

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9QXS1	PLEC_MOUSE	Mus musculus	Plectin	26.100035	T649;T2762	S728;T823;S1055;S1443;S1729;S2639;S2781;T2788;S2809;T2893;T3040;T3369;T3792;T3797;T4037;S4061;S4389;S4391;S4392;S4393;S4396;S4397;S4398;S4399;T4400;S4403;S4413;T4418;T4546;S4614;S4620;T4622;S4623;S4625;S4629;T4630;S4633;S4649;S4682;S21;T26	22517741;36852467;33300544;37507081	MVAGMLMPLDRLRAIYEVLFREGV MVAKKDRRPRSLPHVPGVTNLQV MRAMASLKARGLVRETFAWCHFYW YLTNEGIDHLRQYLHLPPEIVPASLQ RVRRPVAMVIPARRRSPHVQTMQGP LGCPPKRGPLPAEDPAREERQVYRR KEREEGAPETPVVSATTVTGLARPGP EPAPATDERDRVQKTKTKWVNKHL IKHWRAEAQRHISDLYEDLRDGHNL ISLLEVLSGDSLPREKGRMRFHKLQ NVQIALDYLRHRQVKLVNIRNDDIA DGNPKLTLGLIWTIILHFQISDIQVSG QSEDMTAKEKLLLWSQRMVEGYQG LRCDNFTTSWRDGRLFNAIHRHKP MLIDMNKVYRQTNLENLDQAFSVA ERDLGVTRLLDPEDVDVPQPDEKSII TYVSSLYDAMPRVPGAQDGVRADEL QLRWQEYRELVLQLLQWIRHHTAAF EERKFPSFEEIEILWCQFLKFKETE LPAKEADKNRSKVIYQSLGAVQAG QLKIPPGYHPLDVEKEWGKLVHVAILE REKQLRSEFERLECLQRIVSKLQME AGLCEEQLNQADALLQSDIRLLASG KVAQRAGEVERDLKADGMIRLLFN DVQTLKDGRRPQGEQMYRRVYRLH ERLVAIRTEYNLRKAGVVGAPVTQVT LQSTQRRPELEDSTLRYLQDLLAWV EENQRRIDSAEWGVDLPSVEAQLGS HRGMHQSIIEFRAKIERARNDESQ SPATRGAYRDCLGRLDLQYAKLLNS SKARLRSLESLHGFVAAATKELMWL NEKEEEEVGFWDSDRNTNMAAKKE SYSALMRELEMKEKKIKEIQNTGDR LLREDHPARPTVESFQAALQTQWS WMLQLCCCIEAHLKENTAYQFFSD VREAEELQKLQETLRRKYSCDRITIT VTRLEDLLQDAQDEKEQLNEYKGH SGLAKRAKAIQVQLKPRNPAHPVVRGH VPLIACDYKQVEVTVHKGDQCQLV GPAQPSHWKVLSGSSSEAAVPSVCF LVPPPNQEAQEAQVARLEAQHQALVT LWHQLHVDKMSLLAWQSLSRDIQLI RSWSLVTFRTLKPEEQRQALRNLEL HYQAFRLRDSQDAGGFGPEDRLVAER EYGSCSRHYQQLLSLEQGEQEESR CQRCISELKDIRELQLEACETRTVHRL RLPLDKDPARECAQRIAEQQKAQAE VEGLGKGVARLSAEAEKVLALPEPSP AAPTLRSELELTLGKLEQVRSLSAIYL EKLKTISLVIRSTQGAEVVKTHEEQ LKEAQVAPATLQELEATKASLKKLRA QAEAQPVFNTRLRDELGAQEVGER LQQRHGERDVEVERWRERVTQLLE RWQAVLAQTDVQRRELEQLGRQLR

YYRESADPLSAWLQDAKRROEQIQAVPIANCQAAREQLRQEKALLEEIERHGEKVEECQKFAKQYINAIKDYELQLITYKAQLEPVASPAKKPKVQSGSESVI QEYVDLRTRYSELTTLTSQYIKFISET LRRMEEEERLAEQQRAEERERLAEV EAALEKQRQLAEAHAQAKAQAELEA QELQRRMQEEVARREEAAVDAQQQ KRSIQEELQHLRQSSEAEIQAKAQQ VEAARSRMRIEEEEIRVVRLQLETTE RQRGGAEGELQALRARAEEAEAQKR QAQEEAERLRRQVQDESQRKRQAE AELALRVKAEAEAAREKQRALQALD ELRLQAEAAERLLRQAEAEERARQVQ VALETAQRSAEVELQSKRASFAEKTA QLERTLQEEHVTVAQLREEAERRAQ QQAEAEARAREEAERELERWQLKAN EALRLRLQAE EVAQKSLAQADA EK QKEEAEREARRRGKAE EQAVRQREL AEQELEKQRQLAEGTAQQRLAAEQE LIRLRAETEQGEQQRQLLEELARL QHEATAATQKRQELEAE LAKVRAEM EVLLASKARAEESRSTSEKSKORLE AEAGRFRELAEEAARLRALAEAAKR QRQLAEEDAARQRAEAERVLTEKLA AISEATRLKTEAEIALKEKEAENERL RRLAEDEAFQRRRLEEQAALHKADI EERLAQLRKASESELERQKGLVEDT LRQRRQVEEEIMALKVSFEKAAAGK AELELELGRIRSN AEDTMR SKEQAE LEAARQRQLAAEEEQRRREAEERVQ RSLAAEEEAARQRKVALEEVERLKA KVVEARRLRERAEQESARQLQLAQE AAQKRLQAE EKAHAFVVQQREEELQ QTLQQEQNMLDRLRSEAEAARRAA EEAEEAREQAEREAAQSRKQVEEAE RLKQSAEEQAQAQAQAQAAAEKLRK EAEQEAARRAQAEQAALKQKQAADA EMEKHKKFAEQTLRQKAQVEQELTT LRLQLEETDHQKSILDEELQRLKAE VTEAARQRSQVEEELFSVRVQMEEL GKLKARIEAENRALILRDKDNTQRFL EEEAEKMKQVAEEAARLSVAAQEAA RLRQLAEEDLAQQRALAEKMLKEK MQAVQEATRLKAEAE LLQQQKELA QEQARRLQEDKEQMAQQQVVEETQG FORTLEAERQRQLEMSAEERLKL RMAEMSRAQARAEE DAQRFRKQAE E IGEKLRHRT ELATQEKVTLVQTLEIQR QQSDHDAERLREIAE LEREKEK LK QEAKLLQKSEEMQTVQQEQILQET QALQKSFLSEKDSLLQRERFIEQEKA KLEQLFQDEVAKAKQLREEQQRQQ QMEQEKQELMASMEEARRRQRE AEEGVRRKQEELQHLEQQRQQQEK LLAEENQRLRERLQRLEEEHRAALA HSEIATTQAASKALPNGRDAPDGPS

VEAEPEYTFEGLRQKVPAAQQLQEAGI
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SEPSEVRSYVDPSTDERLSYTQLLKR
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GLFDEEMNEILTDPSSDDTKGFFDPN

