

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9HBL0	TENS1_HUMAN	Homo sapiens	Tensin-1	10.169699	S1271;S1441	S463;S489;T491;S503;T504;S558;S746;S826;S889;S894;S919;T985;S1024;T1028;S1032;S1088;S1092;S1228;S1281;T1293;S1296;T1370;S1373;S1398;S1413;S1418;S1485;S1497;S1504;S1550;S1692	33214551;28657654;30379171;38253038;34019948	MTWICLSCMLWPEDLEAPKTHRFK VKTFKKVKPCGICRQVITQEGCTCKV CSFSCHRKQAKVAAPCVPPSNHEL VPITTENAPKNVVDKGEASRGGNT RKSLEDNGSTRVTPSVQPHLQPIRN MSVSRTMEDSCELDLVYVTERIIAVS FPSTANEENFRSNLREVAQMLKSK HGGNYLLFNLSERRPDITKLHAKVL EFGWPDLHTPALEKICSICKAMDTW LNADPHNVVVLHNKGNRGRIGVVIA AYMHYSNISASADQALDRFAMKRFY EDKIVPIGQPSQRRYVHYFSGLLSGSI KMNNKPLFLHHVIMHGIPNFESKG GCRPFLRIYQAMQPVYTSGIYNIPGD SQTSVCITIEPGLLLKGDILLKCYHKK FRSPARDVIFRVQFHTCAIHDLGVVF GKEDLDDAFKDDRFPEYGVKVEFVFS YGPEKIQGMEHLENGPSVSDYNTS DPLIRWDSYDNFSGHRDDGMEEVV GHTQGPLDGSLYAKVKKKDSLHGST GAVNATRPTLSATPNHVEHTLSVSS DSGNSTASTKTDKTDEPVPGASSAT AALSPQEKRELDRLLSGFLEREKQ GAMYHTQHLSRSPAGGSAPVSSGR HVVPAQVHVNGGALASERETDILDD ELPNQDGHSAAGSMGTLSLDGVTN TSEGGYPEALSPLTNGLDKSYPMEP MVNGGGYPYESASRAGPAHAGHTA PMRPSYSAQEGLAGYQREGPHPAW PQPVTTSHYAHDPSGMFRSQSFSEA EPQLPPAPVRGGSSREAVQRGLNSW QQQQQQQQPRPPPRQERAHLES LVASRSPQPLAETPIPSLPEFPRAAS QQEIEQSIETLNMLMLDLEPASAAA PLHKSQSVPGAWPGASPLSSQPLSG SSRQSHPLTQSRSGYIPSGHSLGTPE PAPRASLESVPPGRSYPYDYQPCLA GPNQDFHSKSPASSLPAFLPTTHSP PGPQQPPASLPGLTAQPLSPKEATS DPSRTPEEEPLNLEGLVAHRVAGVQ AREKQPAEPPAPLRRRAASDGQYEN QSPEATSPRSPGVRSPVQCVSPELAL TIALNPGGRPKEPHLSYKEAFEEM EGTSPSSPPPSGVRSPGLAKTPLSA LGLKPHNPADILLHPTGEPRESYVESV ARTAVAGPRAQDSEPKSFSAPATQA YGHEIPLRNGTLGGSFVSPSPLTSS PILSADSTSVGSFSPGESDQGRTP TQPLLESGFRSGSLGQPSAQRNY QSSSPLPTVGSSYSPDYSLQHFSSS PESQARAQFSVAGVHTVPGSPQARH RTVGTNTPSPGFGWRAINPSMAAP SSPSLSHHQMMGPPGTGFHGSTVS SPQSSAATTPGSPSLCRHPAGVYQVS GLHNKVATTPGSPSLGRHPGAHQ

										NLASGLHSNAIASPGSPSLGRHLGG SGSVVPGSPCLDRHVAYGGYSTPED RRPTLSRQSSASGYQAPSTPSFPVSP AYYPGLSSPATSPSPDSAAFROGSPT PALPEKRRMSVGDRAKSLPNYATIN GKVSSPVASGMSSPSGGSTVFSHT LPDFSKYSMPDNPETRAKVKFVQD TSKYWYKPEISREQAIALKQEPGA FIIRDHSFRGAYGLAMKVSSPPPTI MQQNKKGDMTHELVRHFLIETGPR GVKLGKCPNEPNFGSLSALVYQHSII PLALPCKLVIPNRDPTDESKDSSGPA NSTADLLKQGAACNVLFVNSVDME SLTGPQAISKATSETLAADPTPAATIV HFKVSAQGITLTDNQRKLFRRHYP LNTVTFCDLDPQERKWMKTEGGAP AKLFGFVARKQGSTTDNACHLFAEL DPNQPASAIVNFVSKVMLNAGQKR
--	--	--	--	--	--	--	--	--	--	--