

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondri
043432	IF4G3_HUMAN	Homo sapiens	Eukaryotic translation initiation factor 4 gamma 3	18.948827	T168;T211;S232;S258;S277;T278;T283;S284;S285;S288;S289;T294;T295;S736;S806;S1050	T168;S230;S232;S267;S441;S495;S1156;S1218;S1409	23301498;30379171;31492838;39894887;40914422;35138101;22661428;38665916;30620550;39302247;34019948;29351928;39531497;40307207;37340703;32870666;28657654;31637018;35289036;33214551;35254053;32119511;38253038	MNSQPQTRSPFFQRPQIQPPRATIPNSSPSIRPGAQTPTAVVQANQHIMMVNHLPMYPVYVQGPQYQYRHSPPYVGGPPQYVQPPGPGPFYVGGPQGDFFPNAYGTPFYPSQPVVYQSAPIVPTQQQPPPAKREKKTIRIRDPNQGKDI TEEIMSGGGSRNPTPIGRPTSTPTP PQQLPSQVPEHSPVYGVTVSAHLA ASTPVTAAASDQKQEEKPKPDPVLKSP SPVLRVLVLSGKKEQEGQTSETTAIV SIAELPLPPSPTTVSSVARSTIAAPTS SALSSQPIFTTAIDDRCELSSPREDTI PIPSLTSTCTETSDPLPTNENDDICK KPCSVAPNDIPLVSSTNLNINEINGVS EKLSATESIVEIVKQEVLPITLLEIL ENPPEEMKLECIAPITPSTVPSFPPT PPTPPASPPHTPVIVPAAATTVSSPSA AITVQRVLEEDSIRTCLSEDAKEIQ NKIEVEADGQTEEILDSONLNSRRS PVPAQIAITVPKTWKKPKDRTRITTEE MLEAELELKAEEELSIDKVLSEQD KMSQGFHPERDPSDLKVKVAEEN GEEAEPVRNGAESVSEGEIDANS STDSSGDGVTFFPKPESWKPTDTEG KKQYDREFLLDFQFMPACIQKPEGL PPISDVVLDKINQPKLPMRDLDPRL PRGPDFTPAFADFGROTPGGRGVPL LNVGSRSSQPGORREPRKIITVSVKE DVHLKKAENAWKPSQKRDSQADDP ENIKTQELFRKVRILNKLTPQMFN QLMKQVSGLTVDTTEERLKGVIDLVF EKAIDEPSFSVAYANMCRCLVTLKVP MADKPGNTVNFRLNRCQKEFE KDKADDVFEKKQKELEAASAPEER TRLHDELEEAADKARRRSIGNIKFIG ELFKLMLTEAMHDCVVKLLKNHD EESLECLRLTTIGKDLDFEAKAPR MDQYFNQMEKIVKERKTSSRIRFML QDVIDLRLCNWVSRRADQGPKTIEQ IHKEAKIEEQEEQRKVQQLMTKEKR RPGVQRVDEGGWNTVQGAKNRVL DPSKFLKITKPTIDEKIQLVPAQLGS WKGSSGGAKASETDALRSSASSLN RFSALQPPAPSGSTPSTPVEFDSRRT LTSRGSMSGREKNDKPLPSATARPNT FMRGSSKDLLDNQSQEEQRREML ETVKQLTGGVDVERNSTEAERNKTR ESAKPEISAMSAHDKAALSEEELER KSKSIIDEFLHINDFKEAMQCV EELN AQGLLHVFRVGVESTLERSQITRD HMGQLLYQLVQSEKLSKQDFFKGF5 ETLELADDMAIDPHIWLylaELVTP MLKEGGISMRELTIIEFSKPLLPVGRA GVLLSEILHLLCKQMSHKKVGALWR EADLSWKDFLPEGEDVHNFLLEQKL DFIESDPCSSEALSKELSAEELYK RLEKLHEDKANDEQIFDWVEANLDE IQMSSPTFLRALMTAVCKAAIHADSS TFRVDTAVIKQRVPIKLYLSDTEK ELQALYALQASIVKLDQPANLLRMF FDCLYDEEVISEDAFYKWESSKDP EQNGKGVALKSVTAFFTWLREAE SEDN	True	False	4.777	3.405	1.705