Resource Summary Report

Generated by NIF on May 17, 2025

Belvu

RRID:SCR_015989

Type: Tool

Proper Citation

Belvu (RRID:SCR_015989)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/seqtools

Proper Citation: Belvu (RRID:SCR_015989)

Description: Software for multiple sequence alignment viewing, editing and phylogeny. It includes a set of user-configurable modes to color residues used to create high-quality reference alignments.

Resource Type: software application, alignment software, data processing software, image analysis software, software resource

Defining Citation: PMID:26801397

Keywords: editing, phylogeny, sequence, alignment, phylogenetic, viewer, multiple, editor, color, residue, reference

Funding: Wellcome Trust Grant 098051;

NHGRI U54 HG00455

Availability: Free, Available for download

Resource Name: Belvu

Resource ID: SCR_015989

License: GNU GPL version 3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250517T060233+0000

Ratings and Alerts

No rating or validation information has been found for Belvu.

No alerts have been found for Belvu.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Saredi G, et al. (2024) The histone chaperone SPT2 regulates chromatin structure and function in Metazoa. Nature structural & molecular biology, 31(3), 523.

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. Cell, 187(6), 1440.

Cao W, et al. (2023) A sequence-based evolutionary distance method for Phylogenetic analysis of highly divergent proteins. Scientific reports, 13(1), 20304.

Rios-Szwed DO, et al. (2023) FAM111A regulates replication origin activation and cell fitness. Life science alliance, 6(12).

Ferreira P, et al. (2022) Refining the domain architecture model of the replication origin firing factor Treslin/TICRR. Life science alliance, 5(5).

Pejenaute-Ochoa MD, et al. (2021) Structural, Evolutionary, and Functional Analysis of the Protein O-Mannosyltransferase Family in Pathogenic Fungi. Journal of fungi (Basel, Switzerland), 7(5).

Schwabl P, et al. (2020) Culture-free genome-wide locus sequence typing (GLST) provides new perspectives on Trypanosoma cruzi dispersal and infection complexity. PLoS genetics, 16(12), e1009170.

Persson E, et al. (2019) Domainoid: domain-oriented orthology inference. BMC bioinformatics, 20(1), 523.

Castañeda-García A, et al. (2017) A non-canonical mismatch repair pathway in prokaryotes. Nature communications, 8, 14246.

Sarris PF, et al. (2016) Comparative analysis of plant immune receptor architectures uncovers host proteins likely targeted by pathogens. BMC biology, 14, 8.

Fouts DE, et al. (2016) What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. PLoS neglected tropical diseases, 10(2), e0004403.

Prakash A, et al. (2015) Domain atrophy creates rare cases of functional partial protein domains. Genome biology, 16(1), 88.

Creason AL, et al. (2014) Analysis of genome sequences from plant pathogenic Rhodococcus reveals genetic novelties in virulence loci. PloS one, 9(7), e101996.

Hwang WC, et al. (2013) LUD, a new protein domain associated with lactate utilization. BMC bioinformatics, 14, 341.

Fouts DE, et al. (2012) Integrated next-generation sequencing of 16S rDNA and metaproteomics differentiate the healthy urine microbiome from asymptomatic bacteriuria in neuropathic bladder associated with spinal cord injury. Journal of translational medicine, 10, 174.

Margus T, et al. (2007) Phylogenetic distribution of translational GTPases in bacteria. BMC genomics, 8, 15.

Fouts DE, et al. (2005) Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. PLoS biology, 3(1), e15.

Lassmann T, et al. (2005) Kalign--an accurate and fast multiple sequence alignment algorithm. BMC bioinformatics, 6, 298.