

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
Q03001	DYST_HUMAN	Homo sapiens	Dystonin	10.819719	T492;S2551;S2553;S3137;S3462;S3465;T3484;T3657;T3659;T4934;S6292;S6294;T6298;T6868;S7362	S236;S237;S1382;S2229;S2919;S3968;S4749;S7432;S7510;S7513;S7525;S1565;S135;S184	34725712;38665916;34019948;28657654;33214551;39302247;30379171;40596516;40136647;29351928;38253038	MAGYLSPAAYLYVEEQEYLQAYEDV LERYKDERDKVQKKTFTFKWINQHL MKVRKHVNDLYEDLRDGHNLISLLE VLSGDTLPREKGRMRFRHLQNVQIA LDYLKRRQVKLVNIRNDDITDGNPK LTLGLIWTIILHFQISDIHVTGESEDM SAKERLLWTQQATEGYAGIRCENF TTCWRDGLFNAIHKKYRPLIDMN TVAVQSNLANLEHAFYVAEKIGVIRL LDPEDVDVSSPDEKSVITYVSSLYDA FPKVPEGGEGIGANDVEVKWIEYQN MVNYLIQWIRHHVTTMSERTFPNN PVELKALYNQYLQFKETEIPPKETEK SKIKRLYKLEIWIWIEFGRIKLLQGYHP NDIEKEWGLIHAMLEREKALRPEVE RLEMLQOIANRVQRDSVICEDKLILA GNALQSDSKRLESGVQFQNEAIEAG YILECENLLRQHVIDVOILIDGKYQQA DQLVQRVAKLRDEIMALRNECSSVY SKGRILTTEQTKLMISGITQSLNSGF AOTLHPSLTSGLTQSLTPSLTSSSMT SGLSSGMTSRLTPSVTPAYTPGFPSPG LVPNFSSGVPEPNSLQTLKLMQIRKP LLKSSLLDQNLTEENMKFVQDLL NWWDEMQVQLDRTEWGSDLPSVES HLENHKNVHRAIEEFESSLKEAKIS EIQMTAPLKLTYAEKLRLESQYAKL LNTSRNQERHLDTLHNFVSRATNEL IWLNEKEEEEVAYDWSEKNTNIARK KDYHAELMRELDQKEENIKSVQEIA EQLLLENHPARLTIEAYRAAMQTQW SWILQLCQCVEQHIKENTAYFEFFN DAKEATDYLRNLKDAIQKYSCDRS SSIHKLEDLVQESMEEKEELLQYKS TIANLMGKAKTIIQLKPRNSDCPLKT SIPIKAICYRQIEITTYKDDECVLN NSHRAKWKVISPTGNEAMVPSVCF VPPPNKEAVDLANRIEQYQNVLTL WHESHINMKS SVSWHYLINEIDRIR ASNVASIKTMLPGEHQVLSNLQSR FEDFLEDSQESQVFSGSDITOLEKEV NVCKQYYQELLKSAEREEQEE SVYN LYISEVRNIRLRENCEDRLRQIRTP LERDDLHESVFRITEQEKLKKELERL KDDLGTITNKCEEFFSQAAASSVPT LRSELNVVLQNMNQVYSMSSTYIDK LKTVNLVLKNTQAAEALVKLYETKL CEEEAVIADKNNIENLISTLKQWRSE VDEKROVFHALEDELQKAKAISDEM FKTYKERDLDFDWHKEKADQLVER WQNVHVQIDNRLRDLLEGIGKSLKYY RDTYHPLDDWIQQVETTRKRIQENQ PENSKTLATQLNQKMLVSEIEMKQ SKMDECCQYAEQYSATVKDYELQT MTYRAMVDSQOKSPVKRRRMQSSA DLIIQEFMDLRTRYALVLTMTQYIK FAGDSLKRLEEEKSLKEEKEHVE KAKELQKWVSNISKTLKDAEKAGKP PFSKQISSEIISTKKEQLSEALQTIQ LFLAKHGDKMTDEERNELEKQVKT LQESYNLLFSES LKQLQESQTSQGDV KVEEKLDKVIAGTIDQTTGEVLSVFQ AVLRLIDYDTGIRLLETQLMISGLIS PELRKCFDLKDAKSHGLIDEQILCQL KESKAKEIISAASPTTIPVLDALAQ S MITESMAIKVLEILLSTGSLVIPATGE QLTLOKAFQONLVSSALFVKVLERQ NMCKDLIDPCTSEKVS LIDMVQRST LOENTGMWLLPVRPQEGGRITLKCGRNISILRAAHEGLIDRETMRLLSAQ LLSGGLINSNGQRMTVEEAVREGV IDRDTASSILTYQVQTGGI IQSNPAKR LTVDEAVQC DLITSSALLVLEAQRG YVGLIWP HSGEIFPTSSSLQQUELITN ELAYKILNGROKIAALYIPESSOVIGL DAAKQLGIIDNNTASILKNITLPDKM PDLGDLEACKNARRWLSFCCKFPST VHDYRQEEEDVFDGEEPVTITQTSEET KKLFLSYLMINSYMDANTGQRLLLY DGDLEAVGMLLEGCHAEFDGNTA	True	True	4.311	4.037	0.75

IKECLDVSSSGVFLNNASGREKDE
 CTATPSSFNKCHCGEPEHEETPENR
 KCAIDEEFNEMRNTVINSEFQSQSK
 LASTISIDPKVNSSPSVCPVSLISYLT
 QTELADISMLRSDSENILNTNYENQS
 RVETNERANECSSHKNIQNFPSDLI
 ENPIMKSKMSKFCGVNETENEDNT
 NRDSPIFDYSPRLSALLSHDKLMHS
 QGSFNDHTHTPESNGNKCEAPALSFS
 DKTMLSGQRIGEFKQDQFLGIAAINI
 SLPGEQYGOKSLNMISSNPQVQYHN
 DKYISNTSGEDEKTHPGFQQMPEDK
 EDESEIEEYSCAVTPGGDTDNAIVSL
 TCATPLLEDTISASDYETSLNDQQN
 NTGTDDTSDDDFYDTPLFEDDDHDS
 LLLDGGDRDCLHPEDYDTLQEENDE
 TASPADVFDVSKENENSMVPOGAP
 VGSLSVKNKAHCLQDFLMDVEKDE
 LDSGEKIHLNPVGSQKVNQSQSLETG
 SERECTNILEGDESDSLTDYDIVGGK
 ESFTASLKFDDSGSWRGRKEEYVTG
 QEFHSDTDHLDSMQSEESYGDYIYD
 SNDQDDDDDDGIDEEGGIRDENG
 KPRCQVNAEDMDIQLCASILNENSQ
 ENENINTMILLDKMHSCSSLEKQQR
 VNVVQLASPENNLVTEKSNLPEYT
 TEIAGKSKENLLNHMVLKDVLPPII
 KDTESEKTFGPASISHDNNNISSTSE
 LGTDLANTKVLIQGSSELPELTDVSK
 GKDEYFKNMTPKVDSLDHICTEP
 DLIGKPAEESHLSIASVTDKDPQGN
 GSDLIKGRDGKSDILIEDETSIOKMY
 LGEGEVLVEGLVEEENRHLKLLPGK
 NTRDSFKLINSQFPFPQITNNEELN
 QKGSLLKATVTLKDEPNLQHVSKS
 PVQFENLEEIFDTSVSKEISDDITSDI
 TSWEGNTHFEESFTDGPKELDLFT
 YLKHCAKNIAKDVAKPNEDVPSHV
 LITAPPMKEHLQLGVNNTKEKSTST
 QKDSPLNDMIQSNLCSKESISGGG
 TEISQFTPEIEATLSILSRKHVEDVG
 KNDFLQSERCANGLGNDNSNTLN
 TDYSFLEINNKKERIEQQLPKEQALS
 PRSQEKEVQIPELSQVFVEDVKDILK
 SRLKEGHMNPQVEEPSACADTKIL
 IONLIKRIITTSQVNEASTVPSDSQM
 SDSSGVS PMTNSSELKPESRDDPFC
 IGNLKSELLNLIKQDQHSQKITGVF
 ELMRELTHMEYDLEKRGITSKVPL
 QLENIFYKLLADGYSEKIEHVGFDFN
 QKACSTSEMMEEKPHILGDIKSKEG
 NYSPNLETVKEIGLESSTVWASTLP
 RDEKLDLNDPFSHLECTSGSKE
 MASGDSSTEQFSSELQOCLQHTEK
 MHEYLTLLQDMKPPLDNQESLDNN
 LEALKNQLRQLETFELGLAPIAVILR
 KDMKLAEEFLKSLPSDFPRGHVEEL
 SISHQSLKTAFFSSLSNVSSERTQIM
 LAIDSEM SKLAVSHEEFLHLKLSFS
 DWVSEKSKSVKDIEIVNVQDSEYVK
