

PubMLST

Ho Phu Quy

What is PubMLST ?

PubMLST Public databases for molecular typing and microbial genome diversity [MY ACCOUNT](#)

[HOME](#) [ORGANISMS](#) [SPECIES ID](#) [ABOUT US](#) [UPDATES](#)

A collection of open-access, curated databases that integrate population sequence data with provenance and phenotype information for over 100 different microbial species and genera.

22,287,554
ALLELES

805,654
ISOLATES

562,208
GENOMES

Organisms search



Organisms

Choose your organism from a list of over 100 species and genera-specific databases. Access molecular typing and isolate records.



Species ID

Use ribosomal MLST to accurately identify bacterial species from a genome assembly.



Submit data

We welcome submissions to the databases we host. Submissions may consist of new allele sequences, MLST profiles, or isolate records. Isolates may be accompanied by a genome assembly.

PubMLST (Public Multi-Locus Sequence Typing) is a comprehensive online database and bioinformatics platform designed for the storage, analysis, and dissemination of molecular typing data for bacterial species

<https://x.com/PubMLST/status/1308049194972844033>

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MY ACCOUNT

HOME ORGANISMS SPECIES ID ABOUT US UPDATES

Home > Organisms

Organisms

Most popular

	<i>Campylobacter jejuni/coli</i>		<i>Haemophilus influenzae</i>		<i>Neisseria spp.</i>
	<i>Staphylococcus aureus</i>		<i>Streptococcus agalactiae</i>		<i>Streptococcus pneumoniae</i>

Search

PubMLST (Public Multi-Locus Sequence typing) have 139 organisms.

PubMLST hosts databases for a wide range of bacterial species, providing tools for molecular typing and epidemiological analysis. Each organism has a dedicated database containing allelic profiles, sequence types (STs), and metadata.

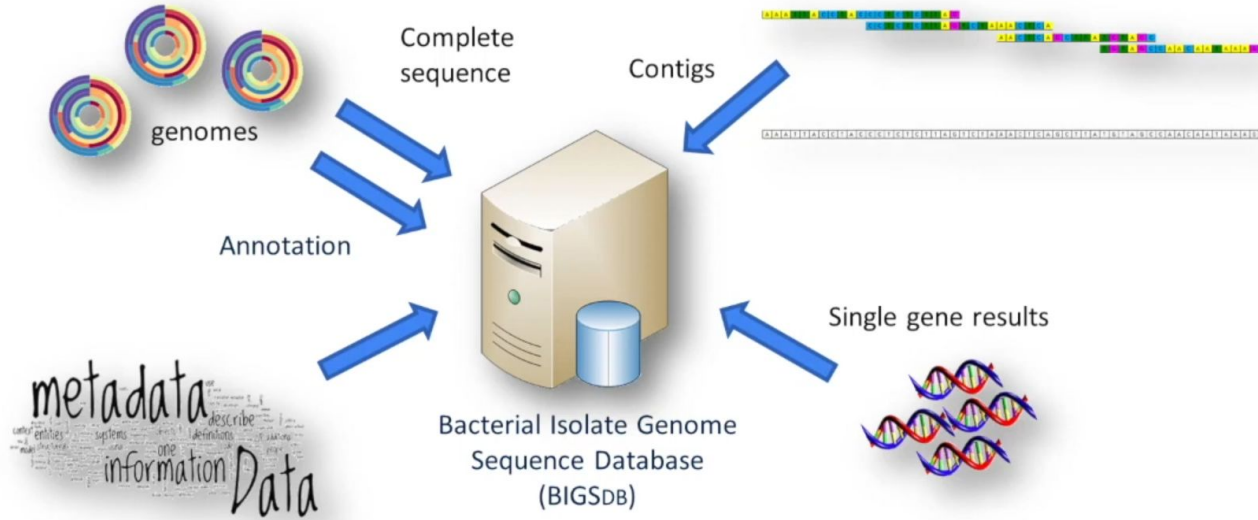
What is PubMLST ?



