

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
095996	APCL_HUMAN	Homo sapiens	Adenomatous polyposis coli protein 2	25.009354	S4	S1585;S1587	31492838;37217939	MASSVAPYEQLVROVEALKAENSHL RQELRDNSSHLSKLETETSGMKVEVL KHLQGGKLEQEARVLVSSGQTEVLEQ LKALQMDITSLYNLKFQPPTLGPPEA ARTPEGSPVHSGSPKDSFGELSRA TIRLLEELDRERCFLLEIEKKEEK LWYYSQLQGLSKRLELPHVETQFS MQMDLIRQQLEFEAQHIRSLMEER FGTSDVMVQRAQIRASRLEQIDKEL LEAQDRVQQTPEQALLAVKSVPVDE DPETEVPTHPEDEGTPQPGNSKVEVV FWLLSMLATRDQEDTARTLLAMSSS PESCVAMRRSGCLPLLQILHGTEA AAGGRAGAPGAPGAKDARMRANAA LHNIVFSQPDQGLARKEMRVLHVLE QIRAYCETCWDWLQARDGGPEGGG AGSAPIEPIQICQATCAVMKLSFDE EYRRAMNELGGLQAVAELLOVDYE MHKMTRDPLNLALRRYAGMTLTLNL TFGDVANKATLCARRGCMEAIVAQL ASDSEELHQVSSILRNLSWRADIN SKKVLREAGSVTALVQCVLRAKST LKSVLALWNLSAHSTENKAAICQV DGALGFLVSTLTYKCSQNSLAHIESG GGILRNVSSLVATREDYRQVLRDHN CLQTLLOHLTSHSLTIVSNACGTLW NLSARSARDQELLWDLGAVGMLRN LVHSHKMIAMGSAALRNLLAHR PAKHQAAATAVSPGSCVPSLYVRKQ RALEAELDARHLAQALEHLEKQGGPP AAEAATKKPLPLRHLGLAODYAS DSGCFDDDDAPSSLAATAATGEPAS PAALSFLGSPFLQQAALARTPPTRR GGKEAEKDTSGEAAVAKAKAKLAL AVARIDQLVEDISALHTSSDDSFSL SGDPGQEAPEGRAQSCSPCRGPEG GRREAGSRAHPLRLKAAHASLND SLNSGSASDGYCPREHMLPCPLAAL ASRREDPRCQPPRSLDLDLPGCQ AEPAREATSADARVRTIKLSPTYQH VPLLEGASRAGAEPLAGPGISPGARK QAWLPADHLSKVPEKLAAPLSVAS KALQKLAQEGPLSLSRCSSLSLSS AGRPGPSEGGDLDDSDSLEGLEEA GPSEALDSTWRAPGATSLPVAIAP RRNRGRGLVEDATPSSSENYVQE TPLVLSRCSVSSLGSEFESPSIASSIP SEPCSGQSGTISPSELPSDPSGQTMP PSRSKTPPLAPAPQGPPEATQFSLQ WESYVCRFLDIADCRERCRLPSELD AGSVRFVTEKPDENFSCASSLSALAL HEHYVQQDVELRLLPSACPERGGGA GGAGLHFAGHRRREEGPAPTGSRPR GAADQELLELLRECLGAAPARLRKV ASALVPRRALPVPVYMLVPAPAPQ EDDSCTDSAEGTPVNFSSAASLDE TLQGPDRDQPGGAPGRQRTGRPTS ARQAMGHRHKAGGAGRSAEQSRGA GKNRAGLELPLGRPPSAPADKDGSK PGRTRGDGALQSLCLTTPTEAVYCF YGNDSDEEPPAAAPTPTHRRSAIPR AFTRERPQGRKEAPAPSKAAPAAPPP ARTQPSLIADETPPCYSLSSASLSE PEPSEPPAVHPRGREPAVTKDPGPG GGRDSSSPRAAEELLQRCISSALPR RRPPVSGLRRRKPRATRLDERPAEG SRERGEAAAGSDRASDLDSVEWRAI QEGANSIVTWLHQAAAATREASSES DSILSFVSGLSVSTLQPPKHRKGRQ AEGEMGSARRPEKRGAAASVKTSGSP RSPAGPEKPRGTQKTPGPAVLRG RTVIYVSPAPRAQPKGTPGPRATPR KVAPPCLAQPAAPAKVPSFGQQRSR SLHRPAKTSSELATLSQPPRSATPPAR LAKTPSSSSQTPASQPLPRKRPPV TQAAGALPGGASPVKTPARTLLAK QHKTQRSVRIPIFMQRPARRGPPPL ARAVPEPGPRGRAGTEAGPGARGGR LGLVVRVASLSSGESSEDRSGFRRO	None	None	None	None	None	None	None		

LTFIKESPLRRRSELSAESAASA  
PQGASPRRGRPALPAVFLCSSRCEEL  
RAAPRQGPAPARQPPAARFSPGER  
PARRTTSESPSRLPVRAPAARFETVK  
RYASLPHISVARRPDGAVPAAPASAD  
AARRSSDGEFRPLPRVAAPGTTWRRRI  
RDEDVPHILRSTLPATALPLRGSTPE  
DAPAGPPRKTSDAVVQTEEVAAPK  
TNSSTSPSLETREPPGAPAGGQLSLL  
GSDVDGPSLAKAPISAPFVHEGLGVA  
VGGFPASRHGSPSRSARVPPFNYP  
SPMVVAATTDAAEKAPATASATLLE