

Resource Summary Report

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BLAST Assembled RefSeq Genomes

RRID:SCR_008420

Type: Tool

Proper Citation

BLAST Assembled RefSeq Genomes (RRID:SCR_008420)

Resource Information

URL: <http://130.14.29.110/BLAST/>

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Description: This portal takes you to the NCBI's BLAST Assembled RefSeq Genomes. The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families. Sponsors: This resource is supported by the National Institutes of Health. Keywords: BLAST, Genome, Search engine, Sequence, Biological, Local, Alignment, Nucleotide, Protein, Program, Database, Stastical, Functional, Evolutionaary, Gene,

Synonyms: BLAST

Resource Type: data or information resource, portal, topical portal

Resource Name: BLAST Assembled RefSeq Genomes

Resource ID: SCR_008420

Alternate IDs: nif-0000-30153

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260903T235000+0000

Ratings and Alerts

No rating or validation information has been found for BLAST Assembled RefSeq Genomes.

No alerts have been found for BLAST Assembled RefSeq Genomes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1139 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Maharramov E, et al. (2025) Exploring the principles behind antibiotics with limited resistance. *Nature communications*, 16(1), 1842.

Li X, et al. (2025) Uncovering de novo polyamine biosynthesis in the gut microbiome and its alteration in inflammatory bowel disease. *Gut microbes*, 17(1), 2464225.

Fujiwara K, et al. (2025) A Near Complete Genome Assembly of the Oshima Cherry *Cerasus speciosa*. *Scientific data*, 12(1), 162.

Daruka L, et al. (2025) ESKAPE pathogens rapidly develop resistance against antibiotics in development in vitro. *Nature microbiology*, 10(2), 313.

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant *Staphylococcus aureus* clone during its transmission in a regional community outbreak in Japan. *Microbial genomics*, 10(7).

Gschwind R, et al. (2024) Inter-phylum circulation of a beta-lactamase-encoding gene: a rare but observable event. *Antimicrobial agents and chemotherapy*, 68(4), e0145923.

Lao HY, et al. (2022) The Clinical Utility of Two High-Throughput 16S rRNA Gene Sequencing Workflows for Taxonomic Assignment of Unidentifiable Bacterial Pathogens in Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry. *Journal of clinical microbiology*, 60(1), e0176921.

Etchegaray E, et al. (2022) The neurodevelopmental gene MSANTD2 belongs to a gene family formed by recurrent molecular domestication of Harbinger transposons at the base of vertebrates. *Molecular biology and evolution*, 39(8).

Knight DR, et al. (2021) Major genetic discontinuity and novel toxigenic species in *Clostridioides difficile* taxonomy. *eLife*, 10.

Blake RC, et al. (2021) Homogeneous Cytochrome 579 Is an Octamer That Reacts Too Slowly With Soluble Iron to Be the Initial Iron Oxidase in the Respiratory Chain of *Leptospirillum ferriphilum*. *Frontiers in microbiology*, 12, 673066.

Pradier L, et al. (2021) PlasForest: a homology-based random forest classifier for plasmid detection in genomic datasets. *BMC bioinformatics*, 22(1), 349.

Bellieny-Rabelo D, et al. (2021) Novel Two-Component System-Like Elements Reveal Functional Domains Associated with Restriction-Modification Systems and paraMORC ATPases in Bacteria. *Genome biology and evolution*, 13(3).

Bonifacio MA, et al. (2020) Insights into Arbutin Effects on Bone Cells: Towards the Development of Antioxidant Titanium Implants. *Antioxidants* (Basel, Switzerland), 9(7).

Russell SL, et al. (2020) Horizontal transmission and recombination maintain forever young bacterial symbiont genomes. *PLoS genetics*, 16(8), e1008935.

Liu C, et al. (2020) TTTCA Repeat Expansion of SAMD12 in a New Benign Adult Familial Myoclonic Epilepsy Pedigree. *Frontiers in neurology*, 11, 68.

Scannapieco AC, et al. (2020) Transcriptome analysis of *Anastrepha fraterculus* sp. 1 males, females, and embryos: insights into development, courtship, and reproduction. *BMC genetics*, 21(Suppl 2), 136.

Retchless AC, et al. (2018) Expansion of a urethritis-associated *Neisseria meningitidis* clade in the United States with concurrent acquisition of *N. gonorrhoeae* alleles. *BMC genomics*, 19(1), 176.

Zhu L, et al. (2015) Chronic methamphetamine regulates the expression of MicroRNAs and putative target genes in the nucleus accumbens of mice. *Journal of neuroscience research*, 93(10), 1600.

Kafkas ??, et al. (2015) Database citation in supplementary data linked to Europe PubMed Central full text biomedical articles. *Journal of biomedical semantics*, 6, 1.

Stacey SN, et al. (2015) New basal cell carcinoma susceptibility loci. *Nature communications*, 6, 6825.