	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q9WTS6	TEN3_MOUSE	Mus musculus	Teneurin-3	25.775171	NaN	NaN	34678516	MDVKERRPYCSLTKSRREKERRYTN SSADNEECRVPTQKSYSSSETLKAF DHDYSRLLYGNRVKDLVHREADEYT RQGQNFTLRQLGVCESATRRGVAFC AEMGLPHRGYSISAGSDADTENEAV MSPEHAMRLWGRGVKSGRSSCLSS RSNSALTLTDTEHENRSDSESEQPS NNPGQPTLQPLPPSHKQHPAQHHP SITSLNRNSLTNRRNQSPAPPAALPA ELQTTPESVQLQDSWVLGSNVPLES RHFLFKTGTGTTPLFSTATPGYTMAS GSVYSPPTRPLPRNTLSRSAFKFKKS SKYCSWRCTALCAVGVSVLLAILLSY FIAMHLFGLNWHLQQTENDTFENG KVNSDTVPTNTVSLPSGDNGKLGGF THENNTIDSGELDIGRRAIQEVPPGI FWRSQLFIDQPQFLKFNISLQKDALI GVYGRKGLPPSHTQYDFVELLDGSR LIAREQRNLVESERAGRQARSVSLH EAGFIQYLDSGIWHLAFYNDGKNPE QVSFNTIVIESVVECPRNCHGNGEC VSGTCHCFPGFLGPDCSRAACPVLC SGNGQYSKGRCLCFSGWKGTECDV PTTQCIDPQCGGRGICIMGSCACNS GYKGENCEEADCLDPGCSNHGVCI HGECHCNPGWGGSNCEILKTMCAD QCSGHGTYLQESGSCTCDPNWTGP DCSNEICSVDCGSHGVCMGGSCRC EEGWTGPACNQRACHPRCAEHGTC KDGKCECSQGWNGEHCTIAHYLDKI VKEGCPGLCNSNGRCTLDQNGWHC VCQPGWRGAGCDVAMETLCTDSKD NEGDGLIDCMDPDCCLQSSCQNQP YCRGLPDPQDIISQSLQTPSQQAAKS FYDRISFLIGSDSTHVLPGESPFNKS LASVIRGQVLTADGTPLIGVNVSFLH YSEYGYTITRQDGMFDLVANGGASL TLVFERSPFLTQYHTVWIPWNVFYV MDTLVMKKEENDIPSCDLSGFVRPS PIIVSSPLSTFFRSSPEDSPIIPETQVL HEETTIPGTDLKLSYLSSRAAGYKSV LKITMTQAVIPFNLMKVHLMVAVVG RLFQKWFPASPNLAYTFIWDKTDAY NQKVYGLSEAVVSVGYEYESCLDLT LWEKRTAVLQGYELDASNMGGWTL DKHHVLDVQNGILYKGNGENQFISQ QPPVVSSIMGNGRRRSISCPSCNGQ ADGNKLLAPVALACGIDGSLYVGDF NYVRRIFPSGNVTSVLELRNKDFRH SSNPAHRYYLATDPVTGDLYVSDTN TRRIYRPKSLTGAKDLTKNAEVVAGT GEQCLPFDEARCGDGGKAVEATLM SPKGMAIDKNGLIYFVDGTMIRKVD QNGIISTLLGSNDLTSARPLTCDTSM HISQVRLEWPTDLAINPMDNSIYVL DNNVVLQITENRQVRIAAGRPMHCQ VPGVEYPVGKHAVQTTLESATAIAVS YSGVLYITETDEKKINRIRQVTTDGEI SLVAGIPSECDCKNDANCDCYQSGD GYAKDAKLNAPSSLAASPDGTLYIAD LGNIRIRAVSKNKPLLNSMNFYEVA SPTDQELYIFDINGTHQYTVSLVTGD YLYNFSYSNDNDVTAVTDSNGNTLR IRRDPNRMPVRVVSPDNQVIWLTIG TNGCLKSMTAQGLELVLFTYHGNSG LLATKSDETGWTTFFDYDSEGRLTN VTFPTGVVTNLHGDMDKAITVDIESS SREEDVSITSNLSSIDSFYTMVQDQL RNSYQIGYDGSLRIFYASGLDSHYQT EPHVLAGTANPTVAKRNMTLPGEN GQNLVEWRFRKEQAQGKVNVFGRK LRVNGRNLLSVDFDRTTKTEKIYDD HRKFLLRIAYDTSGHPTLWLPSSKL MAVNVTYSSTGQIASIQRGTTSEKVD YDSQGRIVSRVFADGKTWSYTYLEKS	None	None	None	None	None	None	None	None	None

									MVLLLHSQRQYIFEYDMWDRLSAIT MPSVARHTMQTIRSIGYYRNIYNPPE SNASIITDYNEEGLLLQTAFLGTSRR VLFKYRRQTRLSEILYDSTRVSFTYD ETAGVLKTVNLQSDGFICTIRYRQIG PLIDRQIFRFSEDGMVNARFDYSYD NSFRVTSMQGVINETPLPIDLYQFD DISGKVEQFGKFGVIYYDINQIISTAV MTYTKHFDAHGRIKEIQYEIFRSLMY WITIQYDNMGRVTKREIKIGPFANTT KYAYEYDVDGQLQTVYLNEKIMWRY NYDLNGNLHLLNPSSSARLTPLRYD LRDRITRLGDVQYRLDEDGFLRQRG TEIFEYSSKGLLTRVYSKGSGWTVIY RYDGLGRRVSSKTSLGQHLQFFYAD LTYPTRITHVYNHSSSEITSLYYDLQG HLFAMEISSGDEFYIASDNTGTPLAV FSSNGLMLKQTQYTAYGEIYFDSNV DFQLVIGFHGGLYDPLTKLIHFGERD YDILAGRWTTPDIEIWKRIGKDPAPF NLYMFRNNNPASKIHDVKDYITDVN SWLVTFGFHLHNAIPGFPVPKFDLT EPSYELVKSQQWEDVPPIFGVQQQV ARQAKAFLSLGKMAEVQVSRRKAGA EQSWLWFATVKSLIGKGVMLAVSQG RVQTNVLNIANEDCIKVAAVLNNAF YLENLHFTIEGKDTHYFIKTTTPESD LGTLRLTSGRKALENGINVTVSQSTT VVNGRTRRFADVEMQFGALALHVR YGMTLDEEKARILEQARQRALARAW AREQQRVRDGEEGARLWTEGEKRQ LLSAGKVQGYDGYYVLSVEQYPELA DSANNIQFLRQSEIGKR									