Resource Summary Report

Generated by NIF on Sep 14, 2026

SeqWare

RRID:SCR_005289
Type: Tool

Proper Citation

SeqWare (RRID:SCR_005289)

Resource Information

URL: http://seqware.github.io/

Proper Citation: SeqWare (RRID:SCR_005289)

Description: A portable software infrastructure designed to analyze massive genomics datasets produced by contemporary and emerging technologies, in particular Next Generation Sequencing (NGS) platforms. It consists of a comprehensive suite of infrastructure tools focused on enabling the end-to-end analysis of sequence data ? from from raw base calling to analyzed variants ready for interpretation by users. SeqWare is tool agnostic, it is a framework for building analysis workflows and does not provide specific implementations out-of-the-box. You use SeqWare to create high-throughput infrastructure for NGS analysis using whatever analysis tools you like. SeqWare currently provides 5 main tools specifically designed to support massively parallel sequencing technologies. All tools can be used together or separately: * MetaDB: provides a common database to store metadata used by all components. * Portal: a LIMS-like web application to manage samples, record computational events, and present results back to end users. * Pipeline: a workflow engine that is capable of wrapping and combining other tools (BFAST, BWA, SAMtools, etc) into complex pipelines, recording metadata about the analysis, and facilitates automation of pipelines based on metadata. * Web Service: a programmatic API that lets people build new tools on top of the project * Query Engine: a NoSQL database designed to store and query variants and other events inferred from sequence data.

Abbreviations: SeqWare

Synonyms: SolexaTools

Resource Type: software resource

Defining Citation: PMID:21210981

Keywords: mapreduce/hadoop, next generation sequencing, genomics

Availability: Acknowledgement requested, GNU General Public License, v3

Resource Name: SeqWare

Resource ID: SCR_005289

Alternate IDs: OMICS_01221

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260912T195624+0000

Ratings and Alerts

No rating or validation information has been found for SeqWare.

No alerts have been found for SeqWare.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

McDonnell B, et al. (2025) Lactococcal mobile genetic elements harbour a diverse phage defensome rich in restriction-modification systems. Nucleic acids research, 53(17).

El-Helbawy NF, et al. (2022) Identification of Age-Associated Transcriptomic Changes Linked to Immunotherapy Response in Primary Melanoma. Current issues in molecular biology, 44(9), 4118.

Murray IA, et al. (2021) Structural and functional diversity among Type III restriction-modification systems that confer host DNA protection via methylation of the N4 atom of cytosine. PloS one, 16(7), e0253267.

Ash JT, et al. (2021) Joint analysis of expression levels and histological images identifies genes associated with tissue morphology. Nature communications, 12(1), 1609.

Liu NQ, et al. (2021) WAPL maintains a cohesin loading cycle to preserve cell-type-specific distal gene regulation. Nature genetics, 53(1), 100.

Hoffmann F, et al. (2020) Prognostic and predictive value of PD-L2 DNA methylation and mRNA expression in melanoma. Clinical epigenetics, 12(1), 94.

Fröhlich A, et al. (2020) Comprehensive analysis of tumor necrosis factor receptor TNFRSF9 (4-1BB) DNA methylation with regard to molecular and clinicopathological features, immune infiltrates, and response prediction to immunotherapy in melanoma.

EBioMedicine, 52, 102647.

Fröhlich A, et al. (2020) Molecular, clinicopathological, and immune correlates of LAG3 promoter DNA methylation in melanoma. EBioMedicine, 59, 102962.

Holderried TAW, et al. (2019) Molecular and immune correlates of TIM-3 (HAVCR2) and galectin 9 (LGALS9) mRNA expression and DNA methylation in melanoma. Clinical epigenetics, 11(1), 161.

Röver LK, et al. (2018) PD-1 (PDCD1) Promoter Methylation Is a Prognostic Factor in Patients With Diffuse Lower-Grade Gliomas Harboring Isocitrate Dehydrogenase (IDH) Mutations. EBioMedicine, 28, 97.

Deptula P, et al. (2017) De novo assembly of genomes from long sequence reads reveals uncharted territories of Propionibacterium freudenreichii. BMC genomics, 18(1), 790.

Blow MJ, et al. (2016) The Epigenomic Landscape of Prokaryotes. PLoS genetics, 12(2), e1005854.

Liu Y, et al. (2015) Correlating bladder cancer risk genes with their targeting microRNAs using MMiRNA-Tar. Genomics, proteomics & bioinformatics, 13(3), 177.