

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

MINSEQE

RRID:SCR_003221

Type: Tool

Proper Citation

MINSEQE (RRID:SCR_003221)

Resource Information

URL: <http://www.fged.org/projects/minseqe/>

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Description: The Minimum Information about a high-throughput nucleotide SEQuencing Experiment that is needed to enable the unambiguous interpretation and facilitate reproduction of the results of the experiment. By analogy to the MIAME guidelines for microarray experiments, adherence to the MINSEQE guidelines will improve integration of multiple experiments across different modalities, thereby maximising the value of high-throughput research. The five elements of experimental description considered essential when making data available supporting published high-throughput sequencing experiments are as follows: # The description of the biological system, samples, and the experimental variables being studied # The sequence read data for each assay # The "final" processed (or summary) data for the set of assays in the study # General information about the experiment and sample-data relationships # Essential experimental and data processing protocols

Abbreviations: MINSEQE

Synonyms: Minimum Information about a high-throughput SEQuencing Experiment

Resource Type: data or information resource, narrative resource, standard specification

Keywords: high-throughput sequencing

Resource Name: MINSEQE

Resource ID: SCR_003221

Alternate IDs: nlx_157258

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132459+0000

Ratings and Alerts

No rating or validation information has been found for MINSEQE.

No alerts have been found for MINSEQE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Osada N, et al. (2023) c-FOS is an integral component of the IKZF1 transactivator complex and mediates lenalidomide resistance in multiple myeloma. Clinical and translational medicine, 13(8), e1364.

Batista D, et al. (2022) Machine actionable metadata models. Scientific data, 9(1), 592.

Zhu H, et al. (2021) MicroRNA biomarkers of type 2 diabetes: A protocol for corroborating evidence by computational genomics and meta-analyses. PloS one, 16(4), e0247556.

Ricard-Blum S, et al. (2020) Omic approaches to decipher the molecular mechanisms of fibrosis, and design new anti-fibrotic strategies. Seminars in cell & developmental biology, 101, 161.

Yuen SC, et al. (2020) A Systematic Bioinformatics Workflow With Meta-Analytics Identified Potential Pathogenic Factors of Alzheimer's Disease. Frontiers in neuroscience, 14, 209.

Kodama Y, et al. (2019) DDBJ update: the Genomic Expression Archive (GEA) for functional genomics data. Nucleic acids research, 47(D1), D69.

Adam-Blondon AF, et al. (2016) Towards an open grapevine information system. Horticulture research, 3, 16056.

Hong EL, et al. (2016) Principles of metadata organization at the ENCODE data coordination center. Database : the journal of biological databases and curation, 2016.

Bagewadi S, et al. (2015) NeuroTransDB: highly curated and structured transcriptomic metadata for neurodegenerative diseases. Database : the journal of biological databases and curation, 2015.

Kolesnikov N, et al. (2015) ArrayExpress update--simplifying data submissions. Nucleic acids research, 43(Database issue), D1113.

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.