

**GenMAPP Gene Database for *Staphylococcus aureus* (strain MRSA252)**  
 Sa-Std\_External\_20100218.gdb  
**ReadMe**

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### 1. Overview of the GenMAPP application and accessory programs

GenMAPP (Gene Map Annotator and Pathway Profiler) is a free computer application for viewing and analyzing DNA microarray and other genomic and proteomic data on biological pathways. MAPPFinder is an accessory program that works with GenMAPP and Gene Ontology to identify global biological trends in gene expression data. The GenMAPP Gene Database (file with the extension *.gdb*) is used to relate gene IDs on MAPPs (*.mapp*, representations of pathways and other functional groupings of genes) to data in Expression Datasets (*.gex*, DNA microarray or other high-throughput data). GenMAPP is a stand-alone application that requires the Gene Database, MAPPs, and Expression Dataset files to be stored on the user's computer. GenMAPP and its accessory programs and files may be downloaded from <http://www.GenMAPP.org>. GenMAPP requires a separate Gene Database for each species. This ReadMe describes a Gene Database for *Staphylococcus aureus* (strain MRSA252) that was built by the Loyola Marymount University (LMU) Bioinformatics Group using the program GenMAPP Builder 2.0, part of the open source XMLPipeDB project <http://xmlpipedb.cs.lmu.edu/>.

### 2. System Requirements and Compatibility:

- This Gene Database is compatible with GenMAPP 2.0 and 2.1 and MAPPFinder 2.0. These programs can be downloaded from <http://www.genmapp.org>.
- System Requirements for GenMAPP 2.0/2.1 and MAPPFinder 2.0:  
 Operating System: Windows 98 or higher, Windows NT 4.0 or higher (2000, XP, etc)  
 Monitor Resolution: 800 X 600 screen or greater (SVGA)  
 Internet Browser: Microsoft Internet Explorer 5.0 or later  
 Minimum hardware configuration:  
     Memory: 128 MB (512 MB or more recommended)  
     Processor: Pentium III  
     Disk Space: 300 MB disk (more recommended if multiple databases will be used)

### 3. Installation Instructions

- Extract the zipped archive and place the file "Sa-Std\_External\_20100218.gdb" in the folder you use to store Gene Databases for GenMAPP. If you accept the default folder during the GenMAPP installation process, this folder will be C:\GenMAPP 2 Data\Gene Databases.

- To use the Gene Database, launch GenMAPP and go to the menu item *Data > Choose Gene Database*. Alternatively, you can launch MAPPFinder and go to the menu item *File > Choose Gene Database*.

#### 4. Gene Database Specifications

##### a. Gene ID Systems

This *Staphylococcus aureus* Gene Database is UniProt-centric in that the main data source (primary ID System) for gene IDs and annotation is the UniProt complete proteome set for *Staphylococcus aureus*, made available as an XML download by the Integr8 resource. In addition to UniProt IDs, this database provides the following proper gene ID systems that were cross-referenced by the UniProt data: OrderedLocusNames (IDs of the form SAR####), GeneId (NCBI), and RefSeq (protein IDs of the form YP\_#####). It also supplies UniProt-derived annotation links from the following systems: EMBL, InterPro, PDB, and Pfam. The Gene Ontology data has been acquired directly from the Gene Ontology Project. The GOA project was used to link Gene Ontology terms to UniProt IDs. Links to data sources are listed in the section below.

Proper ID System	System Code
UniProt	S
OrderedLocusNames	N
GeneId	L
RefSeq	Q

##### b. Species

This Gene Database is based on the UniProt proteome set for *Staphylococcus aureus* (strain MRSA252), taxon ID 282458.

