

Resource Summary Report

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CRowd Extracted Expression of Differential Signatures

RRID:SCR_015680

Type: Tool

Proper Citation

CRowd Extracted Expression of Differential Signatures (RRID:SCR_015680)

Resource Information

URL: <http://amp.pharm.mssm.edu/CREEDS/>

Proper Citation: CRowd Extracted Expression of Differential Signatures (RRID:SCR_015680)

Description: Software resource that allows students or the general public find variants that may be significantly associated with some disease. CREEDS also visualizes and analyzes gene expression signatures.

Abbreviations: CREEDS

Synonyms: CREEDS: CRowd Extracted Expression of Differential Signatures

Resource Type: data processing software, software resource, software application, web application, data visualization software, database, data or information resource

Defining Citation: [PMID:27667448](#)

Keywords: variant, disease expression, disease marker

Funding: NIGMS R01GM098316;
NHLBI U54HL127624;
NCI U54CA189201

Availability: Freely available, Free, Available for download

Resource Name: CRowd Extracted Expression of Differential Signatures

Resource ID: SCR_015680

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Record Creation Time: 20220129T080327+0000

Record Last Update: 20260805T044343+0000

Ratings and Alerts

No rating or validation information has been found for CRowd Extracted Expression of Differential Signatures.

No alerts have been found for CRowd Extracted Expression of Differential Signatures.

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 [RRID](#) .

Zhu B, et al. (2021) Potential Drug Prediction of Glioblastoma Based on Drug Perturbation-Induced Gene Expression Signatures. BioMed research international, 2021, 6659701.

Han Y, et al. (2021) Identification of Potential BRAF Inhibitor Joint Therapy Targets in PTC based on WGCAN and DCGA. Journal of Cancer, 12(6), 1779.

Liu TP, et al. (2018) Systematic polypharmacology and drug repurposing via an integrated L1000-based Connectivity Map database mining. Royal Society open science, 5(11), 181321.