs Sequences

Page: 1 2 3 4 5 6 7 8 > Last

Select the locus that you would like to analyse from the list.

Query Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: [i]

Polymorphic site analysis

This tool will analyse the polymorphic sites in the selected locus for the current isolate dataset.

If more than 50 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

- *16S_rDNA
- 16S_rRNA (SSU rRNA)
- 23S_rRNA
- abcZ
- abcZ (NEIS1015)
- aceF (NEIS1279)
- ackA2 (NEIS1727)
- acnA (NEIS1729)

Options

If both allele designations and tagged sequences exist for a locus, choose how you want these handled: [1]

☒ Use allele sequence retrieved from external database

☐ Use sequences tagged from the bin

☒ Analyse single example of each unique sequence

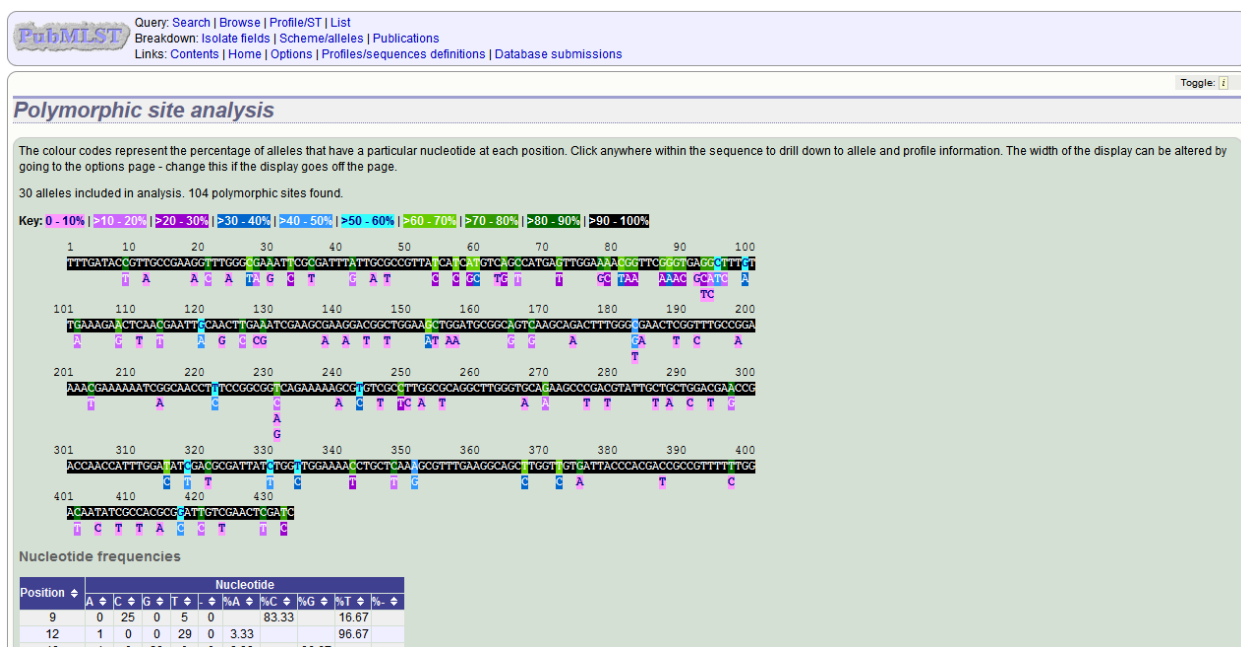
☒ Exclude incomplete sequences

Action

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.



11.12 Presence/absence

This plugin displays the status of loci for isolate records. It will show whether a locus has been designated with an allele name, has a sequence tag, or both.

The function can be selected by clicking the 'Presence/absence status of loci' link in the 'Analysis' section of the main contents page.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29178
- Last updated: 2014-07-17
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs
- Sequences - XMFA / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci**
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

Alternatively, it can be accessed following a query by clicking the 'Presence/Absence' 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.

