

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	p m
Q61315	APC_MOUSE	Mus musculus	Adenomatous polyposis coli protein	46.969581	T879;T881	S105;S109;S742;S746;S778;S906;S985;S1036;S1040;S1359;S1370;S1384;S1391;S1394;T1437;S1565;S1772;S1859;S1861;S1862;S1969;S1971;S2087;S2092;S2125;S2129;S2130;S2132;T2151;S2260;S2270;S2283;S2473;S2535;S2569;S2671;S2674;T2679;S2713;S2726;S2791	22645316;40885482;35822049	MAAASYDQLLKQVEALKMENSNLRFQLEDNSNHLTKLETEASNMKEVLKQLQGSIEDETMTSGQIDLLERLKEFNLDNSNFPQVGLRSLRSMYSYSGREGSVSSRSRSGECSVPVPMGSFPRRTFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYQAQLNLTKRIDSLPLTENFSLQTDMDTRRQLEYEARQIRAAEMEEQLGTCQDMEKRAQRRIARIQIEKDIRVRLQLQSQAEEAERSQRSRHDAASHEAGRQHEGHGVAESNTAASSSGQSPATRVDHETASVLSSTGTHSAPRRLTSHLGTKEVMVYSLLSMLGTHDKDDMSRLLAMSSSQDSCISMRSQSCLPILLIQLLHGNDKDSVLLGNSRSGKEARARASAALHNIHSQPDDKRGRREIRVLHLLQIRAYCETCWEWQEAHEQGMQDQKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGQLQAIALLQVDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDLQVIVASVLRNLSWRADVNSKKTLEVGSVKALMECALEVKKESTLKSVALWNLNSAHCTENKADICAVDGAFLVGTLYRSQNTLAIHESGGILRNVSLLIATNEDHHRQILRENNCLQTLLOHLKSHSLTIVSNACGTLWNLARNPKDQALWDMGAVSMLKNLIHSHKMIAMGSAALRNLMANRPAKYKDNIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQNLGYDYAFDANRHHDSRDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERIGLISAYHPTTENAGTSKRGQLITTTAAQIAKVMEEVSAIHTSQDDRSSASTTEFHCVADDRSAARRSSASHHTSNYNTFKSENSNRTCSPYAKVEYKRSSNDSLNSVTSDDGYGKRGQMKPSVESYSEDDSKFCFSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHVIEDEIKQNEQRQARSONTSYPVYSENTDDKHLKQPHFGQQECVSPYRSRGTSGSETNRMGSSHAINQNVNQSLCQEDDYEDDKPTNYSERYSEEEQHHEEERPTNYSIKYNEEKHHVDQPIDYSLKYATDISSSQKPSFSFSKNSSAQSTKPEHLSPSENTAVPPSNAKRQNLRPSSAQNRNGQTQKGTTCVKVPSINQETIQTYCVEDTPICFSRCSLSSLSSADDEIGCQDTTQEADSANLQTAEVKENDVTRSAEDPATEVPAVSQNRARAKPSRLQASGLSSESTRHNKAVEFSSGAKSPSKGAQTPKSPPEHYVQETPLVFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIHSPLDLPDSPGQTMPPSRSKTPPPPQTVQAKREVPKSKVPAAEKRESGPKQAVNAAVQRVQVLPDVTLLHFATESTPDGFS CSSLSALSLEDPFIQKDVLRIMPPVOENDNGNETESEQPEESNENQDK EVEKPDSEKDLLDDSDDDIEILEECIISAMPTKSSRKAKLAQTASKLPPP VARKPSQLPVYKLLPAQNRLQAQKHVSFTPGDDVPRVYCVETGPIINFSTATSLSDLTIESPPNELATGDGVRAGIQSGEFEKRDITPTEGRSTDDAQRGKISSIVTPDLDDNKAEEGDILAECINSAMPKGKSHKPFVKKIMDQVQASSTSSGANKNQVDTKKKKPTSPVKPMPQNTEYRTRVRKNTDSKVNVTETTFSDNKDSKPSLQTNAKAFNEKLPNNE DRVRGTFALDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVLSREKAELEKESKDSKAEKVTCPREPENSSQAA SKSQASIKHPANRAQSKPVLQKQPTFPQSSKDGPDRAATDEKLQNLAIENTPVCFSRNSSLSSLSDIDQENNNNKESEPIKAEAPANSQGEPSKPQASGY	True	True	2.867	4.692	1.691	1.34	2.581	5.

APKSFHVEDTPVCFSRNSSLSLSID  
SEDDLQECISSAMPKKRPSRLKS  
ESEKQSPRKVGGILAEDLTLDLKDLQ  
RPDSEHAFSPGSENFWDWKAIQEGAN  
SIVSSLHQAAAAACLRSQASSDSDS  
ILSLKSGISLGSPPHLLTPDQEEKPFTS  
NKGPRILKPGKSTLEAKKIESENKG  
IKGGKVKYKSLITGKIRSNSEISSQM  
KQPLPTNMPISIRGRMTMIHIPGLRNS  
SSSTSPVSKKGPPLKTPASKSPSEGP  
GATTSPRGTKPAGKSELSPITRQTSQ  
ISGSNKGSSRSGSRDSTPSRPTQOPL  
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RPDSPTRSQAQTPVLSPLPDMSLST  
HPSVQAGGWRKLPNLSPTIEYNDG  
RPTKRHDIARSHSESPRLPINRAGT  
WKREHSHKSSSLPRVSTWRRTGSSS  
SILSASSESEKAKSEDERHVSSMPA  
PROMKENQVPTKGTWRKIKESDISP  
TGMASQSASSGAASGAESKPLIYQM  
APPVSKTEDVWVRIEDCPINNPRSG  
RSPTGNTPPVIDSVSEKGSSEKIDSK  
DSKDTGKQSVGSGSPVQTVGLETR  
LNSFVQVEAPEQKGTAKPGQSNPV  
SIAETAETCIAERTPFSSSSSKHSSP  
SGTVAARVTFNPNFSPRKSSADSTS  
ARPSQIPTPVSTNTKKRDSKTDITES  
SGAQSPKRHSGSYLVTSV