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Tumor necrosis factor receptor superfamily member 6

Organism: Homo sapiens (Human) | **Gene names:** FAS, APT1, FAS1, TNFRSF6

Entry: P25445

Mass: 37.732 Da

Transmembrane: 1

Subcellular location: [Isoform 1]: Cell membrane {ECO:0000269|PubMed:1713127, ECO:0000269|PubMed:25301068}, Single-pass type I membrane protein {ECO:0000305}. Membrane raft {ECO:0000269|PubMed:25301068}., [Isoform 2]: Secreted., [Isoform 3]: Secreted., [Isoform 4]: Secreted., [Isoform 5]: Secreted., [Isoform 6]: Secreted.

Cofactor: -

Extinction coefficient: 0.735

Isoelectric Point: 8.29

PubMed ID: 1713127, 1375228, 7575433, 7533181, 8598453, 8648105, 17336828, 14702039, 15164054, 15489334, 7538908, 10542291, 10535980, 14759258, 15465831, 18846110, 18691976, 18669648, 19159218, 21109225, 20068231, 21269460, 22171320, 23955153, 24275569, 25301068, 30979585, 8967952, 19118384, 24914971, 7540117, 8929361, 9028321, 9028957, 9322534, 9787134, 9821419, 10090885, 10515860, 10340403, 9927496, 10620127, 11418480, 20935634

Family: -

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Function:

Receptor for TNFSF6/FASLG. The adapter molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted isoforms 2 to 6 block apoptosis (in vitro). {ECO:0000269|PubMed:19118384, ECO:0000269|PubMed:7533181}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	0.188704	DIBMA 12	NaN
DIBMA Glycerol	NaN	DIBMA Glucosamine	NaN
Amphipol 17	0.853371	Amphipol 18	0.962741
AASTY 6-45	NaN	AASTY 11-45	0.0881281
AASTY 6-50	0.478154	AASTY 11-50	NaN
AASTY 6- 55	0.286885	AASTY 11- 55	0.0799744
SMALP 502-E	0.319469	SMALP 140-I	0.392393
SMALP 300	0.467791	SMALP 200	0.767631
SMALP 140	NaN	DDM	0.336623
DM	0.830489	LMNG	0.770784
Fos-12	0.445264	Digitonin-A	0.386274
RIPA	0.575492		

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

DIBMA 10	NaN	DIBMA 12	NaN
DIBMA Glycerol	0.696359873	DIBMA Glucosamine	No data
Amphipol 17	0.862558067	Amphipol 18	0.811264753
AASTY 6-45	No data	AASTY 11-45	0.601687312
AASTY 6-50	0.841077268	AASTY 11-50	No data
AASTY 6- 55	0.441849649	AASTY 11- 55	No data
SMALP 502-E	0.509622216	SMALP 140-I	No data
SMALP 300	0.5578686	SMALP 200	NaN
SMALP 140	No data	DDM	1
DM	No data	LMNG	0.968748152
Fos-12	No data	Digitonin-A	0.504631579
RIPA	No data		

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Involvement in disease:

Autoimmune lymphoproliferative syndrome 1A (ALPS1A) [MIM:601859]: A disorder of apoptosis that manifests in early childhood and results in the accumulation of autoreactive lymphocytes. It is characterized by non-malignant lymphadenopathy with hepatosplenomegaly, and autoimmune hemolytic anemia, thrombocytopenia and neutropenia. {ECO:0000269|PubMed:10090885, ECO:0000269|PubMed:10340403, ECO:0000269|PubMed:10515860, ECO:0000269|PubMed:11418480, ECO:0000269|PubMed:17336828, ECO:0000269|PubMed:20935634, ECO:0000269|PubMed:7540117, ECO:0000269|PubMed:8929361, ECO:0000269|PubMed:9028321, ECO:0000269|PubMed:9028957, ECO:0000269|PubMed:9322534, ECO:0000269|PubMed:9821419, ECO:0000269|PubMed:9927496}. Note=The disease is caused by variants affecting the gene represented in this entry.

Binding site:

-

Tissue specificity:

Isoform 1 and isoform 6 are expressed at equal levels in resting peripheral blood mononuclear cells. After activation there is an increase in isoform 1 and decrease in the levels of isoform 6. {ECO:0000269|PubMed:7575433}.

3D (X-ray crystallography):

Model (1); X-ray crystallography (4); NMR spectroscopy (2)

Pharmaceutical use:

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AS sequence:

MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVP
CQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNSTVCEHCDPCTKCEHGIIKECTLTSNTKCKEEGS
RSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQGSHESPTLNPETVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVN
EAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV

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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)