Resource Summary Report

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UCSD-Nature Signaling Gateway Molecule Pages

RRID:SCR_006907
Type: Tool

Proper Citation

UCSD-Nature Signaling Gateway Molecule Pages (RRID:SCR_006907)

Resource Information

URL: http://www.signaling-gateway.org/molecule/

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Description: A relational database of all significant published qualitative and quantitative information on cell signaling proteins. The Molecule Pages database was developed with the specific aim of allowing interactions, and indeed whole pathways, to be modeled. The goal is to filter the data to present only validated information. In addition, the Gateway is the home of Signaling Update, which provides a one-stop overview of the latest and hottest research in cell signaling for both the specialist and non-specialist alike.

Abbreviations: SGMP

Synonyms: Molecule Pages: A comprehensive signaling database, UCSD - Signaling Gateway Molecule Pages, Alliance for Cellular Signaling Molecule Pages Database

Resource Type: database, data or information resource

Defining Citation: PMID:21505029, PMID:17965093, PMID:12478304

Keywords: database, data model, cell signaling pathway, molecule, protein, signal transduction

Funding: Genentech Inc ;
National Institute of General Medical Sciences

Resource Name: UCSD-Nature Signaling Gateway Molecule Pages

Resource ID: SCR_006907

Alternate IDs: nif-0000-03604, SCR_013230, nif-0000-20810

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250412T055139+0000

Ratings and Alerts

No rating or validation information has been found for UCSD-Nature Signaling Gateway Molecule Pages.

No alerts have been found for UCSD-Nature Signaling Gateway Molecule Pages.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Climer S, et al. (2015) Human gephyrin is encompassed within giant functional noncoding yin-yang sequences. Nature communications, 6, 6534.

Boué S, et al. (2015) Causal biological network database: a comprehensive platform of causal biological network models focused on the pulmonary and vascular systems. Database : the journal of biological databases and curation, 2015, bav030.

Nance T, et al. (2014) Transcriptome analysis reveals differential splicing events in IPF lung tissue. PloS one, 9(3), e92111.

Bateman AR, et al. (2014) Importance of collection in gene set enrichment analysis of drug response in cancer cell lines. Scientific reports, 4, 4092.

Simeone P, et al. (2014) Epigenetic heredity of human height. Physiological reports, 2(6).

Brandao LN, et al. (2013) Inhibition of MerTK increases chemosensitivity and decreases oncogenic potential in T-cell acute lymphoblastic leukemia. Blood cancer journal, 3(1), e101.

De Franceschi L, et al. (2012) Computational identification of phospho-tyrosine sub-networks related to acanthocyte generation in neuroacanthocytosis. PloS one, 7(2), e31015.

Merilahti P, et al. (2012) Endocytosis of integrin-binding human picornaviruses. Advances in virology, 2012, 547530.

Hsiao A, et al. (2008) Bivariate microarray analysis: statistical interpretation of two-channel functional genomics data. Systems and synthetic biology, 2(3-4), 95.

Vastrik I, et al. (2007) Reactome: a knowledge base of biologic pathways and processes. Genome biology, 8(3), R39.

Pradervand S, et al. (2006) Identification of signaling components required for the prediction of cytokine release in RAW 264.7 macrophages. Genome biology, 7(2), R11.

Planque N, et al. (2006) Nuclear trafficking of secreted factors and cell-surface receptors: new pathways to regulate cell proliferation and differentiation, and involvement in cancers. Cell communication and signaling : CCS, 4, 7.