Resource Summary Report

Generated by T1D on Jul 31, 2026

Blixem

RRID:SCR_015994
Type: Tool

Proper Citation

Blixem (RRID:SCR_015994)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/seqtools

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Description: Software for sequence alignments that displays multiple match sequences aligned against a single genomic reference sequence. It can be used for manipulation, display and annotation of genomic data, to check the quality of an alignment, to find missing/misaligned sequence, and to identify splice sites and polyA sites.

Synonyms: SEQtools Blixem

Resource Type: data processing software, software resource, image analysis software, alignment software, software application

Defining Citation: PMID:26801397

Keywords: software, sequence, alignment, annotation, genomic, reference, data, display, manipulation, DNA

Funding: Wellcome Trust Grant 098051;
NHGRI U54 HG00455

Availability: Free, Available for download

Resource Name: Blixem

Resource ID: SCR_015994

License: GNU GPL version 3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260731T042958+0000

Ratings and Alerts

No rating or validation information has been found for Blixem.

No alerts have been found for Blixem.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Djebali S, et al. (2012) Evidence for transcript networks composed of chimeric RNAs in human cells. PloS one, 7(1), e28213.

Frankish A, et al. (2012) The importance of identifying alternative splicing in vertebrate genome annotation. Database : the journal of biological databases and curation, 2012, bas014.