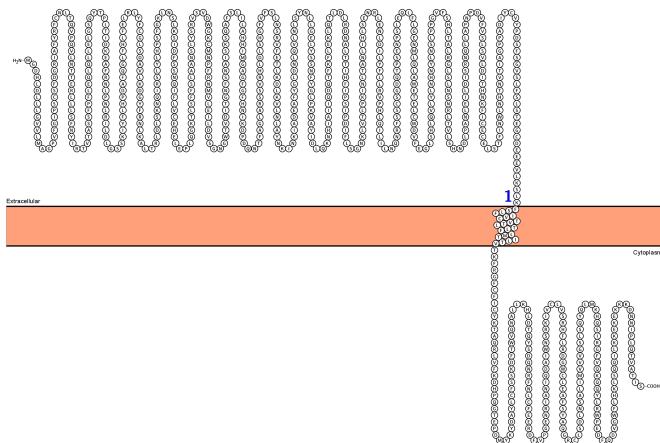


Toll-like receptor 5

Organism: Homo sapiens (Human) | **Gene names:** TLR5, TIL3



Entry: O60602

Mass: 97.834 Da

Transmembrane: 1

Subcellular location: Cell membrane

{ECO:0000269|PubMed:24778236}, Single-pass type I membrane protein {ECO:0000255}.

Cofactor: -

Extinction coefficient: 0.985

Isoelectric Point: 6.21

PubMed ID: 9596645, 18810425, 19179655, 19924287, 16710414, 15489334, 9435236, 15340161, 11489966, 11323673, 16027372, 17157808, 17442957, 18490781, 20855887, 23447684, 24778236, 29934223, 22173220, 14623910

Family: -

Function:

Pattern recognition receptor (PRR) located on the cell surface that participates in the activation of innate immunity and inflammatory response (PubMed:11323673, PubMed:18490781). Recognizes small molecular motifs named pathogen-associated molecular pattern (PAMPs) expressed by pathogens and microbe-associated molecular patterns (MAMPs) usually expressed by resident microbiota (PubMed:29934223). Upon ligand binding such as bacterial flagellins, recruits intracellular adapter proteins MYD88 and TRIF leading to NF-kappa-B activation, cytokine secretion and induction of the inflammatory response (PubMed:20855887, PubMed:11489966). Plays thereby an important role in the relationship between the intestinal epithelium and enteric microbes and contributes to the gut microbiota composition throughout life (By similarity). {ECO:0000250|UniProtKB:Q9JLF7, ECO:0000269|PubMed:11323673, ECO:0000269|PubMed:11489966, ECO:0000269|PubMed:18490781, ECO:0000269|PubMed:20855887, ECO:0000269|PubMed:29934223}.

Data from experiment(s): Hek293 membrane pellets

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		

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:

Systemic lupus erythematosus 1 (SLEB1) [MIM:601744]: A chronic, relapsing, inflammatory, and often febrile multisystemic disorder of connective tissue, characterized principally by involvement of the skin, joints, kidneys and serosal membranes. It is of unknown etiology, but is thought to represent a failure of the regulatory mechanisms of the autoimmune system. The disease is marked by a wide range of system dysfunctions, an elevated erythrocyte sedimentation rate, and the formation of LE cells in the blood or bone marrow. Note=Disease susceptibility is associated with variants affecting the gene represented in this entry.

Binding site:

-

Tissue specificity:

Highly expressed on the basolateral surface of intestinal epithelia (PubMed:11489966). Expressed also in other cells such as lung epithelial cells (PubMed:11489966, PubMed:18490781). {ECO:0000269|PubMed:11489966, ECO:0000269|PubMed:18490781}.

3D (X-ray crystallography):

Model (1); Electron microscopy (1)

Pharmaceutical use:

-

AS sequence:

MGDHLDLLLGVVLMAGPVFGIPSCSFDGRIAFYRFCNLTQVPQVLNTERLLLSFNIRYRTVTASSFPFLEQLQLLELGSQYTPLTID
KEAFRNLPNLRILDGSSKIYFLHPDAFQGLFHLFELRLYFCGLSDAVLKDG YFRNLKALTRDL SKNQIRSLYLHPSFGKLNLSKSI
DFSSNQIFLVCEHELEPLQGKTL SFFSLAANSLSRVSV DWGKCMNPFRNMVLEILDVSGNGWTV DITGNFSNAISKSAFSLIL
AHHIMGAGFGFHNKDPDQNTFAGLARSSVRHLDLSHG FVFSLSNRVFETL KDLKVLNLAYNKINKIAD EAFYGLDNLQVLNLSY
NLLGELYSSNFYGLPKVAYIDLQKNHIAIIQDQTFKFLEKLQTL DLRDNALTTIHFI PSIPDIFLSGNKLVTL PKINLTANLIHLSENRL
ENLDILYFLLRVPHLQILILNQNRFS SCGDQTPSENPSLEQLFL GENMLQLAWETELCWDVFEGLSHLQVLYLNHNYLNSLPPG
VFSHLTALRGLSLNSNRLTVLSHNDLPANLEILDISR NQLLAPNP DVFVSLSVLDITHNKFICECELS TFINWLNHTNVTIAGPPADI
YCVYPDSFSGVSLFSLSTEGCDEEEVLKSLKFS LFIVCTVTLTFLMTILT VTKFRGFCFICYKTAQRLVFKDHPQGTEPDMYKYDAY
LCFSSKDFTWVQNALLKHLDTQYSDQNRFNLCFEERDFVPGENRIANIQDAIWNSRKIVCLVSRHFLRDGWCLEAFSYAQGRCL
SDLNSALIMVVVGSLSQYQLMKHQ SIRGFVQKQYLRWPEDFQDVGWFLHKLSSQQLKKEKEKKKDNNIPLQTVATIS

Creditnotes:

The protein visualizations are generated with the help of Protter:

Omasits, U., Ahrens, C.H., Müller, 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)
