## WHAM

**RRID:** SCR_005497  
**Type:** Tool

### Proper Citation

WHAM (RRID:SCR_005497)

### Resource Information

**URL:** [http://research.cs.wisc.edu/wham/](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
Mentions Count: 157

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 157 mentions in open access literature.

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


Makuch K, et al. (2019) Asymmetric Spontaneous Intercalation of Lutein into a Phospholipid Bilayer, a Computational Study. Computational and structural biotechnology journal, 17, 516-

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


