Resource Summary Report

Generated by dkNET on Apr 16, 2025

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, data processing software, software application, software resource

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

Funding:

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: 20250416T063513+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 1170 mentions in open access literature.

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

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.

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.

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.

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.

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.

Cruchaga C, et al. (2024) Multi-cohort cerebrospinal fluid proteomics identifies robust

molecular signatures for asymptomatic and symptomatic Alzheimer's disease. Research square.

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.

Zhang J, et al. (2024) The association of GNB5 with Alzheimer disease revealed by genomic analysis restricted to variants impacting gene function. American journal of human genetics, 111(3), 473.

Hong Y, et al. (2024) Jnk1 and downstream signalling hubs regulate anxiety-like behaviours in a zebrafish larvae phenotypic screen. Scientific reports, 14(1), 11174.

Miura M, et al. (2024) Programmed cell death-1 is involved with peripheral blood immune cell profiles in patients with hepatitis C virus antiviral therapy. PloS one, 19(5), e0299424.

Cavazzoni A, et al. (2024) Synergic activity of FGFR2 and MEK inhibitors in the treatment of FGFR2-amplified cancers of unknown primary. Molecular therapy : the journal of the American Society of Gene Therapy, 32(10), 3650.

Lizama BN, et al. (2024) CT1812 biomarker signature from a meta-analysis of CSF proteomic findings from two Phase 2 clinical trials in Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(10), 6860.

Rodriguez-Marino N, et al. (2024) Dietary fiber promotes antigen presentation on intestinal epithelial cells and development of small intestinal CD4+CD8??+ intraepithelial T cells. Mucosal immunology.

Voulgarelis D, et al. (2024) Understanding tumour growth variability in breast cancer xenograft models identifies PARP inhibition resistance biomarkers. NPJ precision oncology, 8(1), 266.

Azevedo PL, et al. (2024) SLPI overexpression in hMSCs could be implicated in the HSC gene expression profile in AML. Scientific reports, 14(1), 15550.

Han G, et al. (2024) Bayesian-frequentist hybrid inference framework for single cell RNA-seq analyses. Human genomics, 18(1), 69.

Tavabie OD, et al. (2024) microRNA associated with hepatocyte injury and systemic inflammation may predict adverse outcomes in cirrhotic patients. Scientific reports, 14(1), 23831.

Bagherinia M, et al. (2024) Predictors of social intermediate factors associated with sexual quality of life of women: systematic review and meta-analysis. BMC women's health, 24(1), 64.