

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus
Q91ZU6	DYST_MOUSE	Mus musculus	Dystonin	46.374885	T2483 (Q91ZU6:5);S7184	S236;S237;S1381;S2211;S2862;S3894;S4680;S5488;S7254;S7333;S7336;S7348;S205;S208	22645316;34418053;40885482;40021952	MAGYLSPAAYMYVEEQEYLQAYEDV LERYKDERDKVQKKTFTTKWINQHL MKVRKHVNDLYEDLRDGHNLISLLE VLSGDTLPREKGRMRFRHLQNVQIA LDYLKRRQVKLVNIRNDDITDGNPK LTLGLIWTILHFQISDIHVTGESEDM SAKERLLLWTOQATEGYAGVRCENF TTCWRDGKLFNAIIHKYRPDLIDMN TVAVQSNLANLEHAFYVAEKIGVIRL LDPEDVDVSSPDEKSVITYVSSLYDA FPKVPEGGEGIGANDVEVKWIEYQN MVNYLIQWIRHHVVTMSERTFPNN PLELKALYNQYLOFKEKEIPPKEMEK SKIKRLYKLEWIEFGRKLLQGYHP NDIEKEWCKLIAMLEREKALRPEVE RLDMLQIATRVRDQSVSCEDKLIL ARNALQSDSKRLESGVQFQNEAIEA GYILECENLLRQHVIDVQILIDGKYY QADQLVQRVAKLRDEIMALRNECSS VYSKGRMLTTEQTKLMISGITQSLNS GFAQTLHPSLNSGLTQSLTPSLTSSS VTSGLSSGMTSRLTPSVTPVYAPGFP SVVAPNFSLGVEPNLQTLKLMQIR KPLLKSSLLDQNLTEEEVNMKQVQD LLNWWDEMVOQLDRTEWGSPLPSV ESHLENHKNVHRAIEEFESSLKEAK ISEIQMTAPLKLSTYDKLHRLESQYA KLLNTRSRLQERHLDLTHNFVTRATN ELIWLNEKEESEVAYDWSERNSSVA RKKSYPHAELMRELEQKEESIKAVQEI AEQLLENHPARLTIEAYRAAMQTO WSWILQLCQCVEQHIQENSAYFEFF NDAKEATDYLRLNKDAIQRYKSCDR SSSIHKLEDLVQESMEKEELLQYRS VVAGLMGRAKTVVQLKPRNPDNPLK TSIPIKAICYRQIEITTYKDECVLAN NSHRAKWKVISPTGNEAMVPSVCFT VPPPNKEAVDFANRIEQYQSVLTL WHESHINMKSVMWHYLVNEIDRIR ASNVASIKTMLPGEHQVLSNLQSR LEDFLEDSQESQIFSGDISQLEKEV SVCRKYYQELLKSAEREQEESVYN LYSEVRNIRLRLESCEDRLIRQIRTP LERDDLHESMLRITEQEKLKELDR LKDDLGTITNKCEEFFSQAADSPSPV ALRSELSVVIQSLSQIYSMSSTYIEKL KTVNLVLKNTQAAEALVKLYETKLC EEEAVIADKNNIENLMTLQWRSE VDEKREDFHALEDELQKAKAISDEM FKTHKERDLDFDWHKEKADQLVER WQSVHVQIDNRLRDLEGGKSLKH RDSYHPLDDWQIHIETTQRKIQENQ PENSKALALQLNQKMLVSEIEVKQ SKMDECOQYSEQYSAAVKDYELQ MTYRAMVESQKSPVKKRRRIQSSAD LVIQEFMDLRTRYTALVTLMTQYIKF AGDSLKRLEEEEKSLDEEKKQHIEK AKELQKVVSNISKTLGDGKAGKPL FSKQOMSSKEISTKKEQFSEALQTT QIFLAKHGDKLTTEEERSDLEKQVKT LQEGYNLLFSESLKQQLQPSGESK VPEKPKVIAGTINQTTGEVLSVFOA VLRGLIDYETGIRLLEAQLVITGLISP ELRKCFDLRDAESHGLIDEQVLRQL KELNRAKQLISTASPTSIPVLDSLAQ GMVSESMAIRVLEILLSAGPLLPAT GEHLTLQAFQONLISALFSKYLE RQDTCKDLDIPCTSEKVSITDMVQR SILQENTRMWLLPVRPQEAAGRITLK CGRSVSILRAAHEGLIDRETMFRLLG AQLLSGGLIDCNSGQKMTVEEVAE GVIDRDTASSILTYQVQTGGIVHNSP AKRLTVDEAVQCELTSSALLVLEA QRGYVGLIWPHSGEIFPTSSSLQQL ITNELASKILNCRQKIAALYIPESOV IGLDAKQLGIIDNNTASVLKSVTLP DKMPDLGDLEDCNAKRWLSFCKL QPSTVHDYRQEEGGSDGEEPVTAQS SEQTKKFLSYLMVNSYMDAHTGQ RLLLYDGDLEAVGMLLSCGTELG	True	True	3.098	5.0	1.267	5.0	1.306

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