5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	20	9	F3-1
8	M00242007		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex		14	
9	002184		Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex			
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

Breakdown:

Analysis:

Export:

Page:

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.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Export presence/absence status of loci - *Neisseria* PubMLST

This script will export data showing whether a locus has had an allele designated, a sequence tagged, or both. 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.

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
6

Include in identifier: isolate, country, region, year, epidemiological year, age yr, age mth, sex, disease, source

Loci: 16S_rDNA, 16S_rRNA (SSU_rRNA), 23S_rRNA, abcZ, abcZ (NEIS1015), aceF (NEIS1279), ackA2 (NEIS1727), acnA (NEIS1729)

Schemes: Genetic information processing, Metabolism, Pilin, Typing, MLST, Finotyping antigens, 16S, Antigen genes

Options: Mark present if: ☒ either designations or tags set, ☐ allele designations defined, ☐ sequence tags defined. Symbol for present: O, Symbol for absent: X, ☐ Generate distance matrix

Action:

Click submit. The job will be submitted to the queue and will start running shortly. Click the link to follow the job progress and view the output.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Export presence/absence status of loci - *Neisseria* PubMLST

This analysis has been submitted to the job queue.

[Follow the progress of this job and view the output.](#)

When complete, a single text file will have been generated.

Job status viewer

Status

Job id: BIGSdb_31442_1405591304_69061
 Submit time: 2014-07-17 11:01:44
 Status: finished
 Start time: 2014-07-17 11:01:44
 Progress: 100%
 Stop time: 2014-07-17 11:01:49
 Total time: 4 seconds

Output

- Main output file

Please note that job results will remain on the server for 7 days.

This is a tab-delimited text file that uses ‘O’ to represent presence and ‘X’ to represent a missing locus designation or tag.

id	pgm	adk	abcZ	pdhC	gdh	fumC	aroE
1	O	O	O	O	O	O	O
2	O	O	O	O	O	O	O
3	O	O	O	O	O	O	O
4	O	O	O	O	O	O	O
5	O	O	O	O	O	O	O
6	O	O	O	O	O	O	O
7	O	O	O	O	O	O	O
8	O	O	O	O	O	O	O
9	O	O	O	O	O	O	O
10	O	O	O	O	O	O	O

11.12.1 Options

There are a number of options that can be selected to modify the output.

Options

Mark present if :

☒ either designations or tags set
☐ allele designations defined
☐ sequence tags defined

Symbol for present: O ▼
 Symbol for absent: X ▼

☐ Generate distance matrix

With these you can change the symbols used and whether designations, or tags, or both are counted.

You can also choose to generate a distance matrix based on presence/absence.

11.13 Tag status

The tag status plugin displays a graphical representation of the status of loci designations or tags for isolate data. It is accessed following a query by clicking the ‘Tag status’ button in the Breakdown section at the bottom of the results table.

Isolate provenance/phenotype fields: id < 10

Display/sort options: Order by: id ascending, Display: 25 records per page

Action: Reset Submit

9 records returned. Click the hyperlinks for detailed information.

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FetA VR
1	A4/M1027	B1; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	5-2	10	F1-5
2	120M	B35; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1099		19	15	
4	M1027	B43; Z1043	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV			
5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	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			

Analysis tools:

Breakdown: Fields Two Field Polymorphic sites Combinations Schemes/alleles Publications Sequence bin **Tag status**

Analysis: BURST Codons Presence/Absence Genome Comparator BLAST

Export: Dataset Contigs Sequences

Select the loci you would like to analyse.

PubMLST Query: Search | Browse | Profile/ST | List

Breakdown: Isolate fields | Scheme/alleles | Publications

Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: [i]

Tag status

Select schemes or groups of schemes within the tree. A breakdown of the individual loci belonging to these schemes will then be performed.

- All loci
- Capsule
- Genetic Information Processing
- Metabolism
- Pilin
- Typing

Select

You should see a series of bars representing loci. The colour of these bars designates whether they have an allele designation only, a sequence tag only, both designations or tags, or whether they have flags set.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Tag status

Select schemes or groups of schemes within the tree. A breakdown of the individual loci belonging to these schemes will then be performed.

