

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

DnaA boxes	2283	<a href="#">Protein decay</a>	40	RNA half-lives	525
Short tandem repeats	19	<a href="#">Protein modification</a>	63	Stimulus values	10
Other	3	<a href="#">Replication Initiation</a>	15	Transcr. reg. 2 activity	
<a href="#">Metabolites</a>	722	<a href="#">RNA decay</a>	25	Transcr. reg. 30 affinity	
Amino acids	29	<a href="#">RNA modification</a>	9	<a href="#">Other</a>	154
Antibiotic	21	<a href="#">RNA processing</a>	20	<a href="#">Processes</a>	28
Gases	4	<a href="#">Transcription</a>	4	<a href="#">States</a>	16
Ions	19	<a href="#">Translation</a>	20		
Lipids	32	<a href="#">tRNA aminoacylation</a>	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](mailto:wholecell@lists.stanford.edu).