

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
P55072	TERA_HUMAN	Homo sapiens	Transitional endoplasmic reticulum ATPase	24.423393	S3	S3;S7;S13;S37;T436;S462;S702;S770;S775;S787;T805	30397120;23301498;33214551;26136220;27566657;40596516;22967762;26853435;38665916;34725712;32119511;40914422;30444036;35008409;35083852;34019948;35138101;33465208	MASGADSKGDDLSTAILKQKNRPNR LIVDEAINEDNSVVSLSQPKMDELQ LFRGDTVLLKGGKRRREAVCIVLSDDT CSDEKIRMNRVVRNNLRVRLGDVIS IQPCPDVKYKRIHVLPIDDTVEGITG NLFVEVYLKPYFLEAYRPIRKGDFLVR GGMRAVEFKVVEIDPSPYCIVAPDT VIHCEGEPIKREDFEESLNEVGYDDI GGCRKQLAQIKEMVELPLRHPALFK AIGVKPPRGILLYGPPGTGKTLIARAV ANETGAFFFLINGPEIMSKLAGESES NLRKAFEEAEKNAPAIIFIDELDAIAP KREKTHGEVERRIVSOLLTLMDGLK QRAHVIVMAATNRPN SIDPALRRFG RFDREVDIGIPDATGREILQIHTKN MKLADDVDLEQVANETHGHVGADL AALCSEAAALQAIRKKMDLIDLEDETI DAEVMNSLAVTMDDFRWALSQSNP SALRETVVEVPQVTWEDIGGLEVDK RELQELVQYPVEHPDKFLKFGMTPS KGVLFYGPPEGCKTLLAKAIANECQ ANFISIKGPELLTMWFGESEANVREI FDKARQAAPCVLFFDELDSIAKARG GNIGDGGGAADRVINQILTEMDGMS TKKNVFIIGATNRPDIIIPAILRPGRL DQLIYIPLDEKSRVAILKANLRKSPV AKDVDLEFLAKMTNGFSGADLTEIC QRACKLAIRESESIEIRRRERERQTNP SAMEVEEDDPVPEIRRDHFEEAMRF ARRSVSDN DIRKYEMFAQTLQOSRG FGSFRFPPSGNQGAGPSQSGGGGT GGSVYTEDNDDDLYG	True	True	5.0	5.0	3.051	5.0	2.327