

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q01853	TERA_MOUSE	Mus musculus	Transitional endoplasmic reticulum ATPase	28.027916	NaN	S3;S7;S13;S37;T436;S462;S702;S770;S775;S787;T805	37507081;37453647;33300544;36288343;39627609;39927985	MASGADSKGDDLSTAILKQKNRPNR LIVDEAINEDNSVLSQPKMDELQ LFRGDTVLLKGKKRREAVCIVLSDDT CSDEKIRMNRVVRNLRVRLGDIVS IQPCPDVKYKGRIHVLPIDDTVEGITG NLFEVYLKPYFLEAYRPIRKGDFLVR GGMRAVEFKVVEETDPSPYCIVAPDT VIHCEGEPKREDEEESLNEVGYYDDI GGCRKQLAQIKEMVELPLRHPALFK AIGVKPPRGILLYGPPGTGKTLIARAV ANETGAFFFLINGPEIMSKLAGESES NLRKAFFEEAKNAPAIIFIDELDAIAP KREKTHGEVERRIVSOLLTMDGLK QRAHVIVMAATNRPN SIDPALRRFG RFDREVDIGIPDATGRLEILQIHTKN MKLADDVDLEQVANETHGHVGDAL AALCSEAAQAIRKKMDLIDLEDETI DAEVMNSLAVTMDDFRWALSQSNP SALRETVVEVPQVTWEDIGGLEVDK RELQELVOYPPVEHPDKFLKFGMTPS KGVLFYGPFGCGKTLAKAIANECQ ANFISIKGPELLTMWFGESEANVREI FDKARQAAPCVLFFDELDSIAKARG GNIGDGGGAADRVINQILTEMDGMS TKKNVFIIGATNRPDIDPAILRPGRL DQLIYIPLDEKSRVAILKANLRKSPV AKVDLEFLAKMTNGFSGADLTEIC QRACKLAIRESIESEIRERERQTNP SAMEVEEDDPVPEIRRDHFEEAMRF ARRSVSDNDIRKYEMFAQTLOQSRG FGSFRFPSGNQGGAGPSQSGGGT GGSVYTEDNDDDLYG	True	False	4.586	2.938	0.844	4.0	False