

**GenMAPP Gene Database for *Chlamydia trachomatis* Serovar A str. HAR-13**  
 Ct-Std\_External\_20131122.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 *Chlamydia trachomatis* Serovar A/HAR-13 that was built by the Loyola Marymount University Fall 2013 Biological Databases class using the program GenMAPP Builder 2.0b71, 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 "Ct-Std\_External\_20131122.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 *Chlamydia trachomatis* 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 *Chlamydia trachomatis* A/HAR-13, made available as an XML download. 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	SystemCode
UniProt	S
OrderedLocusNames	N
GeneID (NCBI)	L
RefSeq	Q

##### b. Species

This Gene Database is based on the UniProt proteome set for *Chlamydia trachomatis* Serovar A str. HAR-13, taxon ID 315277.

##### c. Data Sources and Versions

- This *Chlamydia trachomatis* Gene Database was built on November 22, 2013; this build date is reflected in the filename Ct-Std\_External\_20131122.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 *Chlamydia trachomatis* Serovar A str. HAR-13, downloaded from this page:  
<[http://www.uniprot.org/uniprot/?query=organism%3a243277+keyword%3a1185&format=\\* &compress=yes](http://www.uniprot.org/uniprot/?query=organism%3a243277+keyword%3a1185&format=* &compress=yes)>  
Filename: <http://www.uniprot.org/uniprot/?query=organism:315277+keyword:181>  
Version information for the proteome sets can be found at <<http://www.uniprot.org/news/>>  
The proteome set used for this version of the *Chlamydia trachomatis* Gene Database was based on UniProt release 2013\_11 released on November 13, 2013.
- Gene Ontology gene associations are provided by the GOA project:  
<<http://www.ebi.ac.uk/GOA/>> as a tab-delimited text file. The *Chlamydia trachomatis* GOA file was accessed from the GOA proteomes FTP site: <<ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/proteomes/>>  
Filename: "22183.C\_trachomatis\_A.goa". Version 11/12/2013.
- Gene Ontology data is downloaded from <<http://beta.geneontology.org/page/download-ontology>>  
Data is released daily. For this version of the *Chlamydia trachomatis* Gene Database we used the ontology version 2013-111-06. Filename: "go\_daily-termdb.obo-xml.gz".

##### d. Database Report

- UniProt is the primary ID system for the *Chlamydia trachomatis* Gene Database. The UniProt table contains all 917 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. We compared this table with the list of gene IDs in the EnsemblBacteria database site for *Chlamydia trachomatis* Serovar A str. HAR-13. This database recorded 919 coding genes while 917 genes were detected in our database by the TallyEngine and

PostgreSQL queries. This discrepancy in the count is due to the gene ID CTA\_0406/CTA\_0407/CTA\_0408. In the EnsemblDatabase, each of the ordered locus names in this ID are separated. However, the TallyEngine and PostgreSQL does not separate these IDs.

- The following table lists the numbers of gene IDs found in each gene ID system:

ID System	Count
EMBL	4
GeneID (NCBI)	926
GeneOntology	2740
InterPro	1561
OrderedLocusNames	919
Pfam	732
RefSeq	926
UniProt	917

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

- The Gene Database for *Chlamydia trachomatis* was built by the Loyola Marymount University Fall 2013 Biological Databases class 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 *Chlamydia trachomatis* Gene Database, please contact:  
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- 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).

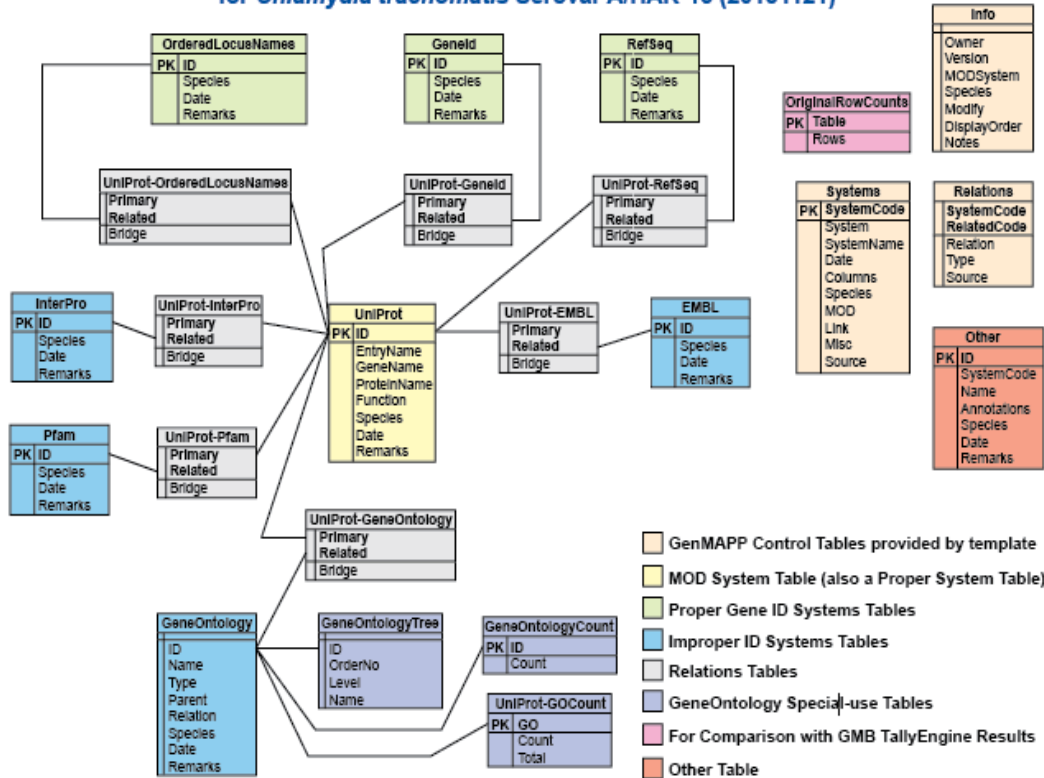
## 6. Release Notes

### a. Current version: Ct-Std\_External\_20131121.gdb

- Hilda Delgadillo, Katrina Sherbina, and Dillon Williams contributed to this release.

## 7. Database Schema Diagram

### GenMAPP Gene Database Schema for *Chlamydia trachomatis* Serovar A/HAR-13 (20131121)



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).