

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext reg
P38080	AKL1_YEAST	Saccharomyces cerevisiae	Serine/threonine-protein kinase AKL1	24.475439	NaN	S10;S407;T471;S504;S541;S574;S801;S846;S953;S960;S1048;S1072	33229814	MSITNGTSRSVSAMGHPAVERYTPG HIVCVGTHKKEVNVNLAEGGFAQIYV VKFLEYLNEFDNTASVPLKIGDVAACL KRVLVQDENGLNEMRNEVEVMKKL KGAPNIQVYFDSNASRRRDGVQGFEE VLLLMELCPNKSLLDYMNQRLSTKL TEAEIVKIMYDVALSISQMHYLPVSLI HRDIKIENVLVDAKNNFKLADFGST STCFPIVTTHQDIALLTQNIYVHTTPO YRSPEMIDLYRCLPINEKSDIWAALGV FLYKLLFFTTTPFEMTGGQFAILHASKYE FPVKNYSKSLINLIIMLAENPNLRP NIYQVLYHLCEILNVEVPIDKYAEG AYNFISKYTFQNKLQNVQLQMYQL QOKKIMQNNKLSDEENLLNDMFL SSFEEISSKLPMNASDGHAASRIPSQ NVGQELLEEKESQSDQRKSTLSEDK SSRTTSNANSSGTANNPQEINTIQSP GIEDKSIFENKTPGELYYPVSELDY LDKELVKQSSDPTISEQSPRLNTQSL PQRQKSTSSYSSGGRSMKSTSYGAA TIGSDEALANEKTAGINKMKQHKSN NPFPMNVAYHSTNELSNDASNFF LEEQQQGRYQQAQNTGTGTGQNTF PDESQYQSRVEQQQQQDQPKGPA NYSQRNFYTGDRSNKPMQLGGTIA GDSGNRRVNFQNISQNYATNSQSG YLPSONSPAIPMVRPVMNQQAQ QIQAOQLQAQQMQAKQMQAKQQ MQVQQQLQVQQMQIQNANNNGT YVSDRTNHTTEDMRNAQGGEPPILA GNSANEPMHSSKNEALLIELSPLK EDAGKQSFQDTNEPQTGGIEDAGGS GTIKGSNNRRNGVLNLSLNEMDLS RDDTGAAVSSFSSSSSASIQAKLS GRKGSSKRNNYSTDELGDSMVSSSES IDIDLDDARRGKTAERRPLHNERGH KDQARSSDASKSNQFKSKDFSSVST RQPRQSLDLNFQEVNLSPTLTQEH RNKNDSPAPNSHHSYRVSPHASTAI TENKRHSTGHELSTRSNGKHETHR TGSKQRHDLERYRHSKDKDSNSSITI STSTPSEMRSFARARQSLDLERVR REAMASSASSGGSNKRRSFFSVF RSEK	None	None	None	None	None	None	None		

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