

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

OXBench

RRID:SCR_005591

Type: Tool

Proper Citation

OXBench (RRID:SCR_005591)

Resource Information

URL: <http://www.compbio.dundee.ac.uk/downloads/oxbench/>

Proper Citation: OXBench (RRID:SCR_005591)

Description: A suite of programs aimed at developers of alignment methods rather than end-users to assess the accuracy of multiple sequence alignment methods. It includes a reference database of protein multiple sequence alignments that were generated by consideration of protein three-dimensional structure.

Abbreviations: OXBench

Resource Type: software resource

Defining Citation: [PMID:14552658](#)

Keywords: alignment, linux, protein, sequence alignment

Availability: Acknowledgement requested

Resource Name: OXBench

Resource ID: SCR_005591

Alternate IDs: OMICS_00983

Old URLs: <http://www.compbio.dundee.ac.uk/Software/Oxbench/oxbench.html> Alt. URL: <http://www.compbio.dundee.ac.uk/software.html>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132538+0000

Ratings and Alerts

No rating or validation information has been found for OXBench.

No alerts have been found for OXBench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Keul F, et al. (2017) PFASUM: a substitution matrix from Pfam structural alignments. BMC bioinformatics, 18(1), 293.

Wright ES, et al. (2015) DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. BMC bioinformatics, 16, 322.