Resource Summary Report

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HPMR - Human Plasma Membrane Receptome

RRID:SCR_007725
Type: Tool

Proper Citation

HPMR - Human Plasma Membrane Receptome (RRID:SCR_007725)

Resource Information

URL: http://receptome.stanford.edu/

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Description: HPMR is a database of human plasma membrane ligands and receptors. Users can search for ligands or receptors to reveal their pairing partners and browse through ligand or receptor families to identify ligand-receptor relationships. Users can also submit their own microarray data to perform online genome-wide online searches for paracrine/autocrine signaling systems. Survey of transcriptomes based on liganded receptome allows the discovery of paracrine/autocrine signaling for known ligand-receptor pairs in previously uncharacterized tissues or developmental stages.

Synonyms: HPMR

Resource Type: database, data or information resource

Keywords: ligand, plasma membrane, receptor

Funding:

Resource Name: HPMR - Human Plasma Membrane Receptome

Resource ID: SCR_007725

Alternate IDs: nif-0000-02985

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250519T204732+0000

Ratings and Alerts

No rating or validation information has been found for HPMR - Human Plasma Membrane Receptome.

No alerts have been found for HPMR - Human Plasma Membrane Receptome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Tsuyuzaki K, et al. (2023) Sctensor detects many-to-many cell-cell interactions from single cell RNA-sequencing data. BMC bioinformatics, 24(1), 420.

Sun H, et al. (2022) Increased circulating microparticles contribute to severe infection and adverse outcomes of COVID-19 in patients with diabetes. American journal of physiology. Heart and circulatory physiology, 323(6), H1176.

Boreggio M, et al. (2022) Unveiling the Bio-corona Fingerprinting of Potential Anticancer Carbon Nanotubes Coupled with D-Amino Acid Oxidase. Molecular biotechnology, 64(10), 1164.

Jung S, et al. (2021) FunRes: resolving tissue-specific functional cell states based on a cell-cell communication network model. Briefings in bioinformatics, 22(4).

Ma F, et al. (2021) Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level. Cell & bioscience, 11(1), 121.

Rakkar K, et al. (2020) Endothelial progenitor cells, potential biomarkers for diagnosis and prognosis of ischemic stroke: protocol for an observational case-control study. Neural regeneration research, 15(7), 1300.

Yan P, et al. (2020) Changes of circulating neuregulin 4 and its relationship with 25-hydroxy vitamin D and other diabetic vascular complications in patients with diabetic peripheral neuropathy. Diabetology & metabolic syndrome, 12, 42.

Ahmad T, et al. (2020) Optimizing performance of GATK workflows using Apache Arrow In-Memory data framework. BMC genomics, 21(Suppl 10), 683.

León López R, et al. (2020) Efficacy and safety of early treatment with sarilumab in hospitalised adults with COVID-19 presenting cytokine release syndrome (SARICOR

STUDY): protocol of a phase II, open-label, randomised, multicentre, controlled clinical trial. BMJ open, 10(11), e039951.

Zhang G, et al. (2020) miR-205 regulates bone turnover in elderly female patients with type 2 diabetes mellitus through targeted inhibition of Runx2. Experimental and therapeutic medicine, 20(2), 1557.

Alghamdi A, et al. (2019) PRe-hospital Evaluation of Sensitive TrOponin (PRESTO) Study: multicentre prospective diagnostic accuracy study protocol. BMJ open, 9(10), e032834.

Meng M, et al. (2018) Enhanced Stability of DNA Oligonucleotides with Partially Zwitterionic Backbone Structures in Biological Media. Molecules (Basel, Switzerland), 23(11).

Turdo F, et al. (2016) CDCP1 is a novel marker of the most aggressive human triple-negative breast cancers. Oncotarget, 7(43), 69649.

Ramilowski JA, et al. (2015) A draft network of ligand-receptor-mediated multicellular signalling in human. Nature communications, 6, 7866.

Ma K, et al. (2012) A statistical model-building perspective to identification of MS/MS spectra with PeptideProphet. BMC bioinformatics, 13 Suppl 16(Suppl 16), S1.

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