CD47
Rabbit Monoclonal antibody(Mab)
Catalog # AD80429

Specification

CD47 - Product info

Application	**IHC-P, IHC**
Primary Accession	[Q08722]
Reactivity	**Human**
Host	**Rabbit**
Clonality	**Monoclonal**
Calculated MW	**35214**

CD47 - Additional info

Gene Name	**CD47**

Other Names
Leukocyte surface antigen CD47, Antigenic surface determinant protein OA3, Integrin-associated protein, IAP, Protein MER6, CD47, CD47, MER6

Dilution
IHC-P~~Ready-to-use
IHC~~Ready-to-use

Storage	**This product is stored at 2-8 °C, please use it within the expiration date.**
Precautions	**CD47 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.**

CD47 - Protein Information

Name CD47

Synonyms	**MER6**
Function	**Has a role in both cell adhesion by acting as an adhesion receptor for THBS1 on platelets, and in the modulation of integrins. Plays an important role in memory formation and synaptic plasticity in the hippocampus (By similarity). Receptor for SIRPA, binding to which prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells. Interaction with SIRPG mediates cell-cell adhesion, enhances superantigen-dependent T-cell-mediated proliferation and costimulates T-cell activation. May play a**

	role in membrane transport and/or integrin dependent signal transduction. May prevent premature elimination of red blood cells. May be involved in membrane permeability changes induced following virus infection.
Cellular Location	**Cell membrane; Multi-pass membrane protein**
Tissue Location	**Very broadly distributed on normal adult tissues, as well as ovarian tumors, being especially abundant in some epithelia and the brain EMBL; X69398; CAA49196.1; -; mRNA EMBL; Z25521; CAA80977.1; -; mRNA EMBL; BT006907; AAP35553.1; -; mRNA EMBL; AK289813; BAF82502.1; -; mRNA EMBL; CH471052; EAW79733.1; -; Genomic_DNA EMBL; CH471052; EAW79734.1; -; Genomic_DNA EMBL; BC010016; AAH10016.1; -; mRNA EMBL; BC012884; AAH12884.1; -; mRNA EMBL; BC037306; AAH37306.1; -; mRNA CCDS; CCDS43125.1; -. [Q08722-3] CCDS; CCDS43126.1; -. [Q08722-1] PIR; A48997; A48997 RefSeq; NP_001768.1; NM_001777.3. [Q08722-1] RefSeq; NP_942088.1; NM_198793.2. [Q08722-3] UniGene; Hs.446414; - PDB; 2JJS; X-ray; 1.85 A; C/D=20-136 PDB; 2JJT; X-ray; 2.30 A; C/D=20-136 PDB; 2VSC; X-ray; 1.90 A; A/B/C/D=20-136 PDB; 4CMM; X-ray; 1.92 A; B=20-136 PDB; 4KJY; X-ray; 1.93 A; A/C=19-135 PDB; 5IWL; X-ray; 2.80 A; C/D=20-132 PDB; 5TZ2; X-ray; 2.30 A; C=19-141 PDB; 5TZT; X-ray; 2.89 A; C/D=20-141 PDB; 5TZU; X-ray; 2.10 A; C=19-141 PDBsum; 2JJS; - PDBsum; 2JJT; - PDBsum; 2VSC; - PDBsum; 4CMM; - PDBsum; 4KJY; - PDBsum; 5IWL; - PDBsum; 5TZ2; - PDBsum; 5TZT; - PDBsum; 5TZU; - ProteinModelPortal; Q08722; - SMR; Q08722; - BioGrid; 107399; 27 CORUM; Q08722; - DIP; DIP-39948N; - IntAct; Q08722; 12 MINT; Q08722; - STRING; 9606.ENSP00000355361; - ChEMBL; CHEMBL3714583; - TCDB; 1.N.1.1.1; the osteoclast fusion complex (ofc) family GlyConnect; 1456; - iPTMnet; Q08722; - PhosphoSitePlus; Q08722; - SwissPalm; Q08722; - BioMuta; CD47; - DMDM; 1171879; - EPD; Q08722; - jPOST; Q08722; - MaxQB; Q08722; - PaxDb; Q08722; - PeptideAtlas; Q08722; - PRIDE; Q08722; - ProteomicsDB; 58643; - ProteomicsDB; 58644; -. [Q08722-2] ProteomicsDB; 58645; -. [Q08722-3] ProteomicsDB; 58646; -. [Q08722-4] DNASU; 961; - Ensembl; ENST00000355354; ENSP00000347512;**

ENSG00000196776. [Q08722-3] Ensembl; ENST00000361309; ENSP00000355361; ENSG00000196776. [Q08722-1] GeneID; 961; - KEGG; hsa:961; - UCSC; uc003dwt.2; human. [Q08722-1] CTD; 961; - DisGeNET; 961; - EuPathDB; HostDB:ENSG00000196776.14; - GeneCards; CD47; - HGNC; HGNC:1682; CD47 HPA; CAB016055; - HPA; HPA044659; - MIM; 601028; gene neXtProt; NX_Q08722; - OpenTargets; ENSG00000196776; - PharmGKB; PA26222; - eggNOG; ENOG410IJTS; Eukaryota eggNOG; ENOG41113GI; LUCA GeneTree; ENSGT00390000007697; - HOGENOM; HOG000013020; - HOVERGEN; HBG003808; - InParanoid; Q08722; - KO; K06266; - OMA; WGQFGIV; - OrthoDB; 1287706at2759; - PhylomeDB; Q08722; - TreeFam; TF336026; - Reactome; R-HSA-202733; Cell surface interactions at the vascular wall Reactome; R-HSA-216083; Integrin cell surface interactions Reactome; R-HSA-391160; Signal regulatory protein family interactions Reactome; R-HSA-6798695; Neutrophil degranulation SIGNOR; Q08722; - ChiTaRS; CD47; human EvolutionaryTrace; Q08722; - GeneWiki; CD47; - GenomeRNAi; 961; - PRO; PR:Q08722; - Proteomes; UP000005640; Chromosome 3 Bgee; ENSG00000196776; Expressed in 230 organ(s), highest expression level in visceral pleura ExpressionAtlas; Q08722; baseline and differential Genevisible; Q08722; HS GO; GO:0009986; C:cell surface; IDA:ARUK-UCL GO; GO:0070062; C:extracellular exosome; IBA:GO_Central GO; GO:0005887; C:integral component of plasma membrane; IBA:GO_Central GO; GO:0005886; C:plasma membrane; TAS:Reactome GO; GO:0035579; C:specific granule membrane; TAS:Reactome GO; GO:0070821; C:tertiary granule membrane; TAS:Reactome GO; GO:0098632; F:cell-cell adhesion mediator activity; IPI:ARUK-UCL GO; GO:0086080; F:protein binding involved in heterotypic cell-cell adhesion; ISS:ARUK-UCL GO; GO:0070053; F:thrombospondin receptor activity; IPI:BHF-UCL GO; GO:0016477; P:cell migration; ISS:ARUK-UCL GO; GO:0071346; P:cellular response to interferon-gamma; ISS:ARUK-UCL GO; GO:0071347; P:cellular response to interleukin-1; ISS:ARUK-UCL GO; GO:0071349; P:cellular response to interleukin-12; IMP:ARUK-UCL GO;