Bars represent loci by schemes arranged in alphabetical order. If a locus appears in more than one scheme it will appear more than once in this graphic. Click on the id hyperlink for a detailed breakdown for an isolate.

Key
Allele designated only | Sequence tagged only | Allele designated + sequence tagged | Flagged

2463 loci selected:

Id	Isolate
1	A4/M1027
2	120M
3	M00242905
4	M1027
5	M00240227
6	M00282207
7	7891
8	M00242007
9	0021/84

Hovering the mouse over the bars will indicate the scheme represented.

Note: Loci will be represented more than once if they are members of multiple selected schemes.

Clicking any of the isolate id hyperlinks navigates to a page that breaks down the exacty status for all loci of that isolate.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Tag status: Isolate id#1 (A4/M1027)

Scheme	Locus	Allele designation(s)	Sequence tag
MLST	abcZ	1	
	adk	3	
	aroE	3	
	fumC	1	
	gdh	4	
	pdhC	2	
Finotyping antigens	pgm	3	
	PorA VR1	5-2	
16S	PorA VR2	10	
	FeA VR	F1-5	
ADP-heptose biosynthesis	SSU rRNA (16S rRNA)	45	
	NEIS0769 (hldA)	2	
	NEIS0773 (hldB)	2	
	NEIS2014 (gmhB)	2	
	NEIS2055 (hldC)	2	
Aminoacyl-tRNA biosynthesis	NEIS2070 (gmhA)		
	NEIS0007	2	
	NEIS0164	2	
	NEIS0326	61	
	NEIS0381	2	
	NEIS0383	2	
	NEIS0672		internal stop codon
	NEIS0676	15	
	NEIS0681	5	
	NEIS0794	5	
	NEIS1277	3	
	NEIS1290 (gatC)	3	
	NEIS1291	13	
	NEIS1293	9	
	NEIS1361	3	
NEIS1408	71		
NEIS1436	5		
NEIS1478	4		
NEIS1518	3		
NEIS1602	3		

There is a column each for allele designations and sequence tags. If an allele designation is defined, the allele identifier is displayed. Cells shaded in blue show that the designation or tag is present, whereas red indicates that they are absent.

Data export plugins

12.1 Isolate record export

You can export the entire isolate recordset by clicking the ‘Export dataset’ link in the Export section of the main contents page.

The screenshot shows the Neisseria PubMLST database main page. At the top, there is a navigation bar with links: Query, Search, Browse, Profile/ST, List, Breakdown, Isolate fields, Scheme/alleles, Publications, and Links: Contents, Home, Options, Profiles/sequences definitions, Database submissions. Below this is the title 'Neisseria PubMLST database' and a descriptive paragraph. The main content area is divided into four sections: Query database, Option settings, General information, and a bottom section with Breakdown, Export, Analysis, and Miscellaneous. The 'Export' section contains two links: 'Export dataset' (highlighted with a red box) and 'Contigs'. The 'Analysis' section contains links for Codon usage, Presence/absence status of loci, Genome comparator, and BLAST. The 'Miscellaneous' section contains a link for Description of database fields.

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.

99 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

Page: [1](#) [2](#) [3](#) [4](#) [>](#) [Last](#)

Isolate fields								MLST		Finotyping antigens		
id	isolate	aliases	country	year	disease	species	serogroup	ST	clonal complex	PorA VR1	PorA VR2	FoTA VR
1	A4M1027	B1; Z1001	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	5-2	10	F1-5
2	120M	B35; Z1035	Pakistan	1967	meningitis and septicaemia	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
3	M00242905		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1099		19	15	
4	M1027	B43; Z1043	USA	1937	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV			
5	M00240227		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	20	9	F3-1
8	M00242007		UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex		14	
9	002184		Czech Republic	1984	invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex			
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968		Neisseria meningitidis	A	1	ST-1 complex/subgroup I/II	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; Z1213	Ghana	1973	invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-4 complex/subgroup IV	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/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	Neisseria meningitidis	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex			

