Resource Summary Report

Generated by dkNET on Apr 29, 2025

Omicsoft Sequence Aligner

RRID:SCR_005270
Type: Tool

Proper Citation

Omicsoft Sequence Aligner (RRID:SCR_005270)

Resource Information

URL: http://omicsoft.com/osa/

Proper Citation: Omicsoft Sequence Aligner (RRID:SCR_005270)

Description: A fast and accurate alignment tool for RNA-Seq data.

Abbreviations: OSA

Synonyms: OSA: a super-fast and accurate alignment tool for RNA-Seq data

Resource Type: commercial organization, software resource

Keywords: alignment, rna-seq

Funding:

Availability: Free for academic use, Commercial use requires license

Resource Name: Omicsoft Sequence Aligner

Resource ID: SCR_005270

Alternate IDs: OMICS_01262

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250426T055749+0000

Ratings and Alerts

No rating or validation information has been found for Omicsoft Sequence Aligner.

No alerts have been found for Omicsoft Sequence Aligner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Wolenski FS, et al. (2017) Identification of microRNA biomarker candidates in urine and plasma from rats with kidney or liver damage. Journal of applied toxicology : JAT, 37(3), 278.

Koenig EM, et al. (2016) The beagle dog MicroRNA tissue atlas: identifying translatable biomarkers of organ toxicity. BMC genomics, 17, 649.

Dong H, et al. (2015) Genomic and transcriptome profiling identified both human and HBV genetic variations and their interactions in Chinese hepatocellular carcinoma. Genomics data, 6, 1.

Zhao S, et al. (2014) Assessment of the impact of using a reference transcriptome in mapping short RNA-Seq reads. PloS one, 9(7), e101374.