

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
A2AGT5	CKAP5_MOUSE	Mus musculus	Cytoskeleton-associated protein 5	21.955739	S568	S816;S1469;S1861	22645316;28528544;30016717	MGDDSEWLKLPVDQKCEHKLWKAR LSGYEEALKIFQKIKDEKSPESKYL GLIKKFVTDSDNAVVLKGLEAALVYV ENAHVAGKTTGEVVSQVSKVFNQP KAKAKELGIEICLMYVEIEKGESVQE ELLKGLDNKNPKIIVACIETLRKALSE FGSKIISLKPPIKVLPLKLFESRDKAVR DEAKLFAIEIYRWNRDVAVKHTLQNI NSVQLKELEEEWVKLPTGAPKPSRF LRSQQELEAKLEQQQSAGGDAEGG GDDGDEVPOVDAYELLDVEILSKLP KDFYDKIEAKKWQERKEALEAVEVL VKNPKLEAGDYADLVKALKKVVGKD TNVMLVALAAKCLTGLAVGLRKKFG QYAGHVPTILEKFKEKKPQVVQAL QEIDAIFLTTTLQNISEDVLAVMDN KNPTIKQOTSLFIARSFRHCTSSTLP KSLKPFCAALLKHINDSAPEVRDAA FEALGTALKVVGEKSVNPFLADVDK LKLDRKECSEKVELVHGKKSGLATE KESKPLPGRAAASGAAGDKDTKDV SGPKPGPLKKTPTAKAGGPSKKGKTT APGGSASAGTKNKKGLETKEIVEPEL SIEVCEEKASAVLPPTCIQLDSSNW KERLACMEEFQKAVELMERTEMPC QALVKMLAKKPGWKETNFQVMQM KLHIVALIAQKGNFSKTSQIVLDGL VDKIGDVKCGNNAKEAMTAIAEACM LPWTAEQVMSMAFSQKNPKNQSET LNWLSNAIKEFGFSELNVKAFISNV KTALAATNPAVRTSAITLLGVMYLYV GPSLRMIFEDEKPALLSQIDAEFQK MQGQSPAPTRGIAKHSTSATDEGE DGEEPGEGGNDVVDLLPRIEISDKIT SELVSKIGDKNWKIRKEGLDEVAGII NEAKFIQPNIGELPTALKGRLNDSN KILVQOTLNILQQLAVAMGANIRQH VKNLGIPVITVLGDSKNNVRAAALAT VNAWAEQTGMKEWLEGEDLSEELK KENPFLRQELLGWLAELPLTRSTP TDLILCVPHLYSCLKDRNGDVRKKA QDALPFFMMHLGYEKMAKATGKLG PTSKDQVLAMLEKAKANMPKPAAP AKAMSKPMGGSAPAKTQPIPAVED SVSSTIEAKPDLKAKAPGVSSKAKS VQGKKVPSKTTTKEDDDKSGPIFIVV PNGKEQRMREKGLKVLKWNFTTP RDEYIEQLKTQMSTCVAKWLQDEM FHSDFQHHNKALAVMVDHLESEKD

GVISCLDLILKWLTLRFFDTNTSVLM
KALEYLKLLFTLLSEEEYHLTENEAS
SFIPYLILKVGEPKDVIRKDVRAILNR
MCLVYPASKMFPPFIMEGTKSKNSKQ
RAECLEELGCLIESYGMNVCQPTPG
KALKEIAIHIGDRDNAVRNAALNTIV
TVYNVHGDQVFKLIGNLSEKDMSM
LEERIKRSKRPSAAPVKQAEKPKQR
TQNINSNANMLRKGPAEDMSSKLN
QARSLSGHPEAAQMVRREFQLDLD
EIENDNGTVRCPELVQHKLDDIF
EPVLIPEPKIRAVSPHFDDMHSNTAS
TINFIIISQVSGDINTSIQALTQIDEVL
RQEDKAEAMSGHIDQFLIATFMQLR
LIYSTHMADEKLDKDEIHKLYSCIIGN
MISLFQIESLAREASTGVKDLMHG
LITLMLDSRIEDLEEGQQVIRSVNLL
VVKVLEKSDQTNILSALLVLLQDSLL
ATASSPKFSELVMKCLWRMVRLLPD
TINSINLDRILLDIHIFMKVFPKEKLN
QCKSEFPRTLKTLHTLCKLKGPKIL
DHLTMIDNKNESELEAHLCRMMKH
SMDQTGSKSDKETEGASRIDEKSS
KAKVNDFLAEIFKKIGSKENTKEGLA
ELYEYKKKYSDDIEPFLKNSSQFFQ
SYVERGLRVIEMERESKGRIPSTGI
SPQMEVTCVPTPTSTVSSLGNTNGE
EVGPSVYLERLKILRQRCGLDNTKQ
DDRPPPLTSLLSKPAIPPVASSTMLH
SKLSQLRESREQHQHSDLDSNQTH
SAGTMTSSSSTTNIDDLKKRLERIKS
SRK