

Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

[sigma-align](#)

RRID:SCR_024337

Type: Tool

Proper Citation

sigma-align (RRID:SCR_024337)

Resource Information

URL: <https://www.imsc.res.in/~rsidd/sigma/>

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Description: Software alignment program with new algorithm and scoring scheme designed specifically for non-coding DNA sequence. This problem is now growing in importance with the increasing number of fully-sequenced species. In particular, studies of gene regulation seek to take advantage of comparative genomics, and recent algorithms (such as PhyloGibbs) for finding regulatory sites in phylogenetically-related intergenic sequence require alignment as a preprocessing step.

Synonyms: Simple greedy multiple alignment

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

Defining Citation: [PMID:16542424](#)

Keywords: alignment program, non-coding DNA sequence,

Availability: Free, Available for download, Freely available,

Resource Name: sigma-align

Resource ID: SCR_024337

Alternate IDs: OMICS_29594

Alternate URLs: <https://sources.debian.org/src/sigma-align/>

License: GNU General Public License, version 2

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260821T194252+0000

Ratings and Alerts

No rating or validation information has been found for sigma-align.

No alerts have been found for sigma-align.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Tang S, et al. (2026) PTEN Loss Promotes PI3K? Phosphorylation and EPHA2/SRC/p-PI3K?Y962 Complex Assembly to Drive Tumorigenesis. Cancer discovery, 16(3), 521.