 KRLEFLKNVLDLGHGHTKMQLTTAF
 DVQFFISEYAQDLSPNQSKQLLRLL
 NTTQKCFLDVQESVTTQVERLETQL
 HLEQDLDQKIVAEERQQEYKELQG
 ICDLLTQENRNLIGHQEAFMIGDGTV
 ELKKYQSKQEELQKDMQGSQAQALA
 EVVKNTENFLKENGKLSQEDKALI
 EQKLNKAEIKCEQLNLKAEQSKKEL
 DKVVTTAIEEETEKVAAVKLEESKT
 KIENLLDWLSNVKDSERAGTKHKQ
 VIEQNGTHFQEGDGKSAIGEEDEVN
 GNLETDVDGQVGTTOENLNQQYQ
 KVKAQHEKIISQHQAVIATQSAQVL
 LEKQGGYLSPEEKELQKNMDELKV
 HYETALAESEKMKLTHSLQEELEK
 FDADYTEFEHWLQQSEQELLENLEA
 GADDINGLMTKLRQKSFSEDEVISH
 KGDRLRYITISGNRVLEAAKSCSKRDG
 GKVDTSATHREVQRKLDHATDRFRS
 LYSKCNVLGNNLKDLVDKYQHYEDA
 SCGLLAGLQACEATASKHLEPIAVD
 PKNLQRQLEETKALQGGQISSQVAV
 EKLKKAIEVLLDARGSLPAKNDIQK

TLDDIVGRYEDLSKSVNERNEKLQIT
LTRSLSVQDGLDEMLDWMGNVSS
LKEQQVPLNSTALQDIIKSNIMLEQ
DIAGROSSINAMNEKVKKFMETDDP
STASSLQAKMKDLSARFSEASHKHK
ETLAKMEELKTKVELFENLSEKLOT
FLETKTQALTEVDVPGKDVTELSQY
MQESTSEFLEHKKHLEVLHSLLEKEI
SSHGLPSDKALVLEKTNLSKFKKE
MEDTIKKEAVTSCQEQLDAFQVL
VKSLKSWIKETTCKVPIVQPSFGAED
LGKSLDTEKLEKWSLKTPEIQKV
NNSGISLNLISAVTTPAKAIAAVKS
GGAVLNGETATNTEEFWANKGLT
SIKKDMTDISHGYEDLGLLKDIAE
LNTKLSKLQKAQEASSAMQWLQK
MNKTATKWQQTAPATDTEAVKTQV
EQNKSFEAELKQNVNKVQELKDKLT
ELLEENPDTPEAPRWKQMLTEIDSK
WQELNQLTIDRQQKLEESSNLTQF
QTVEAQLKQWLVEKELMVSVLGPLS
IDPNMLNTQRQVQVILLQEFATRKP
QYEQTLAAGQGILSRPGEPSLRGIV
KEQLAAVTQKWDSLTGQLSDRCDWI
DQAIKSTQYQSLRLSLDKLSDLDN
KLSSSLAVSTHPDAMNQLETAQK
MKQEIQQEKKQIKVAQALCEDLSAL
VKEEYLKAELSRQLEGLKSFKDVEQ
KAENHVQHLSACASSHQFQQMSR
DFQAWLDTKKEEQNKSHPIAKLDV
LESLIKDHKDFSKTLTAQSHMYEKTI
AEGENLLKTQGEKAALQLQNTI
KTNWDTFNKQVKERENKLESLEK
ALKYKEQVETLWPWIDKQNNLEEI
KFCLDPAEGENSIKLSLQKEMDQ
HFGMVELLNNTANSLLSVCEIDKEV
VTDENKSLIQKVDMMVTEQLHSHKFC
LENMTQKFKFEFQEVSKESKRQLQC
AKEQLDIHDSLGSQAYSNNKYLTMLO
TQOKSLQALKHQVDLAKRLAQDLVV
EASDSKGTSDVLLQVETIAQEHSTLS
QQVDEKCSFLETQKQIGHFQNTIR
EMFSQFAEFDELDSDMAPVGRDAE
TLQKQKETIKAFKLEALMASNDN
ANKTCKMMLATEETSPDLVGIKRD
EALSKQCNKLLDRAQAREEQVEGTI
KRLEEFYKLEKFSILLQKAEHEES
QGPVGMETETINQQLNMFVQFQKE
EIEPLQKQKQDVNWLGGQLISAAK
STSTQGLEHDLDDVNARWKTLNKK
VAQRAAQLOEALLHCGRFQDALESL
LSWVMVDTEELVANQKPPSAEFKVVK
AQIQEQLLQRLDDRKSTVEVIKRE
GEKIATTAEPADKVKILKQLSLLDSR
WEALLNKAETRNRQLEGISVVAQQF
HETLEPLNEWLTTIEKRLVNCPIGT
QASKLEEQAQHKALEDDIHNHKNH