Population genomics: the BIGSdb platform



CHICKEN
JOURNAL
CLUB



Jolley & Maiden 2010. BIGSdb: Scalable analysis of bacterial genome variation at the population level. *BMC Bioinformatics* **11**:595

[No.6 Introduction to PubMLST Database!](#)
(youtube.com)

S. aureus clonal complex designation

We have identified the common, largely non-overlapping clonal complexes within the database associated with ST. Clonal complexes here are defined as those STs that match the central genotype (ST) at four or more loci unless they more closely match another central genotype.

STs are assigned to clonal complexes automatically by a script that runs against the database each evening.

Currently defined complexes

Central ST	Complex name
1	CC1
5	CC5
8	CC8
15	CC15
22	CC22
30	CC30
45	CC45
97	CC97
93	CC93
121	CC121

This is not an exhaustive list of complexes, but those that are seen most frequently in the database and can usually be

<https://pubmlst.org/organisms/staphylococcus-aureus/clonal-complexes>

Staphylococcus aureus MLST primers

Genes

The *S. aureus* MLST scheme uses internal fragments of the following seven house-keeping genes:

- *arcC* (Carbamate kinase)
- *aroE* (Shikimate dehydrogenase)
- *glpF* (Glycerol kinase)
- *gmk* (Guanylate kinase)
- *pta* (Phosphate acetyltransferase)
- *tpi* (Triosephosphate isomerase)
- *yqi* (Acetyl coenzyme A acetyltransferase)

Staphylococcus aureus DNA extraction protocol

1. Resuspend 1/8 of a plate of overnight confluent growth from a blood agar plate in 400 µl lysis solution (see below)
2. Incubate at 37 °C 30 min.
3. Heat to 95 °C for 10 min.
4. Place on ice and add 1 ml phenol/chloroform isoamyl alcohol (25:24:1) and mix thoroughly by inversion.
5. Centrifuge 10,000 g for 20 min.
6. Recover aqueous layer to fresh tube and precipitate DNA with the addition of 1 ml absolute ethanol.
7. Place on ice for 15 min then pellet DNA by centrifugation at 10,000g for 20 min.
8. Resuspend DNA in 50 µl water.

Lysis solution

- 0.5 ml 5000 units/ml lysozyme
- 0.5 ml 500 units/ml lysostaphin
- 0.2 ml 0.5M EDTA
- 0.1 ml 1M Tris
- 8.7 ml de-ionised water

PCR conditions

PCR amplification is carried out on chromosomal DNA using an extension time of 30 s, and an annealing temperature of 55 °C, with Qiagen Taq polymerase. As the same primers are used for amplification and sequencing, it is important that only a single DNA fragment is amplified in the initial PCR. This may involve some optimisation of the annealing temperature.

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arc dn - 5' AGG TAT CTG CTT CAA TCA GCG -3'
aro up - 5' ATC GGA AAT CCT ATT TCA CAT TC -3'
aro dn - 5' GGT GTT GTA TTA ATA ACG ATA TC -3'
glp up - 5' CTA GGA ACT GCA ATC TTA ATC C -3'
glp dn - 5' TGG TAA AAT CGC ATG TCC AAT TC -3'
gmk up - 5' ATC GTT TTA TCG GGA CCA TC -3'
gmk dn - 5' TCA TTA ACT ACA ACG TAA TCG TA -3'
pta up - 5' GTT AAA ATC GTA TTA CCT GAA GG -3'
pta dn - 5' GAC CCT TTT GTT GAA AAG CTT AA -3'
tpi up - 5' TCG TTC ATT CTG AAC GTC GTG AA -3'
tpi dn - 5' TTT GCA CCT TCT AAC AAT TGT AC -3'
yqi up- 5' CAG CAT ACA GGA CAC CTA TTG GC -3'
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glp up - 5' CTA GGA ACT GCA ATC TTA ATC C -3'

glp dn - 5' TGG TAA AAT CGC ATG TCC AAT TC -3'

gmk up - 5' ATC GTT TTA TCG GGA CCA TC -3'

gmk dn - 5' TCA TTA ACT ACA ACG TAA TCG TA -3'

pta up - 5' GTT AAA ATC GTA TTA CCT GAA GG -3'

pta dn - 5' GAC CCT TTT GTT GAA AAG CTT AA -3'

tpi up - 5' TCG TTC ATT CTG AAC GTC GTG AA -3'

