

**SAM**

# Problem: store alignments in a standard format

## Solution:

### Sequence Alignment/Map Format Specification

The SAM/BAM Format Specification Working Group

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The master version of this document can be found at <https://github.com/samtools/hts-specs>.  
This printing is version dfc3e48 from that repository, last modified on the date shown above.

## 1 The SAM Format Specification

SAM stands for Sequence Alignment/Map format. It is a TAB-delimited text format consisting of a header section, which is optional, and an alignment section. If present, the header must be prior to the alignments. Header lines start with '@', while alignment lines do not. Each alignment line has 11 mandatory fields for essential alignment information such as mapping position, and variable number of optional fields for flexible or aligner specific information.