

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	ext reg
Q9BTW9	TBCD_HUMAN	Homo sapiens	Tubulin-specific chaperone D	22.15407	S408;T412	NaN	34725712;31492838;23301498;38665916	<p>MALSDEPAAGGPEEEAEDELAFGA ALEAFGESAEETRALLGRLREHVGGG AEREVALERFRVIMDKYQEQPHLLD PHLEWMMNLLLDIVQDQTSASLV HLAFKFLYIITKVRGYKTFRLRFPHEV ADVEPVLDLVTIQNPKDHEAWETRY MLLLWLSVTCCLIPFDFSRDLGNLLT QPGQARMSIMDRILQIAESYLIVSDK ARDAAAVLVSRFITRPDKQSKMAE FLDWSLCNLRSSFTMQGQVITMD GTLQALAQIFKHGKREDCLYAATVL RCLDGCRLPESNQTLLRKLGVKLVQ RLGLTFLPKVAAWRYQRGCRSLAA NLQLLTQGOSEQKPLILTEDDEDDED DVPEGVERVIEQLLVGLKDKDVTVR WSAAKGIGRMAGRLPRALADDVVG VLDCFSFQETDKAWHGGCLALAE RRGLLLPSRLVDVVAVILKALTYDEK RGACSVGTNVRDAACYVCFWAFARAY EPQELKPFVTAISSALVIAAVFDRDIN CRRASAAAFQENVGROGTFPHGIDI LTTADYFAVGNRSNCFLVISVFIAGF PEYTOPMIDHLVTMKISHWDGVIRE LAARALHNLAQQAPEFSATQVFPRL LSMTLSPDLHMRHGSILACAEVAYA LYKLAQENRPVTDHLDEQAVQGLK QIHQQLYDRQLYRGLGGQLMRQAV CVLIEKLSLSKMPFRGDTVIDGWQW LINDTLRHLHLISSHSRQMKDAAV SALAALCSEYMMKEPGEADPAIQEEL ITQYLAELRNPEEMTRCGFSLALGAL PGFLLKGRLLQVLTGLRAVTHTSPE DVSPAESRRDGLKAIARICQTVGVKA GAPDEAVCGENVSQIYCALLGCMDD YTTDSRGDVGTVWRKAAMTSLMDL TLLLARSQPELIEAHTCERIMCCVAQ QASEKIDRFRAHAASVFLTLLHFDSP PIPHVPHRGELEKLFPRSDVASVNW SAPSOAFPRITQLLGLPTYRYHVLLG LVVSLGGLTESTIRHSTQSLFEYMKG IQSDPQALGSFSGTLLQIFEDNLLNE RVSVPKLLKLDHVLTHGCFDIFTEE DHPFAVKLLALCKKEIKNSKDIQKLL SGIAVFCMVQFPGDVRQALLQLC LLLCHRFPPIRKTASQVYETLLTYS DVVGADVLDEVVTLSDTAWDAELA VVREQRNRLCDLLGVPRLVLPQPG AC</p>	False	False	2.353	2.187	1.377	1.419	1.163	4.25	1.0