

Resource Summary Report

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Platform for Epigenomic and Genomic Research

RRID:SCR_021861

Type: Tool

Proper Citation

Platform for Epigenomic and Genomic Research (RRID:SCR_021861)

Resource Information

URL: <https://github.com/seqcode/pegr>

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Description: Web service platform logging metadata for genomic samples and high throughput sequencing, manages data processing workflows, and provides quality control reporting and visualization. PEGR links people, samples, protocols, sequencing and bioinformatics computation to comply with FAIR best practices for publications and data management plans. Tracks and quality controls experiments from conception to publication ready figures, compatible with multiple assays and bioinformatic pipelines. It supports rigor and reproducibility for biochemists working at wet bench, while continuing to fully support reproducibility and reliability for bioinformaticians through integration with Galaxy platform.

Abbreviations: PEGR

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

Defining Citation: [DOI:10.1101/2021.07.26.453821](https://doi.org/10.1101/2021.07.26.453821)

Keywords: FAIR compliance, platform logging metadata, genomic samples, high throughput sequencing, experiments quality controls, tracking experiments, rigor and reproducibility support

Availability: Free, Available for download, Freely available

Resource Name: Platform for Epigenomic and Genomic Research

Resource ID: SCR_021861

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260813T055245+0000

Ratings and Alerts

No rating or validation information has been found for Platform for Epigenomic and Genomic Research.

No alerts have been found for Platform for Epigenomic and Genomic Research.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Chen H, et al. (2026) Genome-wide rotational and translational phasing of nucleosomes with human transcription factors. *Molecular cell*, 86(14), 2722.

Pugh FB, et al. (2026) A unified framework for causal gene regulatory network inference grounded in orthogonal molecular evidence. *bioRxiv : the preprint server for biology*.

Ranjan A, et al. (2025) Histone acetylation readers Bdf1 and Yaf9 direct SWR1 remodeler to +1 nucleosome. *Science advances*, 11(32), eadt2002.

Louder RK, et al. (2024) Molecular basis of global promoter sensing and nucleosome capture by the SWR1 chromatin remodeler. *Cell*, 187(24), 6849.

van Breugel ME, et al. (2023) Locus-specific proteome decoding reveals Fpt1 as a chromatin-associated negative regulator of RNA polymerase III assembly. *Molecular cell*, 83(23), 4205.

John J, et al. (2022) Genome-wide promoter assembly in *E. coli* measured at single-base resolution. *Genome research*, 32(5), 878.

Mittal C, et al. (2022) An integrated SAGA and TFIID PIC assembly pathway selective for poised and induced promoters. *Genes & development*, 36(17-18), 985.

Shao D, et al. (2022) PEGR: a flexible management platform for reproducible epigenomic and genomic research. *Genome biology*, 23(1), 99.