

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ex re
O94915	FRYL_HUMAN	Homo sapiens	Protein furry homolog-like	26.040516	T627;T632	S844;S1914;S1935;S1941;S1945;S1957;T1959;S1978;S2272;S2454;S2499	34725712;29351928	MSNITIDPDVKKPGEYVIKSLFAEFVQAEKKIEVMMAEPLKLLSRSLSRQGEDLQFDQLISSMSSVAEHCPLSLRRLFDFWYRRQNGTEDESIEYRPRSSKSKGDEQQRERDYLLERRDLAVDFIFCLVLVEVLKQIPVHPVPPDPLVHEVLNLAFFKFKHKEGYSGTNTGNVHHIADLYAEVIGVLAQSKFOAVRKKFVTELELRQKEQSPHVQSVISLIMGMKFFRVKMPVEDFEASFQFMQECAQYFLEVKDKDIKHALAGLFEILIPVAAAANKNEVNVPCLNKVFEMLYQTTFELSSRKKHSLALYPLITCLLCVSOQKOFFLNWHIFLQNCLSHLKKNKDPKMSRVALESYRLLWVYVIRIKCESNTVTQSR LMSIVSALFPKGSRSVVRDTPLNIFVKIIQFIAQERLDFAMKEIIFDLLSVGKSTKTFINPERMNIGLRVFLVIADSLQKQDGEPPMPTTGVLPSGNTLRVKKIFLNKTLTDEEAKVIGMSVYYPQVRKALDSILRHLDKVGRPMCMTSVQMSNKEPEDMITGERKPKIDLFRTCIAIPRLIPDGMSTRDLELLARLTIHMDEELRALAFNTLQALMLDFPDWRE DVLSGFVYFIVREVTDVHPTLLDNAV KMLVQLINQWKQAAQMHNKNQDTHQGVANGASHPPPLERSPYSNVHFVVEGFALVILCSSRPATRRRLAVSVLREIRALFALLEIPKGDDELAIIDVMDRLSPSILESFHILTGADQTTLLYCPSSIDLQTLAEWNSSPISHQFDVISPISHIWIFAHVTQGDWPWISLSSFLKQENLPKH CSTAVSYAWMFAYTRLQLLSPQVDINSPINAKKVNTTSSDSYIGLWRNYLILCCSAATSSSSTSAGSVRCSPPETLASTPDSGYSIDSKIIGIPSPSLFKHIVPMMRSEMEITESLVGLGRTPNGAFRELIEELHPIKEALERRPENMKRRRRRDILRVQLVRIFELLADAGVISHSASGGLDNETHFLNNTLLEYVDLTRQLEAENEKSDTLKDIRCHFSAVANI IQNVVHQRRSIFPQQLRHSLSFMLFSHWAGPFSIMFTPLDRYSDRNMQINRHQYCALKAMSAVLCCGPVADNVGLSSDGYLYKWLNDLSDLKKVHQ LGCEAVTLLLELNPQSNLMYWAVDRCYTGSGRVAAGCFKAIANVFQNRDYQCDTVMLLNILFKAADSSRSIYEVAMQLLQILEPKMFRYAHKLEVQRTDGVLSQLSPLPHLYSVSYQLSEELARAYPELTLAIFSEISQRIQTAHPAGRQVMLHYLLPVMNINELVDLKLPTARRHDEDEDDSLKRELMVTSRRWLRGEGWGSPOATAMVLNLMYMTAKYGDDELAWSEVENVTTLADGWPKNLKILHFLISICGVNSEPSLLPYVKKVIVYLGRDKTMQLLEELVSELQITDPVSSGVTHMDNPPYYRITSSYKIPSVTSGTTSSSNTMVAPT DGNPDNPKPIKENIEESYVHLDIYSGLSHLNRQHHRLESRYSSSSGGSYEEKSDSMPLYSNWRLKVMENQGEPLPFPAGGCWSPLVDYVPETSSPGLPLHRCNIAVILLTDLHDHSVKVEWGSYHLHLLHAIFIGFDHCHPEVYEHCKRLLHLLIVMGPNSNIRTVASVLLRNKEFNEPRVLTVKQVAHLDYNFTAGINDFIPDYQPSMTDSGLSSSSTSSISLGNNSAAISHLHTTILNEVDISVEQDGKVKTLMEFITSRKRGLWNHEDVSAKNPSIKSAEQLTTFPKHVVSVFKQSSSEGHILEHLSEVALQTALSCSSRHYAGRSFQIFRALKQPLTATLSDVLSRLVETVGDPEGDAQGFVIELLTLESAIDT LAETMKHYDLLSALSQTSYHDPIMGNKYAA NRKSTGQLNLSTSPINSSSYLGYN NARSNSLRLSLIGDRRGDRRSNTL DIMDGRINHSSSLARTRSLSLREKGMYDVQSTTEPTNLMATIFWIAASLL ESDYEYELLALRLNKLHLPLDK	False	False	3.52	1.38	0.931	0.839	0.646	2.995	0.9

SESREKIENVQSKLKWTNFPGLQQL
FLKGFTSASTQEMTVHLLSKLISVSK
HTLVDPSQLSGFPLNILCLLPHLIQH
FDSPTQFCKETASRIAKVCAEEKCPT
LVNLAHMMSLYSTHTYSRDCSNWI
NVVCRYLHDSFSDTTFNLVTYLAEL
LEKGLSSMQQSLLOIYSLLSHIDLS
AAPAKQFNLEIHKIGKYVQSPYWKEA
LNILKLVVRSASLVVPSDIPKTYGG
DTGSPEISFTKIFNNVSKELPGKTL
FHFIDISETPIGNKYGDQHSAGRNG
KPKVIAVTRSTSTSSGNSNALVPV
SWKRPQLSQRRTREKLMNVLSLGG
PESGLPKNPSVVFSSNEDLEVGDQQ
TSLISTTEDINQEEVAVEDNSSEQQ
FGVFKDFDFLDVELEDAEGESMDN
FNWGVRRRSLDSIDKGDTPSLQEYQ
CSSSTPSLNLTNQEDTDESSEEEAA
LTASQILSRTQMLNSDSATDETIPDH
PDLLOQSEDSTGSITTEVLQIRDTP
TLEASLDNANSRLPEDTTSVLKEEH
VTTFEDEGSYIIQQEESLVCQGGILD
LEETEMPEPLAPESYPESVCEEDVTL
ALKELDERCEEEADFGSLSSQDEE
EQDGFPEVQTSPLSPFLSAIAAFQP
VAYDDEEAWRCHVNQMLSDTDGS
SAVFTFHVFSRLFQTIQRKFGITNE
AVSFLGDSLQRIQTKFKSSLEVMMML
CSECPVFDVAETLMSCGLETLEKF
GVLELQEHLDYNNVKREAAEQWLD
DCKRTFGAKEDMYRINTDAQMEIL
AELELCRRLYKLHFQLLLFQAYCKL
INQVNTIKNEAEVINMSEELAQLESI
LKEAESASENEEIDISKAAQTITETAI
HSLIETLKNKEFISAVAQVKAFRSLW
PSDIFGSCEDDPVQTLLHIYFHHQTL
GQTGFSFAVIGSNLDMSEANYKLMEL
NLEIRESLRMVQSYQLLAQAKPMGN
MVSTGF