

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
A2A654	A2A654_MOUSE	Mus musculus	NaN	38.922822	S1742;S1743;S1750;T1751;T1754;T1755;T1756;T1760	NaN	21606357;34678516;22645316	MRGRRGRPPKQPAAPAAERCAPAPP PPPPPPPPPPPPPPPPASGPIGGLR SRHRGSSRGRWAAAQAEVAPKTRLS SPRGGGRRKQPPPPPPASGSSASGP GRGGGGGGGGRTGGGGGHLARTTP ARRAVNKVVYDDHESDDDDDEEDM VSEEEEEEDGDAEETQDSEDEEEE DDMEEDDDSDYPEEMEDDDDDAS YCTESSFRSHSTYSSTPGRRKPRVHR PRSPILEEKDIPPLEFPKSSEDLMVP NEHIMNVIAIYEVVRNFGNVLRLSPF CFEDFCAALVSQEQCTLMAEMHVA LLKAVLREEDTSNTTFGPADLKDSV NSTLYFIDGMTWPEVLRVYCESDKE YHHVLPYQEAEDYPYGPVENKIKVL QFLVDQFLTTNIAREELMSEGVIQYD DHCRVCHKLGDLLCCETCSAVYHLE CVKPPLEEVPEDEWQCEVCVAHKVP GVTDCVAEVQKNKPYVRHEPIGYDR SRRKYWFLNRRLIIEEDTDNENEKK VWYYSTKVQLAELIDCLDKGYWEAE LCRVLEDIREEMQQHMDVTEDLTN KARGSNKSFLAAANEIILDSLRIKRG EDIDCDQSPEDPEKDKHEGENNSSK DAEKSREEAEDPSADKDADSKGLEE EPGHGKPEEPTVEGDKGNSVPANLG DNTTNASPEETSPCDGRSPEGCLSE THDSSSMAEKKVASELPPDPEDSN RTCDSSNTSATTASSQPNLETCSSE LTSSQSDSAKAADDPEIGERDSHTPV SVHEEIGDFRLEKSNGEVSESPGAG KGTSGSTRIITRLRNPEKLSQLKSQ QVAAAHEANKLFKEGKEVLVNSQ GEVSRNSTKKEVVMKGNINNYFKLG QEGKYRVYHNQYSTNSFALNKHQH REDHDKRRHLAHKFCLTPAGEFKW NGSVHGSKVLTIISLRLTTIQLESNP SSFLHPNWASHRANWIKAVQMCCK PREFALALAILCAVKPVVMLPIWRE SLGHTRLHRMTSIEREKEKVKKKE KKQEEEEETMQQATWVKYTFPVKHQ VTGYGGWSWISKTHVYRFLPKLPCN TNVNYRKPLDGAKNNTDENKDESE KRKSPRSPKMKTECDSEQGETRDA DATAGAAAGAMELSKEPEKKDQDV KELLSDNDKSFKEEPMIDDTIKTE SHVSSLESTEVDVNVNVEGFLHRTS YKKKTKSSKLDGLLERRIRQFTLEEK QRLEKLESGVKGAGKPPMGALKS SSESPGSKASEGHQGDLSLRQEQSP SSSQASTVDLGLGGSQSDPLVLGISP PSLSTHKPDPKQVLDVDSIQSPGP NCQRQNSVESDLARISEPAGKGLE LSQTKTEVTSSSDDSKPTSADDVGI LICKSRKLHSQDDSTVVSSKSTLP ASVPKSPRDRDARAFSKAVDFDGRG GGDSEYSTLENSSDNMCIRDSAE DMVVQNSSEATSKRFIAPEQGGESV ESTKQVVSSTENCEDKLOGKVTE ANGKKGQHPKPEERAVNRCTDQ VSLRHSVDRKNSEPRESEKKGQKAN KFQINGKDSKAKGYLKGPGTKDGS GKVSSAVEPKVNNINKVIPGNTKSL AGKESAAKPFINGDIIMEELSEQNTS ETNSYLSSSDAKGNHQDGLHTLPS TKESASTQVITPRAPCPDRNLSQVE DMETESPEVKRVIPSPVRTGEGSNL SKGFMDNGLPSSKDENVNGESQR KTVITEVTTMTSTVATESKTIVIVAK GDKQTVVSSSTENCARSTVTTTTTIVT KLSTPSPDTGVDITISVKEQSKTVVTT TVTDSLTTAGSLVTSMTVSKEYSTR DRVLMKFSRFPKTRSGTALPSYRK FVTKSSKSFIVLPNDDLKKLARKGG IREVPYFNYNAPALDIWYPSPRPT FGITWRYRLQTVKSLAGVSLMLRLL WASLRWDDMAAKAPGGGSTRTET SETEITTTTEIHKRRDVGYPYIRSEYICR KIICPIGVPEAPKETPTPQRKGLRSSA LRPKRPETPKQTPVIESVWAAEEL	None	None	None	None	None	None	

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STAP