Resource Summary Report

Generated by RRID on Apr 10, 2025

NIMBL

RRID:SCR_000482
Type: Tool

Proper Citation

NIMBL (RRID:SCR_000482)

Resource Information

URL: https://sites.google.com/site/emesbioinformatics/group-software/nimbl

Proper Citation: NIMBL (RRID:SCR_000482)

Description: MATLAB code to quality control and prioritize differentially methylated markers from illumina infinium arrays.

Abbreviations: NIMBL

Synonyms: NIMBL: Numerical Identification of Methylation Biomarker Lists, Numerical Identification of Methylation Biomarker Lists

Resource Type: software resource

Defining Citation: PMID:22936948

Keywords: quality control, illumina, infinium array, dna methylation, biomarker, dna methylation array, dna methylome, infinium 450k, biomarker discovery, differential methylation, epigenetics, epigenomics

Funding:

Availability: Acknowledgement requested

Resource Name: NIMBL

Resource ID: SCR_000482

Alternate IDs: OMICS_02305

Record Creation Time: 20220129T080201+0000

Record Last Update: 20250410T064611+0000

Ratings and Alerts

No rating or validation information has been found for NIMBL.

No alerts have been found for NIMBL.

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 RRID.

Dedeurwaerder S, et al. (2014) A comprehensive overview of Infinium HumanMethylation450 data processing. Briefings in bioinformatics, 15(6), 929.