

# Resource Summary Report

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## MaxAlign

RRID:SCR\_018552

Type: Tool

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### Proper Citation

MaxAlign (RRID:SCR\_018552)

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### Resource Information

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

**Proper Citation:** MaxAlign (RRID:SCR\_018552)

**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:** service resource, data access protocol, data analysis service, software resource, web service, production service resource, analysis service resource

**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:** 20260731T043032+0000

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## Ratings and Alerts

No rating or validation information has been found for MaxAlign.

No alerts have been found for MaxAlign.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

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.