Resource Summary Report

Generated by NIF on May 15, 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 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: 20250420T014253+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 NIF.

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).

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 ?-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 Methylazanediyl Bisacetamide Derivative Sensitizes Staphylococcus aureus Persisters to a Combination of Gentamicin And Daptomycin. Advanced science (Weinheim, Baden-Wurttemberg, 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.

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

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

Barron MP, et al. (2024) A ?-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.