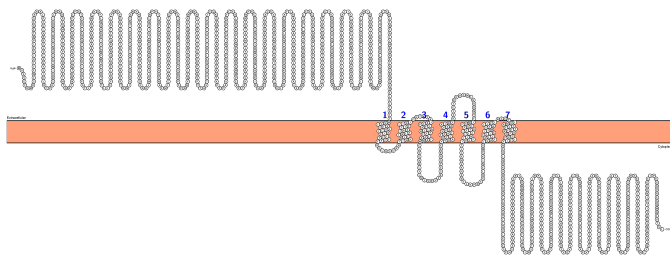


Adhesion G protein-coupled receptor L2

Organism: Homo sapiens (Human) | Gene names: ADGRL2, KIAA0786, LEC1, LPHH1, LPHN2



Entry: O95490

Mass: 163.349 Da

Transmembrane: 7

Subcellular location: Membrane {ECO:0000255}, Multi-pass membrane protein {ECO:0000255}.

Cofactor: -

Extinction coefficient: 1.272

Isoelectric Point: 6.02

PubMed ID: 10030676, 10760572, 16710414, 9872452, 17456239, 19159218, 21269460, 21406692, 24275569, 23647072, 25713288

Family: -

Function:

Calcium-independent receptor of low affinity for alpha-latrotoxin, an excitatory neurotoxin present in black widow spider venom which triggers massive exocytosis from neurons and neuroendocrine cells. Receptor probably implicated in the regulation of exocytosis. {ECO:0000250|UniProtKB:O88923}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	NaN	DIBMA 12	NaN
DIBMA Glycerol	0.291525	DIBMA Glucosamine	NaN
Amphipol 17	0.660427	Amphipol 18	0.28564
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	0.511403	SMALP 140-I	NaN
SMALP 300	NaN	SMALP 200	0.703603
SMALP 140	NaN	DDM	0.681532
DM	0.895506	LMNG	0.849047
Fos-12	0.719306	Digitonin-A	0.49821
RIPA	NaN		

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

DIBMA 10	NaN	DIBMA 12	NaN
DIBMA Glycerol	NaN	DIBMA Glucosamine	No data
Amphipol 17	0.845843315	Amphipol 18	0.77153641
AASTY 6-45	No data	AASTY 11-45	0.756354392
AASTY 6-50	0.678571522	AASTY 11-50	No data
AASTY 6- 55	0.28774339	AASTY 11- 55	No data
SMALP 502-E	NaN	SMALP 140-I	No data
SMALP 300	0.681244433	SMALP 200	0.396282256
SMALP 140	No data	DDM	1
DM	No data	LMNG	0.92064929
Fos-12	No data	Digitonin-A	0.416659087
RIPA	No data		

Involvement in disease:

-

Binding site:

-

Tissue specificity:

Expressed very widely in all normal tissues tested. Expression is variable in tumor cell lines, apparently elevated in some lines and absent or markedly reduced in others. {ECO:0000269|PubMed:10030676}.

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MVSSGCRMRLWFIIVISFLPNTEGFSRAALPFGVLVRRELSCEGYSIDLRCPGSDVIMIESANYGRTDDKICDADPFQMENTDCYL
PDAFKIMTQRCNNRTQCIVVTGSDVFPDPCPGTYKYLEVQYECVPYIFVCPGTLKAIVDSPCIYEAQKAGAWCKDPLQAADKIYF
MPWTPYRTDTLIEYASLEDFQNSRQTTTYKLPNRVDGTGFVVYDGAVFFNKERTRNIVKFDLRTRIKSGEAIINYANYHDTSPYR
WGGKTDIDLAVDENGWLWVIYATEQNNGMIVISQLNPYTLRFEATWETVYDKRAASNAFMICGVLYVVRSVYQDNESETGKNSID
YIYNTRLNRGEYVDVPFPNQYQYIAAVDYNPRDNQLYVWNNNFILRYSLEFGPPDPAQVPTTAVTITSSAELFKTIISTTSTTSQK
GPMSTTVAGSQEGSKGTKPPPAVSTTKIPPITNIFPLPERFCEALDSKGIKWPQTQRGMMVERPCPKGTRGTASYLCMISTGTW
NPKGPDLSNCTSHWVNQLAQKIRSGENAAASLANELAKHTKGPVFAGDVSSSVRLMEQLVDILDAQLQELKPSEKDSAGRSYNK
LQKREKTCRAYLKAIVDTVDNLLRPEALESWKHMNSSEQAHTATMLLDTLEEGAFVLADNLLLEPTRVSMPPTENIVLEVAVLSTE
GQIQDFKFPLGKAGSSISQLSANTVKQNSRNLAKLVFIYRSLGQFLSTENATIKLGADFIGRNSTIAVNSHVISVSINKESSRVYL
TDPVLFTLPHIDPDNYFNANCSFWNYSSERTMMGYWSTQGCKLVDNKTTRTTCACSHLTNFAILMAHREIAYKDGVEHELLTIT
WVGIVISLVCLAICIFTFCFRGLQSDRNTIHKNLCLNLFIAEFIFLIGIDKTKYAIACPIFAGLLHFFFLAAFAWMCLEGVQLYLMLVEV
FESEYSRKYYYYVAGYLPATVVGVSAAIDYKSYGTEKACWLHVDNYFIWSFIGPVTFIILLNIIFLVITLCKMVKHSNTLKPDSRLE
NIKSWVLGAFALLCLLGLTWSFGLLFINEETIVMAYLFTIFNAFQGVFIFHICALQKKVRKEYGKCFRHSYCCGGLPTESPHSSVKA
STTRTSARYSSGTQSRIRRMWNDTVRKQSESSFISGDINSTSTLNQGMTGNYLLTNPLLRPHGTNNPYNTLLAETVVCNAPSAP
VFNSPGHSLNNARDTSAMDTLPLNGNFNNSYSLHKGDYNDVSVQVVDCLSLNDTAFEKMIISELVHNNLRGSSKTHNLELTLP
VKPVGIGSSSEDDAIVADASSLMHSDNPGLELHHKELEAPLIPQRTHSLLYQPQKKVKEGTDVSVSQLTAEAEADHLQSPNRDSL
YTSMPNLRDSPYPESSPDMEEDLSPSRSENEIDIYKSMPNLGAGHQLQMCYQISRGNSDGYIIPINKEGCIPEGDVREGQMQL
VTSL

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)