GO:0030198; P:extracellular matrix organization; TAS:Reactome GO; GO:0007229; P:integrin-mediated signaling pathway; TAS:ProtInc GO; GO:0050900; P:leukocyte migration; TAS:Reactome GO; GO:0035696; P:monocyte extravasation; ISS:ARUK-UCL GO; GO:1905450; P:negative regulation of Fc-gamma receptor signaling pathway involved in phagocytosis; ISS:ARUK-UCL GO; GO:0043312; P:neutrophil degranulation; TAS:Reactome GO; GO:0008228; P:opsonization; IEA:Ensembl GO; GO:0008284; P:positive regulation of cell population proliferation; IDA:UniProtKB GO; GO:0022409; P:positive regulation of cell-cell adhesion; IDA:UniProtKB GO; GO:0050729; P:positive regulation of inflammatory response; IBA:GO_Central GO; GO:0050766; P:positive regulation of phagocytosis; IBA:GO_Central GO; GO:0051496; P:positive regulation of stress fiber assembly; ISS:ARUK-UCL GO; GO:0050870; P:positive regulation of T cell activation; IDA:UniProtKB GO; GO:0032649; P:regulation of interferon-gamma production; IMP:ARUK-UCL GO; GO:0032653; P:regulation of interleukin-10 production; IMP:ARUK-UCL GO; GO:0032655; P:regulation of interleukin-12 production; IMP:ARUK-UCL GO; GO:0032675; P:regulation of interleukin-6 production; IMP:ARUK-UCL GO; GO:0045428; P:regulation of nitric oxide biosynthetic process; ISS:ARUK-UCL GO; GO:0032680; P:regulation of tumor necrosis factor production; IMP:ARUK-UCL GO; GO:0009617; P:response to bacterium; IEA:Ensembl CDD; cd16090; IgV_CD47; 1 Gene3D; 2.60.40.10; -; 1 InterPro; IPR006704; CD47 InterPro; IPR013147; CD47_TM InterPro; IPR013270; CD47_Vset InterPro; IPR007110; Ig-like_dom InterPro; IPR036179; Ig-like_dom_sf InterPro; IPR013783; Ig-like_fold InterPro; IPR037805; IgV_CD47 PANTHER; PTHR10613; PTHR10613; 1 Pfam; PF04549; CD47; 1 Pfam; PF08204; V-set_CD47; 1 SUPFAM; SSF48726; SSF48726; 1 PROSITE; PS50835; IG_LIKE; 1 1: Evidence at protein level; 3D-structure; Alternative splicing; Cell adhesion; Cell membrane; Complete proteome; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunoglobulin domain; Membrane; Phosphoprotein; Pyrrolidone carboxylic acid; Reference proteome; Signal;

Transmembrane; Transmembrane helix SIGNAL 1 18 CHAIN 19 323 Leukocyte surface antigen CD47 /FTId=PRO_0000014880 TOPO_DOM 19 141 Extracellular. TRANSMEM 142 162 Helical. TOPO_DOM 163 176 Cytoplasmic. TRANSMEM 177 197 Helical. TOPO_DOM 198 207 Extracellular. TRANSMEM 208 228 Helical. TOPO_DOM 229 235 Cytoplasmic. TRANSMEM 236 256 Helical. TOPO_DOM 257 268 Extracellular. TRANSMEM 269 289 Helical. TOPO_DOM 290 323 Cytoplasmic. DOMAIN 19 127 Ig-like V-type MOD_RES 19 19 Pyrrolidone carboxylic acid MOD_RES 89 89 Phosphoserine {ECO:0000250|UniProtKB:P97829} CARBOHYD 23 23 N-linked (GlcNAc...) asparagine CARBOHYD 34 34 N-linked (GlcNAc...) asparagine CARBOHYD 50 50 N-linked (GlcNAc...) asparagine CARBOHYD 73 73 N-linked (GlcNAc...) asparagine CARBOHYD 111 111 N-linked (GlcNAc...) asparagine CARBOHYD 206 206 N-linked (GlcNAc...) asparagine DISULFID 33 263 DISULFID 41 114 VAR_SEQ 293 323 Missing (in isoform OA3-293) /FTId=VSP_002535 VAR_SEQ 304 305 KA -> NN (in isoform OA3-305) {ECO:0000303|PubMed:15489334, ECO:0000303|PubMed:7691831, ECO:0000303|Ref.3} /FTId=VSP_002536 VAR_SEQ 306 323 Missing (in isoform OA3-305) {ECO:0000303|PubMed:15489334, ECO:0000303|PubMed:7691831, ECO:0000303|Ref.3} /FTId=VSP_002537 VAR_SEQ 312 323 Missing (in isoform OA3-312) /FTId=VSP_002538 STRAND 26 30 {ECO:0000244|PDB:2JJS} STRAND 35 39 {ECO:0000244|PDB:2JJS} STRAND 42 45 {ECO:0000244|PDB:2JJS} HELIX 51 53 {ECO:0000244|PDB:2JJS} STRAND 54 60 {ECO:0000244|PDB:2JJS} STRAND 63 69 {ECO:0000244|PDB:2JJS} HELIX 70 72 {ECO:0000244|PDB:2JJS} STRAND 74 76 {ECO:0000244|PDB:2JJS} HELIX 79 81 {ECO:0000244|PDB:2JJS} HELIX 88 93 {ECO:0000244|PDB:2JJS} STRAND 98 101 {ECO:0000244|PDB:2JJS} HELIX 102 106 {ECO:0000244|PDB:2JJS} STRAND 110 118 {ECO:0000244|PDB:2JJS} STRAND 121 131 {ECO:0000244|PDB:2JJS} SEQUENCE 323 AA; 35214 MW; 5D20730A2632D550 CRC64; MWPLVAALLL GSACCGSAQL LFNKTKSVEF TFCNDTVVIP CFVTNMEAQN TTEVYVKWKF KGRDIYTFDG ALNKSTVPTD FSSAKIEVSQ LLKGDASLKM DKSDAVSHTG

