

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
Q05707	COEA1_HUMAN	Homo sapiens	Collagen alpha-1(XIV) chain	21.876797	T1390;S1391;S1549	NaN	29485866;38253038;38665916	MKIFQRKMRYWLLPPFLAIVYFCTIV QGQVAPPTRLRYNVISHDSIQISWKA PRGKFGGYKLLVTPTSGGKTNQLNL QNTATKAIHQGLMPDQNYTVQIIAYN KDKEKPAQGGQFRKIDLEKRKDKPK RVKVVDRGNRSRPSSEEVKFCQT PAIADIVILVDSWSIGRFNFRLVRH FLENLVTAFDVGSEKTRIGLAQYSGD PRIEWHLNAFSTKDEVIEAVRNLPYK GGNTLTGLALNYIFENSFKPEAGSRT GVSKIILITDQKSDDDIIPPSRNLR SGVELFAIGVKNADVNLQEIASEPD STHVYNVAEFDLMHTVVESLTRTLC SRVEEQDREIKASAHAITGPPELITS EVTARFVMVNWTHAPGNVEKYRVV YYPTRGGKPEVVVDGTVSSTVLKN LMSLLEYQIAVFAIYAHTASEGLRGT ETTLALPMASDLLLYDVTENSMRVK WDAVPGASGYLILYAPLLEGLAGDEK EMKIGETHDIELSGLLPNTYEYTVTV YAMFGEAEASDPVTGQETTLALSPPR NLRISNVGSNSARLTWDPTSRQING YRIVYNNADGTEINEVEVDPITTFPL KGLTPLYTIAFISYDEGQSEPLTG VFTTEVPAQQYLEIDEVTTDSFRVT WHPLSADEGLHKLWIPVYGGKTE EVLKKEEQDSHVIEGLEPGTEYEVSL LAVLDDGSESEVVTAVGTTLDSFWT EPATTIVPTTSVTSVFQTGIRNLVVG DETTSSLRVKWDISDSVQDFRVTY MTAQGDPEEEVIGTVMVPGSQNNL LLKPLLPDTEYKVTVTPIYTDGEGVS VSAPGKTLPSGGPQNLRVSEEWYNR LRITWDPSSSPVKGYRIVYKPVSVPG PTLETFFGADINTILITNLLSGMDYN VKIFASQASGFSALTMVKTFLFLGV TNLQAKHVEMTSLCAHWQVHRHAT AYRVVIESLQDRQKQESTVGGGTTR HCFYGLQPDSEYKISVYTKLQEIIEGP SVSIMEKTQSLPTRPPTFPPTIPPAKE VCKAAKADLVFMVDGWSWSIGDENF NKIISFLYSTVGALNKIGTDGTQVAM VQFTDDPRTEFKLNAYKTETLLDAI KHISYKGGNTKTGKAIKYVRDTLFTA ESGTRRGPKVIVVITDGRSQDDVNK ISREMQLDGYSIFAIGVADADYSELV SIGSKPSARHVFVDDDFDAFKKIEDE LITFVCETASATCPVVHKDGLAGF KMEMMFLVEKDFSSVEGVSMEPG TFNVFPCYQLHKDALVSQPTRYLHP EGLPSDYTISFLFRILPDTPOEPFAL WEILNKNSDPLVGVILDNGGKTLTY FNVDQSGDFQTVTFEGPEIRKIFYGS FHKLHIVVSETLVKVVVIDCKQVGEKA MNASANITSDGVEVLGKMVRSRCP GGNSAPFQLQMFIVCSTSWANTD KCELPGLRDESCPDLPSCSCSE TNEVALGPAGPPGGPGLRGPKGQQG EPGPKGPDGPRGEIIGLPGQPPGP QGPSGLSIQGMMPGMPGEKGEKGD GLPGPGQIPGGVSPGRDGSFGQRG LPGKDGSSGPPGPPGPIGIPGTPGVP GITGSMGPOGALGPPGVPKAGGERG ERGDLSQAMVRSVARQVCEQLIQS HMARYTAILNQIPSHSSSIRTVQGGP GEPGRPGSPGAPGEGQPPGTPGFP NAGVPGTPGERGLTGKGEKGNPGV GTQGPRGPPGAPGSPGESRPGSPGP PGSPGPRGPPGHLGVPGQPGSPGQP GYCDPSSCSAYGVRAPHPDQPEFTF VQDELEAMELWGPV	False	False	1.287	1.889	1.903	4.332	1.312	3.036