

Resource Summary Report

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m6ASNP: Annotation of genetic variants by m6A function

RRID:SCR_016048

Type: Tool

Proper Citation

m6ASNP: Annotation of genetic variants by m6A function (RRID:SCR_016048)

Resource Information

URL: <http://m6asnp.renlab.org>

Proper Citation: m6ASNP: Annotation of genetic variants by m6A function (RRID:SCR_016048)

Description: Web server implemented in JAVA and PHP for annotating genetic variants by m6A function. It predicts and annotates N6-methyladenosine (m6A) alterations from genetic variants data such as germline SNPs or cancer somatic mutations. It employs two accurate prediction models for human and mouse using Random Forest algorithm. It conducts a statistical analysis for all the predicted m6A alterations. Provides statistical diagrams and a genome browser to visualize the topology characteristics of predicted m6A alterations.

Synonyms: m6ASNP

Resource Type: software application, data analysis software, data access protocol, software resource, data processing software, data visualization software, web service

Defining Citation: [PMID:29617790](#), [DOI:10.1093/gigascience/giy035](#)

Keywords: N6-methyladenosine (m6A), variant annotation, effect prediction, random forest, miclip, m6a, mutant

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Availability: Free, Available for download, Freely available

Resource Name: m6ASNP: Annotation of genetic variants by m6A function

Resource ID: SCR_016048

Alternate URLs: <https://github.com/RenLabBioinformatics/m6ASNP>

License: GNU GENERAL PUBLIC LICENSE

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Record Last Update: 20260729T044407+0000

Ratings and Alerts

No rating or validation information has been found for m6ASNP: Annotation of genetic variants by m6A function.

No alerts have been found for m6ASNP: Annotation of genetic variants by m6A function.

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 [T1D](#) .

Song R, et al. (2024) Variable calling of m6A and associated features in databases: a guide for end-users. Briefings in bioinformatics, 25(5).

Zhao Q, et al. (2020) m6A RNA modification modulates PI3K/Akt/mTOR signal pathway in Gastrointestinal Cancer. Theranostics, 10(21), 9528.

Jiang S, et al. (2018) m6ASNP: a tool for annotating genetic variants by m6A function. GigaScience, 7(5).