

| UniprotKB ID | Entry name | organism     | full name | oglcnacscore | oglcnac sites | phosphorylation sites   | PMIDS   | sequence  | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus |
|--------------|------------|--------------|-----------|--------------|---------------|---|---|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|
| Q8C8R3       | ANK2_MOUSE | Mus musculus | Ankyrin-2 | 41.03029     | S2024;T2931   | S31;S34;T378;T531;S846;T853;S874;T1349;S1426;S1428;S1440;S1467;S1562;S1699;S1700;S1703;S1816;S1819;S1889;S2090;T2202;S2206;T2232;S2238;T2333;S2364;S2399;S2413;S2475;S2480;T2542;S2639;S2661;S2741;S2755;S2913;S3032;T3035;S3226;S3229;S3230;S3343;S3362;S3427;S3686;S3692;T3718;T3739;T3745;T3756;T3759;S3764;S3850;S30;S590;S44 | 22645316;22517741;33300544;34678516;37507081;35822049 | MMNEDAAQKSDSGEKFNQSSQRRK<br>RPKKSDSNASFLRAARAGNLKVVVE<br>YLKGGIDINTCNQNLNALHLLAAKE<br>GHVGLVQELLGRGSSVDSATKKGNT<br>ALHIASLAGQAEVVKVVLKEGANINA<br>QSQNGFTPLYMAAQENHIDVVKYLL<br>ENGANQSTATEDGFTPLAVALQOGH<br>NQAVAILLENDTKGKVRPALHIAAR<br>KDDTKSAALLQNDHNAVQSKMM<br>VNRITTESGFTPLHIAAHYGNVNVAT<br>LLNLRGAADVDFARNGITPLHVASK<br>RGNTNMVKKLLDRGGQIDAKTRDG<br>LTPHCAARSGHDQVVELLERKAP<br>LLARTKNGLSPLHMAAQGDHVECV<br>KHLLOYKAPVDDVTLDYLTALHVAA<br>HCGHYRVTKLLDKRANPNARALN<br>GFTPLHIACKKNRIKVMELLVKYGAS<br>IQAITESGLTPIHVAAFMGHLNIVLLL<br>LQNGASPDVTNIRGETALHMAARAG<br>QVEVVRCLLRNGALVDARAREEQTP<br>LHIASRLGKTEIVQLLQHMAHPDA<br>ATTNGYTPLHISAREGQVDVASVLE<br>AGAAHSLATKKGFTPLHVAAYKGS<br>L<br>DVAKLLQRRRAADSAKNGLTPH<br>VAAHYDNQKVALLLLEKASPHATA<br>KNGYTPLHIAAKKNQMQIASTLLNY<br>GAETNTVTKQGVTPHLSAQEGHTD<br>MVTLLLDKGANIHMSTKSLTLHL<br>AAQEDKVVADILTKHGADRDAYTK<br>LGYTPLIVACHYGNVKMVNFKKQG<br>ANVNAKTKNYGPLHQAAQGGHTH<br>IINVLQHGAKPNATTANGNTALAI<br>KRLGYISVVDTLKVVTEEVTTTTIT<br>EKHKLVNPEMTTEVLVDSDEEGDD<br>TVTGDGGEYLRPEDLKELGDDSLPS<br>SQFLDGMNLYRSLGGRSDSLRSF<br>SSDRSHTLSHASYLRDSAMIDTVVI<br>PSHQVSALAKEAERNRYRLSWGTE<br>LDNVALSSSPIHSGFLVFMVDARG<br>GAMRGCRHNGLRHIIIPPRKCTAPTRV<br>TCRLVKRHRLATMPPMVEGEGLASR<br>LIEVGPSSAQFLGPVIVEIPFAALRG<br>KERELVLRSENGDSWKEHFCDYTE<br>DELNEILNGMDEVLDSPEDLEKKRI<br>CRIITRDFPQYFVAVSRKQDSNLIGP<br>EGGVLSTVVSQVQAVFPEGALTKRI<br>RVGLQAQPMHSELVKKILGNKATFS<br>PIVLEPRRRKFHKPITMTIPVKASS<br>DVMLNGFGGDAPTLRLLCSITGGTT<br>PAQWEDITGTPLTFVNECVSFTTN<br>VSARFWLIDCRQIQESVAFASQVYRE<br>IICVPYMAKFVFAKSHDPIEARLRC<br>FCMTDDKVDKTLEQQENFSEVARS<br>RDVEVLEGGKPIYVDCFGNLVPLTKSG<br>QHIFSFFAFKENRPLFVKVRDIT<br>QEPCGRLSFMKEPKSTRGLVHQAIC<br>NLNITLPIYAKESSESQPEEEIGMT<br>SEKNDETESTETSVLKSHLVNEVPV<br>LASPDLLSEVSEMQLIKMTAILTT<br>DVSDKAGSLKVKELAKAGEEPEGEP<br>FEIVERVKEDLEKVNAILRSGTCMR<br>DEGRARSSQSERELEEEWIVSDEEI<br>QEAQKHAPVEIDEHPCIEVRVDRET<br>KAKVEKDSGLVNYLTDLNSYTS<br>HEKKPHTAPEKSGETSQASAVGKSS<br>ESNKGKATSAAEKQSAQKQLKPGLA<br>IKKPVRRKLEKQKQKESSQSSEE<br>KTELKKGSSSESVDEDRGLVPEPLPT<br>AKATSPLEETPIGSIKDKVKALQKRV<br>EDEQGRSKLPVRVKGKEDVPKRIT<br>PRTHPAVSPSSKSTSSKAERHSSLS<br>SSAKPERHTPVSPSSKNEKLSVPS<br>AKTERHSPVFSGKPEKHSPPSPSTK<br>NERHSPVSSLKTERHTPGSPSGKTD<br>KRPPVPSSGRTEKHPVSPGKTEKH<br>LPGSPSIRTPEKAPGSATGHEKHL<br>PVSPGKTEKQPPISPTSKTERIEETM<br>SVRELMKAFQSGQDPSKHKHTGLFE<br>HKSQKQKQDQKSKSRVEKEKGHT<br>VTQREVTQRETQRIESQTAQRGRF | None          | None          | None    | None    | None          | None                  | None            |

QVSAATESRRFRSTTITVGLRMEDPV  
RERFERTPIKTPPEVVPSVAAEESH  
GSEKIVDEQGDMDQFQISPRKSTSD  
FSEVIKQELEDNNDKYQQFRLTEDTE  
KAQVHLDQVITSPFNATFPLDYMKD  
EFLPALSLQSGALGGSSESLKQEVIA  
GSPCSSLMEGTPQISSEESYKHEGL  
AETPESPESLSFPKKEEQIGAEK  
ETTKVGTPTDIHSEKELPITNDITDSS  
KQKQAGVTRGSEPSTEHSQKEVTQD  
PHKDVCSKQDGCPEQSQSVLASEVF  
TEKGCESQPLVSSAFKQSESET  
QESLTPSEVTKPFPPSDASVKAEGT  
EPKPQGAIRSPQGLELPLPNRSEVL  
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PVEPKMKAGILPSHFPLPAIAKTDL  
VAEVASMRSLLRDPDGAEDDSLE  
QTLMESSGKSPSPDTPSSEEVSYE  
VTPKPSDSSTPKPAVIHECAEEDDSE  
NGEKKRFTPEEEMFKMVTKIKTFDE  
LEQEAQKQRDYKKEPRQDGGSSASD  
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PVLVTSENRKVVSSSSSEPELTQLS  
KGADSGLLTEPVIRVQPPSPSSIDS  
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CETVSPNSATPVSLGVQSPHEKDV  
DKPLAIDKDSLHQDTCENDREERE  
FDPGVESTQADLPNESSLSRCAI  
PEGNESAKEIASPSPVKVEVTITDQ  
ALESMPEDCPIQDSSTTMQTERFAM  
DVPVSELAETDENDSPQIISPYENVP  
SSSFFSAEPSKIQTDTCHSTVVHSPE  
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DAPPLAVAPTASDAASVTGEQASKVI  
ITKTDADADSWSEIREDDAAFARVK  
EEEQKIFGLMVDROSQGTTPDITPA  
RTPTTEEGTPTSEQNPFQEQGLFE  
MTRSGAIDMTKRPYADESLHFFQIG  
QESNEEAISEDLEKATGAEPQTET  
TSESLLESEPKEAMDDGELLPDDV  
SEEDLPAISDANISQVIASASTETP  
TKEAVSTAVEEPPTTQRSDSLSTVKO  
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DDESPESPPEEQKSVIEIPTAPVDNV  
PSAESKPQIPIRTLPTLVPAPPSAEDE  
SAFSDDFPSSLDEDSKEGAKPKSKI  
PVKAPTQRTEWQPSPTDIPLQKTAVP  
QGQETLSRAPDGRSKSESDASSLDA  
KTKCPVKARSYIETETESRERAEGFE  
SESEDGATKPKLFA SRLPVKSRSTSS  
SGRPGTSPTREREHFFDLRNSIEF  
FEEISDEASKLVDRLTQSEREQEPPS  
DDESSALEVSVIESLPPVDIEHSAP  
EDIFDTRPIWDESIETMIERIPDENG  
HDRAEDPQDEQERMEERLAYIADHL  
GFSWTELARELDFTEEQIHQIRIENP  
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VIVESTDDQSQVFERLDGDAAFQKG  
DDMPDIPPETVTEEEYVDENGHTVV  
KKVTRKIIRRYVSSDGTKEEVTMQG  
MPQEPVNIEDGDNYSKVIKRVVLKS  
DTQQSEDNNE