

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q8IVF2	AH NK2_HUMAN	Homo sapiens	Protein AHNAK2	19.853344	T788;S1293;S1567;T1613;S3346;S4425;S4428;S4634;S4636;S4710;S4840;S4851;S4856;T5495;S5504;T5508;S5509;T5513;S5515;S5519;S5712	S280;S294;S593;S842;S1007;S1112;S1337;S1418;S1502;S1667;S1832;S2162;S2243;S2408;S2492;S2738;S2822;S2987;S3068;S3152;S3233;S3408;S3812;S3977;S4142;S4307;S4388;S4472;S4477;S4894;S4897;S5707	30059200;37217939;38253038;39531497;37340703;30379171;28657654;34019948;31492838;36240223;30620550;31373491;39534244;39302247;35254053	<p> MCD CFH MVLPTWP GTPG SVSG RQL QPGEPGAETEDDHSVTEGPADEGIR PRPQGS SPVYEYTTAADFGLQEDAP GRQGSAGR RRSWWKRDSDGSRITFF RMSRPEAVQEATEVTLKTEVEAGAS GYSVTGGDQGI FVKQVLKDS SAAK LFNLREGDQLLSTTVFFENIKYEDAL KILQYSEPKVQFKIRRLQPAPODEE WASSDAQHG PQGKEKEDTDVADGC RETPTKTLEGGDQERLISKPRVGR GRQSQRERLSWPKFQSIKSKRGP GP QRSHSSSEAYEPRDAHDV SPTSTDT EAQLTVERQE QKAGPGSQR RRKFLN LRFRTGSGGQPSSTGQPGR GFQSGV GRAGVLEELGPW GDSLEETGAATGS RREERAEQDREVMPAQSMPLPTEL GDPRLCEGTPQEGGLRAARLHGKTL EGQAQETA VAQRKPRAQPTPGMSRE GEGEGLQSL EIGIARLSLRDTTEGGT QIGPPEIRVRVHDLKTPKFAFSTEKE PERERRLSTPQRGKRQDASSKAGTG LKGEVEGAGWMPGREPTTHAEAQ GDEGDGEEGLQRTRITEEQDKGRED TEGQIRMPKFKIPSLGWSPSKHTKT GREKATEDTEQGREGEATATADRRE QRRTEEGLKDKEDSDSMTNTTKIQL IHDEKRLKKEQILTEKEVATKDSKFK MPKFKMPLFGASAPGKSMEASVDV SAPKVEADVSLLSMOGDLLKTTDL SV QTPSADLEVQDGVKLP EGPPLPE GASLKGHL PKVQRP SLKMPKVDLKG PKLDLKGPKAEV TAPDVKMSLSSME VDVQAPRAKLDGARLEGDLSLADKE VTAKDSKFKMPKFKMPSFGVSAPGK SMEDSVDSAPKVEADVSLSSMOG DLKATDLSIQPPSADLEVQAGQVDV KLPEGPVPEGAGPKVHLPKVEMP SF KMPKVDLKG PQIDVKGPKLDLKGPK AEVTAPDGEVSLPSMEVDVQAQKAK LDGAWLEGDLSLADKDVTA KDSKFK MPKFKMPSFGVSAPGKS IKALVDVS APKVEADLSLPSMQGDLKTTDL SIQP ASTDLKVQADQVDVKLPEGHLPEGA GLKGHLPKVEMPSFKMPKVALKGP QVDVKGPKLDLKS PKAEV TAPDVEV SLPSVEVDVEAPGAKLDSARLEGE LS LADKDVTA KDSRFRKMPKFKMPSFG ASAPGKSIEASVDV SAPKVEADVSLP SMOQDLKTTDL SIQPPSADLEVHAG QVDVKLEGHVPEGAGFKGHLPKVQ MPSLKM PKVDLKG PQVEVRGPKLDL KGHKAEVTAHEVAVSLPSVEVDMQA PGAKLDGAQLDGDLSLADKDVTA KD SKFKMPKFKMPSFGVSAPGKSIEAS VDLSAPKVEADM SLPSMQGDLKTTD LSIQPPSTDL ELQAGQLDVKLPEGPV PEGAGLKGHLPKLQMP SFKVPKVDL KGPEIDIKGPKLDLKD PKVEV TAPDV EVSLPSVEVDVEAPGAKLDGGRLEE DMSLADKDLTTKDSKFKMPKFKMP SFGVSAPGKSIEASVDV SAPKVEADV SLPSMQGDLKATDLSIQPPSADLEV QAGQVDVKLPEGPVSEGAGLKGHL P KVQMP SFKMPKVDLKG PQIDVKGPK LDLKGPKVEV TAPDVKMSLSSMEVD VQAPRAKLDGAQLEGDLSLADKAVT AKDSKFKMPKFKMPSFGVSAPGKSI EASVDVSEPKVEADVSLPSMQGDLK TTDLSIQSPSADLEVQAGQVNVKLPE GPLPEGAGFKGHLPKVQMP SLKMP KVALKGPQMDVKGPKLDLKGPKAEV MAPDVEVSLPSVEVDVEAPGAKLDS VRLEGDLSLADKDVTA KDSKFKMPK FKMPSFGVSAPGKSIEASVDV SAPKV EAEVSLPSMQGDLKTTDL CIPLPSAD LVVQAGQVDMKLP EGQVPEGAGLK GHLPKVDMPSFKMPKVDLKG PQTD VKGAKLDLKGPKAEV TAPDVEVSLPS MEVDVQAQKAKLDGARLEGDLSLA DKDMTAKDSKFKMPKFKMPSFGVS </p>	True	True	4.796	4.322	1.378

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 PSLKMPKVDLKGQVDIKGPKLDLK
 DPKVEMRVPDVEVSLPSMEVDVQAP
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 VSLPSVEVDVKAPGAKLDGARLEGD
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LHDP SRDGNLGLAVGEVGMDSKFK
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FESSILSPCEDVTLTKYQVTV PRAAL
APELAL EIPSGSQAD IPLKTECSTDL
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NEG