

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | er |
|--------------|-------------|--------------|--------------------|--------------|---|--|---|---|---------------|---------------|---------|---------|---------------|----|
| Q61191 | HCFC1_MOUSE | Mus musculus | Host cell factor 1 | 64.846518 | T405;S419;T453;T480;T490;T495;T496;T502;T515;T517;S518;S522;T529;S544;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;T707;T726;S727;T733;T737;T738;T739;T749;S754;S755;T761;T771;S775;T779;T787;S794;T800;T801;T805;S806;T808;T823;T831;T858;T861;T870;T871;T1055;S1058;T1061;S1062;T1138;T1139;T1148;S1195;S1224;T1235;T1238;T1240;T1241;T1243;T1246;T1247;T1495;T1497;T1500;S1506 | S6;S411;S598;S666;S669;S1204;S1223;T1500;S1506;S1516;S1781;S1848 | 22645316;34887587;31227231;40885482;40754593;36064721;36852467;34105348;40128797;36288343;36084651;35822049;21540332;40021952;39927985;39627609;30059200;40997131 | MASAVSPANLPVLLQPRWKRVRVWGSGPVRPRRHGRAVAIKELIVVFGGGNEGIVDELHVYNTATNQWFIQAVRGDIPPGCAAYGFVCDGTRLLVFGGMVEYQKYSNDLYELQASRWKRLKAKTPKNGPPPCPLRGLHSFSLVGNKCYLFGGLANDESDPKNNIPRYLNDLYILELRPGSGVVAWDIPITYGVLPPEPESHTAVVYTEKDNKSKLVVYGGMSGRLGDLWTLDIETLTWNKPSLSGVAPLPRSLHSATTIGNKMYVFGWVPLVMDDVKVATHEKEWKCTNTLACLNLDTMAWETILMDTLEDNIPRARAGHCAVAINTRLYIWSGRDGYRKAOWNQVCCCKDLWYLETEKPPPPARVQLVRANTNSLEVSWGAVATADSYLLQLQKYDIPATAATATSPTPNPVPSVPANPPKSPAPAAAAAPVQPLTQVGITLVPQAATAPPSTTTIQVLPVPGSSISVPTAARTOGVPAVLKVTGPOATTGTPLVTMRPASQAGKAPVTVSLPASVRMVPVTQSAQGTVIGSNPQMSGMAALAAAAAATQKIPSSAPTIVLSPAGTTIVKTVAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAQAQVGTSVSSAANTSTRPIITVHKSGTIVTVAQQAQVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVM SVVQTKPVQTSAVTGOASTGPVTOIITQKGPLPAGTILKLVTSADGKPTIITITQASGAGTKPTILGISSVSPSTTKPGTTTHIKTIPMSAIIITQAGATGVTSPPGKSPITIIITKVMTSGTGAPAKIITAVPKIATGHGQQGVTVVVLKGPAGPQGTILRTVPMGGVRLVTPVTVSAVKPAVITLVVKGTTGVTTLGTVGTVSTSLAGA GAHSTSASLATPITTLGIATLSSQVINPTAITVSAQTTLTAAGGLTPTIITMQPVSQPTQVTLITAPSGVEAQPVDLDPVSILASPTTEQPTATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTATTITVANLGGHPQPTQVQFVCDRQETAASLVTSAVGQQNGNVVRVCSNPPCETHETGTTNTATTATSNMAGQHGCNSPPCETHETGTTSTATTAMSSMGTGQQRDRTRTNTPTVVRITVAPGALERVQGTIVKQCCQQTQNTMTTMTMTVQATGAPCSAGPLLRPSVALES GSHSPAFVQLALPSVRVGLSGPSSKDMPTGRQPETYHTYTTNTPTTTRSI MVAGELGAARVVPTSTYESLQASSPSTMTMTALEALLCPSATVTQVCSNPPCETHETGTTNTATTATSNAGSAQRVCSNPPCETHETGTTHTATTATSNAGGAGQPEGGQQPASGHPCETHQTTSTGTTMSVSVGTLIPDATSSHGTLESGLEVVAVPTVTSQAGSTLLASFPTQRVCSNPPCETHETGTTHTATTVTSNMSSNQDPPPAASDQGEVASTQGDSTNITSASAIITSVSSTLPRAVTIVTQSTPVPVPSVPPPEELQVSPGPRQLPPRQLLQ SASTPLMGESTEVLASQTPELQAAV DLSSTGDPSSGQEPPTS AVVATVVVQ PPPPTQSEVDQLSLPQELMAEAQAGTTTLMVGTGLPEELAVTAAAAEAQA AATEEAQALAIQAVLQAAQAVMGTGEPMDTSEAAAAVTQAEGLHLSAEG QEQGATTIPIVLTQOELAALVQOQQQLQEAQAQAQQHHLPTALAPADSLNDPSIESNCLNELASAVPSTVALLPSTATESLAPSNFVAPQPVVASPAKMQAAATLTEVANGIESLVGKPDLPPPP SKAPVKKENQWFDVGVKGTSMVMTHYFLPPDDAVQSDDDSGTVPDYNQLKKQELQPGTAYKFRVAGINACGRPFSEISAFKTCPLGFPAPCAIKISKSPDGAHLTWEPPSVTSGKIIEYSVYLAIQSSQASGEPKSSTPAQLAFMRVYCGPSPCLVQSSLSNAHIDYTTKPAIIFRIAAARNEKGYGPATQVRWLQETSKDSSGTKPASKRPMSSPEMKSAPKSK | True | False | 2.384 | 5.0 | 2.428 | 1 |

