

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P02462	CO4A1_HUMAN	Homo sapiens	Collagen alpha-1(IV) chain	22.903221	S1095	NaN	38253038	MGPRLSVWLLLLPAALLLHEEHSRA AAKGGCAGSGCCCKDCHGVKQKQK ERGLPGLQGVIGFPGMQGPEGPQGP PGQKGDTEGEPGLPGTKGTRGPPGAS GYPGNPLPGIPGQDPPGPPGIPGC NGTKGERGPGPLPGFAGNPPGPP GLPGMKGDPGEILGHVPGMLLKGE RGFFGIPGTPGPPGLPGLQGVGPPG FTGPPGPPGPPGPPGEEKQOMGLSFQ GPKGDKGDQGVSGPPGVPQAQVQ EKGDFAFKGEKQKGEPPGQGMPPG VGEKGEPPGKPGPRGKPKDKGDKGE KGSPPGFPGEPPGLIGRQGPQGEK GEAGPPGPPGIVGTGGLGEKGERGY PGTPGPRGEPGPKGFPGLPGQPGPP GLPVPQAGAPGFPGERGEKGRDRGF PGTSLPGPSGRDGLPSPGSPGPPG QPGYTNQIVECQPGPPDQGPPIG GQPGFGEIGEKQKGESECLICDIDG YRGPPGPPGPPGPPGPPGPPGAKGD RGLPGRDGVAGVPGQGTPLGIGQP GAKGEPGEFYFDLRLKDKGDPGFP GQPGMPGRAGSPGRDGHPLPGPK GSPGSLKGERGPPGPPGPPGPPGSRG DTGPPGPPGPPGPPGPPGPPGPPGPPG GGPSPGLPGPKGEPGKIVPLPGPPG AEGLPSPGPPGPPGPPGPPGPPGPPG PGLPGEKGAQVQPGGPPGPPGPPGPPG VDGLPGDMGPPGPPGPPGPPGPPGPPG NPGVQGGKGEPPGPPGPPGPPGPPGPPG GIPGTPGKESIGVPGVPEHGAIGP PGLQIRGEPGPPGPPGPPGPPGPPGPPG IGPPGARGPPGGQPPGPPGPPGPPGPPG EKGFPPGPPGPPGPPGPPGPPGPPGPPG PGITGQSGPLPGPPGPPGPPGPPGPPGPPG SKGEMGMGTPGPPGPPGPPGPPGPPGPPG LPGEKGDHGFPGSSGPPGPPGPPGPPGPPG KGDVGLPGKPGSMDKVDMSGMKG QKGDQGEKQIGPIGKESRGGDPGT PGVPGKDGAGQPPGPPGPPGPPGPPGPPG GTPGAPGLPGPKGPPGPPGPPGPPGPPGPPG EKGVGPPGPPGPPGPPGPPGPPGPPGPPG KQAGPPGPPGPPGPPGPPGPPGPPGPPG PGSPGKGEKESIGIPGMPGPPGPPGPPGPPG GSPGPPGPPGPPGPPGPPGPPGPPGPPGPPG LDGIPGVKGEAGLPGTPGTPGPPGPPGPPG KGEPPGSDGPPGPPGPPGPPGPPGPPGPPG FPGPPGAKGDKGSKGEVGFPLGAGS PGIPGSKGEQGFMPGPPGPPGPPGPPGPPG GSPGHATEGPKGDRGPPGPPGPPGPPGPPG PGPMGPPGPPGPPGPPGPPGPPGPPGPPGPPG PGAPGVPPGPPGPPGPPGPPGPPGPPGPPG GITGSKGDMGPPGPPGPPGPPGPPGPPGPPG LQGIKGDQGDQGVPPGPPGPPGPPGPPGPPG PGPYDIKGEPLGPPGPPGPPGPPGPPGPPG GLPGPKGQQQVTGLVGPVPPGPPGPPGPPG DGAPGQKGEKMPGPPGPPGPPGPPGPPGPPG PGPDGLPGSMGPPGPPGPPGPPGPPGPPGPPG RHSQTIDDPQCPSTGKILYHGYSLLY VQGNERAHGQDLGTAGSCLRFKST MPFLFCNINNVCFASRNDYSYWL STPEPMPMSMAPITGENIRPFISCA VCEAPAMVMVHSTQTIQIPPCPSGW SSLWIGYSFVMHTSAGAEKSGQALA SPGSCLEEFRAPIECHRGTCTNYY ANAYSFWLATIERSEMFKKPTPSTLK AGELRTHVSRQCVMRRT	False	True	2.782	3.137	2.331	4.461	1.246	2.588	4.6