

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

[learnMSA](#)

RRID:SCR_022572

Type: Tool

Proper Citation

learnMSA (RRID:SCR_022572)

Resource Information

URL: <https://github.com/Gaius-Augustus/learnMSA>

Proper Citation: learnMSA (RRID:SCR_022572)

Description: Software tool as multiple sequence alignment formulated as statistical machine learning problem, where optimal profile hidden Markov model for potentially very large family of protein sequences is searched and alignment is decoded.

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

Keywords: Multiple sequence alignment, protein sequences, statistical machine learning problem, hidden Markov model

Availability: Free, Available for download, Freely available

Resource Name: learnMSA

Resource ID: SCR_022572

License: MIT License

Record Creation Time: 20220721T050151+0000

Record Last Update: 20260813T055254+0000

Ratings and Alerts

No rating or validation information has been found for learnMSA.

No alerts have been found for learnMSA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Becker F, et al. (2024) learnMSA2: deep protein multiple alignments with large language and hidden Markov models. Bioinformatics (Oxford, England), 40(Suppl 2), ii79.

Becker F, et al. (2022) learnMSA: learning and aligning large protein families. GigaScience, 11.