

Welcome to the *Mycoplasma genitalium* database!

M. genitalium is a gram-positive bacterium and human pathogen. Among all freely-culturable organism, *M. genitalium* has the smallest genome, containing slightly more than 580 kb. Primarily due to its reduced genome size, *M. genitalium* has been the subject of intense research over the past thirty years. *M. genitalium* was the second organism to be completely sequenced, and the first organism to have its genome completely synthesized *de novo* and to be comprehensively modeled. *M. genitalium*'s close relatives have also been the first to have their genome be transplanted into a recipient cell. This PGDB provides a comprehensive description of *M. genitalium* molecular biology.

Cross references

Taxonomy: [243273](#), ATCC: [33530](#), BioProject: [97](#), CMR: [gmg](#), GenBank: [L43967](#), RefSeq: [NC_000908](#)

Genetic code

[Mold, protozoa, coelenterate mitochondria, mycoplasma, and spiroplasma \(4\)](#)

Content

Content	Value	Units	Content	Value	Units	Content	Value	Units
Compartments	6		Proteins	683		Transcriptional regulation		
Chromosomes	1		Monomers	482		Interactions	30	
Length	580076	nt	DNA-binding	5		Transcriptional regulators	5	
GC-content	47	%	Integral membrane	85		Regulated promoters	26	
Transcription units	335		Lipoprotein	14		Pathways	17	
Monocistrons	231		Secreted	20		Stimuli	10	
Polycistrons	104		Terminal organelle	8		Quantitative parameters	1836	
Genes	525		Complexes	201		Cell composition	73	
mRNA	482		DNA-binding	5		Media composition	83	
rRNA	3		Reactions	1857		Reaction K_{eq}	225	
sRNA	4		DNA damage	67		Reaction K_m	483	
tRNA	36		DNA repair	32		Reaction V_{max}	434	
Chromosome features	2305		Metabolic	645		RNA expression	525	

DnaA boxes	2283	Protein decay	40	RNA half-lives	525
Short tandem repeats	19	Protein modification	63	Stimulus values	10
Other	3	Replication Initiation	15	Transcr. reg. 2 activity	
Metabolites	722	RNA decay	25	Transcr. reg. 30 affinity	
Amino acids	29	RNA modification	9	Other	154
Antibiotic	3	RNA processing	20	Processes	28
Gases	4	Transcription	4	States	16
Ions	19	Translation	20		
Lipids	32	tRNA aminoacylation	39		
Vitamins	27	Other	726		

Data sources

- Sources, by type
- Evidence, by species
- Evidence, by media
- Parameter evidence
- Evidence, by pH
- Evidence, by temperature

About WholeCellKB

WholeCellKB is a collection of free, open-source model organism databases designed specifically to enable comprehensive, dynamic simulations of entire cells and organisms. WholeCellKB provides comprehensive, quantitative descriptions of individual species including:

- Cellular chemical composition,
- Growth medium composition,
- Gene locations, lengths, and directions,

- Transcription unit organization and transcriptional regulation,
- Macromolecule composition,
- Reaction stoichiometry, kinetics, and catalysis, and
- Extensive links and cross-links to all references used to construct each database.

WholeCellKB currently contains a single database of *Mycoplasma genitalium*, an extremely small gram-positive bacterium and common human pathogen. This database is the most comprehensive description of any single organism to date, and was used to develop the first whole-cell computational model. The *M. genitalium* database was curated from over 900 primary research articles, reviews, books, and databases over four years by a team of three researchers at Stanford University.

Getting started

The best ways to get started are to browse or search this database using the menu or the search box at the top of this page. See the [tutorial](#) for additional help getting started.

More information

Please see the following for more information or to cite WholeCellKB:

Karr JR, Sanghvi JC, Macklin DN, Arora A, Covert MW. WholeCellKB: Model Organism Databases for Comprehensive Whole-Cell Models. *Nucleic Acids Research* **41**, D787-D792 (2013). [Nucleic Acids Research](#) | [PubMed](#)

Karr JR, Sanghvi JC, Macklin DN, Gutschow MV, Jacobs JM, Bolival B, Assad-Garcia N, Glass JI, Covert MW. A Whole-Cell Computational Model Predicts Phenotype from Genotype. *Cell* **150**, 389-401 (2012). [Cell](#) | [PubMed](#)

Need help?

Please view the [tutorial](#), [about page](#), or contact us at wholecell@lists.stanford.edu.