LHQAVSIGQSLKVLSSREDKDMVQS
KLDIFSQVWYIEIQEKSHRSSELLQQA
LCNAKIFGEDEVELMNLNEVHDK
LSKLSVQDYSTEGLWKQSELRVLQ
EDILLRQNVDAQALLNGLELLKQTT
GDEVLIQDKLEAIKARYKDITKSTD
VAKTLEQALQLARRLHSTHEELCTW
LDKVEVELLSYETQVLKGEASQAO
MRPKELKKEAKNNKALLDSLNEVSS
ALLELVPWRAREGLEKMAEDNER
YRLVSDTTQKVEEIDAAILRSQQFD
QAADAELSWITETEKMLSLGDIRL
EQDQTSALQVQKFTMEILRHKDII
DDLKSGHKIMTACSEEEKQSMKK
KLDKVLKNYDTICQINSERYQLERA
QSLVNQFWETYEELWPWLTETQSII
SQLPAPALEYETLRQQQEEHRLRE
LIAEHKPHIDKMNKTGPQLLELSPG
EGFSIQEKYVAADTLYSQIKEDVKKR
AVALDEAISQSTQFHDKIDQILESLE
RIVERLRQPPSISAEVEKIKEQISENK
NVSVDMEKLOPLYETLKQRGEEMIA
RSGGTDKDISAKAVQDKLDQMVFIW
ENIHTLVEEREAKLLDVMELAEKFW
CDHMSLIVTIKDTQDFIRDLEDPGID
PSVVKQQQAAETIREIDGLQEELD

IVINLGSELIAACGEPDKPIVKKSIDE
LNSAWDSLNAWKDRIDKLEEMQ
AAVQYQDGLQAVFDWVDIAGGLAS
MSPIGTDLETVKQIEELKQFKSEAY
QQQIEMERLNHQAEELLKKVTEESD
KHTVQDPLMELKLIWDSLEERIINR
QHKLEGALLALGQFQHALDELLAWL
THTEGLLSEQKPVGGDPKAIIEELAK
HHVLQNDVLAHQSTVEAVNKAGND
LIESSAGEEASNLQNKLEVLNQRWQ
NVLEKTEQRKQQLDQALRQAKGFH
GEIEDLQQWLTDTERRHLLASKPLGG
LPETAKEQLNVHMEVCAAFEAKEET
YKSLMQKGQQMLARCPKSAETNID
QDINNLKEKWEVETKLNERTKLE
EALNLAMEFHNSLQDFINWLTQAE
QTLNVASRPSLILDTVLFQIDEHKVF
ANEVNSHREQIIELDKTGTHLYFS
QKQDVVLIKLLISVQSRWEKVVQR
LVERGRSLDDARKRAKQFHEAWSK
LMEWLEESEKSLDSELEIANDPDKI
KTQLAQHKEFQKSLGAKHSVYDTTN
RTGRSLKEKTSLADDNLKDDMLSE
LRDKWDTICGKSVERQNKLEALLF
SGQFTDALQALIDWLYRVEPQLAED
QPVHGDIDLVMNLIDNHKAFQKELG
KRTSSVQALKRSARELIEGSRDDSS
WVKVQMQUELSTRWETVCALSISKQT
RLEAALRQAEFEFHSVVHALLEWLAE
AEQTLRFHGVLPDDEDALRTLIDQH
KEFMKLEEKRAELNKATTMGDTV
LAICHPSITTIKHWITIRARFEVLA
WAKQHQQRLASALAGLIAQELLEA
LLAWLQWAEITLTDKKEVIPQEIIE
VKALIAEHQTFMEEMTRKQPDVVKV
TKTYKRRAADPSLSQSHIPVLDKGRA
GRKRFPASSLYPSGSQTQIETKNPRV
NLLVSKWQQVWLLALERRRKLNDL
LDRLEELREFANFDFDIWRKKYMR
WMNHKKSVMDFFRRIDKDQDGKI
TRQEFIDGILSSKFPTSREMSAVAD
IFDRDGDGYIDYYEFVAALHPNKDAY
KPITDADKIEDEVTRQVAKCKCAKRF
QVEQIGDNKYRFFLGNQFGDSQQLR
LVRILRSTVMVRVGGGWMLDEFVLV
KNDPCRHHHGSKMLRSESNSSITT
TQPTIAKGRTNMELREKFIADGASQ
GMAAFRPRGRRSRPSSRGASPNRST
SVSSQAAQAASPQVPATTTPKGTPIQ
GSKLRLPGYLSGKGFHSGEDSGLITT
AAARVRTQFADSKKTPSRPGSRAGS
KAGSRASSRRGSDASDFDIQSVCS
SDVETVPQTHRPTPRAGSRPSTAKPS
KIPTQRKSPASKLDKSSKR