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# WHAM

WISCONSIN'S HIGH-THROUGHPUT ALIGNMENT METHOD

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## What is WHAM

WHAM is a high-throughput sequence alignment tool developed at University of Wisconsin-Madison. It 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. Here is a quick 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

Curious about the name WHAM – it stands for Wisconsin's High-throughput Alignment Method.

WHAM is released under the [GPLv3](#) license. You can download the source code with sample data from the [download page](#).

## How does WHAM compare to BWA and Bowtie

- [Here](#) is a report comparing WHAM to BWA.
- The comparison to Bowtie is in the main reference below.

## Reference

If you need to cite WHAM, please use: “*WHAM: A High-throughput Sequence Alignment Method*, Y. Li, A. Terrel and J. M. Patel, *In Proceedings of the ACM SIGMOD International Conference on Management of Data, SIGMOD 2011, Athens, Greece.*” [[pdf](#)]

## Support

WHAM is supported by a [grant IIS-1110948](#) from the [National Science Foundation](#) and a Fellowship from [Facebook](#).

## The WHAM Team

The WHAM team is: [Yinan Li](#), [Allie Terrell](#) and [Jignesh M. Patel](#).

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### WHAM

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**New release**  
A new version (v0.1.5) of WHAM with lots of improvements is available [...]

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