WHAM
RRID:SCR_005497
Type: Tool

Proper Citation

WHAM (RRID:SCR_005497)

Resource Information

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

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 Name: WHAM

Proper Citation: WHAM (RRID:SCR_005497)

Resource Type: Resource, software resource

Resource ID: SCR_005497

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

Funding Agency: Facebook, NSF

Availability: GNU General Public License, v3

Website Status: Last checked up

Alternate IDs: OMICS_00697

Abbreviations: 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 169 mentions in open access literature.

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


Ogunwa TH, et al. (2019) Insights into the Molecular Mechanisms of Eg5 Inhibition by (+)-Morelloflavone. Pharmaceuticals (Basel, Switzerland), 12(2).


