

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q04637	IF4G1_HUMAN	Homo sapiens	Eukaryotic translation initiation factor 4 gamma 1	43.748332	S60;S61;S64;S198;S1041;S1058;T1073;S1118;T1119	S15;T207;T223;S314;T647;S1028;S1077;S1092;S1145;S1147;S1185;S1187;S1194;S1209;T1211;S1231;S1238;S1596;S509;S705	30379171;33214551;27655845;31492838;32119511;30940748;30620550;30127386;16408927;20068230;30059200;26853435;29351928;31373491;29237092;21158410;34019948;31300553;32574038;32870666;19022411;23301498;28510447	MNKAPQSTGPPAPSPGLPQPAFPFPGQTAPVVFSTPQATQMVNTPSQPRQHFYPSRAQPPSSAASRVQSAAPARPGPAAHVYPAGSQVMMPISQISYPASQGAHYIPGQGRSTYVVPTQYVPVQPGAPGFYPGASPTFEGTYAGAYPAQGVQGFPTGVAPTVPVLMNQPPQIAPKRERKTIRIRDPNQGGKDITEEIMSGARTA STPTPPQTGGGLEPQANGETPOQAVI VRPDDRSQGAIDRPLPGPEHSPSESQSSPSPTPSPSPVLEPGSEPNLA VLSIPGDTMTTIQMSVEESTPISRET GEPYRLSPEPTPLAEPILEVEVTL SKP VPESFSSSPLQAPTPLASHTVEIHE PNGMVPSLEDLEPEVESSELAPPPA CPSESPVPIAPTAQPELLNGAPSP AVDLSPVSEPEEQAKEVTASMAPPTI PSATPATAPSATSPAQEEEMEEEE EEEGEAGEAGEAESEKGGEELLPE STPIPANLSQNLAAAAATQVAVSVK RRRKIKELNKKEAVGDLDFKEAN PAVPEVENQPPAGSNPGPESEGSV PPRPEADETWDSKEDIHNAENIQ PGEQKYEYKSDQWKPLNLEEKKRYD REFLLGFQFIFASMQKPEGLPHISDV VLDKANKTPLRPLDPTLRQGINCGP DFTPSFANLGRITLSTRGPPRGGPG GELPRGPAGLGP RRSGQGP RKEPRK IIATVLMTEDIKLNKAEKAWKPSSKR TAADKDRGEEDADGSKTQDLFRRVR SILNKLTPQMFQQLMKQVTQLAIDT EERLKGVIDLIFEKAISEPNFVAVAN MCRCLMALKVPTTEKPTVTVNFRL LLNRCQKEFEKDKDDDEVFEKKQK EMDEAATAEERGRKKEELEEAR DIA RRRSLGNIKFIGELFKLMLTEAIMH DCVVKLLKNHDEESLECLCRLLTTIG KDLD FEKAKPRMDQYFNQMEKIIKE KKTSSRIRFMLQDVL DLGRSNVWPR RGDQGPKTIDQIHKEAEMEEREHI KVQQLMAKGS DKRRGGPPGPPISRG LPLVDDGGWNTVPISKGSRPIDTSRL TKITKPGSIDSNNQLFAPGGRLSWG KGSSGGGAKPSDAASEAARPATST LNRFSALQQAVPTESDNR RVVQRS SLSRERGEKAGDRGDR LERSERGGD RGDRLDRARTPATKRSFSKEVEERS RERSQPEGLRKAASLTEDRDRGRD AVKREAAALPPV SPLKAALSEELEKK SKAIIIEYLHLNDMKEAVQC VQELA SPSLLFIFVRHGVESTLERSAIAREH MGQLLHQLLCAGHLSTAQYYQGLYE ILELAEDMEIDIPHVWLYLAELVTPIL QEGGVPMGELFREITKPLRPLGKAA SLLLEILGLLCKSMGPKKVGTLWRE AGLSWKEFLPEGQDIGAFVAEQKVE YTLGEESEAPGQRALPSEELNRQLE KLLKEGSSNQRVFDWIEANLSEQQI VSNTLVRALMTAVCYS AIFETPLRV DVAVLKARAKLLQKYL CDEQKELQA LYALQALVVTLEQPPNLLRMFFDAL YDEDVVKEDAFYSWESSKDPAEQQG KGVALKSVTAFFKWLREAEESDHN

