

GenMAPP Gene Database for *Pseudomonas aeruginosa* str. PAO1
Pa-Std_External_20100212.gdb
ReadMe

Last revised: 4/14/10

This document contains the following:

1. Overview of GenMAPP application and accessory programs
2. System Requirements and Compatibility
3. Installation Instructions
4. Gene Database Specifications
 - a. Gene ID Systems
 - b. Species
 - c. Data Sources and Versions
 - d. Database Report
5. Contact Information for support, bug reports, feature requests
6. Release notes
 - a. Current version: Pa-Std_External_20100212.gdb
7. Database Schema Diagram

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 *Pseudomonas aeruginosa* str. PAO1 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 "Pa-Std_External_20100212.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 for *Pseudomonas aeruginosa* 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 *Pseudomonas aeruginosa*, 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, GeneId (NCBI), and RefSeq (protein IDs of the form NP_#####). 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 *Pseudomonas aeruginosa* str. PAO1 (strain LMG 12228 / ATCC 15692 / PRS 101 / 1C / PAO1), taxon ID 208964.

c. Data Sources and Versions

- This *Pseudomonas aeruginosa* Gene Database was built on February 12, 2010; this build date reflected in the filename Pa-Std_External_20100212.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 *Pseudomonas aeruginosa* str. PAO1, made available as an XML download by the Integr8 resource:
<<http://www.ebi.ac.uk/integr8/FtpSearch.do?orgProteomeId=36>>
Filename: "36.P_aeruginosa_LMG_12228.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 *Pseudomonas aeruginosa* Gene Database was based on UniProt Knowledgebase release 15.13 and InterPro Knowledgebase release 24.0 on 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 *Pseudomonas aeruginosa* GOA file was accessed from the Integr8 proteome set download page:
<<http://www.ebi.ac.uk/integr8/FtpSearch.do?orgProteomeId=36>>
Filename: "36.P_aeruginosa_LMG_12228.goa.txt". The GOA file for this version of the *Pseudomonas aeruginosa* Gene Database was based on the GOA Proteome Sets 79.0 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 *Pseudomonas aeruginosa* Gene Database we used the January 28, 2010 release.

Filename: "go_daily-termdb.obo.xml.gz".

d. Database Report

- UniProt is the primary ID system for the *Pseudomonas aeruginosa* Gene Database. The UniProt table contains all 5558 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. Each ID appears once in the form of PA#### (e.g., PA0001). 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=ntpa03>>. There are 5565 protein coding genes listed there. Of the protein coding genes, 5 gene IDs do not appear in our Gene Database because they are not cross-listed in the UniProt XML file.
- The following table lists the numbers of gene IDs found in each gene ID system:

| ID System | ID Count |
|-------------------|----------|
| EMBL | 502 |
| GeneId (NCBI) | 5564 |
| GeneOntology | 4169 |
| InterPro | 4292 |
| OrderedLocusNames | 5570 |
| PDB | 494 |
| Pfam | 2117 |
| RefSeq | 5564 |
| UniProt | 5558 |

