

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q01484	ANK2_HUMAN	Homo sapiens	Ankyrin-2	21.545352	T817;T2496;T3120;T3731;S3817	S31;S34;T378;T531;S846;T853;S874;T1382;S1459;S1461;S1473;S1500;S1596;S1732;S1733;S1736;S1855;S1858;S1929;S2127;T2239;S2243;T2269;S2275;S2405;S2440;S2454;S2516;S2521;T2583;S2679;S2701;S2781;S2795;S2956;S3075;T3078;S3273;S3276;S3277;S3390;S3409;S3474;S3735;T3776;T3797;T3803;T3814;S3823;S3909	30379171;28657654	MMNEDAAQKSDSGEKFNQSSQRRK RPFKSDSNASFLRAARAGNLDKVVVE YLKGGIDINTCNQNLNALHLAAKE GHVGLVQELLGRGSSVDSATKKGNT ALHIASLAGQAEVVKLVKEGANINA QSQNGFTPLYMAAQENHIDVVKYLL ENGANQSTATEDGFTPLAVALQOQH NQAVAILLENDTKGKVRPALHIAAR KDDTKSAALLQNDHNADVQSKMM VNRITTESGFTPLHIAAHYGNVNVAT LLLNRGAAVDFTARNGITPLHVASK RGNTNMVKKLLDRGGQIDAKTRDG LTPHLCAARSGHDQVVELLERLGERGAP LLARTKNGLSPLHMAAQGDHVECV KHLLOHKAPVDDVTLDYLTALHVAA HCGHYRVTKLLDKRANPNARALN GFTPLHIACKNRKVMELLVKYGAS IQAITESGLTPIHVAAFMGHLNIVLLL LQNGASPDVTNIRGETALHMAARAG QVEVVRCLLRNGALVDARAREEQTP LHIASRLGKTEIVQLLQHMHPDA ATTNGYTPLHISAREGQVDVASVLE AGAAHSLATKKGFTPLHVAKYGSL DVAKLLQRRRAADSAKNGLTPHL VAAHYDNQKVALLLLEKASPHATA KNGYTPLHIAAKKNQMIASLLNY GAETNIVTKQGVTPHLASQEGHTD MVTLLLDKGANIHMSTKSLTSLHL AAQEDKVNVDILTCKHADQDAHTK LGYTPLIVACHYGNVKNMVFLLKQG ANVNAKTKNGYTPLHQAAQQGHHTH IINVLLQHGAKPNATTANGNTALAI KRLGYISVVDTLKVVTEEVTTTTTIT EKHKLNVPETMTEVLDSDEEGDD TMTGDGGEYLRPEDLKELGDDSLPS SQFLDGMNLYRSLGGRSDSLRSF SSDRSHTLSHASYLRDSAVMDDSVV IPSHQVSTLAKEAERNYRLSWGTE NLDNVALSSSPIHSGFLVFMVDAR GGAMRGCRRHNLRIIPPRKCTAPTR VTCRLVKRHLATMPPMVEGEGLAS RLIEVGPSPAQFLGKHLPTAPPLN EGESLVSRIQLGPPGKFLGPVIVEI PHFAALRGKERELVLRSENGDSWK EHFCDYTEDELNEILNGMDEVLDSP EDLEKKRICRIITRDFPQYFAVVSRIK QDSNLIGPEGGLVSSVTPVQVAVFP EGALTKRIRVGLAQPMHSELVKKIL GNKATFSPIVLEPRRRKFHKPITMT IPVPKASDVMNLNGFGGDAPTLRL CSITGGTTPAQWEDITGTTPLTFVNE CVSFTTNVSARFWLIDCRQIQESVTF ASQVYREIICVPMYMAKFVVFVAKSHDP IEARLRCFCMTDDKVKLEQQENF AEVARSRDVEVLEGGKPIYVDFGNL VPLTKSQQHIFSFVAFKFNRLPLFV KVRDITQEPGRLSFMKEPKSTRGL VHQAINLNLPIYTKESSESDQEQE EEDMTSEKNDTESTETSVLKSHL VNEVPVLASPDLLSEVSEMKQDLIK MTAILTTDVS DKAGSIKVKELVKAEE EEPGEFPEIVERVKEDLEKVNILRS GTCTRDESSVQSSRSERGLVEEWW IVSDEIEEARQKAPLEITEYPCVEVR IDKEIKGKVEKSTGLVNYLTDLNT CVPLPKEQLQTVQDKAGKCEALAV GRSSEKGGKIPPEDETQSTQKQHKP SLGIKPVRRKLEKQKQKEGLQA SAEKAELKKSSESLGEDPGLAPEP LPTVKATSPLIETPIGSIKDKVKALQ KRVEDEQKGRSKLPIRVKGEDVPK KTTHRPHPAASPLKSERHAPGSPS PKTERHSTLSSSAKTERHPPVSPSSK TEKHSVPSPSAKTERHSPASSSSKTE KHSPVSPSTKTERHSPVSSKTERHP PVSPSGKTDKRPPVSPGRTEKHPPV SPGRTEKRLPVSPSGRTDKHQPVST AGKTEKHLPVSPSGKTEKQPPVSPS KTERIEETMSVRELMKAFQSGQDPS KHKTGLFEHKSQKQKQKQKQKVR	True	True	4.734	3.533	3.976	2.268	1.931

VEKEGPILTQREAQKTENQTIKRGQ  
RLPVTGTAESKRGVVRSSIGVKKEDA  
AGGKEKVLSHKIPEPVQSPVEEESH  
RESEVPKEKMADEQGDMDLQISPD  
RKTSTDFSEVIKQELDNDKYQQFR  
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KNEGVAGSPCGSLMEGTPQISSSES  
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ELALPSRDSEVL SAVADDSLAVSHK  
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KESPCRDSESSPVEPKMAGIFPS  
HFPLPAAVAKTELLTEVASVRSLLR  
DPDGSAAEDDSLEQTSLMESSGKSPL  
SPDTPSSEEVSYEVPKTTDVSTPKP  
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PKHTGSGEDESVPVLTSESRKVS  
SSSESEPELAQLKKGADSGLLPEPVI  
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PDSSPEEQKSVIEIPTAPMENVPFTE  
SKSKIPVRTMPTSTPAPPSAEYESSV  
SEDFLSSVDEENKADEAKPKSKLPV  
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GQDMASIAPDNRKSES DASSLDSK  
TKCPVKTRSYTETETESRRAEELEL  
ESEE GATRPKILTSRLPVKSRSTTSS  
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EEISDEASKLVDRLTQSEREQEIVSD  
DESSALEVSVIENLPPVETEHSVPE  
DIFDTRPIWDESIE TLIERIPDENHGD  
HAEDPQDEQERIEERLAYIADHLGFS  
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LQTP TSSERGGSPHQEPEEPSEHRE  
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KRVVLKSDTEQSEDNNE