Analysis tools:

Breakdown: [Fields](#) [Two Field](#) [Polymorphic sites](#) [Combinations](#) [Schemes/alleles](#) [Publications](#) [Sequence bin](#) [Tag status](#)

Analysis: [BURST](#) [Codons](#) [Presence/Absence](#) [Genome Comparator](#) [BLAST](#)

Export: [Dataset](#) [Contigs](#) [Sequences](#)

Page: [1](#) [2](#) [3](#) [4](#) [>](#) [Last](#)

Select the isolate fields and schemes to include.

Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

Export dataset

This script will export the dataset in tab-delimited text, suitable for importing into a spreadsheet. 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.

Isolate fields

- ☒ id
- ☒ isolate
- ☒ aliases
- ☒ country
- ☐ continent
- ☐ region
- ☐ year
- ☐ epidemiological year
- ☐ age yr
- ☐ age mth
- ☐ sex
- ☐ disease
- ☐ source
- ☐ epidemiology
- ☐ species
- ☐ serogroup
- ☐ MLEE designation
- ☐ serotype
- ☐ sero subtype
- ☐ penicillin
- ☐ penicillin range
- ☐ amoxicillin
- ☐ sulphonamide
- ☐ ceftriaxone
- ☐ ceftriaxone range
- ☐ cefotaxime
- ☐ cefotaxime range
- ☐ rifampicin
- ☐ rifampicin range
- ☐ ciprofloxacin
- ☐ ciprofloxacin range
- ☐ ET no
- ☐ pending assembly
- ☐ assembly status
- ☐ ENA accession
- ☐ private project
- ☐ comments
- ☐ sender
- ☐ curator
- ☐ date entered
- ☐ datestamp

Composite fields

- ☐ strain designation

All None

References

- ☐ references
- ☒ PubMed id
- ☐ Full citation

Loci

- *16S_rDNA
- 16S_rRNA (SSU_rRNA)
- *23S_rRNA
- abcZ (NEIS1015)
- aceF (NEIS1279)
- ackA2 (NEIS1727)
- acnA (NEIS1729)

All None

Schemes

- Genetic information processing
- Metabolism
- Pilin
- Typing
- MLST
- Finotyping antigens
- 16S
- Antigen genes

☒ Include all fields from selected schemes
☒ Include all loci from selected schemes

Options

- ☐ 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

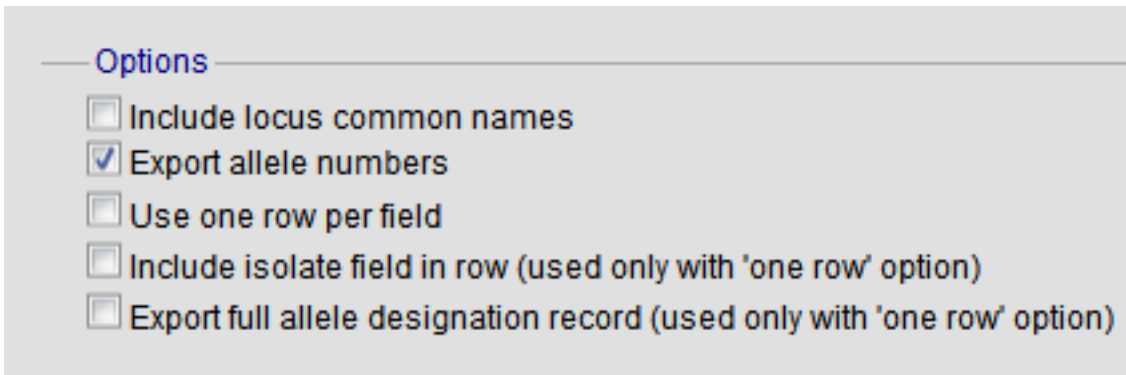
[Submit](#)

Click Submit.