##### c. Data Sources and Versions

- This *Staphylococcus aureus* Gene Database was built on February 18, 2010; this build date reflected in the filename Sa-Std\_External\_20100218.gdb. All date fields internal to the Gene Database (and not usually seen by regular GenMAPP users) have been filled with this build date.
- UniProt complete proteome set for *Staphylococcus aureus* (strain MRSA252), made available as an XML download by the Integr8 resource:  
<<http://www.ebi.ac.uk/integr8/FtpSearch.do?orgProteomeId=19583>>  
Filename: "19583.S\_aureus\_MRSA252.xml" (downloaded as a compressed .gz file and extracted).  
Version information for the proteome sets can be found at  
<<http://www.ebi.ac.uk/integr8/HelpAction.do?action=searchById&refId=5>>.
- The proteome set used for this version of the *Staphylococcus aureus* Gene Database was based on UniProt Knowledgebase release 15.13 and InterPro Knowledgebase release 24.0 from January 19, 2010.
- Gene Ontology gene associations are provided by the GOA project:  
<<http://www.ebi.ac.uk/GOA/>> as a tab-delimited text file. The *Staphylococcus aureus* (strain MRSA252) GOA file was accessed from the Integr8 proteome set download page:  
<<http://www.ebi.ac.uk/integr8/FtpSearch.do?orgProteomeId=19583>>  
Filename: "19583.S\_aureus\_MRSA252.goa". The GOA file for this version of the *Staphylococcus aureus* Gene Database was based on the GOA Proteome Sets 56.0 released January 21, 2010.
- Gene Ontology data is downloaded from <<http://www.geneontology.org/GO.downloads.ontology.shtml>>

Data is released daily. For this version of the *Staphylococcus aureus* Gene Database we used the January 28, 2010 release.

Filename: "go\_daily-termdb.obo-xml".

#### d. Database Report

- UniProt is the primary ID system for the *Staphylococcus aureus* Gene Database. The UniProt table contains all 2640 UniProt IDs contained in the UniProt proteome set for this species.
- The OrderedLocusNames ID system was derived from the cross-references in the UniProt proteome set. The OrderedLocusNames IDs are in the form SAR####. We compared this table with the list of gene IDs in the JCVI Comprehensive Microbial Resource (CMR) at <<http://cmr.jcvi.org/cgi-bin/CMR/GenomePage.cgi?org=ntsa08>>. There are 2659 protein-coding genes listed there, matching our table count for OrderedLocusNames. The following table lists the numbers of gene IDs found in each gene ID system:

ID System	ID Count
EMBL	1
GeneId (NCBI)	2650
GeneOntology	3416
InterPro	2947
OrderedLocusNames	2659
PDB	19
Pfam	1462
RefSeq	2656
UniProt	2640

