

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q6ZWR6	SYNE1_MOUSE	Mus musculus	Nesprin-1	38.570782	S2430;S2437;T5822;S7661	S732;T2268;S5655;S8227;T8278;S8281;S8284;S8308;T8363;S377;S377;S8225	34418053;40885482	MATSRASSRSHRDITNVMQRLODE QEIVQKRTFTTKWINSHLAKRKP VDDLFDKMDGKLLALLEVLGSKQ LPCEQGHVVKRIHAVANIGTALKFLE GRKIKLVNINATDIADGRPSIVLGLM WTILYFQIEELTSNLPQLQSLSSAS SVDSMVSTETASPPSKRKAQKIQG NAKKTLLKVVQHTAGKQMGIEVKD FGKSWRTGLAFHSHVHAIQPELVDLE KVKTRSNRENLEDAFTAETQLGIPR LLDPEDVDVDPDEKSIMTYVAQFL TQYPIHAGAGCDGQEDDVVFGFTN NIALLGFQRDDRLILKETKVVWIEQF ERDFTRAQMTESLQDKYQAFKHFR VOYEMKRKQVEHIIQPLQRDGKLT DQALVKQCWERVSSRLFDWHIQLD KSLPAPLGTIGAWLYRAEVALREEITI QQVHEETANTIQRKLEQHKDLLQNT DAHKRAFHEIYQTRSVNGIPMPDQ LEDMAERFHFVSTSELHLMKMEF LELKYRLLSLLVLAESKLSWIQYGR RESVELLLQSYISFIENSKFFEQYEV YQILKQTADIYVKAEGSVEEAENVM KFMSEATAQWRNLSVEVRSRSM EEVISNWDYRGTVASLQAWLEDAE KMLSQSEHAKKDFFRNLPHWQQH TAMNDAGNFLIETCDEIVSRDLKQ LLLNNGRWRELFMEVKQYARADEM DRMKKEYIDVTTTLFGFATEAHRKL SEPLEVFINVKLLIQDLEDLEKRV VMDAQYKMIAKKAHLFAKESPQEEA NEMLTMSKLEQLSKVKECCSPLL YEAQQLTVPELEETQITSFYDSLGI NEILSVLEQEAQSSTLFKQKHQELLA SQENCKSLTLEKGSQSQVQLVTSS QARKPWDHTKLOKQIADVHHAFO MIKKTGDWKKHVEANSRLMKKFEE SRAELEKVLRAVQEGLEEKGDPEEL LRRHTEFFSQLDQVRLNAFLKACDE LTDILPEQEQQLQEAVRKHLKQWK DLQGEAPYHLLHLKIAVEKDRFSAA VEECRAELEQETKLAPQEGSEKIIKE HRVFFSDKGPPLLCEKRLQIEELC GKLPVQDPVRDTCGACTALKELKA SIDNTYTMLVDDPKWKDYTSRFS FSSWVSAKKACLKKIKDEPIDTGNH DEVKHMVDEIRNDITKKGESLSWLK SRLYLIDISSENEAQKRGDELAELS SSFALVALLSEVEKLLSNFGECVQY KEIVKSSLEGLISGPQESKEEAEMIL DSKNLLEAQQLLHHQKTKMISAK KRDLQEQMEQAQGGQAGPGQEEL RKLESTLTGLEQSRERQERRIQVSLR KWERFETNKETVVRYLQGTGSSHER FLSFSLESLSSELEQTEFSKRTESI ATQAENLVKEAAELPLGPRNKRVLQ RQAKSIKEQVTTLEDTEEDIKTME MVKSKWDHFGSNFETLSIWILEKEN ELSSLEASASAADVQISQIKVTIQEIE SKIDSIVGLEEEAQSFQFVTTGESA RIKAKLTQIRRYWEELQEHARGLEG TILGHLSQQQKFEENLRKIROSVSEF AERLADPIKICSSAAETYKVLQEHMD LCQAVESLSTVTMFSASAQKAVNR ESCTQEAALQQQYEEILHAKEMQ TALEDLLARWQRLKGLSPFLTWLE RCEAIASSPEKDISADRGKVESELQI QALQNEVVSQASLYSNLLQLKEALF SVASKEDVAVMKLQLEQLDERWGD LPQHSKRMHFLQSVLAEHKQFDELL FSPSVWIKQFLGELQRTSEINLRDH QVALTRHKDHAAEIEKKRGEITHLQ GHLSQLRSLGRAQDLHPLQSKVDDC FQLFEEASQVVERRKLALAEFL QSHACMSTLLYQLRQTVEATKSMSK KQSDSLKTDLHSAIQDVKTLESSAIS LDGTLTKAQCHLKSASPEERTSCRA TTDQLSLEVERIQNLLGTQSEADAL VALKEAFREQKEELLRSIEDIEERMD RERLKVPTRALQHRLRVFNQLEDE	True	False	1.495	5.0	1.532	1.768	2.837

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