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

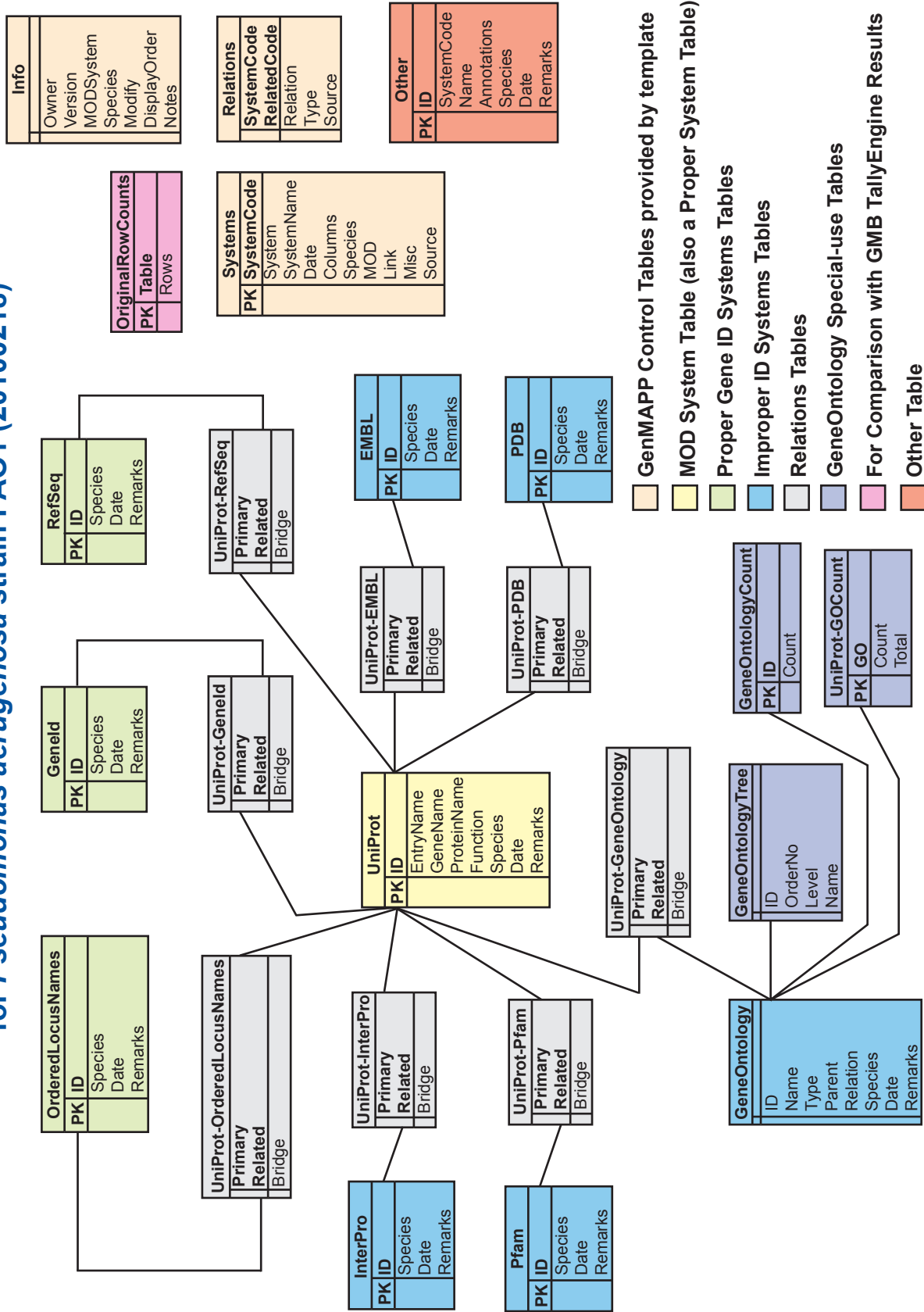
- The Gene Database for *Pseudomonas aeruginosa* was built by the Loyola Marymount University (LMU) Bioinformatics Group using the program GenMAPP Builder, part of the open source XMLPipeDB project <<http://xmlpipedb.cs.lmu.edu/>>.
- For support, bug reports, or feature requests relating to XMLPipeDB 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 *Pseudomonas aeruginosa* Gene Database, please contact:
Kam D. Dahlquist, Ph.D.
Department of Biology
Loyola Marymount University
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 or GenMAPP@googlegroups.com.

6. Release Notes

a. Current version: Pa-Std_External_20100212.gdb

- This release is the first release of a standard *Pseudomonas aeruginosa* Gene Database.
- Kelia McDonald (lead), Kristen Phifer, Lita Gratrix, John David N. Dionisio, and Kam D. Dahlquist contributed to this release.

GenMAPP Gene Database Schema for *Pseudomonas aeruginosa* strain PAO1 (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).