



## Picard.SamToBam Documentation

**Description:** Converts a SAM file to a BAM file.  
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### Summary

The SAM (Sequence Alignment/Map) file format is a generic nucleotide alignment format that describes the alignment of query sequences or sequencing reads to a reference sequence or assembly. BAM is the binary version of the SAM format. For more details on the SAM/Bam format, see the specification here:  
<http://samtools.sourceforge.net/SAM-1.3.pdf>.

This module implements the SamFormatConverter function from Picard. For more information about Picard, see <http://picard.sourceforge.net/>.

### Reference

Sequence Alignment/Map (SAM) Format, Version 0.1.2-draft (20090820).  
<http://samtools.sourceforge.net/SAM1.pdf>

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R; 1000 Genome Project Data Processing Subgroup. [The Sequence alignment/map \(SAM\) format and SAMtools](#). *Bioinformatics*. 2009;25:2078-2079. (<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2723002/?tool=pubmed>)

### Parameters

Name	Description
input.file (required)	The SAM file to be converted. For more details on the SAM format, see the specification here: <a href="http://samtools.sourceforge.net/SAM-1.3.pdf">http://samtools.sourceforge.net/SAM-1.3.pdf</a> .
output.prefix (required)	A label used to name the output file.

### Output File

1. <output.prefix>.bam  
The input SAM file converted to BAM format.

# GenePattern

## Platform Dependencies

**Module type:** Data Format Conversion  
**CPU type:** any  
**OS:** any  
**Language:** Java

## GenePattern module version notes

Date	Version	Description
05/07/13	2	Renamed from SamToBam to Picard.SamToBam