

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Anfo

RRID:SCR_015973

Type: Tool

Proper Citation

Anfo (RRID:SCR_015973)

Resource Information

URL: <https://bioinf.eva.mpg.de/anfo/>

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Description: Anfo is a mapper in the spirit of Soap/Maq/Bowtie, but its implementation takes more after BLAST/BLAT. It's most useful for the alignment of sequencing reads where the DNA sequence is somehow modified (think ancient DNA or bisulphite treatment) and/or there is more divergence between sample and reference than what fast mappers will handle gracefully (say the reference genome is missing and a related species is used instead).

Synonyms: Anfo Short Read Aligner/Mapper

Resource Type: data analysis software, software application, data processing software, sequence analysis software, software resource

Resource Name: Anfo

Resource ID: SCR_015973

Alternate IDs: OMICS_08846

Old URLs: <https://sources.debian.org/src/apollo/>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260903T235329+0000

Ratings and Alerts

No rating or validation information has been found for Anfo.

No alerts have been found for Anfo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.