

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|---|--------------|---------------|---|--|---|
| Q9H4A3-6 | WNK1_HUMAN | Homo sapiens | Isoform 5 of Serine/threonine-protein kinase WNK1 | 41.779992 | NaN | S19;S167;S174;S378;S382;S1261;S1978;S2002;S2011;S2012;S2027;S2029;S2032;S2121;S2270;S2286;S2370;S2372 | 32119511;34725712;35132862;29249144;23301498;32574038;36240223;22661428;31373491;30397120;21740066;30059200;35289036;33214551;29237092;30379171;34019948;35254053;20305658;37340703;27655845;28657654;35138101;34846842;30620550;31492838;29351928 | MSGGAAEKQSSTPGSLFSLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHTMDKDSRGAAATTTTTTEHRFFRRSVICSNATALELPLPLSLPQPSIPAAVPQSNAPPEHRETVTATATSQVAQQPPAAAAAPGEQAVGPA PSTVPSSTSKDRPVSQPSLVGSKEEP PPARSGSGGSAKEPQEERSQQQDD IEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLDTETTVEVAWCELDQRKLTKSERQRFKEEAEMKGLQHPNIVRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVLRSWC RQILKGLQFLHTRTPPIIHRDLKCDN IFITGPTGSVKIGDLGLATLKRASFAK SVIGTPEFMAPEMYEEKYDESVDVY AFGMCMLEMATSEYPYSECQNAAQ IYRRVTSQVGPASFDKVAIPEVKEIIE GCIRQNKDERYSIKDLLNHAFQEE TGVRVELAEEDDGEKIAIKLWLRIED IKKLGKGYKDNEAIEFSFDLERDVPE DVAQEMVESGYCEGDHKTMAKAI KDRVSLIKRKREQRQLVREEQEKKK QEESLQKQVEQSSASQTGIKQLPSA STGIPTASTTSASVSTQVEPEEPEAD QHQQLQYQQPSISVLSDGTVDSDGQSSVFTESRVSSQQTVSYGSOHEQAH STGTVPGHIPSTVQAQSOPHGVYPPS SVPQSMAHPCGGTPTYPESQIFFPTI HERPVSFSPPTCPPKVAISQRRKST SFLEAQTHHFQPLLRTVQSLPPG GSPTNWTPEAVVMLGTTASRVGTGES CEIQVHPMFEPSQVYSDYRPLVLP EEAHYFIPQEAVYVAGVHYQARVAE QYEGIPYNSSVLSSPMKQIPEQKPVQ GGPTSSSVFEFPQAFVLVGHQLQNL RLDSGLGPGSPLSSISAPISTDATRLK FHPVFPVHSAPAVLTHNNESRSNCV FEFHVHTPSSSSGEGGGILPQRVYR NRQVAVDLNQEELPPQSVGLHGYLQ PVTEEKHNYHAPELTVSVVEPIGQN WPIGSPEYSSDSSQITSDPSDFQSP PPTGGAAAPFGSDVSMPIHLPQTVL QESPLFFCFPQGTTSQQVLTASFSSG GSALHPQAQGSQGPSSSSLTGVS SSQPIQHPQQQGGIQQTAPPQQTQVQ YLSQSTSTSSEATTAQPVSQPAPQV LPQVSAGKQGFPPRLPPQYPGDSNIA PSSNVASVCIHSTVLSPPMPTEVLAT PGYFPTVVQPYVESNLLVPMGGVGG QVQVSQPGGSLAQAPTSSQQAVLE STQGVSVQVAPAEPVAVAQTQATQPT TLASSVDSAHSDVASGMSDGNENV PSSSGRHEGRTRTKRHYRKSVRSRSR HEKTSRPKLRILNVSNGDRVVECQ LETHNRKMVTFKFDLDGDNPEEIIAT |

IMVNNDFILAIERESFVDQVREIIEKA
DEMLSEDEVSVPEPEGDQGLSLOQK
DDYGFSGSQKLEGEFKQPIPASSMP
QQIGIPTSSLTQVVHSAGRRFIVSPVP
ESRLRESKVFPSEITDTVAASTAQSP
GMNLSHSASSLSLQAFSELRRAQ
MTEGPNTAPPNFSHTGPTFPVPPF
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VSISTTSPSLQVPTSTSEIVVSSATALY
PSVTVSATSASAGGSTATPGKPPAV
VSQQAAGSTTVGATLTSVSTTTSFPS
TASQLCIQLSSSTSTPTLAETVVVSA
HSLDKTSHSSTTGLAFSLAPSSSSS
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IESTVTPGIPTTAVAPSKLLTSTTSTC
LPPTNLPLGTVALPVPVVTGQVST
PVSTTTSGVKPGTAPSKPPLTKAPVL
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VGPVMAAPTAITEAGTQPQKGV SQ
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SESSVLSSSSPESTLVKPEPNGITIPG
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