Resource Summary Report

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MiST - Microbial Signal Transduction database

RRID:SCR_003166
Type: Tool

Proper Citation

MiST - Microbial Signal Transduction database (RRID:SCR_003166)

Resource Information

URL: http://mistdb.com

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Description: Database which contains the signal transduction proteins for complete and draft bacterial and archaeal genomes. The MiST2 database identifies and catalogs the repertoire of signal transduction proteins in microbial genomes.

Abbreviations: MiST

Synonyms: MiST 2.2, Microbial Signal Transduction Database, Microbial Signal Transduction database (MiST), MiST2

Resource Type: database, data or information resource

Defining Citation: PMID:19900966

Keywords: signal transduction proteins, bacterial genome, archaeal genome, microbial genome, bio.tools

Funding: South Carolina Research Association ;
DOE Office of Science ;
NIH ;
NIGMS GM083177

Resource Name: MiST - Microbial Signal Transduction database

Resource ID: SCR_003166

Alternate IDs: biotools:mist, nif-0000-03140

Alternate URLs: https://bio.tools/mist

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250519T204644+0000

Ratings and Alerts

No rating or validation information has been found for MiST - Microbial Signal Transduction database.

No alerts have been found for MiST - Microbial Signal Transduction database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Xie P, et al. (2024) Multifaceted regulation of siderophore synthesis by multiple regulatory systems in Shewanella oneidensis. Communications biology, 7(1), 498.

Gumerov VM, et al. (2024) MiST 4.0: a new release of the microbial signal transduction database, now with a metagenomic component. Nucleic acids research, 52(D1), D647.

Stuffle EC, et al. (2023) The Aer2 chemoreceptor from Vibrio vulnificus is a tri-PAS-heme oxygen sensor. Molecular microbiology, 119(1), 59.

Ma P, et al. (2021) Membrane Sensor Histidine Kinases: Insights from Structural, Ligand and Inhibitor Studies of Full-Length Proteins and Signalling Domains for Antibiotic Discovery. Molecules (Basel, Switzerland), 26(16).

Ishii E, et al. (2021) Diversity in Sensing and Signaling of Bacterial Sensor Histidine Kinases. Biomolecules, 11(10).

Liu X, et al. (2021) The Hypoxia-Associated Localization of Chemotaxis Protein CheZ in Azorhizorbium caulinodans. Frontiers in microbiology, 12, 731419.

Gavira JA, et al. (2020) How Bacterial Chemoreceptors Evolve Novel Ligand Specificities. mBio, 11(1).

Gumerov VM, et al. (2020) MiST 3.0: an updated microbial signal transduction database with an emphasis on chemosensory systems. Nucleic acids research, 48(D1), D459.

Liu X, et al. (2020) Protein Residues and a Novel Motif Involved in the Cellular Localization of CheZ in Azorhizobium caulinodans ORS571. Frontiers in microbiology, 11, 585140.

Rapun-Araiz B, et al. (2020) The impact of two-component sensorial network in staphylococcal speciation. Current opinion in microbiology, 55, 40.

Coutte L, et al. (2020) Combined RNAseq and ChIPseq Analyses of the BvgA Virulence Regulator of Bordetella pertussis. mSystems, 5(3).

Tran NT, et al. (2019) Defining the regulon of genes controlled by ?E , a key regulator of the cell envelope stress response in Streptomyces coelicolor. Molecular microbiology, 112(2), 461.

Wu Y, et al. (2018) The Core- and Pan-Genomic Analyses of the Genus Comamonas: From Environmental Adaptation to Potential Virulence. Frontiers in microbiology, 9, 3096.

Villanueva M, et al. (2018) Sensory deprivation in Staphylococcus aureus. Nature communications, 9(1), 523.

Liu P, et al. (2018) Concerted Metabolic Shifts Give New Insights Into the Syntrophic Mechanism Between Propionate-Fermenting Pelotomaculum thermopropionicum and Hydrogenotrophic Methanocella conradii. Frontiers in microbiology, 9, 1551.

Ortiz de Ora L, et al. (2018) Regulation of biomass degradation by alternative ? factors in cellulolytic clostridia. Scientific reports, 8(1), 11036.

Mattos-Graner RO, et al. (2017) Two-component signal transduction systems in oral bacteria. Journal of oral microbiology, 9(1), 1400858.

Lin M, et al. (2017) Analysis of complete genome sequence and major surface antigens of Neorickettsia helminthoeca, causative agent of salmon poisoning disease. Microbial biotechnology, 10(4), 933.

Gorshkov V, et al. (2017) Global Gene Expression Analysis of Cross-Protected Phenotype of Pectobacterium atrosepticum. PloS one, 12(1), e0169536.

Tang S, et al. (2016) Sister Dehalobacter Genomes Reveal Specialization in Organohalide Respiration and Recent Strain Differentiation Likely Driven by Chlorinated Substrates. Frontiers in microbiology, 7, 100.