#### 5. Contact Information for support, bug reports, feature requests

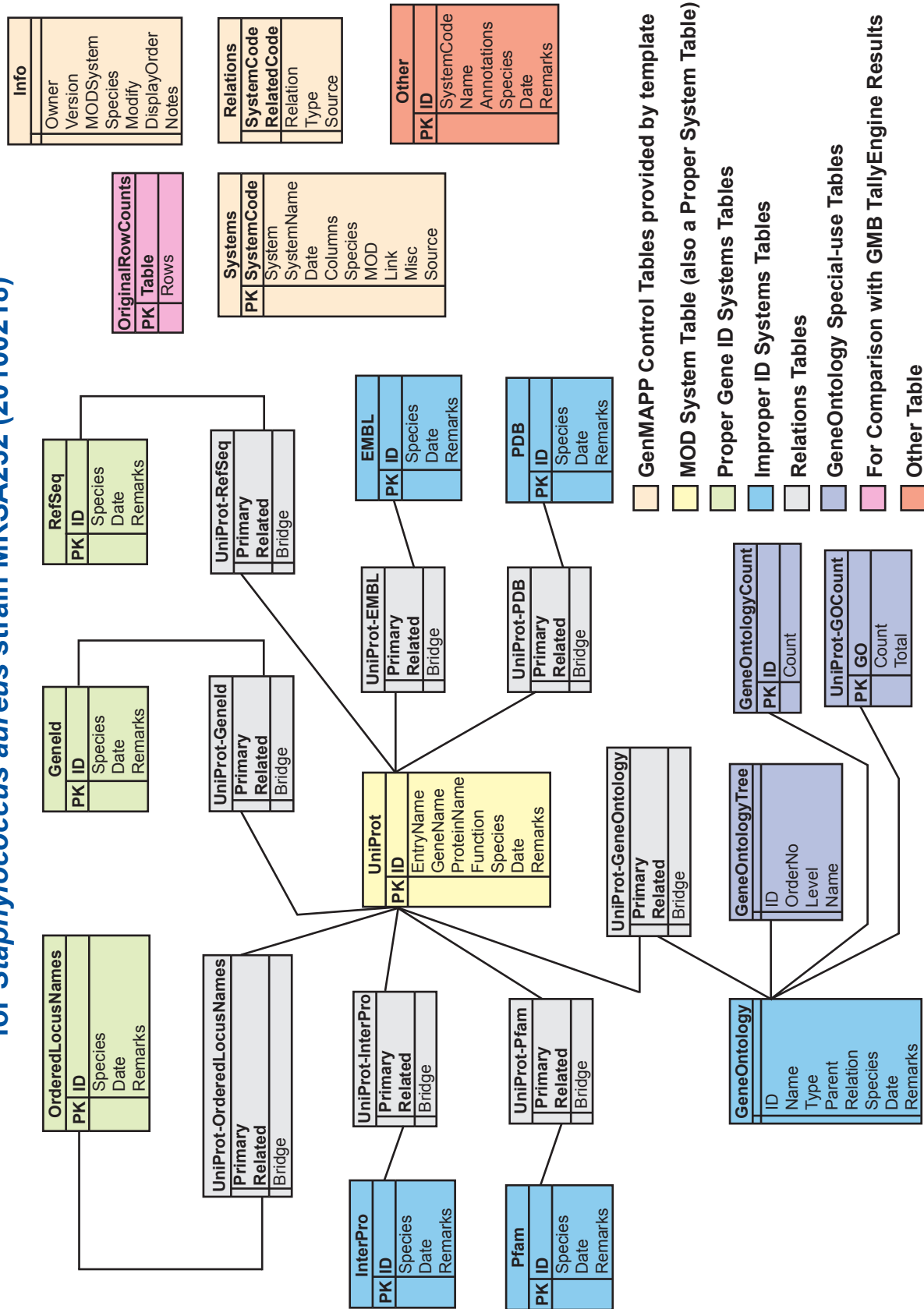
- The Gene Database for *Staphylococcus aureus* (strain MRSA252) was built by the Loyola Marymount University (LMU) Bioinformatics Group using the program GenMAPP Builder 2.0, part of the open source XMLPipeDB project <<http://xmlpipedb.cs.lmu.edu/>>.
- For support, bug reports, or feature requests relating to XMLPipeDB or GenMAPP Builder, please consult the XMLPipeDB Manual found at <<http://xmlpipedb.cs.lmu.edu/documentation.shtml>> or go to our SourceForge site <<http://sourceforge.net/projects/xmlpipedb/>>.
- For issues related to the *Staphylococcus aureus* (strain MRSA252) Gene Database, please contact:  
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1 LMU Drive, MS 8220  
Los Angeles, CA 90045-2659  
kdahlquist@lmu.edu
- For issues related to GenMAPP 2.0/2.1 or MAPPFinder 2.0 please contact GenMAPP support directly by e-mailing [genmapp@gladstone.ucsf.edu](mailto:genmapp@gladstone.ucsf.edu) or [GenMAPP@googlegroups.com](mailto:GenMAPP@googlegroups.com).

#### 6. Release Notes

##### a. Current version: Sa-Std\_External\_20100218.gdb

- This release is the first release of a standard *Staphylococcus aureus* (strain MRSA252) Gene Database
- Kelly Parks (lead), Michael Piña, Andrew Hirning, John David N. Dionisio, and Kam D. Dahlquist contributed to this release.

# GenMAPP Gene Database Schema for *Staphylococcus aureus* strain MRSA252 (20100218)



**NOTE:** Some Relations tables are not shown. All possible pairwise Relations tables exist between Proper ID systems and between Proper and Improper ID systems, but not between Improper ID systems (i.e., Proper-Proper, Proper-Improper, but NOT Improper-Improper).