

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P22105	TENX_HUMAN	Homo sapiens	Tenascin-X	19.836548	T643;T3640 (P22105-1);T3889 (P22105-1);S3892 (P22105-1)	NaN	38253038;28657654;28411811;37217939	MMPAQYALTSSLVLLVLLSTARAGP FSSRSNVTLPAHRPPPQPGGHTVGA GVGSPSSQLYEHTVEGGEKQVVFTH RINLPPSTGCGCPPTEPPVLASEVQ ALRVRLEILEELVKGLKEQCTGGCCP ASAQAGTGQTDVRTLCSLHGVDLS RCTCSCEPGWGGPTCSDPDAEIPP SSPPSASGSCPDDCNDQGRVCVRGRC VCFPGYTGPCGWSPCPGDCQGRG RCVQGVVCVCRAGFSGPDCSQRSCPR GCSQRGRCEGGRCVCDPGYTGDDC GMRSCPRGCSQRGRCENGRCVCNP GYTGEDCGVRSCPRGCSQRGRCKD GRCVCDPGYTGEDCGTRSCPWDCG EGGRCVDGRCVCWPGYTGEDCSTR TCPRDCRGRGRCEDEGECICDTGYSG DDCGVRSCPGDCNQGRGEDGRCV CWPGYTGTDGSRACPRDCRGRGR CENGVCVCNAGYSGEDCGVRSCPG DCRGRGRCESGRMCWPGYTGRDC GTRACPGDCRGRGRCDGRCVCNP GFTGEDCGSRRCPGDCRGHGLCED GVCVCDAGYSGEDCSTRSCPGGCRG RGQCLDGRVCEDGYSGEDCGVRQ CPNDCSQHGVCQDGVICWEGYVS EDCSIRTCPSNCHGRGRCEEGRCLC DPGYTGPTCATRMCPADCRGRGRCV QGVCLCHVGYGGEDCGQEEPPASA CPGGCGPRELCRAGQCVCEGFRGP DCAIQTCPGDCRGRGECHDGSCVCK DGYAGEDCGEEVPTIEGMRMHLE ETTVRTEWTPAPGPVDAYEIQFIPTT EGASPPFTARVPSSASAYDQRGLAPG QEYQVTVRALRGTSWGLPASKTITT MIDGPQDLRVAVTPTTLELGWLRP QAEVDRFVVSYSAGNQRVRLEVPP EADGTLTDLMPGVEYVVTVAERG RAVSYPASVRANTGSSPLGLLGTDE PPPSGPSTTQGAQAPLLQQRPELG ELRVLGRDETGRLRVVWTAQPDTFA YFQLRMRVPEGPGAHEEVLPGDVR QALVPPPPPGTPYELSLHGVPVGGKP SDPIIYQGIMDKDEEKPGKSSGPPRL GELTVTDRTSDSLLLRTVPEGEFD SFVIQYKDRDQGPQVVPVEGPQRSA VITSLDPGRKYKFLYGFVGGKRRHGP LVAEAKILPQSDPSPGTPPHLGNLW VTDPTPDSLHLSWTVPEGFDTFMV QYRDRDGRPQVVPVEGPERSFVSS

LDPDHKYRFTLFGIANKKRYGPLTAD
GTTAPERKEEPPRPEFLEQPLLGET
VTGVTPDSLRLSWTVAQGPFDSEFMV
QYKDAQGQPQAVPVAGDENEVTVP
GLDPDRKYKMNLYGLRGRQRVGPE
SVVAKTAPQEDVDETPSPTLGTAP
ESPEEPLLGETVTGSSPDSLFLWT
VPQGSFDSFTVQYKDRDGRPRAVRV
GGKESEVTVGGLEPGHKYMHLYG
LHEGQRVGPVSAVGVTAPQQEETPP
ATESPLEPRLGELTVTDVTPNSVGLS
WTVPEGQFDSFIVQYKDKDGQPQVV
PVAADQREVTVYNLEPERKYKMNM
YGLHDGQRMGPLSVVIVTAPLPPAP
ATEASKPPLEPRLGELTVTDITPDSV
GLSWTVPEGEFDSFVVQYKDRDGQP
QVVPVAADQREVTIPDLEPSRKYKFL
LFGIQDGKRRSPVSVEAKTVARGDA
SPGAPPRLGELWVTDPTPDSLRLSW
TVPEGQFDSFVVQFKDKDGPQVVPV
EGHERSVTVPLDAGRKYRFLLYGLL
GKKRHGPLTADGTTEARSAMDDTGT
KRPPKRLGEELQVTTVTQNSVGLS
WTVPEGQFDSFVVQYKDRDGQPQV
VPVEGSLREVSVPGLDPAHRYKLLLY
GLHHGKRVGPISAVAITAGREETETE
TTAPTPPAPEPHLGELTVEEATSHTL
HLSWMVTEGEFDSFEIQYTD RDGQL
QMVRI GGDRNDITLSGLES DHRYLV
TLYGFSDGKHVGPVHVEALTVPEEE
KPSEPPTATPEPPIKPRLGELTVDAT
PDSL SLSWTVPEGQFDHFLVQYRNG
DGQPKAVRVPGHEEGVTISGLEPDH
KYKMNLYGFHGGQRMGPVSVVGV
AAEEETPSPTEPSMEAPEPAEEPLL
ELTVTGSSPDSL SLSWTVPQGRFDS
FTVQYKDRDGRPQVVRVGEESEVT
VGGLEPGRKYMHLYGLHEGRRVG
PVSAVGVTAPPEEESPDAPLAKLRLGQ
MTVRDITSDSLSLSWTVPEGQFDHF
LVQFKNGDGQPKAVRVPGHEDGVTI
SGLEPDHKYKMNLYGFHGGQRVGP
VSAVGLTAPGKDEEMAPASTEPTP
EPPIKPRLEELTVTDATPDSL SLSW
VPEGQFDHFLVQYKNGDGQPKATR
VPGHEDRVTISGLEPDNKYKMNLYG
FHGGQRVGPVSAIGVTAEEETPSPT
EPSMEAPEPPEEPLLGETVTGSSPD
SLSLSWTVPQGRFDSFTVQYKDRDG
RPQVVRVGEESEVTVGGLEPGRKY
KMHLYGLHEGRRVGPVSTVGV TAPQ
EDVDETPSPTTEPGTEAPGPPEEPLL

