Resource Summary Report

Generated by RRID on Apr 10, 2025

Haystack

RRID:SCR_017087
Type: Tool

Proper Citation

Haystack (RRID:SCR_017087)

Resource Information

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

Proper Citation: Haystack (RRID:SCR_017087)

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

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

Funding:

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: 20250410T070819+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 2 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.