	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane
0	Q8K4E0	ALMS1_MOUSE	Mus musculus	Centrosome-associated protein ALMS1	24.992371	T750;T1030;T2291	S401;S1305;S1623;S1788;S1916;S1958	36852467	MEPEDLPWPDELEEEEEEEEEGEEEEGKKEVENASAAATEEALTSEESGRLEEFEEAGPDLDFNYESQRQESSDEEEDELAKAWLQAHPDRPGSAFSLPPPTPPPPPPPLSPRLRYTPVEHLGKTEVVPLTCRVWQQSSYQDNSRAQFSNSSTMLLETGVRWGSEEDQRTESWHCLPQERDSSQTLAMSQTEIGRVEGTEVPDLPSQEGGLPAQSQCPGKKPKLNVLCSPLLVIQDNFAAPDLPLLTCLIQDQEEVEPDSLFQQSELEFAPLRGIPDKSEDSEWLARPSEVSEALIQATSETSSDLANSCFSISQHPLTEGLQGKAESGVLTRCGDAKYSSLYENLGAQSERIAVLQREVGCSNLGISQASPSSLPSFVPQEPTSEPEYHSSNLRMLRVSPDTLLTTHTHSAGSADQKIGAAVVSSAYSQEIKPGSFHQEELPDRHLNEEIRKVSPALRTAGQKPEMLPVQSSSYSKGMKSIFYQHPVSHGHQGKEPLSVSAVCGSAGNKAFHQLSTLSDSLLTEETWPVSVIPGLGNQKTPLPSEFSLSYSHRGKNLPEDVVKVSTDSGSAHKKADILTASSRTYQHKMKPANIYHQELPDSRVPIGTRKVAFESGPAGQKSGVSHPYGEMPSVFYQQGLPDRHSAKSPTKTFIPGPADQKTDLSPVPPTSSSHAEKPVSPYQLTLPGSHLPEDVFKASSVCKSSDELSGITALTSASYSYKGRPNSSYQQKFPDSHLNEEAQKILGTTGTVDQKTVTPTMSSSFLQKEKPSIFYQQTLPDGGLSEEDLQVSAVPWPADQNIAIPTVTSAAFSQREKPRIFYQQTLSVDRLPGEPLNVLGTSGPPDQNTGAPTVTPSSYFPGEESIIFYQAGFPGNTLSAMSFKVPRISGSTEQTNVTTGSSSSYSVGEKSIIFYHQALPDGRLPQEASPAPADLNTGEPPMYLASCSVGVKPIIFYQQPMSDSQRTKGHKESDVPGPTDQKTGIATVHSTSQSYIGRRTVSYQKEFPDLSEKALKVLGDVGSTEQKTQIPVVSSALLHKEGPSAYQEDLPDLTEEPLQILGVSEEVSSSSSYQRKLPDHIEVFLKSVGSGSADRKTGAQIVSSSREKSSGFHQQELPNTGTGAPSSSHFHKEKLSDYQKASPHRDLTESSLKASTVPGLSDQKKKPAVSSGFCLHKEKHEISASALLNCQTAELLTVTQRSCLHREDPAISTVIKPDDQKIPLPTTFHGSSDQKVKPVIFVQKQLRDRDQSEDIPKISTVSEPTVVNTVLPVLLPGSYSHREKSDSFYPQELPDGHLTEVDLKVSSGLGQADQISGLPTGIPGTYSHSEKHQLISEHVQELMDNLNSSESSCLSVDSMPLNSQIDDGVIICKPESLGFANAGCEEMQNIDRGSKTLKEIQTLLMEAENAMALKRCNFSVPLVPFRDVNDVSFIRSKKVVCFKESSTTDVCTQRESFVEEVPHIEYVQKDIGTQTNLKYQRGVGNWEFISSATFRSPLQEAEGTARMAYDETFRQYKAARSVMRSEPEGCSTGIGNKMIIPMMTIIKSDSSSDVSDGCCSWDNNLPESLESVSDVFLNFFPYTSPKTSITDSREEEWLSESEDGYGSTDSLAAHVKYLLQCETSLNQAKQILKNAEEEEYRVRTQAWNLKFNLGRDRGYSISELNEDDRRKVEEIKAKLFGHGRATHMSEGLRSPQGIGCLPEAVCSRIIIESHEKGCFRTLTAEQPRPDSCHCAFRSVEPSDLIRGHRSPSSWRGRHINLSRSIEQSNPCFKVGSSFQLQSHPPFQKLLPDDIKISKGVGMPVHAYMDPQPSELVEPTCVPAKEMDFPSSSQILPPEPKKQFTTAITFSSHEHSECISDSSGCKVGVTADSQCSGPSLGVFKPHIPEEQISPRDLKQKTSFQSSLERHGSTPVTILADGSRQRQKLPVDFEHSHQKEKLLQRLGFKVSHSEPNVSTNVSNFKGVQFSGKDTIVSQDKLTSTVEVKEKNVTVTPDLPSCIFLEQPELFEESHTPHTD	False	False	3.663	3.379	1.427	1.304	0.973	1.498

									LQMRKYPSPSCPEIASRIFLEQPKLS EQSKAPHVDREIREDHSFFPKCQDYI VADPSPDFPDQQQCKPPDVVGHTRK QNSLLSEGQDYELEEVQHIPQSYFS NMVNVEAKVSDAISQSAPDHCTAAS TPPSNRKALSCVRITLCPKTSSKLDS GTLGERFHSLDPASKTRINSEFNSD LRIISSRSLEPTSKLLTCKPVAQDQES LVFLGPKSPLDLQVAQSSLPDSKTIF QDLKTKPPQNSQIVTSRQTQVNISHL EGYSKPEGTPVSADGSQEQSKVSFT TSFGKLSSDAITQITTESPEKTTFSSE IFIHADDRGQGILDPMAQKPSRFASS SSVQQIPASHGKDAQPVLLPYKPSGS SKMYYVPLLKRVPSYLDSKSDTTVES SHSGSNDAIAPDFPPQMLGTRDDDL SNTVNIKHKEGIYSKRAATKGKNPS QKGDAAAPVQMPITWDENVLDENQ EEVISRGVVIKMAGPEEMSSLEKDL AGPSDITVQDRKTENLPDTKSIKQKE GSLEIESECHSAFENTAHSVFRSAKF YFHHPVHLPHEQDFCHESLGRSVF MQHSWKDFFHHHSGHSCLPPPGPS SDKLDKTKMDYTRIKSLSINLNLGE HEKIHTIKNQARDPKGKRQANEQKK DQKVTPELTTECPVSLNELWNRYQE RQKQQNPSGACDTKELSLVERLDRL AKLLQNPITHSLRASESAQDDSRGG HRAREWTGRRQQKQKGKQHRKWS KSLERGQSTGDFRKSKVFSPHQGGK SSQFKIEQIKLDKYILRKEPGFNNVS NTSLDSRPSEESVSLTDSPNIFSSTD SPVDSDVLTPTDRDMPLNERSSSIST IDTVRLIQAFGQDRLSLSPRRIKLYST VTSQRRRYLEQPCKHNRKALNTACP QMTSEHSRRRHIQVANHMTSSDSV SSPGSLLSLDSALSNEETVRMVSKG VQAGNLEIVAGVKKYTQDVGVTFPTP SSSEARLEEDSDVTSSSEEKAKEKKF LSNYLQTKNLRKNKPNPCAGVSWF VPVESGQSGSKKENLPKIYRPVISWF EPVTKTKPWREPLREQNWQAQCMN SRGSLGGPGRDSGQVSLRPFVRATL QESLQLHRPDFISHSGERIKRLKLLV QERKLQSLFQSEREALFHSARPLPR RVLLAVQKNKPIGKKEMIQRTRRIYE QLPEVKKKREEEKRKSEYKSYWLRA QHYKMKVTNHLLGRKVPWD								