

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	ex re							
Q61315	APC_MOUSE	Mus musculus	Adenomatous polyposis coli protein	35.313349	NaN	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	35822049;22645316	MAAASYDQLLKQVEALKMENSNLRQLEDNSNHLTKLETASNMKEVLKQLQGSIEDTMTSGQIDLLERLKEFNLDNSNFPVGLRSMKSLRSYGSREGSVSSRSGECSVPVPMGSPFRRTFVNGSRESTGYLEELEKERSLLLDLADLKEEKEKDWWYQQLNLTKRIDSLPLTENFSLQTDMTRRQLEYEARQIRAAEMEEQLGTCQDMEKRAORRIARIQIEKDI LRVRQLLQSQAAEAERSSQSRHDAA SHEAGRQHEGHGVAESNTAASSGQSPATRVDHETASVLSGGTHSAPRRLTSHLGTKVMVYVLSMLGTHDKDDMSRTLLAMSSQDSCISMROSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDCKRGRREIRVLHLEQIRAYCETCWEWQEAHEQGMDQDKNMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AELLQVDCEMYGLTNDHYSVTLRRYAGMALNTLTFGDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLEVGSVKALMECALEVKKESLTKSVLSALWNLSA HCTENKADICAVDGALAFVLVGTLYRSQNTLTAIIESGGILRNVSLLIATNEDHROILRENNCLQTLLOHLKSHSLTIIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNIHSHKHKMIAMGSA AALRNLMANRPKYKDANIMSPGSSLPSLHVRRKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQNLGYDYAFDANRHDDSRSDNFNTGNMTV LSPYLNNTVLPSSSSRGLDSSRSEKDRSLERERIGLSAYHPTTENAGTSKRGLQITTTAAQIAKVMEEVSAIHTSQDDRSSASTTEFHCVADDRSAARRSSASHTHSNTYNTFKSENSNRITCSMPYAKVEYKRSSNDSLNSVTSSDGYGKRGMKPSVESYSEDDSKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHVIEDEIKQNEQRQARSONTSYPVYSENTDDKHLKFQPHFGQCECVSPYRSRGTSSETNRMGSSHAINQNVNQLCQEDDYEDDKPTNYSERYEEEEQHEEEERPTNYSIKYNEEKHHVDQPIDYSLKYATDISSQKPSFSFSKNSSAQSTKPEHLSPSENTAVPPSNAKRQNLPRSSAQRNGQTQKGTCKVPSINQETIQTYCVEDTPICFSRCSSLSLSSADDEIGCDQTTQEADSANLQTAEVKENDVTRSAEDPATEVP AVSQNARAKPSRLQASGLSSESTRHNKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLVFSRCTSVSSLDSEFRSIASSVQSEPCSGMVSGIISPSDLPDS PGQTMPPSRSKTPPPPPQTVQAKREVPKSKVPAAEKRESGPKQTAVNAVQRVQVLPDQVDTLLHFATESTPDGFCSSSLSALSLEPFIQKDVLRIMPVVQENDNGNETESEQPEESNENQDK EVEKPDSEKDLLDSDDDIEILEECIISAMPTKSSRKAKKLAQTASKLPPP VARKPSQLPVYKLLPAQNRQAQKHVSFTPGDDVPRVYCVGTPINFSTATSLSDLTIESPPNELATGDGVRAGIQSGEFKRDITPTEGRSTDDAQRGKISSIVTPDLDDNKAEEDGILAEINSAMPKGKSHKPFVRVKIMDQVQASSTSSGANKNQVDTKKKKTPVVKMPQNT EYRTRVRKNTDSKVNVTETTFSDNKDSKPSLQTNAKAFNEKLPNNE DRVRGTFALDSPHHYTPIEGTPYCFSRNDSLSLDFDDDDVLSREKAELRKGKESKDSEAKVTCRPEPNSSQQAASKSQASIKHPANRAQSKPVLQKQPTFPQSSKDGPDRAATDEKLQNLAIENTPVCFSRNSSLSSLDIDQENNNNKESEPIKEAEPANSQGEPSKPQASGY	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None	N

APKSFHVEDTPVCFSRNSSLSSLSID  
SEDDLQECISSAMPKKRPSRLKS  
ESEKQSPRKVGGILAEDLTLDLKDLQ  
RPDSEHAFSPGSENFWDKAIQEGAN  
SIVSSLHQAAAAACLRSQASSDSDS  
ILSLKSGISLGSPPHLLTPDQEEKPFTS  
NKGPRILKPGKSTLEAKKIESENG  
IKGGKKVYKSLITGKIRSNSEISSQM  
KQPLPTNMPSISRGRMHIHIPGLRNS  
SSSTSPVSKKGPPLKTPASKSPSEGP  
GATTSPRGTKPAGKSELSPITRQTSQ  
ISGSNKGSSRSGSRDSTPSRPTOQPL  
SRPMQSPGRNSISPRNGISPPNKL  
SQLPRTSSPSTASTKSSGSGKMSYTS  
PGRQLSQNLTKQASLSKNASSIPR  
SESASKGLNQMSNGNGSNKKVELS  
RMSSTKSSGSESDSSERPALVRQST  
FIKEAPSPTLRRKLEESASFESLSPSS  
RPDSPTRSQAQTPVLSPSLPDMSLST  
HPSVQAGGWRKLPNLSPTIEYNDG  
RPTKRHDIAARSHSESPRLPINRAGT  
WKREHSHKSSSLPRVSTWRRTGSSS  
SILSASSESEKAKSEDERHVSSMPA  
PRQMKENQVPTKGTWRKIKESDISP  
TGMASQSASSGAASGAESKPLIYQM  
APPVSKTEDVWVRIEDCPINNPRSG  
RSPTGNTPPVIDSVSEKSSSIKDSK  
DSKDTGKQSVGSGSPVQTVGLETR  
LNSFVQVEAPEQKGTAKPGQSNPV  
SIAETAETCIAERTPFSSSSSKHSSP  
SGTVAARVTPFNYPSPRKSADSTS  
ARPSQIPTPVSTNTKKRDSKTDITES  
SGAQSPKRHSGSYLVTSV