Resource Summary Report

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SubtiList

RRID:SCR_007950
Type: Tool

Proper Citation

SubtiList (RRID:SCR_007950)

Resource Information

URL: http://genolist.pasteur.fr/SubtiList/

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Description: Subtilist is a database dedicated to the analysis of the genome of Bacillus subtilis. It provides a complete dataset of DNA and protein sequences derived from the paradigm strain B. subtilis 168, linked to the relevant annotations and functional assignments. It also allows one to easily browse through these data and retrieve information, using various criteria (gene names, location, keywords, etc.). The purpose of the website is to collate and integrate various aspects of the genomic information from B. subtilis, the paradigm of sporulating Gram-positive bacteria. The data contained in SubtiList originated mainly from the worldwide collaborative B. subtilis genome sequencing project, supplemented with information from the B. subtilis entries present in the EMBL/GenBank/DDBJ databanks, as well as observations either published in international journals or communicated directly to us by individual researchers.

Abbreviations: SubtiList, SUBTILISTG

Synonyms: SUBTILISTG

Resource Type: data or information resource, data analysis service, service resource, database, analysis service resource, production service resource

Defining Citation: PMID:11752255, PMID:7704253

Keywords: bacillus subtilis, bacillus subtilis genome, b. subtilis, b. subtilis genome, b. subtilis protein, gram-positive bacteria, sporulating bacteria

Funding: European Union Biotechnology program contract BIO2-CT93-0272; European Union Biotechnology program contract BIO2-CT94-2011;

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Resource Name: SubtiList

Resource ID: SCR_007950

Alternate IDs: nif-0000-03506

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250521T061213+0000

Ratings and Alerts

No rating or validation information has been found for SubtiList.

No alerts have been found for SubtiList.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Tork SE, et al. (2020) A new uricase from Bacillus cereus SKIII: Characterization, gene identification and genetic improvement. International journal of biological macromolecules, 165(Pt B), 3135.

Othoum G, et al. (2019) Comparative genomics study reveals Red Sea Bacillus with characteristics associated with potential microbial cell factories (MCFs). Scientific reports, 9(1), 19254.

Sassine J, et al. (2017) Functional redundancy of division specific penicillin-binding proteins in Bacillus subtilis. Molecular microbiology, 106(2), 304.

Abolbaghaei A, et al. (2017) How Changes in Anti-SD Sequences Would Affect SD Sequences in Escherichia coli and Bacillus subtilis. G3 (Bethesda, Md.), 7(5), 1607.

Habib C, et al. (2017) Characterization of the regulation of a plant polysaccharide utilization operon and its role in biofilm formation in Bacillus subtilis. PloS one, 12(6), e0179761.

Ling HL, et al. (2017) Data for proteome analysis of Bacillus lehensis G1 in starch-containing medium. Data in brief, 14, 35.

Zalucki YM, et al. (2017) Signal peptidase I processed secretory signal sequences: Selection for and against specific amino acids at the second position of mature protein. Biochemical and biophysical research communications, 483(3), 972.

Mamou G, et al. (2017) Deficiency in Lipoteichoic Acid Synthesis Causes a Failure in Executing the Colony Developmental Program in Bacillus subtilis. Frontiers in microbiology, 8, 1991.

Gómez-Lunar Z, et al. (2016) Microevolution Analysis of Bacillus coahuilensis Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. Frontiers in microbiology, 7, 58.

Tork SE, et al. (2015) Purification and characterization of gamma poly glutamic acid from newly Bacillus licheniformis NRC20. International journal of biological macromolecules, 74, 382.

Schneider J, et al. (2015) Spatio-temporal remodeling of functional membrane microdomains organizes the signaling networks of a bacterium. PLoS genetics, 11(4), e1005140.

Gunka K, et al. (2013) Selection-driven accumulation of suppressor mutants in bacillus subtilis: the apparent high mutation frequency of the cryptic gudB gene and the rapid clonal expansion of gudB(+) suppressors are due to growth under selection. PloS one, 8(6), e66120.

Zafra O, et al. (2012) Extracellular DNA release by undomesticated Bacillus subtilis is regulated by early competence. PloS one, 7(11), e48716.

Tagami K, et al. (2012) Expression of a small (p)ppGpp synthetase, YwaC, in the (p)ppGpp(0) mutant of Bacillus subtilis triggers YvyD-dependent dimerization of ribosome. MicrobiologyOpen, 1(2), 115.

Yousefi-Nejad M, et al. (2011) Proteomics of early and late cold shock stress on thermophilic bacterium, Thermus sp. GH5. Journal of proteomics, 74(10), 2100.

Galián C, et al. (2011) Optimized purification of a heterodimeric ABC transporter in a highly stable form amenable to 2-D crystallization. PloS one, 6(5), e19677.

Ondrusch N, et al. (2011) Blue and red light modulates SigB-dependent gene transcription, swimming motility and invasiveness in Listeria monocytogenes. PloS one, 6(1), e16151.

Yu WB, et al. (2011) Comparative transcriptome analysis of Bacillus subtilis responding to dissolved oxygen in adenosine fermentation. PloS one, 6(5), e20092.

Helianti I, et al. (2010) Constitutive high level expression of an endoxylanase gene from the newly isolated Bacillus subtilis AQ1 in Escherichia coli. Journal of biomedicine &

biotechnology, 2010.

Huang Y, et al. (2009) Selection for minimization of translational frameshifting errors as a factor in the evolution of codon usage. Nucleic acids research, 37(20), 6799.