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glp dn - 5' TGG TAA AAT CGC ATG TCC AAT TC -3'

gmk up - 5' ATC GTT TTA TCG GGA CCA TC -3'

gmk dn - 5' TCA TTA ACT ACA ACG TAA TCG TA -3'

pta up - 5' GTT AAA ATC GTA TTA CCT GAA GG -3'

pta dn - 5' GAC CCT TTT GTT GAA AAG CTT AA -3'

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glp up - 5' CTA GGA ACT GCA ATC TTA ATC C -3'

glp dn - 5' TGG TAA AAT CGC ATG TCC AAT TC -3'

gmk up - 5' ATC GTT TTA TCG GGA CCA TC -3'

gmk dn - 5' TCA TTA ACT ACA ACG TAA TCG TA -3'

pta up - 5' GTT AAA ATC GTA TTA CCT GAA GG -3'

pta dn - 5' GAC CCT TTT GTT GAA AAG CTT AA -3'

tpi up - 5' TCG TTC ATT CTG AAC GTC GTG AA -3'

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glp dn - 5' TGG TAA AAT CGC ATG TCC AAT TC -3'

gmk up - 5' ATC GTT TTA TCG GGA CCA TC -3'

gmk dn - 5' TCA TTA ACT ACA ACG TAA TCG TA -3'

pta up - 5' GTT AAA ATC GTA TTA CCT GAA GG -3'

pta dn - 5' GAC CCT TTT GTT GAA AAG CTT AA -3'

tpi up - 5' TCG TTC ATT CTG AAC GTC GTG AA -3'

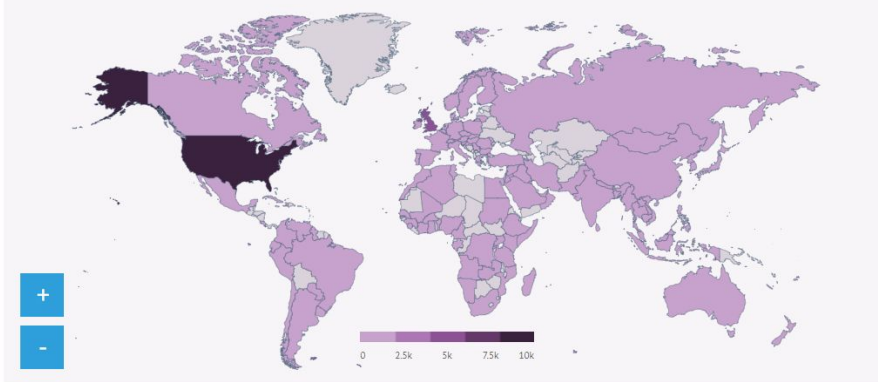
tpi dn - 5' TTT GCA CCT TCT AAC AAT TGT AC -3'

yqi up - 5' CAG CAT ACA GGA CAC CTA TTG GC -3'

yqi dn - 5' CGT TGA GGA ATC GAT ACT GGA AC -3'

Staphylococcus aureus

Source of isolates submitted to the *Staphylococcus aureus* database



↑ SUBMIT

This MLST scheme was developed by Mark Enright in the laboratory of Brian Spratt, Imperial College London, in collaboration with the laboratories of Nick Day and Sharon Peacock. It is described in Enright *et al.* 2000 *J Clin Microbiol* **38**:1008-15.

- Primers
- Clonal complexes

Database curated by Yvonne Pannekoek.

