

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondri
Q9Y4K1	CRBG1_HUMAN	Homo sapiens	Beta/gamma crystallin domain-containing protein 1	9.770501	T530;S639;T840;T841;S841;S979;S1317;S1444;S1447	S483;S489;S737;S756;S892;T933	38665916;34019948;39302247;31492838;30379171;39531497;40307207;35132862;40596516;29351928;38253038;39534244;35254053	MPLSPPAQDGPPEPSPCRPPKHTT FHLWRSKKKQPPAPDCGVFVPHPL PAPAGEARALDVVDGKYVVRDSQEF PLHCGESQFFHTTSEALGSLLESGI FKKSRAPQPPEDNRRKPVLGKLGTLF TAGRRRNSRNGLESPTRSNAKPLSP KDVVASPKLPERESERSRSQSSQLK QTDTSSEEGSPRENPREAEGELPESG GPAAPPDAELSPRWSSAAAIVAVQQ CHENDSPQLEPLEAEGEPDPDATTT AKQLHSSPGNSSRQENAETPARSPG EDASPGAGHEQEAF LGVRGAPGSPT QERPAGGLGEAPNGAPSVCAEEGSL GPRNARSQPPKGASDLPGEPPEAGA AHTASSAQADCTARPKGHAHPAKVL TLDIYLSKTEGAQVDEPVVITPRAED CGDWDDMEKRSSGRRSGRRRGSQK STDSPGADAELPESAARDDAVFDDE VAPNAASDNASAEKKVKSRAALDG GVASAASPESKPSPGTKGQLRGESD RSKQPPASSPTKRKGRSRALEAVPA PPASGPRAPAKE SPPKRVDPSPVTK GTAAESGEEAARAIPREL PVKSSLL PEIKPEHKGRLPNHFNRAEAGGRS RELGRAAGAPGASDADGLKPRNHFG VGRSTVTTKVTLPAPKPHVELNLKTP KNLDSLGNHNPFSQPVHKGNTAT KISLFENKRTNSSPRHTDIRQRNTP ASSKTFVGRAKLNLAKKAKEMEQPE KKVMPNSPQNGVLKETAIEKVTV SEEEILPATRGMNGDSSENQALGPQ PNQDDKADVQTDAGCLSEPVASALI PVKDHKLEKEDSEAADSKSLVLEN VDTAQDIPITTVDTKDLPTAMPKPQ HTFSDSQSPAESSPGPSLSAPAPG DVPKDTCVQSPISFPCTDLKVSINH KGCVLPVSRQNNKEMPLELGGETT PPLSTERSPEAVGSECP SRVLVQVRS FVLPVESTQDVSSQVIPESSEVREVQ LPTCHSNPEVVSVASCAPPQEEVL GNEHSHCTAELAAKSGPVIPPASE KTLPIQAQSQSRTPLMAESSPTNSP SSGNHLATPQRPDQVTNGQDSPA LLNISAGSDDSVFDSSDMEKFTI KQMDSAVCMMPKRRKARMPNSPA PHFAMPPIHEDHLEKVFDPKVFTFG LGKKKESQPEMSPALHMLQNLDTK SKLRPKRASAEQSVLFKSLHTNTNG NSEPLVMPEINDKENRDTVNGGIK SRLEKALFSSLLSSLPQDKIFSPSVT SVNTMTAFSTSQNGLSQSSVSQP TTEGAPPCGLNKEQSNLLPDNSLKV FNFNSSSTSHSLKSPSHMEKYPQK EKTKELDLRSNLHLPETKFSLSK LKNDDMEKANHIESVIKSNLPCAN SDTDFMGLFKSSRYDPSISFSGMSL SDTMTLRGVSQKLNPRPGKVVIYS EPDVSEKCIIEVFSIDIQDCSSWSLSPV ILIKVVRGCWILYEQPNFEGHSIPLE EGELESLGLWGIEDILERHEEAESD KPVVIGSIRHVVDYRVSHIDLFTEP EGLGILSSYFDDTEEMQGFVGMQKT CSMKVHWGTWLIYEPPGQGVPFIL EPGEYDLSFWDTEAYIGSMRPLK MGRKVEFPDTPKVVYKPFPEGK CVELETGMCSFVMEGGETEATGD DHLPFTSVGSMKVLRIWVAYEKPG FTGHQYLLEEGEYRDWKAWGGYNG ELQSLRPILGDFSNAHMIMYSEKNF GSKGSSIDVLGIVANLKETGYGVKTQ SINVLGVSVVAYENPDFTGEQYILDK GFYTSFEDWGGKNCISSVQPICLD SFTGPRRRNQIHLFSEPQFQGHSSQ FEETTSQIDDSFSTKSCRVS GGSWV VYDGENFTGNQYVLEEGHYPLSA MGCPPGATFKSLRFIDVEFSEPTILF EREDFKGKKIELNAETVNLRLGPN TQIRSVQVIGGIWVTYEYGSYRGRQF LLSPAEPNWWYEFSGCRQIGSLRPFV QKRIYFRLRNKATGLFMSTNGNLED	False	False	1.721	3.292	0.281