ELTVTGSSPDSLSLWVTPQGRFDS
FTVQYKDRDGRPQAVRVGGQESKVT
VRGLEPGRKYMHLYGLHEGRRLG
PVSAVGVTEDEAETTQAVPTMTPEP
PIKPRLGELTMTDATPDSLSLWVTP
EGQFDHFLVQYRNGDGQPKAVRVP
GHEDGVTISGLEPDHXYKMPLYGFH
GGQRVGPISVIGVTAEEETPSPTL
STEAPEPEEPLLGETVTGSSPDSL
SLSWTIPQGHFDSFTVQYKDRDGRP
QVMRVRGEESEVTGGLEPGRKYK
MHLYGLHEGRRVGPVSTVGTAPED
EAETTQAVPTTTPPEPNKPRLGELTV
TDATPDSLSLWVPEGQFDHFLV
QYRNGDGQPKVVRVPGHEDGVTISG
LEPDHXYKMPLYGFHGGQRVGPISV
IGVTAEEETPAPTEPSTEAPEPEEP
LLGETVTGSSPDSLSLWVTPQGRF
DSFTVQYKDRDGRPQVVRGEESE
VTVGGLEPGCKYMHLYGLHEGQR
VGPVSAVGVTAAPKDEAETTQAVPTM
TPEPPKPRLGELTVTDATPDSLSL
WVPEGQFDHFLVQYRNGDGQPKA
VRVPGHEDGVTISGLEPDHXYKMNL
YGFHGGQRVGPVSAIGVTEETPSPT
EPSTEAPEAPEEPLLGETVTGSSPD
SLSLWVTPQGRFDSFTVQYKDRDG
QPQVVRGEESEVTGGLEPGRKY
KMHLYGLHEGQRVGPVSTVGITAPL
PTPLPVEPRLGELAVAAVTSDSVGLS
WTVAQGFDSFLVQYRDAQQQPQA
VPVSGDLRAVAVSGLDPARKYKFLLF
GLQNGKRHGVPVVEARTAPDTKPS
RLGELTVTDATPDSVGLSWTVPEGE
FDSFVQYKDKDGRLOVVPVAANQR
EVTVQGLEPSRKYRFLLYGLSGRKRL
GPISADSTTAPLEKELPPHGLGELTVA
EETSSSLRLSWTVAQGFDSFVQY
RDTDGQPRAVPVAADQRTVTVEDLE
PGKKYKFLLYGLLGGKRLGPVSALG
MTAPEEDTPAPELAPEAPEPEEPRL
GVLTVTDTPDSMRLSWSVAQGFDS
SFVQYEDTNGQPQALLVDGDQSKI
LISGLEPSTPYRFLLYGLHEGKRLGP
LSAEGTTGLAPAGQTSEESRPRLSQL
SVTDVTTSSLRLNWEAPPGAFDSFL
LRFVPSPTLEPHRPLLQRELMV
PGTRHSAVLRDLRSGTLYSLTYGLR
GPHKADSIQGTARTLSPVLESPRDLQ
FSEIRETSKVNWMPPPSRADSFKV
SYQLADGGEPQSVQVDGQARTQKLQ
GLIPGARYEVTVSVRGESEPLTG

