

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## OXBench

RRID:SCR\_005591

Type: Tool

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### Proper Citation

OXBench (RRID:SCR\_005591)

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### 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:** 20260801T190255+0000

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### Ratings and Alerts

No rating or validation information has been found for OXBench.

No alerts have been found for OXBench.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.