

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Haystack

RRID:SCR_017087

Type: Tool

Proper Citation

Haystack (RRID:SCR_017087)

Resource Information

URL: <https://github.com/lucapinello/Haystack>

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Description: Software suite of computational tools implemented in Python to study epigenetic variability, cross cell type plasticity of chromatin states and transcription factors motifs providing mechanistic insights into chromatin structure, cellular identity and gene regulation. Epigenetic variability and transcription factor motifs analysis pipeline.

Synonyms: haystack, haystack_bio

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Keywords: epigenetic, variability, cell, plasticity, chromatin, transcription, factor, motif, structure, gene, regulation, analysis

Availability: Free, Available for download, Freely available

Resource Name: Haystack

Resource ID: SCR_017087

Alternate URLs: https://github.com/pinellolab/haystack_bio

License: GNU AGPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260905T132818+0000

Ratings and Alerts

No rating or validation information has been found for Haystack.

No alerts have been found for Haystack.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Bhattacharya S, et al. (2025) Intestinal secretory differentiation reflects niche-driven phenotypic and epigenetic plasticity of a common signal-responsive terminal cell. *Cell stem cell*, 32(6), 952.

Singh PNP, et al. (2024) Transcription factor dynamics, oscillation, and functions in human enteroendocrine cell differentiation. *Cell stem cell*, 31(7), 1038.

Jadhav U, et al. (2019) Extensive Recovery of Embryonic Enhancer and Gene Memory Stored in Hypomethylated Enhancer DNA. *Molecular cell*, 74(3), 542.