WHAM
RRID:SCR_005497
Type: Tool

Proper Citation

WHAM (RRID:SCR_005497)

Resource Information

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

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Description: A 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

Resource Type: Resource, software resource

Keywords: bio.tools

Parent Organization: University of Wisconsin-Madison; Wisconsin; USA

Funding Agency: Facebook, NSF

Availability: GNU General Public License, v3

Website Status: Last checked up

Abbreviations: WHAM

Resource Name: WHAM

Resource ID: SCR_005497
Alternate IDs: OMICS_00697, biotools:wham
Alternate URLs: https://bio.tools/wham

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 203 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Rashid MH, et al. (2021) Molecular simulation of the Kv7.4[?S269] mutant channel reveals that ion conduction in the cavity is perturbed due to hydrophobic gating. Biochemistry and biophysics reports, 25, 100879.


Black KA, et al. (2020) A constricted opening in Kir channels does not impede potassium


Tong L, et al. (2020) Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. Scientific reports, 10(1), 17925.


