	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion
0	Q9P219	DAPLE_HUMAN	Homo sapiens	Protein Daple	23.873835	S1496;T1519;S1521;T1522;S1523;T1525;S1791	S227;S239;S486;S1444;S1601;S1806;T1954	39531497;37340703;30379171;34019948;31492838;29237092;30059200;35254053	MDVTVSELLELFLQSPLVTWVKTFG PFGSGSQDNLTMYMDLVDGIFLNQI MLQIDPRPTNQRINKHVNNDVNLRI QNLTILVRNIKTYYQEVLQQLIVMNL PNVLMIGRDPLSGKSMEEIKKVLLL VLGCAVQCERKEEFIERIKQLDIETQ AGIVAHIQEVTHNQENVFDLQWLEL PDVAPEELEALSRSMVLHLRRLIDQ RDECTELIVDLTQERDYLQAQHPPSP IKSSSADSTPSPTSSLSSEDKQHLAV ELADTKARLRRVRQELEDKTEQLVD TRHEVDQLVLELQKVKQENIQLAAD ARSARAYRDELDSLREKANRVERLE LELTRCKEKLHDVDFYKARMEELRE DNIILIETKAMLEEQLTAARARGDKV HELEKENLQLKSKLHDLELDRDTDK KRIEELLEENMVLEIAQKQSMNESA HLGWELEQLSKNADLSDASRKSFVF ELNECASSRILKLEKENQSLQSTIQG LRDASLVLEESGLKCGELEKENHQL SKKIEKLQTQLEREKQSNQDLETLS EELIREKEQLQSDMETLKADKARQI KDLEQEKDHLNRAMWSLRERSQVS SEARMKDVEKENKALHQTVTEANG KLSQLEFEKRQLHRDLEQAKEKGER AEKLERELQRLQEENGRLARKVTSL ETATEKVEALEHESQGLQLENRTLR KSLDTLQNVSLQLEGLERDNKQLDA ENLELRRLVETMRFTSTKLAQMERE NQQLEREKEELRKNVDLLKALGKKS ERLELSYQSVSAENLRLQQSLESSS HKTQTLESELGELEAERQALRRDLE ALRLANAQLEGAEKDRKALEQEVAQ LEKDKKLLEKEAKRLWQQVELKDAV LDDSTAKLSAVEKESRALDKELARC RDAAGKLKELEKDNRDLTKQVTVHA RTLTTLREDLVLEKLKSQQLSSELDK LSQELEKVGLNRELLLQEDDSGSDT KYKILEGRNESALKTTLAMKEEKIVL LEAQMEEKASLNRQLESELQMLKK ECETLRQNQGEGQHLQNSFKHPAG KTAASHQGKEAWGPGHKEATMELL RVKDRAIELERNNAALQAEKQLLKE QLQHLETQNVTFSSQILTLQKQSAFL QEHNTTLQTQTAKLQVENSTLSSQS AALTAQYTLLQNHHTAKETENESLQ RQQEQLTAAYEALLQDHEHLGTLHE RQSAEYEALIRQHSCLKTLHRNLEL EHKELGERHGDMLKRKAELEEREK VLTTEREALQQEQRTNALAMGENQ RLRGELDRVNFLHHQLKGEYEELH AHTKELKTSLNNAQLELNRWQARF DELKEQHQTMDISLTKLDNHCELLS RLKGNLEEENHHLLSQIQLLSQQNQ MLLEQNMENKEQYHEEQKQYIDKL NALRRHKEKLEEKIMDQYKFYDPPP KKKNHWIGAKALVKLIKPKKEGSRE RLKSTVDSPPWQLESSDPASPAASQ PLRSQAENPDTPALGSNCAEERDAH NGSVGKGPGDLKPKRGSPHRGSLD RTDASTDLAMRSWPSELGSRTCSTS ATTTAPSNSTPIARHPGRTKGYNSDD NLCEPSLEFEVPNHRQYVSRPSSLE SSRNTSSNSSPLNLKGSSEQLHGRS ESFSSEDLIPSRDLATLPREASTPGR NALGRHEYPLPRNGPLPQEGAQKRG TAPPYVGVRPCSASPSSEMVTLEEFL EESNRSSPTHDTPSCRDDLLSDYFR KASDPPAIGGQPGPPAKKEGAKMPT NFVAPTVKMAAPTSEGRPLKPGQYV KPNFRLTEAEAPPSVAPRQAQPPQSL SLGRPRQAPVPPASHAPASRSASLSR AFSLASADLLRASGPEACKQESPQK LGAPEALGGRETGSHTLQSPAPPSS HSLARERTPLVGKAGSSCQGPGPRS RPLDTRRFSLAPPKEERLAPLHQSAT APAIATAGAGAAAAGSGSNSQLLHF SPAAAPAARTKPKAPPRSGEVATITP VRAGLSLSEGDGVPGQGCSEGLPAK SPGRSPDLAPHLGRALEDCSRGSVS	False	False	2.447	3.794	0.82

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