

Resource Summary Report

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SAMtools Text Alignment Viewer

RRID:SCR_005611

Type: Tool

Proper Citation

SAMtools Text Alignment Viewer (RRID:SCR_005611)

Resource Information

URL: <http://samtools.sourceforge.net/tview.shtml>

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Description: Text alignment viewer software based on the GNU ncurses library that works with short indels and shows MAQ consensus. It uses different colors to display mapping quality or base quality, subjected to users' choice.

Abbreviations: SAMtools tview

Synonyms: Text Alignment Viewer

Resource Type: software resource

Keywords: text alignment, viewer, maq consensus, indel

Resource Name: SAMtools Text Alignment Viewer

Resource ID: SCR_005611

Alternate IDs: OMICS_00893

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132538+0000

Ratings and Alerts

No rating or validation information has been found for SAMtools Text Alignment Viewer.

No alerts have been found for SAMtools Text Alignment Viewer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Dhanwani R, et al. (2022) Transcriptional analysis of peripheral memory T cells reveals Parkinson's disease-specific gene signatures. NPJ Parkinson's disease, 8(1), 30.