

# Resource Summary Report

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## Belvu

RRID:SCR\_015989

Type: Tool

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### Proper Citation

Belvu (RRID:SCR\_015989)

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### 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:** alignment software, data processing software, image analysis software, software application, software resource

**Defining Citation:** [PMID:26801397](#)

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

**Funding:** NHGRI U54 HG00455;  
Wellcome Trust Grant 098051

**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:** 20260919T195315+0000

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### Ratings and Alerts

No rating or validation information has been found for Belvu.

No alerts have been found for Belvu.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 18 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.

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

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

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.