

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q15149	PLEC_HUMAN	Homo sapiens	Plectin	27.535839	S305;T638;S757;S1216;S1218;S1435;S2361;T4539;S4673	T113;S125;S149;S720;S1047;S1435;S1721;S1732;S2631;S2782;S2802;T2886;T3033;S3036;T3362;S3580;T3785;T4030;S4054;S4382;S4384;S4385;S4386;S4389;S4390;S4391;S4392;T4393;S4396;S4400;S4406;T4411;T4539;S4607;S4613;T4615;S4616;S4618;S4622;T4623;S4626;S4642;S4672;S4675;S42;S42;S20;S21;T26	23301498;30379171;31492838;22121020;28411811;35083852;28657654;29351928;35008409;33465208;35254053;33214551;30444036;26853435;30397120;34019948	MVAGMLMPRDQLRAIYEVLFRGV MVAKKDRRPRSLPHVPGVTNLQV MRAMASLRARGLVRETFAWCHFVW YLTNEGIAHLRQYLHLPPEIVPASLQ RVRRPVAMVMPARRTPHVQAVQGP LGSPPKRGPLPTEEQRVYRRKELEE SPETPVVPATTQRTLARPGPEPAPAT DERDRVQKKTFTKWNKHLIKAQR HISDLYEDLRDGHNLISLLEVLSGDS LPREKGRMRFHKLQNVQIALDYLRLH RQVKLVNIRNDDIADGNPKLTLGLI WTIILHFQISDIQVSGQSEDMTAKEK LLLWSQRMVEGYQGLRCDNFTSSW RDGRLFNAIHRHKLPLIDMNVYR QTNLENLDQAFSVAERDLGVTRLLD PEDVDVPPQDEKSIITYVSSLYDAMP RVPDVQDGV RANELQLRWQEYREL VLLLLQWMRHHTAAFEERRFPSSF EIEILWSQFLKFKEMELPAKEADKN RSKGIYQSELEGAVQAGQLKVP PLDVEKEWGKLVAILEREKQLRSE FERLECLQRIVTKLQMEAGLCEEQ NQADALLQSDVRLAAGKVPORAGE VERDLKADSMIRLLFNDVQTLKDG RHPQGEQMYRRVYRLHERLVAIRTE YNLRLKAGVAAPATQVAQVTLQSVQ RRPELEDSTLRYLQDLLAWVEENQH RVDGAEWGVDLPSVEAQLGSHRGL HQSIIEFRAKIERARSDEGQLSPATR GAYRDLGRLDLQYAKLLNSSKARL RSLESLSHFSVAAATKELMWLNEKEE EEVGFWDSDRNTNMTAKKESYSAL MRELELKEKKIKELQAGDRLLRED HPARPTVESFQAALQTQWSWMLQL CCCIEAHLKENAAYFQFFSDVREAE GQLQKLQEALRRKYSCDRSATVTRL EDLLQDAQDEKEQLNEYKGLSGLA KRAKAVVQLKPRHPAHPMRGRPLL AVCDYKQVEVTVHKGDECCQLVGP PSHWKVLSSSGSEAAVPSVCFLVPP PNQEAQEA VTRLEAQH QALVTLWH QLHVDMSLLAWQSLRRDVQLIRS WSLATFRTLKPEEQRQALHSLELHY QAFLRDSQDAGGFGPEDRLMAERE YGSCSHHYQQLLSLEQGAQEESRC QRCISELKDIRELQLEACETRTVHRLR LPLDKEPARECAQRIAEQKQAEV EGLGKGVARLSAEAEKVLALPEPSPA APTLRSELETLGKLEQVRSLSAIYLE KEAQAVPATLPELEATKASLKKLRAQ AEAQQPTFDALRDELRGAQEVGERL QQRHGERDVEVERWRERVAQLLER WQAVLAQTDVVRQRELEQLGRQLRYY RESADPLGAWLQDARRRQEQIQAM PLADSQAVREQLRQEALLEEIERH GEKVEECQRFAKQYINAIKDYELQLV TYKAQLEPVASPAKKPKVQSGSESVI QEYVDLRTHYSELTTLTSQYIKFISET LRRMEEEEERLAEQRAEERERLAEV EAALKEQRQLAEHAQAQAQAERA

KELQQRMQEEVVRREEAAVDAQQ
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