

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q61191	HCFC1_MOUSE	Mus musculus	Host cell factor 1	38.292269	T405;S419;T480;T490;T495;T496;T502;T515;T517;S518;S522;T529;S562;S563;T579;T583;T586;T587;T588;T592;S597;S603;T612;T619;S620;S622;S623;T627;T629;T634;S638;T640;T642;T651;T652;T658;S666;S669;S685;T689;T694;S695;T698;S702;T703;T726;S727;T733;T738;T739;S754;S755;T761;T771;S775;T779;T787;S794;T800;T801;T805;S806;T808;T823;T831;T858;T861;T870;T871;T1055;S1058;T1061;T1138;T1148;T1235;T1238;T1240;T1241;T1243;T1246;T1247;T1495;T1497;T1500;S1506	S6;S411;S598;S666;S669;S1204;S1223;T1500;S1506;S1516;S1781;S1848	36064721;21540332;36084651;31227231;22645316;36852467;34105348;34887587;36288343;35822049;30059200	MASAVSPANLPAVLLQPRWKRVVG WSGPVPRPRHGHRAVAIKELIVVFG GGNEGIVDELHVYNTATNQWFIPAV RGDIPPGCAAYGFVCDGTRLLVFGG MVEYGKYSNDLYELOQSRWEWKRL KAKTPKNGPPPCPRLGHSFSLVGNK CYLFGGLANDSEVDPKNNIPRYLNDL YILELRPGSGVVAWDIPITYGVLPPPR ESHTAVVYTEKDNKKSCLVIYGGMS GCRLGDLWTLDIETLTWNKPSLSGV APLPRSLHSATTIGNKMYVFGGWVP LVMDDVKVATHEKEWKCTNLTACL NLDTMAWETILMDTLEDNIPRARAG HCAVAINTRLYIWSGRDGYRKAOWNN QVCKDLWYLETEKPPPARVQLVR ANTNSLEVSWGAVATADSYLLQLQK YDIPATAATATSPTPNPVPSVPANPP KSPAPAAAAPAVQPLTQVGITLVPQA ATAPPSTTTIQVLPVPGSSISVPTAA RTQGVPAVLKVTGPQATTGTPLVTM RPASQAGKAPVTVTSLPASVRMVVP TQSAQGTVIGSNPQMSGMAALAAAA AATQKIPSSAPTLSVPAGTTIVKTV AVTPGTTTTLPATVKVASSPVMVSNPA TRMLKTAQAQVGTSSAANTSTRPI ITVHKSGTIVTAAQQAQVVTTVVGGV TKTITLVKSPISVPGGSALISNLGKVM SVVQTKPVQTSAVTGQASTGPVTQII QTKGPLPAGTILKLVTSADGKPTTIIT TTQASGAGTKPTILGISSVSPSTTKPG TTTIKTIIPMSAIIQAGATGVTSSPGI KSPITIIITKVMSTSGTGAPAKIITAVPK IATGHGQQGVTVVVLKGAPGQPGTI LRTVPMGGVRLVPTVSAVKPAVTT LVVKGTTGVTTLGTVTGTVSTSLAGA GAHSTSASLATPITTLGTIATLSSQVI NPTAITVSAQAQTTLAAGGLTTPIT MQPVSQPTQVTLITAPSGVEAQPVH DLPVSILASPTTEQPTATVTIADSGQG DVQPGTVTLVCSNPPCETHETGTTN TATTTVVANLGGHPQPTQVQFVCDR QETAASLVTSAVGQQNGNVVRVCS NPPCETHETGTTNTATTATSNMAGQ HGCSNPPCETHETGTTSTATTAMSS MGTGQQRDRTRTNTPTVVVITVAP GALERVQGTVKPQCQTQQTNMTT TMTVQATGAPCSAGPLLRPSVALES GSHSPAFVQLALPSVRVGLSGPSSK DMPTGRQPETYHTYTTNTPTTTRSI MVAGELGAARVVPTSTYESLQASSP SSTMTMTALEALLCPSATVTQVCSN PPCETHETGTTNTATTSNAGSAQRV CSNPPCETHETGTTHTATTATSNNG AGQPEGGQQPASGHPCETHQTTSTG TTMSVSVGTLLIPDATSSHGTLESGL VVAVPTVTSQAGSTLLASFPTQRVCS NPPCETHETGTTHTATTVTSNMSSN QDPPPAASDQGEVASTQGDSTNITS ASAITTSVSSTLPRAVTTVTQSTPVPG PSVPPPEELQVSPGPRQQLPPRQLLQ SASTPLMGESTEVLSASQTPELQAAV

