Resource Summary Report

Generated by RRID on Aug 12, 2026

ReMM score

RRID:SCR_023095
Type: Tool

Proper Citation

ReMM score (RRID:SCR_023095)

Resource Information

URL: https://remm.bihealth.org

Proper Citation: ReMM score (RRID:SCR_023095)

Description: Software tool that scores positions in human genome in terms of their regulatory probability. Regulatory Mendelian Mutation score was created for relevance prediction of non-coding variations (SNVs and small InDels) in human genome (hg19) in terms of Mendelian diseases.

Abbreviations: ReMM score

Synonyms: Regulatory Mendelian Mutation score

Resource Type: software application, software resource

Defining Citation: DOI:10.1101/2022.03.14.484240

Keywords: positions in human genome scoring, regulatory probability, relevance prediction, non-coding variations, SNVs and small InDels, Mendelian diseases, human genome

Availability: Free, Available for download, Freely available

Resource Name: ReMM score

Resource ID: SCR_023095

Alternate URLs: https://charite.github.io/software-remm-score.html, https://search.datacite.org/works/10.5281/zenodo.1197579

Record Creation Time: 20230104T050211+0000

Record Last Update: 20260810T040830+0000

Ratings and Alerts

No rating or validation information has been found for ReMM score.

No alerts have been found for ReMM score.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Godinez-Zamora GF, et al. (2025) Contribution of next generation sequencing to the diagnosis of inborn errors of immunity in a pediatric cohort. Frontiers in immunology, 16, 1638544.

Nakamura T, et al. (2024) Topologically associating domains define the impact of de novo promoter variants on autism spectrum disorder risk. Cell genomics, 4(2), 100488.

Pagnamenta AT, et al. (2023) Structural and non-coding variants increase the diagnostic yield of clinical whole genome sequencing for rare diseases. Genome medicine, 15(1), 94.

Schubach M, et al. (2022) The Regulatory Mendelian Mutation score for GRCh38. GigaScience, 12.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. GigaScience, 12.

Schwarz JM, et al. (2021) Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 33(2), 133.