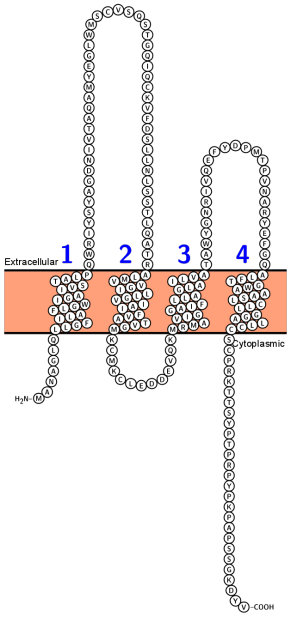
Claudin-1

Organism: Homo sapiens (Human) | **Gene names:** CLDN1, CLD1, SEMP1, UNQ481/PRO944



Entry: O95832

Mass: 22.744 Da

Transmembrane: 4

Subcellular location: Cell junction, tight junction {ECO:0000269|PubMed:20375010, ECO:0000269|PubMed:23407391}. Cell membrane {ECO:0000269|PubMed:23704991}, Multi-pass membrane protein {ECO:0000255}. Basolateral cell membrane {ECO:0000269|PubMed:20375010}. Note=Associates with CD81 and the CLDN1-CD81 complex localizes to the basolateral cell membrane. {ECO:0000269|PubMed:20375010}.

Cofactor: -

Extinction coefficient: 1.821

Isoelectric Point: 8.41

PubMed ID: 9931503, 10828592, 11071387, 12975309, 15489334, 15521008, 16619213, 17325668, 20375010, 21269460, 21516087, 23407391, 24074594, 23704991, 24038151

Family: -

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Function:

Claudins function as major constituents of the tight junction complexes that regulate the permeability of epithelia. While some claudin family members play essential roles in the formation of impermeable barriers, others mediate the permeability to ions and small molecules. Often, several claudin family members are coexpressed and interact with each other, and this determines the overall permeability. CLDN1 is required to prevent the paracellular diffusion of small molecules through tight junctions in the epidermis and is required for the normal barrier function of the skin. Required for normal water homeostasis and to prevent excessive water loss through the skin, probably via an indirect effect on the expression levels of other proteins, since CLDN1 itself seems to be dispensable for water barrier formation in keratinocyte tight junctions (PubMed:23407391). {ECO:0000269|PubMed:23407391}.; (Microbial infection) Acts as a co-receptor for hepatitis C virus (HCV) in hepatocytes (PubMed:17325668, PubMed:20375010, PubMed:24038151). Associates with CD81 and the CLDN1-CD81 receptor complex is essential for HCV entry into host cell (PubMed:20375010). Acts as a receptor for dengue virus (PubMed:24074594). {ECO:0000269|PubMed:17325668, ECO:0000269|PubMed:20375010, ECO:0000269|PubMed:24038151, ECO:0000269|PubMed:24074594}.

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	NaN
SMALP 140	NaN	DDM	1
DM	NaN	LMNG	NaN
Fos-12	NaN	Digitonin-A	NaN
RIPA	NaN		

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

DIBMA 10	NaN	DIBMA 12	NaN
DIBMA Glycerol	NaN	DIBMA Glucosamine	No data
Amphipol 17	NaN	Amphipol 18	NaN
AASTY 6-45	No data	AASTY 11-45	NaN
AASTY 6-50	0.349717706	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	NaN	SMALP 200	NaN
SMALP 140	No data	DDM	0.933603942
DM	No data	LMNG	0.777378619
Fos-12	No data	Digitonin-A	0
RIPA	No data		

Involvement in disease:

Ichthyosis-sclerosing cholangitis neonatal syndrome (NISCH) [MIM:607626]: A rare autosomal recessive complex ichthyosis syndrome characterized by scalp hypotrichosis, scarring alopecia, mild diffuse ichthyosis, sclerosing cholangitis and leukocyte vacuolization. {ECO:0000269|PubMed:15521008, ECO:0000269|PubMed:16619213}. Note=The disease is caused by variants affecting the gene represented in this entry.

Binding site:

-

Tissue specificity:

Strongly expressed in liver and kidney. Expressed in heart, brain, spleen, lung and testis. {ECO:0000269|PubMed:9931503}.

3D (X-ray crystallography):

-

Pharmaceutical use:

-

AS sequence:

MANAGLQLLGFILAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQIQCKVFDSLLNLSSTLQATRALMV
VGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYDPMTPVNARYEFGQALFTGWA
AASLCLLGGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV

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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)