

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: data or information resource, database

Keywords: ligand, plasma membrane, receptor

Resource Name: HPMR - Human Plasma Membrane Receptome

Resource ID: SCR_007725

Alternate IDs: nif-0000-02985

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260912T200151+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 17 mentions in open access literature.

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

Zhang J, et al. (2025) Single-cell and bulk transcriptome analysis unveils a ligand-receptor-based signature for prognostication and reveals that TREM1 controls the malignant behaviors of hepatocellular carcinoma. *Acta biochimica et biophysica Sinica*, 57(11), 1847.

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.