AMAP
RRID:SCR_015969
Type: Tool

Proper Citation
AMAP (RRID:SCR_015969)

Resource Information

URL: http://code.google.com/p/amap-align/

Description: Source code that performs multiple alignment of peptidic sequences. It utilizes posterior decoding and a sequence-annealing alignment, instead of the traditional progressive alignment method.

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

Keywords: software, peptide, sequence, alignment, annealing, bioinformatics, multiple, svn, posterior, decoding

Resource ID: SCR_015969

Parent Organization: University of California; Berkeley; USA

Funding Agency: NHGRI, NSF

References: PMID:17237099

Availability: Free, Available for download

Website Status: Last checked up

Alternate URLs: http://baboon.math.berkeley.edu/amap/
Ratings and Alerts

No rating or validation information has been found for AMAP.

No alerts have been found for AMAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

Listed below are recent publications. The full list is available at scicrunch.


