

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9ERB4	CSPG2_RAT	Rattus norvegicus	Versican core protein	23.439218	NaN	S1963;S1964	38843836	MLINMNGILWMCSTLLLTHALHKA KMEENPPVKGSLSGKVLPCHFSTL PTLPPDYNTSEFLRIKWSKIEVDKNG KDIKETTTLVAQDGNIKIGQDYKGRV SVPTHPDDVGDASLTMVKLRASDAG VYRCDEVMYGIEDTQNTMSLAVDGVV FHYRAATSRYTLNFESAQQACLIDIGA VIATPEQLFAAYEDGFEQCDAGWLS DQTVRYPIRAPREGCYGDMMGKEG VRTYGFRRSPQETYDVVYCYVDHLDGD VFHITAPSKFTFEEAAEACANRDARL ATVGELHAAWRNGFDQCDYGWLSD ASVRHPVTVARAQCGGGLLVRTLY RFENQTCFPLPDSRFDAYCFKRSP SIIPKTEWSVSETSVPLEDEVLGKSD QDTLEQTHLEATMSPEALSTIEVTO GETQEEPPQTPGIPFALSSTAVMTKE TTAFEEEEGEGSTYTLSEDRMLTDSEI VPSLETTVPVGTSYPGGAMTQQEVEM DTMVTQMSSIRPTVVLSTEPEVSYEA EGSSPMEFASTLKPFGTQVTQLVEE TTEEGKKTPLDYTDLGSGLFEQPRVT ELPDFSMTPSDISVFTAIDSLHRITP LRPPSPFTEEPHIFKEPSEKTTGDII LPRESVTQHPLTTLMDIIAKKTESDI DHEYHMTSKPPVMQPTRPSVVERK TTSKPOELSTSPPPAGTKFHPDINVYI IEVRENKTGRMSDMVNVNGHPIDSES KEEEPCSEETDPLHDLFAEILPELPD SFEIDYHSEEDDEGEDCVNATDVT TTPSVQYITGKPHVTTVPKNPEAAEA RRGLYESVAPSQNFNTSATDTHQF IPAETELSTTMQFTKSKEATELLEIT WKPETYPETPEHFSSGEPDVFPPLPS HDGKTTKWSEFITESNPNTENPEHK QPKPIPLFPEEFGGGAIDQASQQTIF SRATEVALGKETDQSPTISTSSIRSGS VSVHALEEDPIALTGISQTDSESMSTV ESWVEMTPSQTVFESGSSSAPTIEG SGEVEEYTNKIFNTVTDLPQREPTDT LIPLDMSNIMITDHHIYTPATTAPLD SQLPSTDARPTQFGIQTTTSEWVSST SFEGRKTEEDKERDTNAAHTGEVQP ATERSDRLLLTSELESSNVAASSPLD TWEGFVPETTSTVSEKEMANTTPVF TETSDVANLETQSFHSSSSSQPRVQ EELTTLGKPPPLIFMDLGS GDASTD MEFITASSFTLDLES DTKVKELPST LSPSVETSSSSEPIGLAPSTVLDIEIVE VMNQTSKKT LISELSGKPTSQA EVR DLYPGLGEDFGDSSEYPTVSSTTM KEETVGMGGSENERVKDTQTLSSIP PTSDNINPVPDSKFGSTVASTTAFP WEEFMTSAEGSGEELSSVRSVSLV LPLGVDILPTTESPYFDQEFEEAAV TEAGKQSALPIAVSGNTVDLTENRDI EVNSTMSVDLPQTMPEAKLWSKPE VNPEKQEIGSETVTQDKAQGQKSFE SLHSSLAPEQTTLSESQSLIETEVQTS YYSMLTTMKTYNTNEEVEEEGTSIA HMSTPGPGIKGLESYPTHPPEATGKS YFSASALVTESGPARSVVMDSSSTQ EEESIKLFQKDMILTHKESNDLSFS GLGSGEALPPLPTTSVSLTDMGKINS TLYPETSHMESLGT SILGDNHERMK NVSNEVRTLISETGSISQDSTEAPNT TLDSTRTEESTTSP LPFMKLMDTEH SPKQTLRWEEEIQT HRPQMTGQM TNDNSSVSEAEAAATSAPAFLPETYS VEMTKAFATSPSQTSDLFDANS GEG SGEVDGLDLVYTSRTTQASSQGDSM FASHGFIEKHPEVSRTEGTATDGSPT ASAMFLHQSEYNESSLYPTSTLPSTV TYESPSEGIADGLQDHIRFEVSTLKP	False	True	2.0	2.947	1.348	1.14	0.709	1.984	4.501

SRRKATESVIIDLKEDSKDLGLAITE  
SAIVEILPELTSDRNIIDIDHTKPVYE  
YIPGIQTDLDSDIPLGSHGSSEESLEV  
QEKYEATINLSPTTEAFDGS GDALPA  
GHTQAIYNE SVTPSDGKQPEDISFSF  
ATGIPV SSTETELNTFFPTVSTLHIPS  
KLTTASPEIDKPNIEAISLDDIFESST  
LSDGQAIADQSEVISTLGHLEKTQEE  
YEEKKYGGPSFQPEFFSGVGEVFTD  
APAYV SIGRTYSVAQPLTEFPNVVGO  
SDSTHYEATS AVSSVTELSPQTPSS  
PSPVVIDSGVSEFTEVPHKSAQPAPT  
AASSQK LIEGSFKKVRANIEATIKSLG  
ENDHGTESPMS SPALDISED DSK  
PKLLEDLETSPTKTETSQDSPNKAN  
DQIPGKTAGILAGIKTTESGPVVTAAD  
DMELGDATQRPHSASAPAAFRVETS  
MVPQIPQEPERPTFPSLEINHETHHT  
SLFEESILATSEKQVSRILDYSNQA  
TVSTL DLNTEHSIPPSILDNSNETA  
FLIGSEETVEGTAVYLPDPDLCKTN  
PCLNGGTCYPTETS YVCTCAPGYSG  
DQCELD FDECHSNPCRN GATCVDG  
LNTFRCLCLPSYVGALCEQDTETCD  
YGW HKFQGQCYKYFAHRRTWDAAE  
RECR LQGAHLTSILSHEEQMFVNRV  
GHDYQWIGLNDKMF EHFRRWTDG  
SALQYENWRPNQ PDSFFSAGEDCV  
VIWHENGQWNDVPCNYHLTYTCK  
KGTVACGQPPVENAKTFGKMKPRY  
EINSLIRYHCKDGF IQRHLPTIRCLG  
NGRWAMPKITCMNPSAYQRTYSKK  
YLKNSSSVKDNSINTSKHEHRWSRR  
WQETR