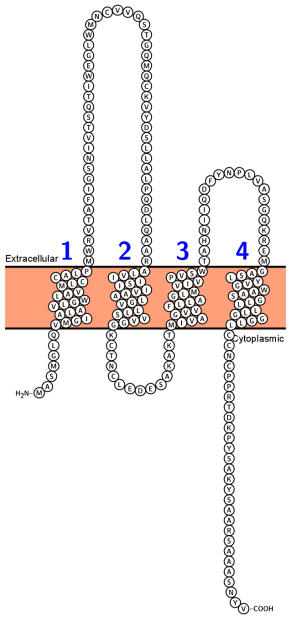
Claudin-4

Organism: Homo sapiens (Human) | **Gene names:** CLDN4, CPER, CPETR1, WBSCR8



Entry: O14493

Mass: 22.077 Da

Transmembrane: 4

Subcellular location: Cell junction, tight junction {ECO:0000250|UniProtKB:O35054}. Cell membrane {ECO:0000269|PubMed:20375010}, Multi-pass membrane protein {ECO:0000255}. Note=CLDN4 is required for tight junction localization in the kidney. {ECO:0000250|UniProtKB:O35054}.

Cofactor: -

Extinction coefficient: 1.922

Isoelectric Point: 8.38

PubMed ID: 9334247, 15489334, 16236711, 20375010, 21269460, 27647526

Family: -

Function:

Channel-forming tight junction protein that mediates paracellular chloride transport in the kidney. Plays a critical role in the paracellular reabsorption of filtered chloride in the kidney collecting ducts. Claudins play a major role in tight junction-specific obliteration of the intercellular space, through calcium-independent cell-adhesion activity. {ECO:0000250|UniProtKB:O35054}.

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Data from experiment(s): Hek293 membrane pellets

DIBMA 10	0.263698	DIBMA 12	0.297544
DIBMA Glycerol	0.349633	DIBMA Glucosamine	0.488168
Amphipol 17	0.367378	Amphipol 18	0.624801
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	0.513197	SMALP 140-I	NaN
SMALP 300	NaN	SMALP 200	0.65147
SMALP 140	NaN	DDM	0.67855
DM	0.830982	LMNG	0.722431
Fos-12	0.722711	Digitonin-A	0.575347
RIPA	0.373794		

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:

Note=CLDN4 is located in the Williams-Beuren syndrome (WBS) critical region. WBS results from a hemizygous deletion of several genes on chromosome 7q11.23, thought to arise as a consequence of unequal crossing over between highly homologous low-copy repeat sequences flanking the deleted region.

Binding site:

-

Tissue specificity:

-

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3D (X-ray crystallography):

X-ray crystallography (2)

Pharmaceutical use:

-

AS sequence:

MASMGLQVMGIALAVLGWLAVMLCCALPMWRVTAFIGSNIVTSQTIWEGLWMNCVVQSTGQMQCKVYDSLLALPQDLQAAR
ALVIISIIVAALGVLLSVVGGKCTNCLEDESAKAKTMIVAGVVFLLAGLMVIVPVSWTAHNIIQDFYNPLVASGQKREMGASLYVG
WAASGLLLLGGGLLCCNCPPRTDKPYSAKYSAARSAAASNYV

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)