

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracell region
P13611	CSPG2_HUMAN	Homo sapiens	Versican core protein	24.77561	T3141	S2116;S2608;T2617	28411811;28657654;38665916	MFINIKSILWMCSTLIVTHALHKVKV GKSPVPRGSLSGKVSLPCHFSTMP LPPSYNTSEFLRIKWSKIEVDKNGKD LKETTTLVAQNGNIKIGQDYKGRVSV PTHPEAVGDAASLTVVKLLASDAGLYR CDVMYGIEDTQDQTVSLTVDGVVFHY RAATSRYTLNFEEAAQKACLDVGVAVIA TPEQLFAAYEDGFEQCDAGWLADQT VRYPIRAPRVGCYGDKMKGAVRTY GFRSPQETYDVYCYVDHLDGDFVHL TVPSKFTFEEAAKECENQDARLATV GELQAAWRNGFDQCDYGLWSDASV RHPVTVARAQCGGGLLVGRTLYRFE NQTGFPPDSRFDAYCFKPKKEATTID LSILAETASPSLSKEPQMVSDRTPPII PLVDELPIVTEFPPVGNIVSFEQKAT VQPQAITDSLATKLPPTGSKKPPWD MDDYSPSASGPLGKLDISEIKEEVLQ STTGVSHYATDSDWDGVVEDKQTOES VTQIEQIEVGPLVTSMEILKHIPSKEF PVTEPLVTARMILESKTEKMMVSTV SELVTTGHYGFTEGEEDEDRITV GSDESTLIFDQIPEVITVSKTSEDTHI THLEDLESVASTTVSPLIMPDDNNG SSMDDWEERQTSGRITEEFLGKYL TTPFPSQHRTEIELFPYSGDKILVEGI STVIYPSLQTEMTHRRRETELIPEM RTDYTDEIQEITKSPFMGKTEEEV FSGMKLSTSLSEPIHVTESSVEMTKS FDFPTLITKLSAEPTEVRDMEEDFTA TPGTTKYDENITVLLAHGTLVVEAA TVSKWSWDEDNTTSKPLESTEPSAS SKLPPALLTTVGMNGKDKDIPSFTE DGADEFLLIPDSTQKQLEEVTDEDIA AHGKFTIRFQPTTSTGIAEKSTLRDS TTEEKVPPITSTEGQYYATMEGSALG EVEDVDLSKPVSTVPQFAHTSEVEG LAFVYSSTQEPTTYVDSHTIPLSVI PKTDWGVLVSPVSEDEVLGEPSSQD ILVIDQTRLEATISPETMRTTKITEGT TQEEFPWKEQTAEKVPVPSSTAWT PKEAVTPLDEQEGDGSAYTVSEDEL LTGSERVVLETPVVGKIDHSVSYP GAVTEHKVKTDEVVTLTPRIGPKVSL SPGPEQKYETEGSSTTGFTSSLSPFS THITQLMEETTTEKTSLEDIDLGSGL FEKPKATELIEFSTIKVTVPSDITTA SSVDRLHTSAFKPSSAITKKPLIDR EPGEETTSDMVIGESTSHVPPTTLE DIVAKETETDIDREYFTTSSPPATQPT RPPTVEDKEAFGPQALSTPQPPASTK FHPDINVYIEVRENKTRMSDLSVI GHPIDSEKEDPCSEETDPVHDL AEILPEFPDIIIDLYHSENEEEEE CANATDVITTPSVQYINGKHLVTTVP KDPEAAEARRGQFESVAPSQNFSDS SESHTHPFVIAKTELSAVQPNESTE TTESLEVTWKPETYPETSEHFSGGE PDVFPVTFHEEFESGTAKKGAESV TERDTEVGHQAHEHTEPVSFLPEES SGEIAIDQESQKIAFARATEVTFGEE VEKSTSVTYTPTIVPSSASAYVSEEEA VTLIGNPWPDDLSTKESWVEATPR