You can then download the data in tab-delimited text or Excel formats.



12.1.1 Advanced options

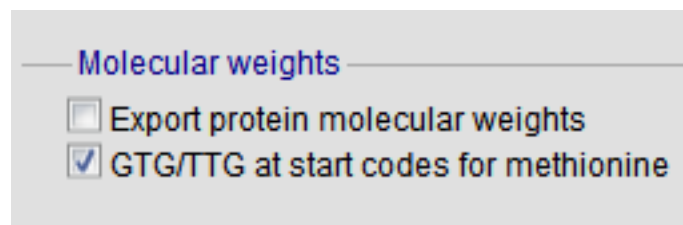


The options fieldset has the following options.

- 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 datestamp information as separate rows when exporting allele designation data.

12.1.2 Molecular weight calculation

The plugin can also calculate the predicted molecular weight of the gene product of any allele designated in the dataset.



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.

12.2 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 clicking the ‘Sequences’ link in the Export section of the contents page.

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.

ID	Accession	Country	Year	Invasiveness	Locus	Allele	Scheme	ST
4	M102/1	USA	1951	Invasive (unspecified/other)	Neisseria meningitidis	A	4	ST-1 complex/subgroup IV
5	M00240227	UK	2000	Invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex
6	M00282207	UK	2000	Invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex
7	7891	B54; Z1054	Finland	1975	Invasive (unspecified/other)	Neisseria meningitidis	A	5
8	M00242007	UK	2000	Invasive (unspecified/other)	Neisseria meningitidis	B	1102	ST-18 complex
9	0021/84	Czech Republic	1984	Invasive (unspecified/other)	Neisseria meningitidis	W	114	ST-22 complex
10	6748	B73; Z1073	Canada	1971	Invasive (unspecified/other)	Neisseria meningitidis	A	1
11	129	B92; Z1092	Germany	1964	Invasive (unspecified/other)	Neisseria meningitidis	A	1
12	0090/89	Czech Republic	1989	Invasive (unspecified/other)	Neisseria meningitidis	B	1015	ST-32 complex/ET-5 complex
13	139M	B99; Z1099	Philippines	1968	Invasive (unspecified/other)	Neisseria meningitidis	A	1
14	0120/95	Czech Republic	1995	Invasive (unspecified/other)	Neisseria meningitidis	X	117	ST-1 complex/subgroup III
15	1	Germany	1999	carrier	Neisseria meningitidis	E	864	ST-18 complex
16	2	Germany	1999	carrier	Neisseria meningitidis	B	854	ST-174 complex
17	3	Germany	1999	carrier	Neisseria meningitidis	W	174	ST-18 complex
18	4	Germany	1999	carrier	Neisseria meningitidis	B	19	ST-18 complex
19	S3131	B213; Z1213	Ghana	1973	Invasive (unspecified/other)	Neisseria meningitidis	A	4
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/ET-5 complex
24	S4355	B227; Z1227	Denmark	1974	Invasive (unspecified/other)	Neisseria meningitidis	A	5
25	9	Germany	1999	carrier	Neisseria meningitidis	B	930	ST-334 complex

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.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Export allele sequences in XMFA/concatenated FASTA formats - Neisseria PubMLST

This script will export 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. 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.

Include in identifier

Loci

Schemes

Options

Action **Submit**

Click submit.

Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Export allele sequences in XMFA/concatenated FASTA formats - Neisseria PubMLST

This analysis has been submitted to the job queue.

Please be aware that this job may take a long time depending on the number of sequences to align and how busy the server is. Alignment of hundreds of sequences can take many hours!

Follow the progress of this job and view the output.

Please note that the % complete value will only update after the alignment of each locus.

The job will be submitted to the job queue. Click the link to follow the progress and download the resulting files.

