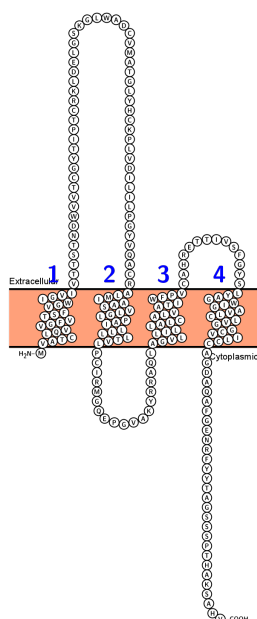


Claudin-11

Organism: Homo sapiens (Human) | Gene names: CLDN11, OSP, OTM



Entry: 075508

Mass: 21.993 Da

Transmembrane: 4

Subcellular location: Cell junction, tight junction. Cell membrane {ECO:0000269|PubMed:20375010}, Multi-pass membrane protein {ECO:0000255}.

Cofactor: -

Extinction coefficient: 1.826

Isoelectric Point: 8.22

PubMed ID: 10700007, 14702039, 15489334, 20375010

Family: -

Function:

Plays a major role in tight junction-specific obliteration of the intercellular space, through calcium-independent cell-adhesion activity. {ECO:0000250}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	No data
DIBMA Glycerol	No data
Amphipol 17	No data
AASTY 6-45	No data
AASTY 6-50	No data
AASTY 6- 55	No data
SMALP 502-E	No data
SMALP 300	No data
SMALP 140	No data
DM	No data
Fos-12	No data
RIPA	No data

DIBMA 12	No data
DIBMA Glucosamine	No data
Amphipol 18	No data
AASTY 11-45	No data
AASTY 11-50	No data
AASTY 11- 55	No data
SMALP 140-I	No data
SMALP 200	No data
DDM	No data
LMNG	No data
Digitonin-A	No data

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

DIBMA 10	No data	DIBMA 12	No data
DIBMA Glycerol	No data	DIBMA Glucosamine	No data
Amphipol 17	No data	Amphipol 18	No data
AASTY 6-45	No data	AASTY 11-45	No data
AASTY 6-50	No data	AASTY 11-50	No data
AASTY 6- 55	No data	AASTY 11- 55	No data
SMALP 502-E	No data	SMALP 140-I	No data
SMALP 300	No data	SMALP 200	No data
SMALP 140	No data	DDM	No data
DM	No data	LMNG	No data
Fos-12	No data	Digitonin-A	No data
RIPA	No data		

Involvement in disease:

-

Binding site:

-

Tissue specificity:

-

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MVATCLQVVGFVTSFVGWIGVIVTTSTNDWVVTGTYIPTCRKLDELGSKGLWADCVMATGLYHCKPLVDILILPGYVQACRALM
IAASVLGLPAILLTTLVPCIRMGQEPGVAKYRRAQLAGVLLILLALCALVATIWFVCAHRETTIVSFGYSLYAGWIGAVLCLVGGC
VILCCAGDAQAFGENRFYYTAGSSSPTHAKSAHV

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)
