

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](http://FDI.Lab-SciCrunch.org) on Apr 18, 2025

WHAM

RRID:SCR_005497

Type: Tool

Proper Citation

WHAM (RRID:SCR_005497)

Resource Information

URL: <http://research.cs.wisc.edu/wham/>

Proper Citation: WHAM (RRID:SCR_005497)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. High-throughput sequence alignment tool that aligns short DNA sequences (reads) to the whole human genome at a rate of over 1500 million 60bps reads per hour, which is one to two orders of magnitudes faster than the leading state-of-the-art techniques. Feature list for the current version (v 0.1.5) of WHAM: * Supports paired-end reads * Supports up to 5 errors * Supports alignments with gaps * Supports quality scores for filtering invalid alignments, and sorting valid alignments * finds ALL valid alignments * Supports multi-threading * Supports rich reporting modes * Supports SAM format output

Abbreviations: WHAM

Synonyms: Wisconsin's High-throughput Alignment Method

Resource Type: software resource

Keywords: bio.tools

Funding: Facebook ;
NSF IIS-1110948

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: WHAM

Resource ID: SCR_005497

Alternate IDs: OMICS_00697, biotools:wham

Alternate URLs: <https://bio.tools/wham>, <https://sources.debian.org/src/wham-align/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250410T065301+0000

Ratings and Alerts

No rating or validation information has been found for WHAM.

No alerts have been found for WHAM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 341 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Coquille S, et al. (2025) Allosterity and Evolution: A Molecular Journey Through the Structural and Dynamical Landscape of an Enzyme Super Family. *Molecular biology and evolution*, 42(1).

Goutam RK, et al. (2025) Impact of frequent ARID1A mutations on protein stability provides insights into cancer pathogenesis. *Scientific reports*, 15(1), 3072.

Truong DT, et al. (2025) Presence of EGF ligand restricts the binding ability of EgB4 nanobody to EGFR extracellular domain. *Scientific reports*, 15(1), 2420.

Truong DT, et al. (2024) Imidazole[1,5-a]pyridine derivatives as EGFR tyrosine kinase inhibitors unraveled by umbrella sampling and steered molecular dynamics simulations. *Scientific reports*, 14(1), 12218.

Angelo M, et al. (2024) In silico π -dynamics predicts protein binding specificities to modified RNAs. *bioRxiv : the preprint server for biology*.

Shabanpour Y, et al. (2024) Protein-free domains in native and ferroptosis-driven oxidized cell membranes: a molecular dynamics study of biophysical properties and doxorubicin uptake. *Frontiers in molecular biosciences*, 11, 1494257.

Le?niewski M, et al. (2024) Assessment of Two Restraint Potentials for Coarse-Grained

Chemical-Cross-Link-Assisted Modeling of Protein Structures. *Journal of chemical information and modeling*, 64(4), 1377.

Liu T, et al. (2024) Reconciling ASPP-p53 binding mode discrepancies through an ensemble binding framework that bridges crystallography and NMR data. *PLoS computational biology*, 20(2), e1011519.

Prabhakaran A, et al. (2024) Triplet-Triplet Annihilation Upconverting Liposomes: Mechanistic Insights into the Role of Membranes in Two-Dimensional TTA-UC. *ACS applied materials & interfaces*, 16(22), 29324.

Benoit A, et al. (2024) STAT6 mutations enriched at diffuse large B-cell lymphoma relapse reshape the tumor microenvironment. *International journal of hematology*, 119(3), 275.

Gu X, et al. (2024) Empowering AlphaFold2 for protein conformation selective drug discovery with AlphaFold2-RAVE. *eLife*, 13.

Kollár L, et al. (2024) Boronic acid inhibitors of penicillin-binding protein 1b: serine and lysine labelling agents. *Journal of enzyme inhibition and medicinal chemistry*, 39(1), 2305833.

Lyukmanova EN, et al. (2024) Structure and dynamics of the interaction of Delta and Omicron BA.1 SARS-CoV-2 variants with REGN10987 Fab reveal mechanism of antibody action. *Communications biology*, 7(1), 1698.

DeLuca M, et al. (2024) Mechanism of DNA origami folding elucidated by mesoscopic simulations. *Nature communications*, 15(1), 3015.

Heo HY, et al. (2024) A MethylazanediyI Bisacetamide Derivative Sensitizes *Staphylococcus aureus* Persists to a Combination of Gentamicin And Daptomycin. *Advanced science (Weinheim, Baden-Wurtemberg, Germany)*, 11(9), e2306112.

Hornberger MI, et al. (2024) A biodynamic model predicting copper and cadmium bioaccumulation in caddisflies: Linkages between field studies and laboratory exposures. *PloS one*, 19(2), e0297801.

Lichtinger SM, et al. (2024) The mechanism of mammalian proton-coupled peptide transporters. *eLife*, 13.

Dadsena S, et al. (2024) Lipid unsaturation promotes BAX and BAK pore activity during apoptosis. *Nature communications*, 15(1), 4700.

Barron MP, et al. (2024) A γ -dynamics investigation of insulin Wakayama and other A3 variant binding affinities to the insulin receptor. *bioRxiv : the preprint server for biology*.

Babu CS, et al. (2024) Solution Ionic Strength Can Modulate Functional Loop Conformations in *E. coli* Dihydrofolate Reductase. *The journal of physical chemistry. B*, 128(17), 4111.