Sequences will be export in XMFA and FASTA file formats.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Job status viewer

Status

Job id:	BIGSdb_29565_1405601815_9307
Submit time:	2014-07-17 13:56:55
Status:	finished
Start time:	2014-07-17 13:57:10
Progress:	100%
Stop time:	2014-07-17 13:57:23
Total time:	12 seconds

Output

- XMFA output file (not aligned)
- Concatenated FASTA (not aligned)
- Tar file containing output files

Please note that job results will remain on the server for 7 days.

12.2.1 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: i

☒ 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 i

☒ Align sequences
 Aligner: MAFFT ▼

☐ 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.

12.3 Contig export

The contig export plugin can be accessed by clicking the 'Contigs' link in the Export section of the contents page of isolate databases.

Query: Search | Browse | Profile/ST | List
 Breakdown: Isolate fields | Scheme/alleles | Publications
 Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Neisseria PubMLST 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 - advanced queries.
- Browse database - peruse all records.
- Search by combinations of loci (profiles) - including partial matching.
- List query - find isolates by matching a field to an entered list.

Option settings

- Set general options - including isolate table field handling
- Set display and query options for locus, schemes or scheme fields.

General information

- Isolates: 29178
- Last updated: 2014-07-17
- Update history
- About BIGSdb

Breakdown

- Single field
- Two field
- Unique combinations
- Scheme and alleles
- Publications
- Sequence bin

Export

- Export dataset
- Contigs**
- Sequences - XMF / concatenated FASTA formats

Analysis

- Codon usage
- Presence/absence status of loci
- Genome comparator
- BLAST

Miscellaneous

- Description of database fields

Alternatively, it can be accessed following a query by clicking the 'Contigs' button in the Export section at the bottom of the results table.

5	M00240227	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	B	1100	ST-32 complex/ET-5 complex	7	16	
6	M00282207	UK	2000	invasive (unspecified/other)	Neisseria meningitidis	W	1101	ST-22 complex			
7	7891	B54; Z1054	Finland	1975	invasive (unspecified/other)	A	5	ST-5 complex/subgroup III	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)	W	114	ST-22 complex			
10	6748	B73; Z1073	Canada	1971	invasive (unspecified/other)	A	1	ST-1 complex/subgroup I/II	18-1	3	F5-1
11	129	B92; Z1092	Germany	1964	invasive (unspecified/other)	A	1	ST-1 complex/subgroup I/II	5-2	10	F3-6
12	0090/89		Czech Republic	1989	invasive (unspecified/other)	B	1015	ST-32 complex/ET-5 complex	7	16	
13	139M	B99; Z1099	Philippines	1968	invasive (unspecified/other)	A	1	ST-1 complex/subgroup I/II	5-2	10	F5-1
14	0120/95		Czech Republic	1995	invasive (unspecified/other)	X	117			14	
15	1		Germany	1999	carrier	E	864				
16	2		Germany	1999	carrier	B	854	ST-18 complex			
17	3		Germany	1999	carrier	W	174	ST-174 complex			
18	4		Germany	1999	carrier	B	19	ST-18 complex			
19	S3131	B213; Z1213	Ghana	1973	invasive (unspecified/other)	A	4	ST-4 complex/subgroup IV	7	13-1	F1-5
20	5		Germany	1999	carrier	NG	198	ST-198 complex			
21	6		Germany	1999	carrier	NG	198	ST-198 complex			
22	7		Germany	1999	carrier	E	60	ST-60 complex			
23	8		Germany	1999	carrier	B	32	ST-32 complex/ET-5 complex			
24	S4355	B227; Z1227	Denmark	1974	invasive (unspecified/other)	A	5	ST-5 complex/subgroup III	5-1	9	F3-1
25	9		Germany	1999	carrier	B	930	ST-334 complex			

Analysis tools:

Breakdown: Fields Two Field Polymorphic sites Combinations Schemes/alleles Publications Sequence bin Tag status

Analysis: BURST Codons Presence/Absence Genome Comparator BLAST

Export: Dataset **Contigs** Sequences

Page: 1 2 3 4 > Last

Select the isolates for which you wish to export contig data for. If the export function was accessed following a query, isolates returned in the query will be pre-selected.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

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) A4/M1027
☐ 2) 120M
☐ 7) 7891
☐ 10) 6748
☐ 11) 129
☐ 13) 139M
☐ 19) S3131
☐ 24) S4355

Options
 Identify contigs with \geq 0 % of sequence untagged
 FASTA header line: original designation

Filter by
 Sequence method:
 Project:
 Experiment:
 Minimum length:

Action

At its simplest, press submit.

