

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
E9Q8I9	FRY_MOUSE	Mus musculus	Protein furry homolog	24.474581	NaN	T213;S1382;S1383;S1936;S1940;S2427;S2428;S2495;T2516;S2815	33300544	MASQQDSGFFEISIKYLLKSWSNAS PVGNGYKPPVPPASGTHREKGGPPA MLPINVDPDPSKPGVEYLVKSLFVNFTT QAERKIRIIMAEPLEKPLTKSLQRGE DPQFDQVSSMSLSEYCLPSILRTL FDWYKRQNGIEDESHEYRPRTSNKS KSDEQQRDYLMEERRDLAIDFIFSLVL IEVLKQIPLHPVIDSLIHDIIINLAFKHF KYKEGYLGPNTGNMHIVADLYAEVI GVLAQAKFPAVKKKFMKELRHK EQSPYVVQSIHSLIMGMKFFRIKMYP VEDFEASLQFMQECACHYFLEVKDK DIKHALAGLFEIVLPVAAAVKNEVN VPCLRNFVESLYDTTLELSRKKHSL ALYPLVTCLLCVSQKQLFLNRWHVF LNNCLSNLKNKDPKMARVALESY RLLVVYMRIRKCESNTATQSRLLITITT TLFPKGSRGVPRDMLNIFVKIQFI AQERLDFAMKEIIFDFLCVGPAPAKAF SLNPERMNIQLRAFLVIADSLQOKD GEPMPVTVGAVLPSGNTLRVKKTYL SKLTTEEEAKMIGMSLYYSQVRKAV GNILRHLDKEVGRCMMLTNVQMLN KEPEDMITGERKPKIDLFRTCVAAP RLLPDGMSKLELIDLLARLSIHMDD ELRHIAQNSLQGLLVDFSDWREDVL FGFTNFLLREVNDMHHTLLDSSLK LLQLLTQWKLVITQGRAYEQANKI RNSELIPNGSSHRMQSERGPHCSVL HAVEGFALVLLCSFQVATRKLVLIL KEIRALFLALGQPEDDRPMIDVMD QLSSSILESFIVAVSDSATLPPTHN VDLQWLVEWNAVLVNSHYDVKSPS HVWIFAQSVKDPWVLCFLFRQEN LPKHCPTALSYAWPYAFTRLQSVMP LVDPNSPVNAKKTSTASSGDNYVTL WRNYLLCFGVAKPSIMSPGHLRAS TPEIMATTPDGTVSYDNKAIGTPSVG VLLKQLVPLMRLESIEITESLVLFVGF RTNSLVFRELVEELHPLMKEALERR PENKRRERRDLLRLQLRIFELLAD AGVISDSTNGALERDTLALGALFLEY VDLTRMLLEAENDKEVEILKDIRAH FSAMVANLIQCVVHRRRFLFPQOS LRHHLFILFSQWAGPFSIMFTPLDRY SDRNHQITRYQYCALKAMSAVLCGG PVFDNVGLSPDGYLYKWLNDILACQ DLRVHQLGCEVVMLLLELNPQINL FNWAIIDRCYTGSYQLASGCFAIATV CGNRNYPFDIVTLLNLVLFKASDTN REIYEVSMQLMQILEAKLFVHSKKV AEQRPGSILYGTGHPPLPLYSVSLAL LSCELARMYPELTLPLFSEVSQRFTT THPNGRQIMLTYLPLWLNHIELVDS RLLLPGSSPSSPEDEVKDRGEVITAS HGLKGNWGSPEATSLVNLNLMYM TAKYGDEVPGAEMENAWNALANNE KWSNNLRVTLQFLISLCGVSSDTILL PYIKKVATYLCRNNTIQTMEELLFEL QQTEPVNPIVQHCDNPPFYRFTASS KASAAAAGTTSSSNTVVAGQDSFPD PEESKILKESDDRFNSVIRAHTRLES RYSNSSGGSYDEKNDPISPYTGWL LSITEAKQPQPLPMPGSGGCWAPLV DYLPEITTPRGLHRCNIAVIFMTEM VVDHSVREDWALHLLPLLLHAVFLGL DHYRPEVFEHSHKLLHLLIALSCNS NFHAIASVLLQREMGEAKLTMQP AYQPEYLYTGGDFLREDQSSPVPDS GLNSSSTSSSISLGGSSGNLPQMTQ EVEDVEAATETDEKASKLIEFLTTRA FGPLWCHEDITPKNQNSKSAEQLSN FLRHVVSVFKDSRSGFHLEQHLSEV ALQATALASSRHYAGRSFQIFRALKQ PLSAHALSDLLSRLVEVIGEHGDEIQ GYVMEALLTLEAAVDNLSDCCLKNSD LFTVLSRSSPDLSSSSKLTASRKST GQLNVNPGTPGSGGGGGSGNNTT AERSRHQRFSVPPKFGVDRSSDP	None	None	None	None	None	None	None	None	

PRSATLDRIQACTQQGLSSKTRSNSS
LKESLTDP SHVSHPTNLLATIFWVTV
ALMESDFEF EYLMALRLLNRLLAH
MPLEKAENREKLEKLAQLKWADF
PGLQQLLLKGFTSLTTTDLTLQLFSL
LTSVSKVPMVDSSQAIGFPLNVLCLL
PQLIQHFENPNQFCKDIAERIAQVCL
EENPKLSNLAHVMTLYKTHSYTRD
CATWVNVVCRYLHEAYADITLNMVT
YLAELLEKGLPSMQOPLLQVIYSLLS
YMDLSVVPVKQFNMEVLKTIKEYVQ
SIHWREALNILKLVVRSASLVLP
QHSDSLKIELHRVWTSASKELPGKT
LDFHFDISETPIIGRRYDELQNSSGR
DGKPRAMAVTRSASSTSSGSNSNVL
VPVSWKRPQYSOKRTKEKLVHVL
CGQEVGLSKNPSVIFSSCGDLDLPE
HQTSLVSEEDGPREQENMDDTNSE
QQFRVFRDFDFLDVELEDGEGESM
DNFNWGVRRRSLDSLKCDMQILE
ERQLSRSTPSLNKMSHEDSDESSEE
DLTASQILEHSDLMNLSPEEANP
MELLTSACDSAPADPHSFNTRMAN
FEASLPDINNLOISEGSKAEAVPEEE
DTTVHEDDLSSINELPAAFECSDSF
SLDMTEAEEKGNRGLDQYTLASFGE
GDRGVSPPPSPFFSAILAAFPAAACD
DAEEAWRSHINQLMCDSDGSCAVY
TFHFVSSLFKNIQKRFCLTCDAAASY
LGDNLRGIGSKFVSSQMLTSCSEC
PTLFVDAETLLSCGLLDKLFVLEL
QEYLDTYNNRKEATLSWLANCKATF
AGGSRDGVITCQPGDSEKQLELCQ
RLYKLFQLLLLYQSYCKLIQVHEV
SSVPELLNMSRELSDLKRNKKEATA
AIATDPLYIEGAWSEPTFTSTEAAIQS
MLECLKNNELGKALRQIKECRSLWP
NDIFGSSDDEVQTLNIFYFRHQTG
QTGTVALVGSNHSLEICTKLMELN
MEIRDMIRRAQNYRVLTAFLPDSSV
SGTSL