Resource Summary Report

Generated by RRID on Apr 8, 2025

BLASTatlas - Mapping of whole genome homology

RRID:SCR_005891
Type: Tool

Proper Citation

BLASTatlas - Mapping of whole genome homology (RRID:SCR_005891)

Resource Information

URL: http://www.cbs.dtu.dk/ws/ws.php?entry=BLASTatlas

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Description: The BLASTatlas is a tool that is useful for mapping and visualizing whole genome homology of genes and proteins within a reference strain compared to other strains or species of one or more prokaryotic organisms using either blastp, blastn, tblastn, or blastx. DNA structural information is also included in the atlas to visualize the DNA chromosomal context of regions. Additional information can be added to these plots. The tool is SOAP compliant and WSDL (web services description language) files are available with programming examples available in Perl. The resolution is per-residue or per nucleotide depending on the regime of the blast search: For each annotation in the reference genome, the best hit in the database genome is found using one of the above algorithms. Each matching or mismatching residue/nucleotide of the best hit (based on BLAST score) is then mapped back to the genome sequence, using the coordinates provided in the annotations. By providing an interoperable method to carry out whole genome visualization of homology, this service offers bioinformaticians as well as biologists an easy-to-adopt workflow that can be directly called from the programming language of the user, hence enabling automation of repeated tasks. This tool can be relevant in many pangenomic as well as in metagenomic studies, by giving a quick overview of clusters of insertion sites, genomic islands and overall homology between a reference sequence and a data set.

Abbreviations: BLASTatlas

Resource Type: data access protocol, software resource, web service

Defining Citation: PMID:18414733

Keywords: genome, homology, dna, proteome, orf, blastp, blastn, tblastn, blastx, residue, nucleotide

Funding:

Resource Name: BLASTatlas - Mapping of whole genome homology

Resource ID: SCR_005891

Alternate IDs: nlx_149461

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250404T060444+0000

Ratings and Alerts

No rating or validation information has been found for BLASTatlas - Mapping of whole genome homology.

No alerts have been found for BLASTatlas - Mapping of whole genome homology.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Lauritano C, et al. (2024) Salinity Stress Acclimation Strategies in Chlamydomonas sp. Revealed by Physiological, Morphological and Transcriptomic Approaches. Marine drugs, 22(8).

Yan H, et al. (2022) Oxidative stress facilitates infection of the unicellular alga Haematococcus pluvialis by the fungus Paraphysoderma sedebokerense. Biotechnology for biofuels and bioproducts, 15(1), 56.

Ventura-López C, et al. (2022) Sex-specific role of the optic gland in octopus maya: A transcriptomic analysis. General and comparative endocrinology, 320, 114000.

Ji X, et al. (2021) Integrated Analysis of the Metabolome and Transcriptome on Anthocyanin Biosynthesis in Four Developmental Stages of Cerasus humilis Peel Coloration. International journal of molecular sciences, 22(21).

Zolfaghari Emameh R, et al. (2021) Application of beta and gamma carbonic anhydrase

sequences as tools for identification of bacterial contamination in the whole genome sequence of inbred Wuzhishan minipig (Sus scrofa) annotated in databases. Database : the journal of biological databases and curation, 2021.

Zhang M, et al. (2019) De novo transcriptome assembly of a facultative parasitic nematode Pelodera (syn. Rhabditis) strongyloides. Gene, 710, 30.

Zhou S, et al. (2019) Full-length transcriptome sequences of Agropyron cristatum facilitate the prediction of putative genes for thousand-grain weight in a wheat-A. cristatum translocation line. BMC genomics, 20(1), 1025.

Nithya N, et al. (2017) Analysis of beta-lactamases, blaNDM-1phylogeny & plasmid replicons in multidrug-resistant Klebsiella spp. from a tertiary care centre in south India. The Indian journal of medical research, 146(Supplement), S38.

Giardina G, et al. (2017) Radiation damage at the active site of human alanine:glyoxylate aminotransferase reveals that the cofactor position is finely tuned during catalysis. Scientific reports, 7(1), 11704.

Sun L, et al. (2015) Cryo-EM structure of the bacteriophage T4 portal protein assembly at near-atomic resolution. Nature communications, 6, 7548.

Qiao C, et al. (2012) Structural basis of LaDR5, a novel agonistic anti-death receptor 5 (DR5) monoclonal antibody, to inhibit DR5/TRAIL complex formation. BMC immunology, 13, 40.

Bouvet P, et al. (1997) RNA recognition by the joint action of two nucleolin RNA-binding domains: genetic analysis and structural modeling. The EMBO journal, 16(17), 5235.