

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

[split_pairs.pl](#)

RRID:SCR_015707

Type: Tool

Proper Citation

split_pairs.pl (RRID:SCR_015707)

Resource Information

URL: https://github.com/eead-csic-compbio/split_pairs

Proper Citation: split_pairs.pl (RRID:SCR_015707)

Description: Software for processing NGS sequence reads in FASTQ and FASTA formats. split_pairs.pl is suited particularly for the task of sorting pair end reads and for modifying their headers with Perl-style regular expressions.

Synonyms: split_pairs

Resource Type: data processing software, software resource, software application

Keywords: ngs sequence read, fasta file, fastq file, pair end sorting, perl-style regular expression

Availability: Free, Available for download, Runs on Linux, Runs on Mac OS

Resource Name: split_pairs.pl

Resource ID: SCR_015707

License: MIT License

License URLs: https://github.com/eead-csic-compbio/split_pairs/blob/master/LICENSE

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260813T055114+0000

Ratings and Alerts

No rating or validation information has been found for split_pairs.pl.

No alerts have been found for split_pairs.pl.

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 [RRID](#) .

Decena M??, et al. (2024) Expansions and contractions of repetitive DNA elements reveal contrasting evolutionary responses to the polyploid genome shock hypothesis in Brachypodium model grasses. Frontiers in plant science, 15, 1419255.