

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

GramAlign

RRID:SCR_024032

Type: Tool

Proper Citation

GramAlign (RRID:SCR_024032)

Resource Information

URL: <http://bioinfo.unl.edu/gramalign.php>

Proper Citation: GramAlign (RRID:SCR_024032)

Description: Software tool as time efficient progressive Multiple Sequence Alignment algorithm. Sequence distance estimation step is determined by the natural grammar present in nucleotide and amino acid sequences.

Synonyms: gramalign

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

Keywords: Multiple Sequence Alignment, progressive Multiple Sequence Alignment, sequence distance estimation, nucleotide and amino acid sequences,

Availability: Free, Freely available

Resource Name: GramAlign

Resource ID: SCR_024032

Alternate IDs: OMICS_05314

Old URLs: <https://sources.debian.org/src/gramalign/>

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260810T040844+0000

Ratings and Alerts

No rating or validation information has been found for GramAlign.

No alerts have been found for GramAlign.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Humble JL, et al. (2019) Genome-wide survey of cytochrome P450 genes in the salmon louse *Lepeophtheirus salmonis* (Krøyer, 1837). *Parasites & vectors*, 12(1), 563.

Lundström JO, et al. (2019) Sindbis virus polyarthritis outbreak signalled by virus prevalence in the mosquito vectors. *PLoS neglected tropical diseases*, 13(8), e0007702.

Lopez-Jimena B, et al. (2018) Development of a single-tube one-step RT-LAMP assay to detect the Chikungunya virus genome. *PLoS neglected tropical diseases*, 12(5), e0006448.

Lopez-Jimena B, et al. (2018) Development and validation of four one-step real-time RT-LAMP assays for specific detection of each dengue virus serotype. *PLoS neglected tropical diseases*, 12(5), e0006381.