Segemehl
RRID:SCR_005494
Type: Tool

Proper Citation

Segemehl (RRID:SCR_005494)

Resource Information

URL: http://www.bioinf.uni-leipzig.de/Software/segemehl/

Description: A software to map short sequencer reads to reference genomes. It is able to detect not only mismatches but also insertions and deletions. Furthermore, it is not limited to a specific read length and is able to map primer- or polyadenylation contaminated reads correctly. Segemehl implements a matching strategy based on enhanced suffix arrays (ESA). Segemehl now supports the SAM format, reads gziped queries to save both disk and memory space and allows bisulfite sequencing mapping and split read mapping.

Resource Name: Segemehl
Proper Citation: Segemehl (RRID:SCR_005494)
Resource Type: Resource, software resource
Resource ID: SCR_005494
Parent Organization: University of Leipzig; Saxony; Germany
Related resources: ANNOgesic
References: PMID: 24512684, PMID: 22581174, PMID: 19750212
Availability: Acknowledgement requested, Free, Public
Website Status: Last checked up
Alternate IDs: OMICS_00683
Abbreviations: Segemehl

Mentions Count: 25

Ratings and Alerts

No rating or validation information has been found for Segemehl.

No alerts have been found for Segemehl.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Guo Q, et al. (2019) Arabidopsis TRM5 encodes a nuclear-localised bifunctional tRNA guanine and inosine-N1-methyltransferase that is important for growth. PloS one, 14(11), e0225064.


Liu L, et al. (2018) Overexpression of Promotes Stress Resistance and Biofilm Formation of L-
ZS9 by Regulating the Expression of Multiple Genes. Frontiers in microbiology, 9, 2628.


Ustianenko D, et al. (2016) TUT-DIS3L2 is a mammalian surveillance pathway for aberrant structured non-coding RNAs. The EMBO journal, 35(20), 2179-2191.