Resource Summary Report

Generated by dkNET on Apr 29, 2025

IMA

RRID:SCR_010955
Type: Tool

Proper Citation

IMA (RRID:SCR_010955)

Resource Information

URL: http://www.rforge.net/IMA/

Proper Citation: IMA (RRID:SCR_010955)

Description: A software package designed to automate the pipeline for analyzing site-level and region-level methylation changes in epigenetic studies utilizing the 450K DNA methylation microarray.

Abbreviations: IMA

Resource Type: software resource

Funding:

Resource Name: IMA

Resource ID: SCR_010955

Alternate IDs: OMICS_00795

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014516+0000

Ratings and Alerts

No rating or validation information has been found for IMA.

No alerts have been found for IMA.

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 dkNET.

Wei S, et al. (2021) Ten Years of EWAS. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 8(20), e2100727.

Li T, et al. (2020) Genome-wide analysis of DNA methylation identifies S100A13 as an epigenetic biomarker in individuals with chronic (? 30?years) type 2 diabetes without diabetic retinopathy. Clinical epigenetics, 12(1), 77.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Huang SK, et al. (2014) Lung fibroblasts from patients with idiopathic pulmonary fibrosis exhibit genome-wide differences in DNA methylation compared to fibroblasts from nonfibrotic lung. PloS one, 9(9), e107055.

Patil VK, et al. (2013) Interaction of prenatal maternal smoking, interleukin 13 genetic variants and DNA methylation influencing airflow and airway reactivity. Clinical epigenetics, 5(1), 22.

Wessely F, et al. (2012) Identification of DNA methylation biomarkers from Infinium arrays. Frontiers in genetics, 3, 161.