

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

Maintain refrigerated at 2-8°C

Precautions

CD47 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

CD47 - Protein Information

Name CD47

Synonyms

Function

MER6

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

Cellular Location

Tissue Location

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.

Cell membrane; Multi-pass membrane protein

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;
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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;
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Phosphoprotein; Pyrrolidone carboxylic

acid; Reference proteome; Signal;
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surface antigen CD47
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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
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(GlcNAc...) asparagine CARBOHYD 50 50
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73 73 N-linked (GlcNAc...) asparagine
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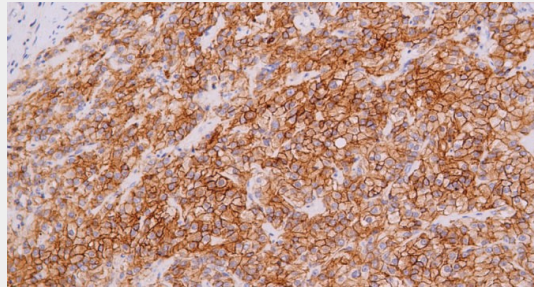
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NYTCEVTELT REGETIIELEK YRVVSWFSPN
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EYSLKNATGL GLIVTSTGIL ILLHYYVFST
AIGLTSFVIA ILVIQVIAYI LAVVGLSLCI
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NDE

CD47 - Protocols

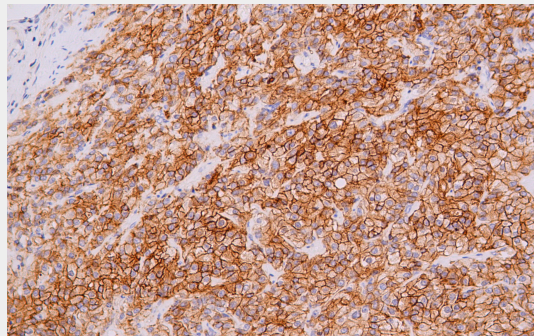
Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [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 (pH 9.0). Samples were incubated with primary antibody (Ready-to-use) for 15 min at room temperature. AmpSee™ Detection Systems [Abcepta:AR005] was used as the secondary antibody.