HISAT2 is **a fast and sensitive alignment program for mapping next-generation sequencing reads (both DNA and RNA) to a population of human genomes as well as to a single reference genome**.

*package* hisat2

**Versions**

2.2.1-4,  2.2.1-3,  2.2.1-2,  2.2.1-0,  2.2.0-4,  2.2.0-3,  2.2.0-2,  2.2.0-1,  2.2.0-0,

**Depends**

* [**libgcc-ng**](https://github.com/conda-forge/libgcc-ng-feedstock) >=10.3.0
* [**libstdcxx-ng**](https://github.com/conda-forge/libstdcxx-ng-feedstock) >=10.3.0
* [**perl**](https://github.com/conda-forge/perl-feedstock)
* [**python**](https://github.com/conda-forge/python-feedstock) >3.5

**Required By**

* [**hocort**](https://bioconda.github.io/recipes/hocort/README.html#hocort)
* [**funannotate**](https://bioconda.github.io/recipes/funannotate/README.html#funannotate)
* [**smartmap**](https://bioconda.github.io/recipes/smartmap/README.html#smartmap)
* [**piret**](https://bioconda.github.io/recipes/piret/README.html#piret)
* [**bismark**](https://bioconda.github.io/recipes/bismark/README.html#bismark)

**Installation**

With an activated Bioconda channel, install with:

conda install hisat2

and update with:

conda update hisat2

or use the docker container:

docker pull quay.io/biocontainers/hisat2:<tag>

Notes

Pre-built indices for HISAT2 can be downloaded from https://daehwankimlab.github.io/hisat2/download/.

Download stats

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To install this package with conda run one of the following:  
conda install -c bioconda hisat2  
conda install -c bioconda/label/cf201901 hisat2

*recipe*star

An RNA-seq read aligner.

**Homepage**

<https://github.com/alexdobin/STAR>

**License**

GPLv3

**Recipe**

/[star](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/star)/[meta.yaml](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/star/meta.yaml)

**Links**

biotools: [star](https://bio.tools/star), usegalaxy-eu: [rna\_starsolo](https://usegalaxy.eu/?tool_id=rna_starsolo), usegalaxy-eu: [rna\_star](https://usegalaxy.eu/?tool_id=rna_star)

*package*star

**Versions**

2.7.10a-0,  2.7.9a-0,  2.7.8a-1,  2.7.8a-0,  2.7.7a-0,  2.7.6a-0,  2.7.5c-0,  2.7.5b-0,  2.7.5a-0,

**Required By**

* [**knock-knock**](https://bioconda.github.io/recipes/knock-knock/README.html#knock-knock)
* [**fusion-inspector**](https://bioconda.github.io/recipes/fusion-inspector/README.html#fusion-inspector)
* [**squire**](https://bioconda.github.io/recipes/squire/README.html#squire)
* [**rmats**](https://bioconda.github.io/recipes/rmats/README.html#rmats)
* [**clinker**](https://bioconda.github.io/recipes/clinker/README.html#clinker)
* [**star-fusion**](https://bioconda.github.io/recipes/star-fusion/README.html#star-fusion)
* [**tritimap**](https://bioconda.github.io/recipes/tritimap/README.html#tritimap)
* [**discasm**](https://bioconda.github.io/recipes/discasm/README.html#discasm)
* [**drop**](https://bioconda.github.io/recipes/drop/README.html#drop)
* [**ctat-mutations**](https://bioconda.github.io/recipes/ctat-mutations/README.html#ctat-mutations)
* [**fusion-filter**](https://bioconda.github.io/recipes/fusion-filter/README.html#fusion-filter)
* [**fusioncatcher**](https://bioconda.github.io/recipes/fusioncatcher/README.html#fusioncatcher)
* [**icount**](https://bioconda.github.io/recipes/icount/README.html#icount)
* [**mockinbird**](https://bioconda.github.io/recipes/mockinbird/README.html#mockinbird)
* [**arriba**](https://bioconda.github.io/recipes/arriba/README.html#arriba)
* [**riboraptor**](https://bioconda.github.io/recipes/riboraptor/README.html#riboraptor)
* [**rnaquast**](https://bioconda.github.io/recipes/rnaquast/README.html#rnaquast)
* [**imfusion**](https://bioconda.github.io/recipes/imfusion/README.html#imfusion)

