

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## FAST Analysis of Sequences Toolbox

RRID:SCR\_024074

Type: Tool

---

### Proper Citation

FAST Analysis of Sequences Toolbox (RRID:SCR\_024074)

---

### Resource Information

**URL:** <https://metacpan.org/dist/FAST>

**Proper Citation:** FAST Analysis of Sequences Toolbox (RRID:SCR\_024074)

**Description:** Software Fast Analysis of Sequences Toolbox (FAST) is a set of UNIX utilities (for example fasgrep, fascut, fashead and fastr) that extends the UNIX toolbox paradigm to bioinformatic sequence records. FAST workflows are designed for serial processing of flatfile biological sequence record databases per-sequence, rather than per-line, through UNIX pipelines. The default data exchange format is multifasta (specifically, a restriction of BioPerl FastA format). FASTQ format is supported. FAST is designed for learnability, interoperability, interface consistency, rapid prototyping, fine-tuned control, and reproducibility. FAST tools expose the power of Perl and BioPerl to users in an easy-to-learn command-line paradigm.

**Abbreviations:** FAST

**Synonyms:** libfast-perl, Fast Analysis of Sequences Toolbox, FAST - FAST Analysis of Sequences Toolbox, fast

**Resource Type:** software resource, software toolkit

**Keywords:** Analysis of sequences, UNIX utilities, UNIX toolbox paradigm to bioinformatic sequence records, serial processing, flatfile biological sequence record databases per-sequence, FASTQ format, learnability, interoperability, interface consistency, rapid prototyping, fine-tuned control, reproducibility

**Availability:** Free, Available for download, Freely available,

**Resource Name:** FAST Analysis of Sequences Toolbox

**Resource ID:** SCR\_024074

**Old URLs:** <https://sources.debian.org/src/libfast-perl/>

**License:** perl\_5

**Record Creation Time:** 20230824T050211+0000

**Record Last Update:** 20260725T191107+0000

---

## Ratings and Alerts

No rating or validation information has been found for FAST Analysis of Sequences Toolbox.

No alerts have been found for FAST Analysis of Sequences Toolbox.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.