Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

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 errores * 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: 20260725T190604+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 345 mentions in open access literature.

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

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.

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

Pultar F, et al. (2025) Neural Network Potential with Multiresolution Approach Enables Accurate Prediction of Reaction Free Energies in Solution. Journal of the American Chemical Society, 147(8), 6835.

Kanervisto A, et al. (2025) World and Human Action Models towards gameplay ideation. Nature, 638(8051), 656.

Panda S, et al. (2025) Diffusion-programmed catalysis in nanoporous material. Nature communications, 16(1), 1231.

Co NT, et al. (2025) Implementation of Time-Averaged Restraints with UNRES Coarse-Grained Model of Polypeptide Chains. Journal of chemical theory and computation, 21(3), 1476.

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

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.

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.

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

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.

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.

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.

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.

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.

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.

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 Methylazanediyl Bisacetamide Derivative Sensitizes Staphylococcus aureus Persisters to a Combination of Gentamicin And Daptomycin. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(9), e2306112.