

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

MaxAlign

RRID:SCR_018552

Type: Tool

Proper Citation

MaxAlign (RRID:SCR_018552)

Resource Information

URL: <http://www.cbs.dtu.dk/services/MaxAlign/>

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Description: Web tool for maximizing usable data in alignment. Maximizes number of characters that are present in gap free columns alignment area by selecting optimal subset of sequences. Removes sequences with many gaps in post process of alignments in order to improve alignment area.

Synonyms: MaxAlign 1.1, MaxAlign 1.1 Server

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

Defining Citation: [PMID:17725821](#)

Keywords: Maximizing data, post process alignment, gap free column alignment area, sequence subset selection, improve alignment area, bio.tools

Funding: Foundation for Science and Technology Portuguese Ministry of Science.

Availability: Free, Available for download, Freely available

Resource Name: MaxAlign

Resource ID: SCR_018552

Alternate IDs: biotools:maxalign

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

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260905T132839+0000

Ratings and Alerts

No rating or validation information has been found for MaxAlign.

No alerts have been found for MaxAlign.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Sonoda GG, et al. (2023) Venomous Noodles: The Evolution of Toxins in Nemertea through Positive Selection and Gene Duplication. *Toxins*, 15(11).

Fisch D, et al. (2023) PIM1 controls GBP1 activity to limit self-damage and to guard against pathogen infection. *Science (New York, N.Y.)*, 382(6666), eadg2253.

Nemudraia A, et al. (2022) Sequence-specific capture and concentration of viral RNA by type III CRISPR system enhances diagnostic. *Nature communications*, 13(1), 7762.

Nemudraia A, et al. (2022) Sequence-specific capture and concentration of viral RNA by type III CRISPR system enhances diagnostic. *Research square*.

Santiago-Frangos A, et al. (2021) Distribution and phasing of sequence motifs that facilitate CRISPR adaptation. *Current biology : CB*, 31(16), 3515.

Czarkwiani A, et al. (2021) FGF signalling plays similar roles in development and regeneration of the skeleton in the brittle star *Amphiura filiformis*. *Development (Cambridge, England)*, 148(10).

Aoyagi Blue Y, et al. (2021) Copy number analyses of DNA repair genes reveal the role of poly(ADP-ribose) polymerase (PARP) in tree longevity. *iScience*, 24(7), 102779.

Nemudryi A, et al. (2020) Temporal detection and phylogenetic assessment of SARS-CoV-2 in municipal wastewater. *medRxiv : the preprint server for health sciences*.

Velez G, et al. (2020) Structural Insights into the Unique Activation Mechanisms of a Non-classical Calpain and Its Disease-Causing Variants. *Cell reports*, 30(3), 881.

Roux J, et al. (2014) Patterns of positive selection in seven ant genomes. *Molecular biology and evolution*, 31(7), 1661.

Gouveia-Oliveira R, et al. (2007) MaxAlign: maximizing usable data in an alignment. *BMC bioinformatics*, 8, 312.