

Resource Summary Report

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FSA

RRID:SCR_016114

Type: Tool

Proper Citation

FSA (RRID:SCR_016114)

Resource Information

URL: <http://fsa.sourceforge.net/>

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Description: Software for a statistical multiple sequence alignment algorithm which uses a "distance-based" approach to align homologous protein, RNA or DNA sequences. The GUI, MAD (Multiple Alignment Display), can display the intermediate alignments produced by FSA, where each character is colored according to the probability that it is correctly aligned.

Abbreviations: FSA

Synonyms: Fast Statistical Alignment, FSA: Fast Statistical Alignment

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

Defining Citation: [PMID:19478997](#)

Keywords: multiple, sequence, alignment, algorithm, distance, approach, homologous, protein, DNA, RNA, accurate, fast

Availability: Free, available for download

Resource Name: FSA

Resource ID: SCR_016114

Alternate URLs: <https://sources.debian.org/src/fsa/>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260905T132804+0000

Ratings and Alerts

No rating or validation information has been found for FSA.

No alerts have been found for FSA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Chouleur T, et al. (2024) PTP4A2 Promotes Glioblastoma Progression and Macrophage Polarization under Microenvironmental Pressure. Cancer research communications, 4(7), 1702.

Guo H, et al. (2022) Phosphoregulation of DSB-1 mediates control of meiotic double-strand break activity. eLife, 11.

Wilburn DB, et al. (2019) Indirect sexual selection drives rapid sperm protein evolution in abalone. eLife, 8.