

Resource Summary Report

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Secreted Protein Database

RRID:SCR_013448

Type: Tool

Proper Citation

Secreted Protein Database (RRID:SCR_013448)

Resource Information

URL: <http://spd.cbi.pku.edu.cn>

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Description: A collection of secreted proteins from Human, Mouse and Rat proteomes, which includes sequences from SwissProt, Trembl, Ensembl and Refseq. The 18,152 entries are classified into fourteen functional categories, including "apolipoprotein", "cytokine", "protease", "toxin", etc. To make the dataset more comprehensive, nine related datasets were also collected, such as SPDI, Riken mouse secretome, SwissProt vertebrate secreted proteins, SubLoc etc.

Abbreviations: SPD

Synonyms: Secreted Protein Database

Resource Type: data or information resource, database

Resource Name: Secreted Protein Database

Resource ID: SCR_013448

Alternate IDs: nif-0000-03449

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260729T044316+0000

Ratings and Alerts

No rating or validation information has been found for Secreted Protein Database.

No alerts have been found for Secreted Protein Database.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Kessler BE, et al. (2019) Resistance to Src inhibition alters the BRAF-mutant tumor secretome to promote an invasive phenotype and therapeutic escape through a FAK>p130Cas>c-Jun signaling axis. *Oncogene*, 38(14), 2565.

Wang R, et al. (2016) Phenotype-Genotype Association Analysis of ACTH-Secreting Pituitary Adenoma and Its Molecular Link to Patient Osteoporosis. *International journal of molecular sciences*, 17(10).

Meinken J, et al. (2015) MetazSeckB: the human and animal secretome and subcellular proteome knowledgebase. *Database : the journal of biological databases and curation*, 2015.

Wang GX, et al. (2014) The brown fat-enriched secreted factor Nrg4 preserves metabolic homeostasis through attenuation of hepatic lipogenesis. *Nature medicine*, 20(12), 1436.

Cantacessi C, et al. (2013) TIMPs of parasitic helminths - a large-scale analysis of high-throughput sequence datasets. *Parasites & vectors*, 6, 156.

Reinhold WC, et al. (2013) Commentary on "MelanomaDB: a web tool for integrative analysis of melanoma genomic information to identify disease-associated molecular pathways". *Frontiers in genetics*, 4, 156.

Shin SW, et al. (2013) Elevation of Eosinophil-Derived Neurotoxin in Plasma of the Subjects with Aspirin-Exacerbated Respiratory Disease: A Possible Peripheral Blood Protein Biomarker. *PloS one*, 8(6), e66644.

Cantacessi C, et al. (2012) Insights into SCP/TAPS proteins of liver flukes based on large-scale bioinformatic analyses of sequence datasets. *PloS one*, 7(2), e31164.

Cantacessi C, et al. (2011) The transcriptome of *Trichuris suis*--first molecular insights into a parasite with curative properties for key immune diseases of humans. *PloS one*, 6(8), e23590.

Yan H, et al. (2010) Proteomic analysis of astrocytic secretion that regulates neurogenesis using quantitative amine-specific isobaric tagging. *Biochemical and biophysical research communications*, 391(2), 1187.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.