

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[sei](#)

RRID:SCR_022571

Type: Tool

Proper Citation

sei (RRID:SCR_022571)

Resource Information

URL: <https://github.com/FunctionLab/sei-framework>

Proper Citation: sei (RRID:SCR_022571)

Description: Web server for systematically predicting sequence regulatory activities and applying sequence information to human genetics data. Provides global map from any sequence to regulatory activities, as represented by sequence classes, and each sequence class integrates predictions for chromatin profiles like transcription factor, histone marks, and chromatin accessibility profiles across wide range of cell types.

Resource Type: web service, data access protocol, software resource

Defining Citation: [PMID:35817977](#)

Keywords: systematically predicting sequence regulatory activities, applying sequence information, human genetics data, sequence class predictions

Funding: National Science Foundation Graduate Research Fellowship Program ;
NHGRI R01HG005998;
NHLBI U54HL117798;
NIGMS R01GM071966

Availability: Free, Available for download, Freely available

Resource Name: sei

Resource ID: SCR_022571

Alternate URLs: <https://hb.flatironinstitute.org/sei>

Record Creation Time: 20220720T050146+0000

Record Last Update: 20260804T043802+0000

Ratings and Alerts

No rating or validation information has been found for sei.

No alerts have been found for sei.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Hosseini R, et al. (2025) Ultra-fast variant effect prediction using biophysical transcription factor binding models. Nucleic acids research, 53(18).

Dalla-Torre H, et al. (2025) Nucleotide Transformer: building and evaluating robust foundation models for human genomics. Nature methods, 22(2), 287.

Wang L, et al. (2025) Whole-exome sequencing study of opioid dependence offers novel insights into the contributions of exome variants. Translational psychiatry, 15(1), 380.

Kathail P, et al. (2024) Current genomic deep learning models display decreased performance in cell type specific accessible regions. bioRxiv : the preprint server for biology.

Wang X, et al. (2024) Deep learning approaches for non-coding genetic variant effect prediction: current progress and future prospects. Briefings in bioinformatics, 25(5).

Gao Y, et al. (2023) Hypothyroidism and rheumatoid arthritis: a two-sample Mendelian randomization study. Frontiers in endocrinology, 14, 1179656.