

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P83741-2	WNK1_MOUSE	Mus musculus	Isoform 2 of Serine/threonine-protein kinase WNK1	49.649624	NaN	T17;S165;S172;S378;S382;S1256;S1973;S2006;S2007;S2022;S2024;S2027;S2116;S2265;S2281;S2365;S2367	36064721;22645316;22826440;22517741;30016717;36852467;33300544;34887587;36288343;30059200;35822049;26192747;23443134;34678516	MSDGAAEKQSGTPGFLTPPAPVPKN GSSSDSSVGEKLGATVADSGVGRTE EYRRRRHTMDKDSRGA AATTTPTTEH RFFRRSVIDCSNATALELPLPLSIP QPSVPAVVPQSAPPEPHREETLTATV ASQVSQQPSAAASPGEQAVVGSATT TVPSSTSKDRPVSQPSLVGSKEEPPP SRSGSGGGASAKEAQEDRSQQQD DIEELETKAVGMSNDGRFLKFDIEIG RGSFKTVYKGLDTETTVEVAWCELO DRKLTKSERQRFKEEAEMLKGLQHP NIVRFYDSWESTVKGKKCIVLVTEL MTSGTLKTYLKRFKVMKIKVLRSWC RQILKGLQFLHTRTPPIIHRDLKCDN IFITGPTGSVKIGDLGLATLKRASFAK SVIGTPEFMAPEMYEKEYDESVDVY AFGMCMLEMATSEYPYSECQNAAQ IYRRVTSQVGPASFDKVAIPEVKEIIE GCIRQNKDERYSIKDLLNHAFQEE TGVRELAEEDDGEKIAIKLWLRID IKKLKGYKDNEAIEFSFDLERDVPE DVAQEMVESGYVCEGDHKTMAKAI KDRVSLIKRKREQRQLVREEQEKRK QEESFKQNEQQASVSQAGIQQLS AASGTAPATSASVSTQVEPEEPE ADQHQQLOYYQPSISVLSGDTIDSG QGSSVFTESRVSSQQTVSYGSQHEQ AHSTGTAPGHTVSSIQASQPHGVY PPSSMPRRGRMSVCVPHLSAVPSL SRISPSAPSTPPPVL SAPLCPSSLRTA PEETF AEKLSKALESVLPMHSASQR KHRRSSLPSLFVTTTPQSM AHPCGGT PTYPESQIFFPTIHERPVFSPPPTCP PKVAISQRRKSTSFLEAQRHFQPLL RTVGQNHLLPGSSPTNWTPEAIVML GATANRVNRELCEMQVPVFEPTQI YSDYR PGLVLAEEAHYFIPQETVYLA GVHYQAQVAGQYEGISYNSPVLSSP MKQISEQKPVPGGPASSSVFEFPPSG QAFVLVGHLLQNLRLDSGSPASPLSSI SAPNSTDATHLKFHPVFPVPHSAPAV LTNSNENRSNCVFEFHAQTPSSSGE GGGILPQRVYRNRQVAVDSNQEELS PQSVGLHCHLQPVTEEQRNHHAPE LTISVVEPMGQIWPISPEYSSDSSQI TSSDLSDFSPPPTGGTAAPFGSDVS LPFIRLPQTVLQESPLFFCFPQGTTT QQVLSASYSSGGSTLHPQAQGNQ GQPSSSLAGVLSSQPIQHPQQGIQP TVPSQQAVQYSLPQAASSSEGTTAQP VSQPQVSAGTQSTQGVSAAPPEQT PITQSQPTQPVLVTSADSAHSDVAS GMSDGNENAPSSSGRHEGRTTKRH YRKSVRSRSRHEKTSRPKLRILNVSN KGDRVVECQLETHNRKMTFKFDL DGDNP EEIATIMVNNDFILAIERESF

VAQVREIIEKADEMLSEDVSVPEPEGD
QGLSLQKDDYGFPGSQKLEGEFK
QPIAVSSMPQQIGVPTSSLTQVVHSA
GRRFIVSPVPESRLRESKVFTSDISDP
VVASTSQAPGMNLSHSASSLSLQQA
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GPTFSPFLASIAGVQTVAASTPSVSV
PITSSPLNDISTSVMQSETALPTEKGI
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SSSAVSSSTVPAVTVSTPSQPVOAS
TSGSIASSTGSFPPTFTSTTTATTMG
SVVAPDAKPPTVLLQQVASNTAGVAI
VTSVSTTTTFFPGMASQPSLPLSSSTS
APTLAETMVVSAHSLDKASHSSTAG
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SSSPESTLVKPEPNGISIGISLDVPD
STHKAPTPEAKSDAQPTKVGRFQV
TTTANKVGRFVSRTEDKVTELKKE
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LAEPShLNGPSSDLEAAFLSRGTED
GSGSPHSPHLC SKSLPVQNLSQSL
SNSFNSSYMSSDNESDIEDEDLRL
LRLREKHLKEIQDLQSRQKHEIESL
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GQSGT SVLHPQOTLHPAGNTPETGH
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STPISAASATSLGHFTKSMCPPQQYG
FPPAPFGTQWSGTGGPAPQLGQFQ
PVGTASLQNFNISNLQKSISNPPGSN
LRTT