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: 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 Agency: Facebook, NSF

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: WHAM

Resource ID: SCR_005497
Alternate IDs: OMICS_00697, biotools:wham


Record Creation Time: 20220129T080230+0000

Record Last Update: 20240424T182814+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 314 mentions in open access literature.

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


Wei K, et al. (2024) Analyzing (3-Aminopropyl)triethoxysilane-Functionalized Porous Silica


