

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O75970	MPDZ_HUMAN	Homo sapiens	Multiple PDZ domain protein	5.263779	NaN	S230;S483;S790;S1078;S1818;S1824	34019948	MLEAIDKNRALHAAERLQTKLRERG DVANEDKLSLLKSVLQSPFLFSQILSL QTSVQQLKDQVNIATSATSNIIEYAHV PHLSPAVIPTLQNESFLLSPNNGNLE ALTGPGIPHINKPACDEFDQLIKN MAQGRHVEVFELKPPSGGLGFSV GLRSENRGELGIFVQEIQEGSVAHR DGRLKETDQILAINQALDQTITHQQ AISILQKAKDTVQLVIARGSLPQLVSP IVSRSPSAASTISAHSNPVHWQHME TIELVNDGSGLGFIIIGKATGVIVKT ILPGGVADQHGRLCSGDHILKIGDTD LAGMSSEQVAQVLRQCGNRVKLMI ARGAIEERTAPTALGITLSSSPTSTPE LRVDASTQKGESETFDVELTKNVQ GLGITIAGYIGDKKLEPSGIFVKSITKS SAVEHDGRIQIGDQIIAVDGTNLQGF TNQQAVEVLRHTGQTVLLTLMRRG MKQEAELMSREDVTKDADLSPVNA SIIKENYEKDEDFLSSTRNTNILPTEE EGYPLLSAEIEEIEDAQKQEAALLTK WQRIMGINYEIVVAHVSKFSENSGL GISLEATVGHHFIRSVLPEGPVGHSG KLFSGDELLEVNGITLLGENHQDVV NILKELPIEVTMVCCRRTVPPTTQSE LDSDLCDIELTEKPHVDLGEFIGSS ETEDPVLAMTDAGQSTEEVQAPLAM WEAGIQHIELEKGSKGLGFSILDYQD PIDPASTVIIIIRSLVPGGIAEKDGRLLP GDRLMFVNDVNLENSSEAVEAL KGAPSGTVRIGVAKPLPLSPEEGYVS AKEDSFLYPPHSCEEAGLADKPLFR ADLALVGTNDADLVDESTFESPSP ENDSIYSTQASILSLHGSSCGDGLNY GSSLPSSPKDVIENSCDPVLDLHM SLEELYTQNLQRQDENTPSVDISM GPASGFTINDYTPANAIEQQYECENT IVWTESHLPSEVISSAELPSVLPDSA GKGSEYLLEQSSLACNAECVMLQNV SKESFERTINIAKGNSSLGMTVSAN KDGLGMIVRSIIHGGAISRDRGRIAGD CILSINEESTISVTNAQARAMLRHS LIGPDIKITYVPAEHLLEEFKISLGQOS GRVMALDIFSSYTGRDIPELPEREEG EGESELQNTAYSNWNQPRRVELW REPSKSLGISIVGGRGMGSRLSNGE VMRGIFIKHVLEDSPAGKNGTLKPG DRIVEVDGMDLRDASHEQAVEAIRK AGNPVVMVQSIINRPRKSPLPSLLH

NLYPKYNFSSTNPFADSLQINADKA  
PSQSESEPEKAPLCSVPPPPSAFAE  
MGSDHTQSSASKISQDVKEDFEFGY  
SWKNIRERYGTLTGELHMIELEKGH  
SGLGLSLAGNKDRSRMSVFIVGIDP  
NGAAGKDGRLQIADELLEINGQILYG  
RSHQNASSIICKAPSKVKIIFIRNKDA  
VNQMAVCPGNAVEPLPSNSENLQN  
KETEPTVTTSDAAVDLSSFKNVQHL  
ELPKDQGGGLGIAISEEDTLSGVIKSL  
TEHGVAATDGRLKVGQILAVDDEI  
VVGYPKIEKFISLLKTAKMTVKLTIHAE  
NPDSQAVPSAAGAASGEKKNSSQSL  
MVPQSGSPEPESIRNTRSSTPAIFA  
SDPATCPIIPGCETTIEISKGRGLGL  
SIVGSDTLLGAIHHEVYEEGAACKD  
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INVLRQTPQRVRLTLRDEAPYKEEE  
VCDTLTIELQKKPGKGLGLSIVGKRN  
DTGVFVSDIVKGGIADADGRLMQGD  
QILMVNGEDVRNATQEAVAALLKCS  
LGTVTLEVGRKAGPFHSERRPSQSS  
QVSEGLSSFTFPLSGSSTSESLESS  
SKKNALASEIQGLRTVEMKKGPTDS  
LGISIAGGVGSPLGDVPIFIAMMHPT  
GVAAQTQKLRVGDRIVTICGTSTEG  
MHTHTQAVNLLKNASGSIEMQVVAG  
GDVSVVTGHQQEPASSLSFTGLTS  
SSIFQDDLGPPOCKSITLERGPDGLG  
FSIVGGYGSPHGDLPYVKTVFAKGA  
ASEDGRLKRGDQIIAVNGQSLEGVT  
HEEAVAILKRTKGTVTLMVLS