

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
E9PY55	E9PY55_MOUSE	Mus musculus	NaN	29.185005	NaN	NaN	22645316	MSGSTQPVAQTWRAAEPYPPHGIS YPVQIARSHTDVGLLEYQHHPDYT SHLSPGSIHQPRRRPSSLSEFQPGS ERSQELHLRPESTRFLPELGKPDIEF TESKRPRLELLPDTLLRPSPLLATGQ PSGSEDLTKDRSLAGKLEPVSPSP HADPELELAPSRLSKEELIQNMDRV DREITMVEQQISKLKKKQQLLEEA AKPPEPEKPVSPPIESKHRSLVQIY DENRKKAAEAHRILEGLGPQVELPL YNQPSDTRQYHENIKINQAMRKKLI LYFKRRNHARKQWEQRFQRYDQL MEAWEKKVERIENPRRRAKESKV REYYEKQFPEIRKQRELQERMQSRV GQRGSGLSMSAARSEHEVSEIIDGL SEQENLEKQMRQLAVIPPMLYDADQ QRIKFINMNGLMDDPMKVYKDRQV TNMWSEQERDTFREKFMQHPKNF GLIASFLERKTVAECVLYYLTKKNE NYKSLVRRSYRRRGKSQQQQQQQQ QQQQQQMARSSQEEKEEKEKEKEA DKEEEKQDAENEKEELSKETDDTS GEDNDEKEAVASKGRKTANSQGRR KGRITRSMANEANHEETATPQOSSE LASMENNESSRWTEEMETAKKGL LEHGRNWSAIARMVGSKTVSQCKN FYFNYKKRQNLDEILQHQHKLMEKE RNARRKKKTPAAASEETAFFPAAE DEEMASGASANEELAEAEASQA SGNEVPRVGECSGPAAVNNSSDTE VPSRSEATKDTGPKPTGTEALPAAT QPPVPPPEPAVAPAEPSPVDPASGP PSPEPSPSPAAPPATVDKDEQAPAA PAPQTEDAKEQKSEAEIDVKGPEEP EASEEPPESVSDHKEETEEPEDEK AKGTEAIETVSEAPLKVEEAGSKAAV TKGSSSGATQDSDSATCSADEVDE PEGGDKGRLLSPRPSLLTPAGDPRAS TSPQKPLDLKQLKQRAAAIPPIVTKV HEPPREDTVPPKPVPPVPTOHLQP EGDVSQQGGSPRGKRSRSPVPPAEK EAEKPAFFPAFPTGPKLPTEPPRWS SGLPFPPIPREVIKTSHPHADPSAFSY TPPGHPLPLGLHDSARPVLP RPPI PPPLISSAKHPGLERQLGAISSQGM VQLRVPHSEHAKAPMGPLTMGLPLA VDPKKGALGSATSGSITKGLPSTR AADGPSYRGSITHGTPADVLYKGTIS RIVGEDSPSRLDRAREDITLPGHVIY EGKKGHVLSYEGGMSVVSQCSKEDG RSSSGPPHETAAPKRTYDMMEGRV GRTVTSASIEGLMGRAIPEQHSPLK EQHHIRGSITQGIPRSYVEAQEDYLR REAKLLKREGTTPPPPPRDLTETYK PRPLDPLGPKLKPTEGVVATVKEA GRSIEHPREELRRTPELPLAPRPLKE GSITQGTPLKYDSGAPSTGKHKHDVR SIIGSPGRFPFALHPLDIMADARALE RACYEESLKSRSSTSGAGGSITRGA PVVPELGKPRQSPLTYEDHGAPFTS HLPRGSPVTTREPTRLQEGSLLSSK ASQDRKLTSTPREIAKSPHSTVPEHH PHPISPYEHLLRGVTGVDLYRGHIPL AFDPTSIPRGIPLAAAAAYLPRHLA PSPTYPHLYPPYLIRGYPDTAALNR QTIINDYITSQQMHNAASAMAQRA DMLRGLSPRESSLALNYAAGPRGIID LSQVPHLPVLPPTPGTPATAIDRLA YLPATAPPFSSRHSSSPLSPGGPHTL AKPTATSSSERERERERERERDKSILTS TTTVEHAPIWRPGTEQSSGAGGSSR PASHTHQHSPISPRTQDALQQRPSV LHNTSMKGVVTSVEPGTPTVLRSTS TSSPVRPAATFPPATHCPLGGTLEGV	True	False	3.001	5.0	2.228	1.772	1.119	2.083	2.117

YPTLMEPVLLPKETS RVARPERPRVD
AGHAFLTKPPAREPASSPKSSEPRS
LAPPSSHTAIARTPAKNLAPHHASP
DPPAPTSASDLHREKTQSKPFSIQEL
ELRSLGYHSGAGYSPDGVEPISPVSS
PSLTHDKGLSKPLEELEKSHLEGEL
RHKQPGPMKLSAEAAHLPHLRPLPE
SQPSSPLLQTAPGIKQHQRVVTLAQ
HISEVITQDYTRHHPQQLSGPLPAPL
YSFPGASCPVLDLRRPPSDLYLPPPD
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LGSSDAIEPVSPPEGMTTEPGHARS
TAYPLLYRDGEQGEPRMGSKSPGNT
SQPPAFFSKLTESNSAMVSKKQEI
NKKLNTHNRNEPEYNIGQPGTEIFN
MPAITGAGLMTCRSQAVQEHASTN
MGLEAIIRKALMGKYDQWEEPPPLG
ANAFNPLNASASLPAAAMPITTADG
RSDHALTSPGGGKAKVSGRPSSRK
AKSPAPGLASGDRPPSVSVHSEGD
CNRRTPLTNRVWEDRPSSAGSTPPFP
YNPLIMRLQAGVMASPPPPGLAAGS
GPLAGPHHAWDEEPKLLCSQYETL
SDSE