The preferred citation for this website is:

Jolley *et al. Wellcome Open Res* 2018, **3**:124 [version 1; referees: 2 approved]

Typing

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Allele sequences: 954,696

Last updated: 2024-06-13

Isolate collection

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Isolates: 42,787

Last updated: 2024-06-19

Genome collection

A subset of records within the isolate database may contain genomes assemblies. You can access these from the isolate database by filtering on sequence bin size in a query.

Genomes: 30,785

Last updated: 2024-06-12

Analysis with PubMLST

Home > Organisms > *Staphylococcus aureus* > *Staphylococcus aureus* typing > Sequence query



Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences. ⓘ

Please select locus/scheme

Order results by

MLST

locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

or enter Genbank accession

Select FASTA file: ⓘ

Click to select or drag and drop...

Action

RESET

SUBMIT

Uploaded file: *Staphylococcus aureus*_strain_HC1340.fasta

7 exact matches found.

Locus	Allele	Length	Contig	Start position	End position	Flags
arcC	2	456	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	2948666	2949121	
aroE	3	456	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	1832909	1833364	
glpF	1	465	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	1448319	1448783	
gmk	1	417	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	1342835	1343251	
pta	4	474	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	731881	732354	
tpi	4	402	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	933071	933472	
yqiL	3	516	NZ_CP012011.1_Staphylococcus_aureus_strain_HC1340_chromosome_complete_genome	462415	462930	

Only exact matches are shown above. If a locus does not have an exact match, try querying specifically against that locus to find the closest match.



MLST



Matching profile

ST: 239

clonal complex: CC8

https://pubmlst.org/bigsdb?db=pubmlst_saureus_seqdef&l=1&page=sequenceQuery

Sequence attribute search

You can also search using the [locus-specific query](#) page. Use this page for access to the sequence analysis or export plugins.

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 Display

locus = arcC + i

Order by: locus ascending

Display: 25 records per page i

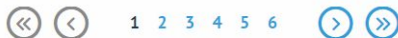
Filter query by Action

[RESET](#) [SEARCH](#)

1,044 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.



locus	allele id	sequence	sequence length	type	allele	flags
arcC	1	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	2	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	3	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	4	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	5	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	6	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	7	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	8	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	9	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	10	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	11	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	12	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	13	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	14	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	15	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	16	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	17	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	18	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	19	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	20	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	21	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	453			<input type="checkbox"/>
arcC	22	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	23	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	24	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>
arcC	25	TTATTAATCCAACAA ... GAAGGTGTTGAAGCG	456			<input type="checkbox"/>



Analysis with PubMLST

Search by locus combinations



Schemes

Please select the scheme you would like to query:

MLST [Select](#)

Please enter your allelic profile below. Blank loci will be ignored.

arcC	aroE	glpF	gmk	pta	tpi	yqjL
2	3	1	1	4	4	3

Autofill profile

ST: [Autofill](#)

Options

Search: [Exact or nearest match](#)

Display/sort options

Order by: ST ascending

Display: 25 records per page

Action

[RESET](#)

[SEARCH](#)

Exact matches found (7 loci).

1 record returned. Click the hyperlink for detailed information.

ST	arcC	aroE	glpF	gmk	pta	tpi	yqjL	clonal complex
239	2	3	1	1	4	4	3	CC8

Profile information for ST-239 (MLST)



ST	arcC	aroE	glpF	gmk	pta	tpi	yqjL	clonal complex
239	2	3	1	1	4	4	3	CC8

sender: Keith Jolley

curator: Keith Jolley, University of Oxford, UK

update history: [1 update](#) [show details](#)

date entered: 2016-01-26

timestamp: 2016-01-26



Client database

PubMLST S. aureus: Contains data for a collection of isolates that represent the total known diversity of *Staphylococcus aureus*. 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. [3086 isolates](#)



Tools

Export: [Profiles](#) [Sequences](#)

https://pubmlst.org/bigsdbs/db=pubmlst_saureus_seqdef

Isolates collection

PubMLST

Public databases for molecular typing
and microbial genome diversity

MY

HOME

ORGANISMS

SPECIES ID

ABOUT US

UPDATES

Home > Organisms > *Staphylococcus aureus* > *Staphylococcus aureus* isolates

Logged in

Tooltips

Expand

Modify dashboard

Index page

Staphylococcus aureus isolates database

Record versions: current; Record creation: all time

Isolate count

42,787

▲ 10 [month]