**Installation**

With an activated Bioconda channel (see [2. Set up channels](https://bioconda.github.io/user/install.html#set-up-channels)), install with:

conda install star

and update with:

conda update star

or use the docker container:

docker pull quay.io/biocontainers/star:<tag>

(see [star/tags](https://quay.io/repository/biocontainers/star?tab=tags) for valid values for <tag>)

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To install this package with conda run one of the following:  
conda install -c bioconda star  
conda install -c bioconda/label/cf201901 star

*recipe*tophat

A spliced read mapper for RNA-Seq

**Homepage**

<http://ccb.jhu.edu/software/tophat/index.shtml>

**License**

Boost Software License

**Recipe**

/[tophat](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/tophat)/[meta.yaml](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/tophat/meta.yaml)

**Links**

biotools: [tophat2](https://bio.tools/tophat2), usegalaxy-eu: [tophat2](https://usegalaxy.eu/?tool_id=tophat2)

*package*tophat

**Versions**

2.1.1-3,  2.1.1-2,  2.1.1-1,  2.1.1-0,  2.1.0-0,  2.0.14-0,  2.0.13-6,  2.0.13-5,  2.0.13-4,

**Depends**

* [**bowtie2**](https://bioconda.github.io/recipes/bowtie2/README.html#package-bowtie2) <=2.2.5
* [**python**](https://github.com/conda-forge/python-feedstock) >=2.7,<2.8.0a0

**Required By**

* [**rop**](https://bioconda.github.io/recipes/rop/README.html#rop)
* [**imfusion**](https://bioconda.github.io/recipes/imfusion/README.html#imfusion)

**Installation**

With an activated Bioconda channel (see [2. Set up channels](https://bioconda.github.io/user/install.html#set-up-channels)), install with:

conda install tophat

and update with:

conda update tophat

or use the docker container:

docker pull quay.io/biocontainers/tophat:<tag>

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To install this package with conda run one of the following:  
conda install -c bioconda tophat  
conda install -c bioconda/label/cf201901 tophat

**Bowtie** is a software package commonly used for [sequence alignment](https://en.wikipedia.org/wiki/Sequence_alignment) and [sequence analysis](https://en.wikipedia.org/wiki/Sequence_analysis) in [bioinformatics](https://en.wikipedia.org/wiki/Bioinformatics).[[3]](https://en.wikipedia.org/wiki/Bowtie_(sequence_analysis)#cite_note-bowtie-paper-3) The source code for the package is distributed [freely](https://en.wikipedia.org/wiki/Free_software) and compiled binaries are available for [Linux](https://en.wikipedia.org/wiki/Linux), [macOS](https://en.wikipedia.org/wiki/MacOS) and [Windows](https://en.wikipedia.org/wiki/Windows) platforms. As of 2017, the [*Genome Biology*](https://en.wikipedia.org/wiki/Genome_Biology) paper describing the original Bowtie method has been cited more than 11,000 times.[[3]](https://en.wikipedia.org/wiki/Bowtie_(sequence_analysis)#cite_note-bowtie-paper-3) Bowtie is [open-source software](https://en.wikipedia.org/wiki/Open-source_software) and is currently maintained by [Johns Hopkins University](https://en.wikipedia.org/wiki/Johns_Hopkins_University).

*recipe*bowtie

An ultrafast memory-efficient short read aligner

**Homepage**

<https://github.com/BenLangmead/bowtie>

**License**

Artistic-2.0-only

**Recipe**

/[bowtie](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/bowtie)/[meta.yaml](https://github.com/bioconda/bioconda-recipes/tree/master/recipes/bowtie/meta.yaml)

**Links**

biotools: [bowtie](https://bio.tools/bowtie), doi: [10.1186/gb-2009-10-3-r25](https://doi.org/10.1186/gb-2009-10-3-r25)

*package*bowtie

**Versions**

1.3.1-1,  1.3.1-0,  1.3.0-2,  1.3.0-1,  1.3.0-0,  1.2.3-2,  1.2.3-1,  1.2.3-0,  1.2.2-1,

