

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
Q9P273	TEN3_HUMAN	Homo sapiens	Teneurin-3	18.417951	S1923;T1926;S1967	NaN	38665916;37217939;29351928	MDVKERRPYCSLTKSRREKERRYTN SSADNEECRVPTQKSYSSSETLKAF DHDSSRLLYGNRVKDLVHREADEFT RQGQNFTRQLQGVCEPATRRGLAFC AEMGLPHRGYSISAGSDADTENEAV MSPEHAMRLWGRGVKSGRSSCLSS RSNSALTLTDEHENKSDSENEQPA SNQGOSTLQPLPPSHKQHSAQHHP SITSLNRNLSLNRNNSQPAPPAALPA ELQTTPEVQLQDSWVLGSNVPLES RHFLFKTGTGTTPLFSTATPGYTMAS GSVYSPTRPLPRNTLSRSFAFKKKS SKYCSWKCTALCAVGVSVLLAILLSY FIAMHLFGLNWQLQOTENDTFENG KVNSDTMPTNTVSLPSGDNGKLG FTQENNTIDSGELDIGRRAIQEIPPGI FWRSQLFIDQPQFLKFNISLQKDALI GVYGRKGLPPSHTQYDFVELLDGSR LIAREQRSLLETERAGRQARSVSLHE AGFIQYLDSGIWHLAFYNDGKNAEQ VSFNTIVIESVVECPRNCHGNGECV SGTCHCFPGFLGPDCSRACPVLC GNGOYSKGRCLCFSGWKTECDVP TTQCIDPQCGGRGICIMGSCACNSG YKGESCEEADCIDPGCSNHGVCIHG ECHCSPGWGGSNCEILKTMCPDQC SGHGTYLQESGSCTCDPNWTGPDC SNEICSVDCGSHGVCMMGGTCRCEE GWTGPACNQRACHPRCAEHGTCKD GKCECSQGWNGEHCTIEGCPGLCN SNGRCTLQNGWHVCVCPGWVWGA GCDVAMETLCTDSKDNEDGLIDC MDPDCCLQSSCQNPYCRGLPDQP DIISQSLQSPSQAAKSFYDRISFLIG SDSTHVIPGESPFNKSLASVIRGQVL TADGTPLIGVNVVFFHYPEYGYTITR QDGMFDLVANGGASLTLVFERSPFL TQYHTVWVWVNVFYVMDLVMKKE ENDIPSCDLSGFVRPNPIVSSPLSTF FRSSPEDSPIIPETQVLHEETTIPGTD LKL.SYLSRAAGYKSVLKITMTQSIIP FNLMKVHLMVAVVGRFLQKWFPPAS PNLAYTFIWDKTDAYNQKVYGLSEA VVSVGYEYESCLDLTLWEKRTAILQG YELDASNMGWVTLDKHHVLDVQN GILYKNGENQFISQPPVSSIMG NGRRRSISPCSCNGQADGNKLLAPV ALACGIDGSLYVGFNYVRRIFPSGN VTSVLELSSNPAHRYLATDPVTGDL YVSDTNTRRIYRPKSLTGAKDLTKNA EVAAGTGEQCLPFDEARCGDGGKAV EATLMSPKGMAVDKNGLIYFVDTG MIRKVDQNGIISTLLGSNDLTSARPL TCDTSMHISQVRLWPTDLAINPMD NSIYVLDNNVVLQITENRQVRIAAGR PMHCQVPGVEYVPGKHAVQTTLESA TAIAVSYSGVLYITETDEKKINRIRQV TTDGEISLVAGIPSECDCKNDANCD CYQSGDGYAKDAKLSAPSSLAASPD GTLYIADLGNIRIRAVSKNKPLLNSM NFYEVASPTDQELYIFDINGTHQYTV SLVTGDYLYNFYSYNDNDITAVTDS NGNTLRIRRDPNRMPVRVWVSPDNQ VIWLTIGTNGCLKSMTAQGLELVLF YHGNSGLLATKSDETGWTTFFDYDS EGRLTNVTFPTGVVTNLHGDMDKAI TVDIESSSREEDVSITSNLSSIDSFYT MVQDQLRNSYQIGYDGLRIIYASGL DSHYQTEPHVLAGTANPTVAKRNM TLPGENGQNLVWVRFKQQAQGV NVFGRKLRVNGRNLVDFDRITKT EKIYDHRKFLRLRIAYDTSGHPTLWL PSSKLMVAVVYVSTGQIASIQRGTT SEKVDYDGGGRIVSRVFADGKTWSY TYLEKSMVLLLHSQRQYIFEDMWD RLSAITMPSVARHTMQTIRSIGYYRN IYNPPESNASHITDYN EEGLLQTAFL GTSRRVLFKYRRQTRLSEILYDSTRV SFTYDETAGVLKTVNLQSDGFICTIR YRQIGLIDRQIFRFSEDMVNARFD	False	True	1.452	3.02	1.439	0.867	0.588	4.441

YSYDNSFRVTSMQGVINETPLPIDLY
QFDDISGKVEQFGKFGVIYYDINQHS
TAVMTYTKHFDAHGRIKEIQYEIFRS
LMYWITIQYDNMGRVTKREIKIGPFA
NTTKYAYEYDVGQLQTVVYLNEKIM
WRYNYDLNGNLHLLNPSNSARLTP
LRYDLRDRITRLGDVQYRLDEDGFL
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WTVIYRYDGLGRRVSSKTLGQHLQ
FFYADLTYPTRITHVYNHSSSEITSLY
YDLQGHLFAMEISSGDEFYIASDNT
GTP LAVSSNGLMLKQIQYTAYGEIY
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FGERDYDILAGRWTTPDIEIWKRIK
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ALHVRYGMTLDEEKARILEQARQRA
LARAWAREQQRVRDGEEGARLWTE
GEKRQLLSAGKVQYDGYVLSVEQ
YPELADSANNIQFLRQSEIGRR