Resource Summary Report

Generated by RRID on Sep 10, 2026

SEQanswers

RRID:SCR_004808
Type: Tool

Proper Citation

SEQanswers (RRID:SCR_004808)

Resource Information

URL: http://seqanswers.com/

Proper Citation: SEQanswers (RRID:SCR_004808)

Description: An information resource and user-driven community focused on all aspects of next-generation genomics. They hope to become the central location for next generation sequencing technology discussion and education. The site will always attempt to cater to everyone, regardless of scientific background or knowledge. The High-Throughput Sequencing Map site was conceived by James Hadfield (Cancer Research UK, Cambridge) and built by Nick Loman (University of Birmingham). The database is as only as good as you, the users.

Abbreviations: SEQanswers

Synonyms: SEQanswers: the next generation sequencing community

Resource Type: community building portal, data or information resource, database, discussion, narrative resource, portal, topical portal

Defining Citation: PMID:22419780

Keywords: genomics, sequencing, high-throughput sequencing, next-generation genomics, next generation sequencing

Resource Name: SEQanswers

Resource ID: SCR_004808

Alternate IDs: OMICS_01710, nlx_143910

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T132524+0000

Ratings and Alerts

No rating or validation information has been found for SEQanswers.

No alerts have been found for SEQanswers.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Islam S, et al. (2021) Ten simple rules for navigating the computational aspect of an interdisciplinary PhD. PLoS computational biology, 17(2), e1008554.

Malandrino D, et al. (2019) Social support for collaboration and group awareness in life science research teams. Source code for biology and medicine, 14, 4.

Grabowski P, et al. (2019) A Primer on Data Analytics in Functional Genomics: How to Move from Data to Insight? Trends in biochemical sciences, 44(1), 21.

Li H, et al. (2018) Expression of microRNAs in the serum exosomes of methamphetamine-dependent rats vs. ketamine-dependent rats. Experimental and therapeutic medicine, 15(4), 3369.

Brown AV, et al. (2018) Ten quick tips for sharing open genomic data. PLoS computational biology, 14(12), e1006472.

Lotterhos KE, et al. (2018) Analysis validation has been neglected in the Age of Reproducibility. PLoS biology, 16(12), e3000070.

Liu W, et al. (2018) RGAAT: A Reference-based Genome Assembly and Annotation Tool for New Genomes and Upgrade of Known Genomes. Genomics, proteomics & bioinformatics, 16(5), 373.

Chakraborty C, et al. (2017) Rising Strengths Hong Kong SAR in Bioinformatics. Interdisciplinary sciences, computational life sciences, 9(2), 224.

Yu M, et al. (2017) Ten simple rules to make the most out of your undergraduate research career. PLoS computational biology, 13(5), e1005484.

Namjoshi SV, et al. (2017) Screening the Molecular Framework Underlying Local Dendritic mRNA Translation. Frontiers in molecular neuroscience, 10, 45.

Gnimpieba EZ, et al. (2017) Bio-TDS: bioscience query tool discovery system. Nucleic acids research, 45(D1), D1117.

Ison J, et al. (2016) Tools and data services registry: a community effort to document bioinformatics resources. Nucleic acids research, 44(D1), D38.

da Fonseca RR, et al. (2016) Next-generation biology: Sequencing and data analysis approaches for non-model organisms. Marine genomics, 30, 3.

Kotze AC, et al. (2014) Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. International journal for parasitology. Drugs and drug resistance, 4(3), 164.

Sen SK, et al. (2014) Identification of candidate genes involved in coronary artery calcification by transcriptome sequencing of cell lines. BMC genomics, 15, 198.

Ekblom R, et al. (2014) A field guide to whole-genome sequencing, assembly and annotation. Evolutionary applications, 7(9), 1026.

Lindahl BD, et al. (2013) Fungal community analysis by high-throughput sequencing of amplified markers--a user's guide. The New phytologist, 199(1), 288.

Li JW, et al. (2013) The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. Briefings in bioinformatics, 14(5), 548.

Schliesky S, et al. (2012) RNA-Seq Assembly - Are We There Yet? Frontiers in plant science, 3, 220.

Kalari KR, et al. (2012) Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. Frontiers in oncology, 2, 12.