

Resource Summary Report

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

F-Seq

RRID:SCR_010880

Type: Tool

Proper Citation

F-Seq (RRID:SCR_010880)

Resource Information

URL: <http://fureylab.web.unc.edu/software/fseq/>

Proper Citation: F-Seq (RRID:SCR_010880)

Description: A software package that generates a continuous tag sequence density estimation allowing identification of biologically meaningful sites whose output can be displayed directly in the UCSC Genome Browser.

Abbreviations: F-Seq

Resource Type: software resource

Resource Name: F-Seq

Resource ID: SCR_010880

Alternate IDs: OMICS_00482

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T132649+0000

Ratings and Alerts

No rating or validation information has been found for F-Seq.

No alerts have been found for F-Seq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Zhang Y, et al. (2026) Architectural and evolutionary features of TE-derived TSSs shape tissue-specific promoter activity in the human genome. *Nature communications*, 17(1).

Sakai S, et al. (2025) In vivo transition in chromatin accessibility during differentiation of deep-layer excitatory neurons in the neocortex. *Development (Cambridge, England)*, 152(13).

Weiß E, et al. (2025) HSV-1 infection induces a downstream shift of the +1 nucleosome. *Journal of virology*, 99(4), e0208624.

Paquette A, et al. (2024) A genome scale transcriptional regulatory model of the human placenta. *Science advances*, 10(26), eadf3411.

Fang C, et al. (2024) Dynamics of accessible chromatin regions and subgenome dominance in octoploid strawberry. *Nature communications*, 15(1), 2491.

Cheng S, et al. (2024) Review and Evaluate the Bioinformatics Analysis Strategies of ATAC-seq and CUT&Tag Data. *Genomics, proteomics & bioinformatics*, 22(3).

Djakovic L, et al. (2023) The HSV-1 ICP22 protein selectively impairs histone repositioning upon Pol II transcription downstream of genes. *Nature communications*, 14(1), 4591.

Kuwayama N, et al. (2023) HMGA2 directly mediates chromatin condensation in association with neuronal fate regulation. *Nature communications*, 14(1), 6420.

Friedel CC, et al. (2021) Dissecting Herpes Simplex Virus 1-Induced Host Shutoff at the RNA Level. *Journal of virology*, 95(3).

Espeso-Gil S, et al. (2021) Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. *Frontiers in molecular neuroscience*, 14, 664912.

Zhao Z, et al. (2021) Comprehensive characterization of somatic variants associated with intronic polyadenylation in human cancers. *Nucleic acids research*, 49(18), 10369.

Keele GR, et al. (2020) Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. *PLoS genetics*, 16(1), e1008537.

Funk CC, et al. (2020) Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. *Cell reports*, 32(7), 108029.

Nagahama K, et al. (2020) Setd1a Insufficiency in Mice Attenuates Excitatory Synaptic Function and Recapitulates Schizophrenia-Related Behavioral Abnormalities. *Cell reports*, 32(11), 108126.

Deniz Ö, et al. (2020) Endogenous retroviruses are a source of enhancers with oncogenic potential in acute myeloid leukaemia. *Nature communications*, 11(1), 3506.

van der Burg KRL, et al. (2019) Contrasting Roles of Transcription Factors Spineless and EcR in the Highly Dynamic Chromatin Landscape of Butterfly Wing Metamorphosis. *Cell reports*, 27(4), 1027.

Pearl JR, et al. (2019) Genome-Scale Transcriptional Regulatory Network Models of Psychiatric and Neurodegenerative Disorders. *Cell systems*, 8(2), 122.

Alvarez JM, et al. (2019) Local Changes in Chromatin Accessibility and Transcriptional Networks Underlying the Nitrate Response in Arabidopsis Roots. *Molecular plant*, 12(12), 1545.

Yi G, et al. (2019) Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. *Cell reports*, 26(4), 1059.

Yevshin I, et al. (2019) GTRD: a database on gene transcription regulation-2019 update. *Nucleic acids research*, 47(D1), D100.