

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

readseq

RRID:SCR_024313

Type: Tool

Proper Citation

readseq (RRID:SCR_024313)

Resource Information

URL: <https://github.com/rdpstaff/ReadSeq>

Proper Citation: readseq (RRID:SCR_024313)

Description: Software package as Java based common sequence file format reader and sequence file manipulation.

Resource Type: software resource, software toolkit

Keywords: Java, common sequence file format reader, sequence file manipulation,

Availability: Free, Available for download, Freely available,

Resource Name: readseq

Resource ID: SCR_024313

Alternate URLs: <https://sources.debian.org/src/rdp-readseq/>

License: GPL-3.0 license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260912T200117+0000

Ratings and Alerts

No rating or validation information has been found for readseq.

No alerts have been found for readseq.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Winter AD, et al. (2015) A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites. BMC genomics, 16(1), 331.

Liu L, et al. (2014) Induced and natural variation of promoter length modulates the photoperiodic response of FLOWERING LOCUS T. Nature communications, 5, 4558.

Cardinale DJ, et al. (2013) Base composition and translational selection are insufficient to explain codon usage bias in plant viruses. Viruses, 5(1), 162.

Campoli C, et al. (2013) HvLUX1 is a candidate gene underlying the early maturity 10 locus in barley: phylogeny, diversity, and interactions with the circadian clock and photoperiodic pathways. The New phytologist, 199(4), 1045.

Creevey CJ, et al. (2011) Identifying single copy orthologs in Metazoa. PLoS computational biology, 7(12), e1002269.

Obermeier C, et al. (2009) Gene expression profiling via LongSAGE in a non-model plant species: a case study in seeds of Brassica napus. BMC genomics, 10, 295.