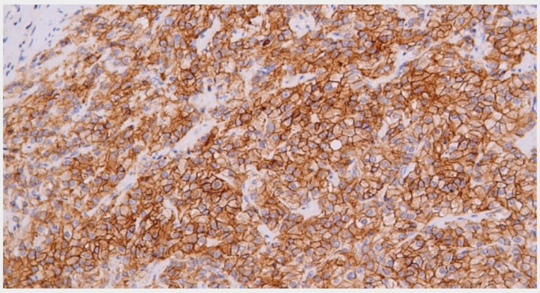
**NYTCEVTELT REGETIIELK YRVVSWFSPN
ENILIVIFPI FAILLFWGQF GIKTLKYRSG
GMDEKTIALL VAGLVITVIV IVGAILFVPG
EYSLKNATGL GLIVTSTGIL ILLHYYVFST
AIGLTSFVIA ILVIQVIAYI LAVVGLSLCI
AACIPMHGPL LISGLSILAL AQLLGLVYMK
FVASNQKTIQ PPRKAVEEPL NAFKESKGMM
NDE**

CD47 - Protocols

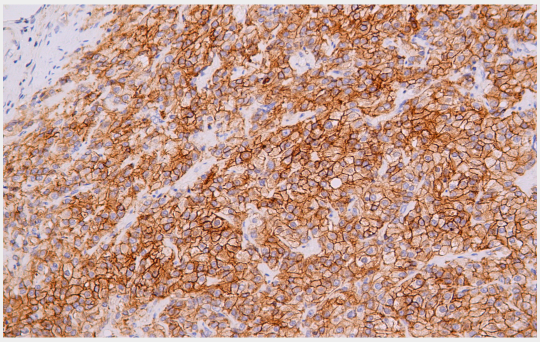
Provided below are standard protocols that you may find useful for product applications.

- Western Blot
- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

CD47 - Images



Prostate cancer



Immunohistochemical analysis of paraffin-embedded prostatic cancer tissue using AD80429 performed on the Abcarta® FAIP-30 Fully automated IHC platform.Tissue was fixed with formaldehyde at room temperature, antigen retrieval was by heat mediation with a EDTA buffer (pH9. 0). Samples were incubated with primary antibody(Ready-to-use) for 15 min at room temperature. AmpSeeTM Detection Systems（Abcepta:AR005） was used as the secondary antibody.