Genome count

30,785

▲ 1 [month]

Country

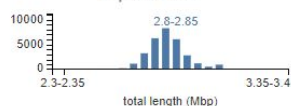


Continent

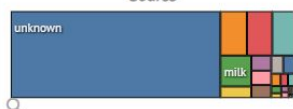
Top 5 values

Value	Frequency
Europe	11,635
North America	8,418
Asia	5,681
Africa	1,679
South America	1,232

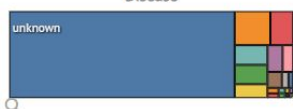
Sequence size



Source



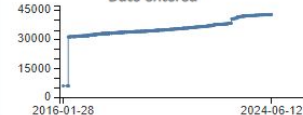
Disease



Source category



Date entered



Year



LOG OUT

SEARCH

SUBMISSIONS

YOUR PROJECTS

EXPORT

ANALYSIS

CUSTOMISE

INFORMATION

TYPING

https://pubmlst.org/bigsdb?db=pubmlst_saureus_isolates

Genome collection

Search or browse database

Logged in Help Tooltips Expand Modify form Modify dashboard

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

Isolate provenance/primary metadata fields

Sequence bin

Display/sort options

id = Enter value... + ⓘ

total length (Mbp) >= 1 + ⓘ

Order by: id ascending

Display: 25 records per page ⓘ

Action

RESET

SEARCH



30,785 records returned (1 - 25 displayed). Click the hyperlinks for detailed information.

id	isolate	aliases	Isolate fields				MLST											clonal complex
			country	year	disease	source	category	source	arcC	aroE	glpF	gmk	pta	tpi	yqjL	ST		
3532	Saitama9		Japan	2012	other	human	pus	3	124	1	1	1	410	40	1558	CC97		
3533	Saitama11		Japan	2013	other	human	pus	3	549	1	1	1	1	40	1566	CC1		
3625	ERR1197981		Unknown		unknown	unknown	unknown	2	2	2	2	6	3	2	30	CC30		
3882	ERR410047		Unknown		unknown	unknown	unknown	2	2	2	2	2	2	2	39	CC30		
5329	ERR410050		Unknown		unknown	unknown	unknown	3	3	1	1	4	4	3	8	CC8		
5959	ERR410059		Unknown		unknown	unknown	unknown	8	2	2	2	6	3	2	34	CC30		
5960	ERR410074		Unknown		unknown	unknown	unknown	8	2	2	2	6	3	2	34	CC30		
5965	ERR410082		Unknown		unknown	unknown	unknown	1	1	1	1	1	1	1	1	CC1		
5966	ERR410106		Unknown		unknown	unknown	unknown	7	6	1	5	8	8	6	22	CC22		
6087	ERR211639		Unknown		unknown	unknown	unknown	6	57	45	2	7	58	52	130			
6088	ERR163446		Unknown		unknown	unknown	unknown	14	16	11	2	13	336	14	3121			
6089	SRR445025	199/08	Slovenia	2008	unknown	unknown	unknown	3	35	19	2	20	26	39	398			

https://pubmlst.org/bigssdb?db=pubmlst_saureus_isolates&page=query&genomes=1

Run demo workflow for **coregenome-MLST** analysis

Data using: 50 genome example downloaded from ncbi.

(<https://www.ncbi.nlm.nih.gov/datasets/genome/?taxon=1280>)

Tools using:

chewbbaca(https://chewbbaca.readthedocs.io/en/latest/user/getting_started/overview.html) and

PHYLOViZ Online(<https://online.phyloviz.net/index>)

Exercise: using this workflow to run dataset.

Link: https://zenodo.org/records/10694715/files/chewBBACA_tutorial.zip