

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
E9PWM3	E9PWM3_MOUSE	Mus musculus	NaN	29.185005	NaN	NaN	22645316	MGRVQDVGWATAGLVIWAGTCYCIY RLTKGRTQSVSGHARNNGSRIETETV VGEQNQTLATSEAMAGREAEITRVKT EPETGEGGEPVAEVDKVPVLRSS GNCQAKTMLEEEIETQSETSSLVET MVMTEAVTLTESTSQAKEVTMKEAV TQTDAAEAEAVGKKEAVTQTKAKAWA MAGRAEVKKEAMTQTKAEARTLAE KETEINRVTVTQSEVLAVTKEVVKIG TMNETGVVAEAMIRPLEETVSVTRT QSEARLDAAVDTKENLNDMSVVVT GVDTKSCAQSQAVAIHQNDDMAGAE ADKEDLKNMSKAGSGIDMKVPGQP HIAANNLAEAVPGAKNDAWDNAKDI CEAEADIRTLIQSETVAKIETEATSS ATMDGGKDNAMKAMTDVNVTDTOP QAVTSDQTEAMPDAKVKKGNASA MAKAGAKANTKTSSQTDALPDAGDK NRSDNNVTAKAETGIDMVSTQTEP VAKDNANTTSKEGAQATGQSQGEAL PNTKKGKARGKAKAKCKAAAGTDTKT CAQPQAGTKTQAEALSQSKVDSKSD SNGVSKAGAKADQKASGQPOPVAN CQNEALPGTKNKVKGNPNPTPKTEA GTATTSSAQTNVTSSQGETTPGAKN KAKGNRNSVPAKAGPDTTGSASQSQ TVANSHSEALPGAKNKVKSNSNVVP KAEAGVGCAPQSVPASQGTALTGTK TKVKGNSSAVSKPDAGAGTMSAH AKTAANSQGETLPGSKNKVKGNSN AVPKAEAGAGTTEPNQPQAEALLGA RNKVKGNSNSVPAKESGASTILALA SSQAEALLGARNKVRGSSNAAPKAE AGVGARGSAQSQAVVSSQNEALLGA RNKIRSNAGTKSGARTGTRGSAQPQ AVVSSQNEALLGARDKGLSSSQVEA TGDNRVYAKPMVGAASEMVTVA GAQPNVHDYYWNGIGVEDWIAAER WIKFRFQIDGDWENSVSWTEDES GATIGPWTGAANDKAGLVSSWAVAC DESSIKSWTGARPENEVALGSWVSA GDQATGAIWAGAQTDTGTWVADKA SAGSWTGAENQISAGSWVVSQNGQAI AGPWAVSQVTDGSWPAVQASGVSW VVDQATGTWVAENQGTAVSWAGA GNIVSIGYWTGAVDQTNVSWTGT DQVGVVEKPRFEDQASEKGSWVVA GVQTSGETRLGSEDQSSGRSWTETV DQANAASRLGTVDQAGGTSWAGTG DQVGGVSTSGSADQSSSGSWAGTR NLAGERSWTGTDQSDGAAPGFE NQTSDEGSWAGTIGQPSGGSKSVSE AQSAGRSWADSADQLSGGFLVGPLD QANGESQPVSSELAAAGVDQTSGGG CWTGSGDQSGGESRLGPRDQSNGE SWPGTGDQGGWYCTYTGQTIGGG PWVGVSGQDVGGPKPVHMQATG GAWLGTGTQVSAVSWTGDQVGGCS KPGFEDQAIGGGFWAGAGDQTTGG SRPAVSEDQSSGVSVWGGAGGHVIG GSRTDQSSGTSWPMGMSQVSGGSW IGSVDQTSGCTKSGFEDQTCAGGSW VGTGEQTSGDSPGSRASNEASGG SRLDPODQASGGSWIRSEDQASGRF LVSAEVEANEGFWFGPGEAFIGSW CWTEEATILPVAGMKDEASTESTSG TREETSISSSGLGDEKKTSPESWTRSE EAALTGTCDGGEAKTVAGAEAEVDP ESKTRAEAKAEAEAEATKVEAEVRVE TRAEAGAAATTASEAGAEAGARVEA GAGAEAGMGFWPWNGDDTTKGSR LGAEAEAGAGGGAEAGAEATENSMG FWFWNGDAATKCKLCTEAEAEETGI GTGTGAGTGTGTGTGTGVGAGVEVQ AVADTSMGFVWFDGAGATKGSRLG	None	None	None	None	None	None	None		

TEAEAGVGAGAQAQAGAEAVGGTSME
FWSWDGDEATKGSRLGAEAEPTG
VVAEPGAETSMGFVFWNEDSTTKG
SGLGTEVGAGLGSWTFSTNVNDGE
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CKRTVNLDPHDLEKLCMIEMTEDP
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GGISVIOQLLSNPYPNVRQKALNALN
NISVAAENHRTVKTYLSQVCEDTVY
PLNSNVQVAGLRLIKHLTITSEYQH
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GMLVNFSKNPSMTRDLLIANAPTAL
INIFSKKETKENILNALLLFENINRH
FKKRGKTYPQDRFSKTSLYFLFQRPK
ACAKKLRALAADCSDPEVKERVEVLI
NKL