

Resource Summary Report

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Motif Alteration Genome wide to Globally Investigate Elements

RRID:SCR_021903

Type: Tool

Proper Citation

Motif Alteration Genome wide to Globally Investigate Elements (RRID:SCR_021903)

Resource Information

URL: <https://github.com/zeyang-shen/maggie>

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Description: Software Python package for identifying motifs mediating transcription factor binding and function. Links mutations of motif to changes of epigenomic feature without assuming linear relationship.

Abbreviations: MAGGIE

Resource Type: software toolkit, software resource

Defining Citation: [PMID:32657363](#)

Keywords: Identifying motifs mediating transcription factor binding, identifying motifs mediating transcription factor function, motif mutations, epigenomic feature changes

Funding: NIDDK R01 DK091183;
Foundation Leducq ;
Netherlands Organization for Scientific Research ;
Amsterdam Cardiovascular Sciences

Availability: Free, Available for download, Freely available

Resource Name: Motif Alteration Genome wide to Globally Investigate Elements

Resource ID: SCR_021903

License: GNU General Public License v3.0

Record Creation Time: 20220421T050137+0000

Ratings and Alerts

No rating or validation information has been found for Motif Alteration Genome wide to Globally Investigate Elements.

No alerts have been found for Motif Alteration Genome wide to Globally Investigate Elements.

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 [dkNET](#) .

Yuan J, et al. (2024) Single-nucleus multi-omics analyses reveal cellular and molecular innovations in the anterior cingulate cortex during primate evolution. Cell genomics, 4(12), 100703.

Duttke SH, et al. (2024) Position-dependent function of human sequence-specific transcription factors. Nature, 631(8022), 891.

Shen Z, et al. (2022) Systematic analysis of naturally occurring insertions and deletions that alter transcription factor spacing identifies tolerant and sensitive transcription factor pairs. eLife, 11.