

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus |
|--------------|------------|--------------|--------------------------------------|--------------|---------------|--|-------------------------------------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|
| Q9H1A4 | APC1_HUMAN | Homo sapiens | Anaphase-promoting complex subunit 1 | 27.480873 | S286;S298 | S51;S60;S202;S286;T291;S313;S341;S343;S355;S362;S373;S377;T537;S547;S555;T571;S686;S688;S916 | 35289036;23301498;35254053;30059200 | MSNFYEERTTMIARDLQEFVFPFGR DHCKKHPNALNLQRLQLPASELW SSDGAAGLVGSLQEVETIHEKQKESW QLRKGVSEIGEDVDYDEELYVAGNM VIWSKGSQSALAVYKAFVDSVPVQ QALWCDFIISQDKSEKAYSSNEVEK CICILQSSCINMHSIEGKDYIASLPFQ VANVWPVKYGLLFERSASSHEVPPG SPREPLPTMFSMLHPLDEITPLVCKS GSLFGSSRVQYVVDHAMKIVFLNTD PSIVMTYDAVQNVHVSVWTLRRVKSE EENVVLFKFEQGGTPQNVATSSSLT AHLRSLSKGDSFVTSFQNYSSHSIQ SRSTSSPSLHRSFSPISNMAALSRH SPALGVHSFSGVQRFNISHNOSP RHSISHSPNSNSNGSFLAPETEPV ELCIDHLWTETITNIREKNSQASKVF ITSDLCGQKFLCFLVESQLQRCVKF QESNDKTLQIFGVSNTIPAKDAAPVE KIDTMLVLEGSGLVLYTGVVRVVK VFIPGLPAPSLTMSNTMPRPSTPLDG VSTPKPLSKLLGSLDEVLLSPVPEL RDSSKLHDSLYNEDCTFQQLGTYIH SIRDPVHNRTLELSNGSMVRITPE IATSELVQTCQAIKFLPKIEIAVQML VKWYNVHSAPGGPSYHSEWNLFVT CLMNMGMGYNDRDLAWTRNDFEG SLSPIVAPKARPSETGSDDDWEYLL NSDYHQNVESHLLNRSCLSPSEAS QMKDEDFSQNLSLSDSSTLLFTHIPAI FFVLHLVYELKLNLMGEGICSLVE LLVQLARDLKLGPYVDHYRDYPTLV RTTGQVCTIDPGQTFGMHHSFFTS EPPSIYQWVSSCLKGEGMPPYPYLP GICERSRLVLSIALYLGDSESLVSD SSOYLTRITIAPOKQLQVEQENRFSF RHSTSVSSLAERLVVWMTNVGFTLR DLETLPFGIALPIRDYIHCREQPASD WPEAVCLLIGRQDLKQACEGNLKP GKSVLSSDVPSTETEEEDGMND MNHVMSLIWSEDLRVQDVRRLQ SAHPVRVNVQYPELSDHEFIEEKE NRLQLCQRTMALPVGGRGMFTLFSY HPVPTPLPIPKNLTGRAPPRNTIV DLNSGNIDVPPNMTSWASFHNGVA AGLKIAPASQIDSAWIVYKPKHAEL ANEYAGFLMALGLNGHLTKLATLNI HDYLTGHEMTSIGLLLGVSAKLG TMDMSITRLLSIHYPALLPPTSTELDV PHNVQVAAVVGIGLVYQGTARHTA EVLLAEIGRPPGPEMEYCTDRESYSL AAGLALGMVCLGHGNSLIGMSDLN VPEQLYQYMGVGHRRFOTGMHREK HKSPSYQIKEGDTINVDVTCPGATLA LAMIYKTNRSIADWLRAPDTMYL LDFVKPEFLLRRLARLILWDDILP NSKWVDSNVPQIIRENSISLSEIPL CSEDLNLETLQAHVYIAGACLSLG FRFAGSENLSAFNCLHKFAKDFMTY LSAPNASVTGPHNLETCLSVLLSLA MVMAGSGNLKVLQCRFLHMKTTGG EMNYGFHLAHHMALGLLFLGGGRY SLSTSNSSIAALLCALYPHFAHSTD NRYHLQALRHLVLAAPRLLVPVD VDTNTPCYALLEVYKGTQWYEQTK EELMAPTLLPELHLLKQIKVKGPRY WELLIDLKSGTQHLKSKDGLVYV KLKAGQLSYKEDPMGWQSLLAQTV ANRNSEARAFKPETISAFSTDPALLS FAEYFCPTVNMGQKQEIIDLFSV LYECVTQETPEMLPAYIAMDQAIRRL GRREMSSETSELWQIKLVLEFFSSRS HQERLQNHKRGFLFMNSEFLPVVK CTIDNTLDQWLQVGGDMCVHAYLS GQPLEESQLSMLACFLVYHSPVAPQ HLPPIGLEGSTSFAELLFKFKQLKMP VRALLRLAPLLLGNPQPMVM | True | False | 4.178 | 5.0 | 1.193 | 0.825 | 0.759 |