

Resource Summary Report

Generated by [NIF](#) on Sep 17, 2026

[psychromVAR](#)

RRID:SCR_027456

Type: Tool

Proper Citation

psychromVAR (RRID:SCR_027456)

Resource Information

URL: <https://github.com/pinellolab/psychromVAR>

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Description: Software Python package for inferring transcription factor binding variability from scATAC-seq data by implementing algorithm proposed in chromVAR. It is built on anndata and mudata therefore can work seamlessly with scanpy and muon pipeline.

Resource Type: software resource, software toolkit

Keywords: inferring transcription factor binding variability, scATAC-seq data,

Availability: Free, Available for download, Freely available

Resource Name: psychromVAR

Resource ID: SCR_027456

License: MIT license

Record Creation Time: 20250926T061848+0000

Record Last Update: 20260912T200527+0000

Ratings and Alerts

No rating or validation information has been found for psychromVAR.

No alerts have been found for psychromVAR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. Nature methods, 23(5), 946.