QVVELSGSSIPITEGSGEAEDEDED MFTMVDLSQRNTDITLITLDTSR TESFFVPPATTIYVSEQPSAKVVPTK FVSETDTSSEWISSSTVEEKKRKEEG TTGTASTFEVYSSTQRSQDLILPFEL ESPNVATSSDSGTRKFSMLTTPTO SEREMTDSTPVFTEINTLENLGAQT TEHSSIHQPGVQEGTLTLPSPASVF MEQSGEAAADPETTTVSSFSNLVE YAIQAEKEVAGTLLSPHVETTFSTPT GLVLSVMDRVVAENITQTSREIVIS ERLGEPNYGAIEIRGFSTGFPLEEDFS GDFREYTSVSHPIAKEETVMMEGSG DAAFRDTQTSPTVPTSVHISHISDS EGPSSMTVSTSAFPWEEFTSAEAGS GEQLVTVSSSVVPLPSAVQKFSGTA SSIIDGLGVEGTVNEIDRRSTILPTA	False	True	2.396	2.951	2.663	4.364	4.309	2.809	5.0

EVEGTPKAPVEKEEVKVSQTVSTNFP
QTIEPAKLWSRQEVNPNVPRQIESETT
SEEQIQEEKSFESFQNSPATEQTIIFD
SOTFTETELKTTDYSVLTTKKTYSD
KEMKEEDTSLVNMSTPDPDANGLE
SYTTLPEATEKSHFFLATALVTESIPA
EHVVTDSPIKKEESTKHFPKGMRP
QESDTELLFSGLGSSEVPLTLP
VNFTEVEQINNNTLYPHTSQVESTS
DKIEDFNRMENVAKVGLVPLVQTDI
FEGSGSVTSTTLIEILSDTGAEGPTVA
PLPFSTDIGHQPQNQTVRWAEEIQTS
RPQTITEQDSNKNSSAEINETTSS
TDFLARAYGFEMAKEFVTSAPKPSD
LYYEPSGEGSSEVDIVDSFHSTATTQ
ATRQESSTTFVSDGSLEKHPEVPSAK
AVTADGFPTVSVMLPLHSEQNKSSP
DPTSTLNTVSYERSTDGSGFQDRFR
EFEDSTLKNRKKPTENIIIDLKED
KDLILTTTESTILEILPELTSKNTIIDI
DHTKPVYEDILGMQTDIDTEVPSEP
HDSNDESNDDSTQVQEIYAAVNL
LTEETFEGSADVLASYTQATHDESM
TYEDRSQDLHMGFFHTTGIPAPSTE
TELDVLLPTATSLPIPRKSATVPIEIG
IKAEAKALDDMFESSTLSDGQAIAD
QSEIHTLQGFERTQEEYEDKKHAGP
SFQPEFSSGAEALVDHTPYLSIATT
HLMQDQSVTEVPDVMEGSNPPYTD
TTLAVSTFAKLSSQTPSSPLTIYSGSE
ASGHTEIPQPSALPGIDVGSVMSPQ
DSFKIHNIEATFKPSSEYHLHITEP
PSLSPDTKLEPSEDDGKPELLEEME
ASPTELIAVEGTEILQDFQNKTDGQV
SGEAIKMFPTIKTPEAGTVITTADEIE
LEGATQWPHSTASATYVEAGVVP
WLSPTSERPTLSSSPEINPETQAAL
IRGQDSTIAASEQQVAARILDSNDQA
TVNPFVFNTEVATPPFSLLETSNETD
FLIGINEESVEGTAIYLPDPDRCKMN
PCLNGGTCYPTETSYVCTCVPGYSG
DQCELDDECHSNPCRNATCVDG
FNTFRCLCLPSYVGCALCEQDTETCD
YGWKFKOGQCYKYFAHRRTWDAAE
RECLQGAHLTSILSHEEQMFVNRV
GHDYQWIGLNDKMFHDFRWTG
STLQYENWRPNQPDFSFFSAGEDCVV
IHWENGQWNVPCNYHLTYTCKK
GTVACGQPPVVENAKTFGKMKPRYE
INSLIRYHCKDGFQIRHLPTIRCLGN
GRWAIPKITCMNPSAYQRTYSMKYF
KNSSAKDNSINTSKHHRWSRRW
QESRR