

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitoc
Q80XP9	WNK3_MOUSE	Mus musculus	Serine/threonine-protein kinase WNK3	46.434157	T566;T571;S589;S1156;S1161;S1392	S62;S303;S307;T540;S1039;S1550;S1553;S1595	34887587;22645316;40885482;36852467	MATDSGEPASTEDSEKPDGVSFENR AARAVAPLTVEARIKEKYSTFSASGE NIERKRFRKSVEMTEDDKVAESSR RDERKAATNISRVDKVPNTVLRGGQ EVKYEQCCKATSESSKDCFKKTEK EMEEEEAEKAVATSPSGRFLKFDIE LGRGAFKTVYKGLDTEWVVEVAWCE LQDRKLTAEQQRFKEEAEMLKGL QHPNIVRFYDSWESTLKGKCCIVLVT ELMTSGTLKTYLKRKFKVMKPKVLRS WCRQILKGLQFLHTRTPPIHRDLKC DNIFITGPTGSVKIGDLGLATLMRTS FAKSVIGTPEFMAPEMYEEHYDESV DVYAFGMCMLEMATSEYPYSECQN AAQIYRKVTSGIKPAFNFKVTDPVVK EIEGCIQNKSERLSIKDLLNHAFH AEDTGLRVELAEEDDCSNSSLALRL WVEDPKKLGKHKDNEAIEFSFNLE ADTPEEVAYEMVKSGFHESDSKAV AKSIRDVTLIKKIREKKPAGCLEER RDSQCKYVRNVLPQQQTATLQPTPG PHTAAEYEEETEVDQHVRQQFLQKQP QQQSSSVRGDTSSSEPTAGPVLHSDT SSHPTVAYSSNQTTSSQEQPKLTQSP VLPVVQGSVMPPIYAAGVGVVSQS QISPLTIQKVSQIKPVSQPIGAEQQAT LQNPDFVRSLNQDVTSVKENTNNP DTPSGNGKQDRNKQRRASCPRPEK GTFKQLTVLQVSVSGDNMVEQLET HNNKMVTFKFDVDGDAPEDIAADYM VEDNFVLENEKEKFEELRAIVGQA QEILHVHSAVEKSIGVDSVALESNSN QTGSSEQVLINSASTQTSNESAPQSS PVGRWRFCINQTIKNREAQSPPSLO PSMAMVPLHPPFSSRNTSNQAIISQ NTVFTIENNPGHRELFTSKLDHKDV VDGKIGEHASIEEQSSISYQVEDDR QIMTPATDNNYSAAALVCPVPGECE ALTSQAGMFMPTYPNQQAALVADV HIAYPGESVPIGGNAALTSVLVSSDQ KPQSLSVQOPTIDAEFISKEGETTVN TETSSPKAVIATQTPGFPAVILPATI LES DGERPPKMEFADNRIKTLDEKL RNLLYQEHSSICPEQKDTQSIDS PFSSAEDILSYSMPEVIAISHCGIQD SPAQSPNFQQTGSKILSNVAASQPA HISVFKDLNVITSVPSLCLHEMSP DASLPGDPEAYPAVSSDGTIHLQTG GGYFGLSFTCPSLKNPISRKSWTRKL KSWAYRLRQSTSFKRSKVRQVETE DKRSAIASDPIPLTRFSSDTRALSRC KAMSGSFQGRGFQVITVPQQQPVK MMSFGKDRPPFNKTTVQSSEQAL TFAEAAVSQLIEVEPAMPPTHKASVSS RKLRTLLETFKEDKGDPEQGDIVSYS TACETSVSSVATEKNVTSTTEVSQS GSEPLDKEKNESTPGKQCTNEFSA TLAGNRKSVTKTRPEGDQYLPREE QAYAQTQNSLFYSPSSPMSSDNESE IEDEDLKVLELQRLREKHIOEVVSLQ QQNKELQELYERLRATKDNKAQSSE VPLSPASPRRPRSFKSLRRPQSM HSDNLVVKDALGVESNTVSCQQSPA SKKGMFTDDLHKLVDWTRVTVGH FPSKPSLNQLKQSQKSEENWNK SCESTPSTMGYTSNWISSLSQIRGAA PTSLPOGLPLPSFHGLASYGMPHV COYNAVGAAGYPVQVWVIGSIPAQQS VVLPTQSGGLFQPGMNLQSFAPPV QNPASIPPGPK	False	False	1.206	1.19	0.673