	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitoc
0	P83741	WNK1_MOUSE	Mus musculus	Serine/threonine-protein kinase WNK1	69.731061	S1229;S1230;T1239;T1270;S1274;S1280;S1282;S1290;T1680;T1681;T1801;T1806;T1808;S1817;T1818;T1825;T1836;T1841;T1843;S1844;S1845;S1858;T1860;T1944;T1945;S2281;T2291;S2292;S2297;T2298;S2301;T2306;S2365;S2367;T2376;T2377	T17;T58;S165;S172;S378;S382;S1256;T1843;S1973;S2006;S2007;S2022;S2024;S2027;S2116;S2265;S2281;S2365;S2367	22517741;22645316;33300544;40885482;26192747;34887587;36852467;36064721;22826440;36288343;23443134;35822049;40021952;39927985;34678516;39627609;30059200;30016717	MSDGAAEKQSGTPGFLTPPAPVPKN GSSSDSSVGEKLGATVADSGVGRTE EYRRRRHTMDKDSRGAAATTTPTEH RFFRRSVICDSNATALELPGLPLSIP QPSVPAVVPQSAPPEPHREETLTATV ASQVSQQPSAAASPGEQAVVGSATT TVPSSTSKDRPVSQPSLVGSKEEPPP SRSGSGSGGASAKEAQEDRSQQQD DIEELETKAVGMSNDGRFLKFDIEIG RGSFKTVYKGLDTETTVEVAWCELQ DRKLTKSERQRFKEEAEMLKGLQHP NIVRFYDSWESTVKGKKCIVLVTEL MTSGTLKTYLKRFKVMKIKVLRSWC RQILKGLQFLHTRTPPIIHRDLKCDN IFITGPTGSVKIGDLGLATLKRASFAK SVIGTPEFMAPEMYEEKYDESVDVY AFGMCMLEMATSEYPYSECQNAAQ IYRRVTSGVKPASFDKVAIPEVKEIIE GCIRQNKDERYSIKDLLNHAFFQEE TGVRVELAEEDDGEKIAIKLWLRIED IKKLKGKYKDNEAIEFSFDLERDVPE DVAQEMVESGYVCEGDHKTMAKAI KDRVSLIKRKREQRQLVREEQEKRK QEESSFKQQNEQQASVSQAGIQQLS AASTGIPTAPATSASVSTQVEPEEPE ADQHQQLQYQQPSISVLSDGTIDSG QGSSVFTESRVSSQQTVSYGSQHEQ AHSTGTAPGHTVSSIQAQSQPHGVY PPSSMAQGQNQGQPSSSLAGVLSSQ PIQHPQQQGIQPTVPSQQAVQYSLPQ AASSSEGTTAQPVSQPQVSAGTQLP VSQTVATVQGEPHIPVSTQPSVVPVH SGAHFLPMGQPIPTSLLPQYPVSQIPI STPHVSTAQTGFSSVPITMAAGINQP LLTLASSATASSIPGGSPVVPNQLPTL LQPVNQLQSQVHPQLLQPTTVQSIGI PANLGQAAEGPLPSGDVLYQGFPSR LPPQYPGDSNIAPSSNVASVCIHSTV LAPPSMPTEALATQGYFPTVVQPYVE STPLVPMGSVGGQVQVSQPAVSLTQ QPPTTSSQQAVLESTQGVSQAAPPE QTPITQSQPTQPVPLVTSADSAHSDV ASGMSDGNENAPSSSGRHEGRTTK RHYRKSVRSRSRHEKTSRPKLRILN VSNKGDRVVECQLETHNRKMVTFK FDLDGDNPEEIATIMVNNDFILAIER ESFVAQVREIIEKADEMLSEDVSVEP EGDQGLESLQGKDDYGFPGSQKLEG EFKQPIAVSSMPQQIGVPTSSLTQVV HSAGRRFIVSPVPESRLRESKVFTSD ISDPVVASTSQAPGMNLSHSASSLSL QQAFSELKHGQMTEGPNTAPPNFN HMAGPTFSPFLASIAGVQTVAASTPS VSVPITSSPLNDISTSVMQSETALPT EKGIVGVTTTSTGVVASGGLTTMSVS ESPTSSSAVSSSTVPAVVTVSTPSQP VQASTSGSIASSTGSFPPGTFSTTTAT TMGSVVAPDAKPPTVLLQQVASNTA GVAIVTSVSTTTPFPGMASQPSLPLS SSTSAPTLAETMVVSAHSLDKASHS STAGLGLSFCAPSSSSSSGTAVSTSV SQPGMVHPLVISSAVVSTPGLPQPVV PTSTPLLPQVPNIPPLVQPVVNVPAV QQTLIHSQPQPALLPNQPHTHCPEM DADTQSKAPGIDDIKTLEEKLRSLFS EHSSSGTQHASVSLETPLVVETTVTP GITTTAVAPSKLMTSTTSTCLPPTSLP LGAAGMPVMPVGTPGQVSTPGTHA SAPVGTATGVKPGTTPPKPTKTVVPP VGTELSAGTVPCEQLPPFPGPSLIQS QQPLEDLDAQLRRTLSPETITVAPAV GPLSTMSSTTVTEAGTRLQKDGTEG HVTATSSGAGVVKMGRFQVSVTMD DAQKERKNRSEDTKSVHFESSTSES SVLSSSSPESTLVKPEPNGISISGISL DVPDSTHKAPTPEAKSDAGQPTKVG RFQVTTTANKVGRFSVSRTEDKVTE LKKEGPVTSPPFRDSEQTVIPAVIPKK EKPELAEPSHLNGPSSDLEAAFLSR GTEDGSGSPHSPPHLCSKSLPVQNL	True	False	3.668	4.68	1.595

									SQSLSNSFNSSYMSSDNESDIEDED LRLELRRLREKHLKEIQDLQSRQKH EIESLYTKLGKVPPAVIIPPAAPLSGR RRRPTKSKGSKSSRSSSLGNKSPQL SGNLSGQSGTSVLHPQQTLHPAGNT PETGHNQLLQPLKPSPSSDNLYSAF TSDGAISVPSLSAPGQGTSSTNTVGG TVSSQAAQAQPPAMTSSRKGTFTDD LHKLVDNWARDAMNLSGRRGSKG HMNYEGPGMARKFSAPGQLCVPMT SNLGGSTPISAASATSLGHFTKSMCP PQQYGFPPAPFGTQWSGTGGPAPQP LGQFQPVGTASLQNFNISNLQKSIS NPPGSNLRTT					