**Depends**

* [**libgcc-ng**](https://github.com/conda-forge/libgcc-ng-feedstock) >=10.3.0
* [**libstdcxx-ng**](https://github.com/conda-forge/libstdcxx-ng-feedstock) >=10.3.0
* [**perl**](https://github.com/conda-forge/perl-feedstock)
* [**python**](https://github.com/conda-forge/python-feedstock) >=3.6,<3.7.0a0
* [**python\_abi**](https://github.com/conda-forge/python_abi-feedstock) 3.6.\* \*\_cp36m
* [**tbb**](https://github.com/conda-forge/tbb-feedstock) >=2020.2,<2021.0.0a0

**Required By**

* [**fusioncatcher**](https://bioconda.github.io/recipes/fusioncatcher/README.html#fusioncatcher)
* [**mirge-build**](https://bioconda.github.io/recipes/mirge-build/README.html#mirge-build)
* [**phyluce**](https://bioconda.github.io/recipes/phyluce/README.html#phyluce)
* [**cap-mirseq**](https://bioconda.github.io/recipes/cap-mirseq/README.html#cap-mirseq)
* [**mirdeep-p2**](https://bioconda.github.io/recipes/mirdeep-p2/README.html#mirdeep-p2)
* [**emirge**](https://bioconda.github.io/recipes/emirge/README.html#emirge)
* [**mockinbird**](https://bioconda.github.io/recipes/mockinbird/README.html#mockinbird)
* [**mirdeep2**](https://bioconda.github.io/recipes/mirdeep2/README.html#mirdeep2)
* [**trnanalysis**](https://bioconda.github.io/recipes/trnanalysis/README.html#trnanalysis)
* [**mirge3**](https://bioconda.github.io/recipes/mirge3/README.html#mirge3)
* [**virema**](https://bioconda.github.io/recipes/virema/README.html#virema)
* [**dunovo**](https://bioconda.github.io/recipes/dunovo/README.html#dunovo)
* [**hmmcopy**](https://bioconda.github.io/recipes/hmmcopy/README.html#hmmcopy)
* [**methylpy**](https://bioconda.github.io/recipes/methylpy/README.html#methylpy)
* [**hicup**](https://bioconda.github.io/recipes/hicup/README.html#hicup)
* [**repenrich**](https://bioconda.github.io/recipes/repenrich/README.html#repenrich)
* [**trinity**](https://bioconda.github.io/recipes/trinity/README.html#trinity)
* [**capc-map**](https://bioconda.github.io/recipes/capc-map/README.html#capc-map)
* [**plastid**](https://bioconda.github.io/recipes/plastid/README.html#plastid)
* [**imfusion**](https://bioconda.github.io/recipes/imfusion/README.html#imfusion)
* [**seq2hla**](https://bioconda.github.io/recipes/seq2hla/README.html#seq2hla)
* [**ngseqbasic**](https://bioconda.github.io/recipes/ngseqbasic/README.html#ngseqbasic)
* [**fastq-screen**](https://bioconda.github.io/recipes/fastq-screen/README.html#fastq-screen)
* [**mir-prefer**](https://bioconda.github.io/recipes/mir-prefer/README.html#mir-prefer)
* [**shortstack**](https://bioconda.github.io/recipes/shortstack/README.html#shortstack)
* [**splicemap**](https://bioconda.github.io/recipes/splicemap/README.html#splicemap)
* [**umap**](https://bioconda.github.io/recipes/umap/README.html#umap)

**Installation**

With an activated Bioconda channel (see [2. Set up channels](https://bioconda.github.io/user/install.html#set-up-channels)), install with:

conda install bowtie

and update with:

conda update bowtie

or use the docker container:

docker pull quay.io/biocontainers/bowtie:<tag>

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https://bioconda.github.io/recipes/hisat2/README.html

https://anaconda.org/bioconda/hisat2

https://bioconda.github.io/recipes/star/README.html

https://anaconda.org/bioconda/star

https://bioconda.github.io/recipes/tophat/README.html

https://anaconda.org/bioconda/tophat

https://bioconda.github.io/recipes/bowtie/README.html