# Resource Summary Report

Generated by kravitz2 on Jul 31, 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:** data access protocol, web service, 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:** 20260731T043112+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 kravitz2 .

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.