

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 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/>

**Proper Citation:** sigma-align (RRID:SCR\_024337)

**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:** 20260903T235947+0000

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## Ratings and Alerts

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

No alerts have been found for sigma-align.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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.