

Resource Summary Report

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Sybil

RRID:SCR_005593

Type: Tool

Proper Citation

Sybil (RRID:SCR_005593)

Resource Information

URL: <http://sybil.sourceforge.net/>

Proper Citation: Sybil (RRID:SCR_005593)

Description: A web-based software package for comparative genomics.

Abbreviations: Sybil

Synonyms: Sybil: Web-based software for comparative genomics

Resource Type: data or information resource, database, software resource

Defining Citation: [PMID:22121156](#)

Keywords: comparative genomics, genome, synteny, protein cluster, protein, gene, genomic region, synteny gradient, bio.tools

Resource Name: Sybil

Resource ID: SCR_005593

Alternate IDs: OMICS_00945, biotools:sybil

Alternate URLs: <https://bio.tools/sybil>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260811T043235+0000

Ratings and Alerts

No rating or validation information has been found for Sybil.

No alerts have been found for Sybil.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Chinnasamy P, et al. (2025) Blockchain based electronic educational document management with role-based access control using machine learning model. Scientific reports, 15(1), 18828.

Kruse CPS, et al. (2025) A multi-omic characterization of the physiological responses to salt stress in *Scenedesmus obliquus* UTEX393. Communications biology, 8(1), 1632.

Baccega D, et al. (2024) Enhancing COVID-19 forecasting precision through the integration of compartmental models, machine learning and variants. Scientific reports, 14(1), 19220.

Rai HM, et al. (2024) Enhancing data security and privacy in energy applications: Integrating IoT and blockchain technologies. Heliyon, 10(19), e38917.

Dell'Olio A, et al. (2024) Tailored impact of dietary fibers on gut microbiota: a multi-omics comparison on the lean and obese microbial communities. Microbiome, 12(1), 250.

Burtneck MN, et al. (2024) Identification of *Burkholderia cepacia* strains that express a *Burkholderia pseudomallei*-like capsular polysaccharide. Microbiology spectrum, 12(3), e0332123.

Simon J, et al. (2023) Role of sex in lung cancer risk prediction based on single low-dose chest computed tomography. Scientific reports, 13(1), 18611.

Scott WT, et al. (2023) A structured evaluation of genome-scale constraint-based modeling tools for microbial consortia. PLoS computational biology, 19(8), e1011363.

Villada JC, et al. (2022) Integrative Genome-Scale Metabolic Modeling Reveals Versatile Metabolic Strategies for Methane Utilization in *Methylobacterium album* BG8. mSystems, 7(2), e0007322.

Henneke L, et al. (2022) A dietary carbohydrate - gut *Parasutterella* - human fatty acid biosynthesis metabolic axis in obesity and type 2 diabetes. Gut microbes, 14(1), 2057778.

Arshad A, et al. (2021) A survey of Sybil attack countermeasures in IoT-based wireless sensor networks. PeerJ. Computer science, 7, e673.

Malik IT, et al. (2020) Functional Characterisation of ClpP Mutations Conferring Resistance to Acyldepsipeptide Antibiotics in Firmicutes. Chembiochem : a European journal of chemical biology, 21(14), 1997.

Tretina K, et al. (2020) Theileria parasites subvert E2F signaling to stimulate leukocyte proliferation. Scientific reports, 10(1), 3982.

Kraševac N, et al. (2020) Unconventional Secretion of Nigerolysins A from Aspergillus Species. Microorganisms, 8(12).

Peiro C, et al. (2019) Chemical and Metabolic Controls on Dihydroxyacetone Metabolism Lead to Suboptimal Growth of Escherichia coli. Applied and environmental microbiology, 85(15).

Valverde JR, et al. (2018) Modelling the metabolism of protein secretion through the Tat route in Streptomyces lividans. BMC microbiology, 18(1), 59.

Amara A, et al. (2018) Development and validation of an updated computational model of Streptomyces coelicolor primary and secondary metabolism. BMC genomics, 19(1), 519.

Launay H, et al. (2018) Cryptic Disorder Out of Disorder: Encounter between Conditionally Disordered CP12 and Glyceraldehyde-3-Phosphate Dehydrogenase. Journal of molecular biology, 430(8), 1218.

Reichenbach T, et al. (2018) Structural and biochemical characterization of the Cutibacterium acnes exo- α -1,4-mannosidase that targets the N-glycan core of host glycoproteins. PloS one, 13(9), e0204703.

Botero K, et al. (2018) A genome-scale metabolic model of potato late blight suggests a photosynthesis suppression mechanism. BMC genomics, 19(Suppl 8), 863.