

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	extracellular region
Q2WGJ9	FR1L6_HUMAN	Homo sapiens	Fer-1-like protein 6	27.979371	S847;S1041	NaN	38253038;29351928	MFGLKVKKKRNKAEGKLILANKAAK DSQGDTEALQEEPSHQEGPRGDLV HDDASIFPVPSASPKRRSKLLTKIHD GEVRSQNYQIAITTEARQLVGENID PVVTEIEGDEKKQSTVKEGTNSPFYN EYFVDFDFIGPQVHLFDKIIKISVFHHK LIGSVLIGSFKVDLGTVYNQPGHQFC NKWALLTDPGDIRTGTGKYLKCDISV MGKGDVLKTSPKTSDTEEPKLNLLI PNGFPLERPWARFYVRLYKAEGLPK MNSSIMANVTKAFVGDSDKLDVDPFV EVSFAGQMGRTTVQKNCADPVWHE QVIFKEMFPPLCRRVKIQVWDEGSM NDVALATHFIDLKKSNEQDGDGKF LPTFGPAWINLYGSPRNHSLMDDYQ EMNEGFEGVSVFRGRILVEIAVEILS GRAQESKFSKALKELKLPKDKDSDK SSKGDADKADKTEDGKSSQASNKTN STEVEVESFDVPEIVPEKNEEFLLF GAFFEATMIDRKIGDKPISFEVSGN FGNLIDGGSHHGSKSAESAEDLL PLLHEGGQDVAHDVPIPMASHTHPE KPLVTEGNRRNYNLPFEAKKPCVYFI SSWGDQTFRLHWSNMLEKMADFL EESIEEVRELKISQEAPEEKMTVLS DFISRSSAFISEAEKKPKMLNQTLLD KKRLTLCWQLEAMCKEAKGIIQQQ KKKLSVDEMIHEAQNFVEKIRFLVD EPQHTIPDVFIWMLSNRRRVAYARI ASKDLLYSPVAGQMGKHCCKIKTHF LKPPGKRPAGWSVQAKVDVYLWLS IKHASAILDNLVPGYEAEMSSKGACT NHPPSNLLYQEQHVFLRAHMYQA RGLIAADSNGLSDPFKAVTFLSHCQ TTKIIISQTLSPWNQMLLFNDLVH GDVKELAESPLVVELYDSDAVGK PEYLGATVAAPVVKLADQDYEPRLC YHPIFCGNLSGGDLLAVFELLQVPPS GLQGLPVEPPDITQIYVPANIRPVL SKYRVEVLFWGVREMKKVQLLSVD RPQALIECGGQGVKSCVIQSYKNNP NFSIQADAFEVELPENELHPPLSIC VVDWRAFGRSTLVGYTINYLKQFL CKLREPLAPITQVDGTQPGHDISDSL TATESSGAHSSQDPPADHIYVDVEP PPTVVPDQAQAQPAILDVDPDSSPML EPEHTPVAQEPKDGKPKDPRKPSR RSTKRRKRTIADESAENVIDWWSKY YASLKAQAKAKERNPKGKKGNTKAK PDEVVVDIEDGPKKKKDKMLKKKPK DDGIPNALILQIYDGDLESEFNMFED WVKTFELFRGKSTEDDHGLDGRVI GKFKGSFCIYKSPQDSSSEDGQLRI QQGIPPNHPVTLIRVYVAAFNLSP ADPDGKSDPYIVIKLKGTEIKDRDKYI PKQLNPVFGRSFEIQATFPKESLLSIL IYDHDIMIGTDDLIGETKIDLENRFYS KHRAICGLSQYEIEGYNAWRDTSK PTEILTKLCKDNKLDGPFYFHPGKIQI GNQVFSGKTIFTEEDTDETVESYEHL ALKVLHSHWEDIPEVGCRLVPEHIETR PLYHKDKPGMEQGRLOMWDMMFP KDMPPQPPVDISPRRPGYELRVTI WNTEDVILEDENIFTGQKSSDIYVKG WLKGLEDDKQETDVHYNLSLTGEGN FNWRFLFPFQYLPKAEKQMVITKREN IFSLEKMECKTPAVLVLQVWDFERL SSDDFLGTLEMNLSFPRAAKSAKA CDLAKFENASEETKISIFQKRVRG WWPFSKSKELTGKVEAEFHLVTAEE AEKNPVGKARKEPELAKPNRPDTS FSWFMSPFKCLYLIWKNYKYYIIIA FILILILFVLFIYTLPGAISRRIVVGS	False	False	2.785	1.348	1.021	0.526	0.889	1.288	0.706