

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[SEQanswers Wiki](#)

RRID:SCR_004810

Type: Tool

Proper Citation

SEQanswers Wiki (RRID:SCR_004810)

Resource Information

URL: <http://seqanswers.com/wiki/>

Proper Citation: SEQanswers Wiki (RRID:SCR_004810)

Description: Wiki forum providing an extensive catalogue of manually categorized analysis tools, technologies and information about service providers, maintained by the members of the SEQanswers community. * Minimum Information about a high-throughput Sequencing Experiment * Software Hub: The place to add to, edit or browse the software database on SEQwiki. * Service Providers: Browse or edit the list of NGS service facilities. * How-to Hub: Mini reviews for the most used tools broken down by common tasks. * Developers Hub: The place to discuss the development of the SEQwiki site and its associated data. See also publishing SEQ*. * Publications: Publication about SEQwiki and selected citations.

Abbreviations: SEQwiki

Resource Type: data or information resource, narrative resource, software repository, software resource, wiki

Defining Citation: [PMID:22086956](#)

Keywords: sequencing, high-throughput sequencing, service provider, next generation sequencing, next-generation genomics, genomics, data set, wiki, software

Availability: The community can contribute to this resource

Resource Name: SEQanswers Wiki

Resource ID: SCR_004810

Alternate IDs: OMICS_01743, nlx_143911

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T132524+0000

Ratings and Alerts

No rating or validation information has been found for SEQanswers Wiki.

No alerts have been found for SEQanswers Wiki.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Abugessaisa I, et al. (2016) FANTOM5 transcriptome catalog of cellular states based on Semantic MediaWiki. Database : the journal of biological databases and curation, 2016.