

Resource Summary Report

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MetaCore

RRID:SCR_008125

Type: Tool

Proper Citation

MetaCore (RRID:SCR_008125)

Resource Information

URL: <http://thomsonreuters.com/metacore/>

Proper Citation: MetaCore (RRID:SCR_008125)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 17, 2022. An integrated software suite for functional analysis of experimental data. The scope of data types includes microarray and SAGE gene expression, SNPs and CGH arrays, proteomics, metabolomics, pathway analysis, Y2H and other custom interactions. MetaCore is based on a proprietary manually curated database of human protein-protein, protein-DNA and protein compound interactions, metabolic and signaling pathways and the effects of bioactive molecules in gene expression.

Resource Type: data analysis software, software resource, software application, data processing software

Keywords: expression, gene, dna, interaction, metabolomics, microarray, pathway, protein, proteomic, software

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: MetaCore

Resource ID: SCR_008125

Alternate IDs: nif-0000-20874

Alternate URLs: <http://www.genego.com/metacore.php>

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260810T040457+0000

Ratings and Alerts

No rating or validation information has been found for MetaCore.

No alerts have been found for MetaCore.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1182 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Kulkarni AJ, et al. (2025) L-Phenylalanine is a metabolic checkpoint of human Th2 cells. *Cell reports. Medicine*, 6(12), 102466.

Soudy M, et al. (2025) Sex-dependent molecular landscape of Alzheimer's disease revealed by large-scale single-cell transcriptomics. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14476.

Svinin G, et al. (2025) Causal network analysis of omics data using prior knowledge databases. *Briefings in bioinformatics*, 26(6).

Ali M, et al. (2025) Temporal transcriptomic changes in the THY-Tau22 mouse model of tauopathy display cell type- and sex-specific differences. *Acta neuropathologica communications*, 13(1), 93.

Ali M, et al. (2025) Multi-cohort cerebrospinal fluid proteomics identifies robust molecular signatures across the Alzheimer disease continuum. *Neuron*, 113(9), 1363.

Zagare A, et al. (2025) MIRO1 mutation leads to metabolic maladaptation resulting in Parkinson's disease-associated dopaminergic neuron loss. *NPJ systems biology and applications*, 11(1), 37.

Ramamoorthi G, et al. (2025) Antitumor CD4+ T Helper 1 Cells Target and Control the Outgrowth of Disseminated Cancer Cells. *Cancer immunology research*, 13(5), 729.

Shen L, et al. (2025) Marginal interaction test for detecting interactions between genetic marker sets and environment in genome-wide studies. *G3 (Bethesda, Md.)*, 15(1).

Cohen JD, et al. (2025) In vitro human ion channel assays predictive of drug-induced seizure. *Toxicological sciences : an official journal of the Society of Toxicology*, 203(2), 253.

Le Bars S, et al. (2025) Single-cell analysis reveals shared and distinct molecular signatures in brain organoid models of neurodegeneration and neuroinflammation. *Alzheimer's research & therapy*, 18(1), 1.

Ren J, et al. (2025) Targeting EPHB2/ABL1 restores antitumor immunity in preclinical models of ependymoma. *Proceedings of the National Academy of Sciences of the United States of America*, 122(4), e2319474122.

Lizama BN, et al. (2025) Sigma-2 receptor modulator CT1812 alters key pathways and rescues retinal pigment epithelium (RPE) functional deficits associated with dry age-related macular degeneration (AMD). *Scientific reports*, 15(1), 4256.

Oosterwijk-Wakka JC, et al. (2025) Kinomic profiling to predict sunitinib response of patients with metastasized clear cell Renal Cell Carcinoma. *Neoplasia* (New York, N.Y.), 60, 101108.

Mannini A, et al. (2025) Ganglioside GD2 Contributes to a Stem-Like Phenotype in Intrahepatic Cholangiocarcinoma. *Liver international : official journal of the International Association for the Study of the Liver*, 45(1), e16208.

Ozuna H, et al. (2025) Proteomics profiling of inflammatory responses to elxacaftor/tezacaftor/ivacaftor in cystic fibrosis. *Frontiers in immunology*, 16, 1486784.

Helmuth ME, et al. (2025) Phenotyping Men With Lower Urinary Tract Symptoms: Results From the Symptoms of Lower Urinary Tract Dysfunction Research Network. *Neurourology and urodynamics*, 44(1), 178.

Zhong C, et al. (2025) Chemoresistance mechanisms to 5-Fluorouracil and reversal strategies in lung and breast cancer. *Scientific reports*, 15(1), 6074.

Doulamis IP, et al. (2025) Transcriptomic signatures of subcutaneous adipose tissue in patients with diabetes and coronary artery disease: a pilot study. *Frontiers in cardiovascular medicine*, 12, 1524605.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. *Neoplasia* (New York, N.Y.), 60, 101104.

Ali M, et al. (2024) Single cell transcriptome analysis of the THY-Tau22 mouse model of Alzheimer's disease reveals sex-dependent dysregulations. *Cell death discovery*, 10(1), 119.