

SNAP Quick Start

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If you received SNAP as a compressed file, first decompress it with `gunzip`. Then use the following commands:

To build an index:

```
snap index hg19.fa index-dir
```

You can also give the `-s` option to set seed size. We recommend seed size 20 for 100 bp reads and 22 for larger reads. Both indices are around 39 GB, but the indexing process itself works best with 64 GB RAM.

To align unpaired reads:

```
snap single index-dir reads.fq -o output.sam
```

To align paired-end reads:

```
snap paired index-dir read1.fq read2.fq -o output.sam
```

The align commands take several parameters that affect accuracy and performance. The default ones work well for 100 bp reads with about 2% sequencing error rate. Generally for longer reads you want to increase `-d` (the maximum number of differences allowed) and decrease `-h` (the number of hits to consider per seed). Please refer to the Running SNAP document for more details. That document also explains how to run SNAP in multithreaded mode and how other parameters affect performance.