A table will be produced with download links. Clicking these will produce the contigs in FASTA format.

PubMLST Query: [Search](#) | [Browse](#) | [Profile/ST](#) | [List](#)
 Breakdown: [Isolate fields](#) | [Scheme/alleles](#) | [Publications](#)
 Links: [Contents](#) | [Home](#) | [Options](#) | [Profiles/sequences definitions](#) | [Database submissions](#)

Toggle: [?](#)

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) A4/M1027
☐ 2) 120M
☐ 7) 7891
☐ 10) 6748
☐ 11) 129
☐ 13) 139M
☐ 19) S3131
☐ 24) S4355

Options
 Identify contigs with \geq 0 % of sequence untagged
 FASTA header line: original designation

Filter by
 Sequence method:
 Project:
 Experiment:
 Minimum length:

Action

Contigs with $\geq 0\%$ sequence length untagged

id	isolate	contigs	matching contigs		non-matching contigs	
			count	download	count	download
1	A4/M1027	364	364	download	0	
2	120M	359	359	download	0	
7	7891	199	199	download	0	
10	6748	652	652	download	0	

- Download table in tab-delimited text format
- Batch download all contigs from selected isolates (tar format)

You can also download all the data in a tar file by clicking the 'Batch download' link.

PubMLST Query: Search | Browse | Profile/ST | List
Breakdown: Isolate fields | Scheme/alleles | Publications
Links: Contents | Home | Options | Profiles/sequences definitions | Database submissions

Toggle: [?]

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) A4/M1027
- 2) 120M
- 7) 7891
- 10) 6748
- 11) 129
- 13) 139M
- 19) S3131
- 24) S4355

Options

Identify contigs with \geq 0 % of sequence untagged
FASTA header line: original designation

Filter by

Sequence method: [?]
Project: [?]
Experiment: [?]
Minimum length: [?]

Action

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	

Download table in tab-delimited text format
Batch download all contigs from selected isolates (tar format)

12.3.1 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 50 % of sequence untagged
FASTA header line: original designation

The resulting table has two download links for each isolate, one for contigs matching the condition, and one for contigs that don't match.

Contigs with $\geq 50\%$ sequence length untagged

id	isolate	contigs	matching contigs		non-matching contigs	
			count	download	count	download
1	A4/M1027	364	175		189	
2	120M	359	99		260	
7	7891	199	56		143	
10	6748	652	423		229	

Frequently asked questions (FAQs)

13.1 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 (bigsdb.pl and bigscurate.pl respectively) must match. This prevents somebody from accessing a private database using an instance of bigsdb.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/bigsdb/bigsdb.pl> then you can set script_path_includes to something like "/bigsdb/" (which is the default), or "/cgi-bin/" or just "/" if you don't care about this check.

13.2 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/bigsdb/dbases/). The database view accessed by each of these configurations can be different as can the access restrictions.

Example:

We have a database 'bigsdb_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 postgresql user. We will name this view 'public':

```
sudo su postgres
psql bigsdb_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/bigsdb/dbases/test_private`. This will be accessible from http://IP_ADDRESS/cgi-bin/bigsdb/bigsdb.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/bigsdb/dbases/test_public`. This will be accessible from http://IP_ADDRESS/cgi-bin/bigsdb/bigsdb.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*.

14.1 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.
- <
 - Less than 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).

14.2 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:

- 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.
- 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.
- 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).

14.3 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:

- 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.

- 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.
- 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).

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- Isolate database

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