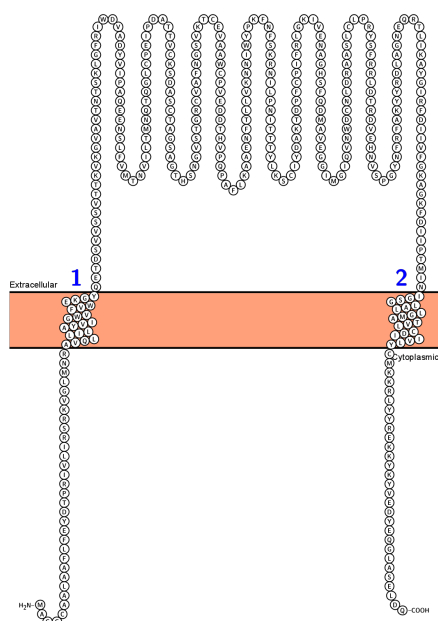


P2X purinoceptor 4

Organism: Homo sapiens (Human) | Gene names: P2RX4



Entry: Q99571

Mass: 43.369 Da

Transmembrane: 2

Subcellular location: Membrane

{ECO:0000269|PubMed:10515189,
ECO:0000269|PubMed:23303206,
ECO:0000269|PubMed:28326637}, Multi-pass
membrane protein {ECO:0000255}.

Cofactor: -

Extinction coefficient: 1.399

Isoelectric Point: 8.29

PubMed ID: 9016352, 16541075, 15489334, 10515189,
19159218, 22068874, 23303206, 28326637

Family: -

Function:

Receptor for ATP that acts as a ligand-gated ion channel. This receptor is insensitive to the antagonists PPADS and suramin. {ECO:0000269|PubMed:10515189, ECO:0000269|PubMed:22068874, ECO:0000269|PubMed:28326637}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	 NaN	DIBMA 12	 NaN
DIBMA Glycerol	 NaN	DIBMA Glucosamine	 NaN
Amphipol 17	 NaN	Amphipol 18	 NaN
AASTY 6-45	 NaN	AASTY 11-45	 NaN
AASTY 6-50	 NaN	AASTY 11-50	 NaN
AASTY 6- 55	 NaN	AASTY 11- 55	 NaN
SMALP 502-E	 NaN	SMALP 140-I	 NaN
SMALP 300	 NaN	SMALP 200	 0.37689
SMALP 140	 NaN	DDM	 0.624955
DM	 0.330648	LMNG	 0.789235
Fos-12	 0.655156	Digitonin-A	 NaN
RIPA	 0.355976		

Data from experiment(s): Hek293 membrane pellets 1 %

DIBMA 10	 NaN	DIBMA 12	 NaN
DIBMA Glycerol	 NaN	DIBMA Glucosamine	 No data
Amphipol 17	 0.527391374	Amphipol 18	 0.278689295
AASTY 6-45	 No data	AASTY 11-45	 NaN
AASTY 6-50	 0.324162185	AASTY 11-50	 No data
AASTY 6- 55	 NaN	AASTY 11- 55	 No data
SMALP 502-E	 NaN	SMALP 140-I	 No data
SMALP 300	 0	SMALP 200	 NaN
SMALP 140	 No data	DDM	 0.986557543
DM	 No data	LMNG	 0.93171823
Fos-12	 No data	Digitonin-A	 0.037874434
RIPA	 No data		

Involvement in disease:

-

Binding site:

-

Tissue specificity:

-

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MAGCCAALAAFLFEYDTPRIVLIRSRKVGLMNRVQLLILAYVIGWVFWWEKGYQETDSVSSVTTKVKGVAVTNTSKLGFRIWD
VADYVIPAQEENSLFVMTNVILTMNQTTQGLCPEIPDATTVCKSDASCTAGSAGTHSNGVSTGRCVAFNGSVKTC EVAAWCPVED
DTHVPQPAFLKAAENFTLLVKNNIWYPKFNFSKRNLPNITTTYLKSCIYDAKTDPF C PIFRLGKIVENAGHSFQDMAVEGGIMGI
QVNWDCNLDRAASLCLPRYSFRRLDTRDVEHNVSPGYNFRFAKYRDLAGNEQRTLIKAYGIRFDIIVFGKAGKFDIIPTMINIGS
GLALLGMATVLCDIIVLYCMKKRLYYREKKYKYVEDYEQGLASELDQ

Creditnotes:

The protein visualizations are generated with the help of Protter:

Omasits, U., Ahrens, C.H., MÃ¼ller, S., Wollscheid, B. "Protter: interactive protein feature visualization and integration with experimental proteomic data". *Bioinformatics*. 2014 Mar 15; **30**(6):884-6. doi: 10.1093/bioinformatics/btt607.

IP and extinction coefficients are gathered from Protparam by ExPASy:

Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D., Bairoch, A. "Protein Identification and Analysis Tools on the ExPASy Server". (In) *John M. Walker (ed): The Proteomics Protocols Handbook*, Humana Press (2005). pp. 571-607

The basic knowledge is found on UniProt:

The UniProt Consortium. "UniProt: the universal protein knowledgebase in 2021". *Nucleic Acids Res.* **49**:D1 (2021)