Resource Summary Report

Generated by NIF on Aug 25, 2026

Blixem

RRID:SCR_015994
Type: Tool

Proper Citation

Blixem (RRID:SCR_015994)

Resource Information

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

Proper Citation: Blixem (RRID:SCR_015994)

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

Defining Citation: PMID:26801397

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

Funding: NHGRI U54 HG00455;
Wellcome Trust Grant 098051

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: 20260821T194032+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 NIF .

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.

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