

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8IVF2	AHNK2_HUMAN	Homo sapiens	Protein AHNK2	12.642916	T788;S1567;T1613;S4636;S4710;S4856;T5495;S5504;S5509;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	30379171;30059200;31492838;28657654;31373491;34019948;30620550	MCDCFHMVLPWPPTPGSVSGRQL QPPEGAETEDDHSVTEGPADEGIR PRPQGSPPVYEYTTAAADFGLEDAP GRQGSAGRRRSWWKRDSGDSRTFF RMSRPEAVQEATEVTLKTEVEAGAS GYSVTGGGQDGIFVKQVLDSSAAK LFNLREGDQLLSTTVFFENIKYEDAL KILQYSEPYKVQFKIRRLPAPQDEE WASSDAQHGPQKKEKEDTDVADGC RETPTKTLEGGDQERLISKPRVGR GRQSQRERLSWPKFQSIKSKRGP QRSHSSSEAYEPRDAHDVSPTSTDT EAQLTVERQEQAQKAGPSQRRRFLN LRFRTGSGQGPSSTGQPRGFQSGV GRAGVLEELGPWGSLEETGAATGS RREERAEQDREVMQAQSMPLPTL GDPRLCEGTPQEGGLRAARLHGKTL EGQAQETAQAQRKPRAQPTPGMSRE GEGEGLQSLEIGIARLSLRDTTEGGT QIGPPEIRVRVHDLKTPKFAFSTEKE PERERRLSTPQRGKRQDASSKAGTG LKGEEVEGAGWMPGREPTTHAEAQ GDEGDGEEGLQRTRITEEQDKGRED TEGQIRMPKFKIPSLGWSKHTKT GREKATEDTEQGREGEATATADRRE QRRTEGLKDKEDSDSMTNTTKIQL IHDEKRLKKEQILTEKEVATKDSKFK MPKFKMPLFGASAPGKSMEASVDV SAPKVEADVSLSMQDGLKTTDLV QTPSADLEVQDQVQVVKLPEGPLPE GASLKGHLPKVQRPVSLKMPKVDLKG PKLDLKGPKAEVTAPDVKMSLSSME VDVQAPRAKLDGARLEGDLSLADKE VTAKDSKFKMPKFKMPSFGVSAPGK SMEDSVQVAPKVEADVSLSSMQG DLKATDLSIQPPSADLEVQAGQVDV KLPEGPVPEGAGPKVHLPKVEMPSF KMPKVDLKGPKQIDVKGPKLDLKGPK AEVTAPDGEVSLPSMEVDVQAQKAK LDGAWLEGDLSLADKDVTAKDSKFK MPKFKMPSFGVSAPGKSIKALVDVS APKVEADLSLPSMQDGLKTTDLSIQP ASTDLKVQADQVQVVKLPEGHLPEGA GLKGHLPKVEMPSFKMPKVALKGP QVDVKGPKLDLKSPEAEVTAPDVEV SLPSVEVDVEAPGAKLDSARLEGELS LADKDVTAKDSRFKMPKFKMPSFG ASAPGKSIEASVDVSAPKVEADVSLP SMQDGLKTTDLSIQPPSADLEVHAG QVDVKLLEGHVPEGAGFKGHLPKVQ MPSLKMPKVDLKGQVEVRGPKLDL KGHKAEVTAHEVAVSLPSVEVDMQA PGAKLDGAQLDGDLSLADKDVTAKD SKFKMPKFKMPSFGVSAPGKSIEAS VDLSAPKVEADMSLPSMQDGLKTTD LSIQPPSTDLELQAGQLDVKLPEGPV PEGAGLKGHLPKLQMPKFKVQVVDL KGPEIDIKGPKLDLKDPKVEVTAPDV EVSLSVEVDVEAPGAKLDGGRLEE DMSLADKDLTTKDSKFKMPKFKMP SFGVSAPGKSIEASVDVSAPKVEADV SLPSMQDGLKATDLSIQPPSADLEV

QAGQVDVKLPEGPVSEAGLKGHLPL
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LHDP SRDGNLGLAVGEVGMDSKFK
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NEG