

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endo retic
P42858	HD_HUMAN	Homo sapiens	Huntingtin	20.151289	S1177;S1347;S1348;S1789;T1796;S2382;T2389	S411;S417;S419;S432;S640;S643;S1179;S1199;S1870;S1874	30379171;23301498;29351928	MATLEKLMKAFESLKSFQQQQQQQ QQQQQQQQQQQQPPPPPPPPPP PQLPQPPPAQPLLPQPPPPPPPP PPGPAVAEEPLHRPKKELSATKKDR VNHCLTICENIVAQSVRNSPEFQKLL GIAMELFLLCSDDAESDVRMVADEC LNKVIKALMDSNLPRLQLELYKEIKK NGAPRSLRAALWRF AEL AHLVLRPQK CRPYLVNLLPCLTRTSKRPEESVQET LAAAVPKIMASFGNFANDNEIKVLL KAFIANLKSSSPTIRRTAAGSAVSICQ HSRRTQYFYSWLLNVLGLLVVVED EHSTLLILGVLLTLRYLVPLLQQQVK DTSLKGSFQVTRKEMEVSPSAEQLV QVYELTLHHTQH QDHNVTGAELELL QQLFRTPPELLOTLTAVGGIGQLTA AKEESGGRSRSGSIVELIAGGGSSCS PVLRRKQKGVLLGEEEALEDDSES RSDVSSSALTASVKDEISGELAASSG VSTPGSAGHDIITEQPRSQHTLQADS VDLASCDLTSSATDGEDDILSHSSS QVSAVPSDFAMDNDGTQASSPISD SSQTTTEGPD SAVTPSDSSEIVLDGT DNQYLGLOIGQPQDEDEEATGILPD EASEAFRNSMALQQAHLKNMNSH CRQPSDSSVDFVLRDEATEPGDQE NKPCRKGDIGQSTDDDSAPLVHCV RLLSASFLLTGGKNVLPDRDVRVS VKALALSCVGAVALHPESFFSKLYK VPLDTTEYPEEQYVSDILNYIDHGD QVRGATAILCGTILCSILSRFRHVG DWMGTIRTLTGNTFSLADCIPLLRKT LKDESSVTCKLACTAVRNCVMSLCS SSYSELGLQLIIDVLT LRNSSYWLVR TELLLETLAEIDFRLVSFLEAKAENLH RGAHHYTGLLKLQERVLNNVVIHLL GDEDPRVRHVAAASLIRLVPKLFYKC DQOQADP VVAVARQSSVYLKLLM HETQPPSHFVSVTITRIYRGYNLLPSI TDVTMENNLSRVIAAVSHELITSTTR ALTFGCCEALCLLSTAFPVCIWSLG WHCGVPPLSASDESRSCTVGMAT MILTLLSSAWFPDL SAHQDALILAG NLLAASAPKSLRSSWASEEEANPAA TKQEEVWPALGDRALVPMVEQLFS HLLKVINICAHVLDVAPGPAIKAAL PSLTNPPSLPIRRKGEKEPEGEQAS VPLSPKKGSEASAASRQSDTSGPVTT SKSSSLGSFYHLP SYLKLHDV LKATH ANYKVTLDLQNSTEKFQGGFLRSALD VLSQILELATLQDIGKCV EILGYLKS CFSREPMMATVCVQQLLKT LFGTNL ASQFDGLSSNPSKSGRAQRLGSSS VRPGLYHYCFMAYTHFTQALADAS LRNMVQAEQENDTSGWFDV LQKVS TQLKTNLTSVTKNRADKNAIHNHIR LFEPLVIKALKQYTTTTCVLQKQVL DLAQLVQLRVNYCLLDSQVFIGF VLKQFEYIEVQGFRESEAIPIFFFL VLLSYERYHKSQIIGIPKIIQLCDGIM ASGRKAVTHAIPALQPIVHDLFVLRG TNKADAGKELETOKEVVVSMLRLI QYHQVLEMFILV LQQCHKENEDKW KRLSRQIADIIPLAKQMHIDSHE ALGVLNTLFEILAPSSLRPVDMLLRS MFVTPNTMASVSTVQLWISGILAILR VLISQSTEDIVLSRIQELSFSPYLISCT VINRLRDGDSTSTLEHSE GKQIKNL PEETFSRFLQLV GILLEDIVTKOLKV EMSEQQHTFYCQELGTLMLCLIHIF KSGMFRRITAATRLFRSDGCGGSF YTLDSLNLRRARSMITTHPALVLLWC QILLVNHTDYRWWAEVQQTPKRH SLSSTKLLSPOMSGEEEDS LAAKL GMCNREIVRRGALILFCDYVCQNLH DSEHLTWLVNHIQDLISLSHEPPVQ DFISAVHRNSAASGLFIQAIQSRCEN LSTPTMLKKTLCLEGIHLSQSGAVL TLYVDRLLCTPFRVLARMVDILACRR VEMLLAANLQSSMAQLPMEELNRI	True	True	5.0	5.0	3.091	5.0

QEYLQSSGLAQRHQRLYSLLDLDRFRL
STMQDSLSPPVSSHPLDGDGHVS
LETVSPDKDWYVHLVKSQCWTRSD
SALLEGAELVNRIPAEDMNAFMN
SEFNLSLLAPCLSLGMSEISGGQKSA
LFEAAREVTLARVSGTVQQLPAVHH
VFQPELPAEPAAYWSKLNDFGDAA
LYQSLPTLARALAQYLVVWSKLP
HLPPEKEKDIVKFVVATLEALS
HEQIPLSLDLQAGLDCCCLALQPL
WSVVSSTEFVTHACSLIYCVHFILE
VAVQPGEQLLSPERRINTPKAISEEE
EEVDPNTQNPKYITAACEMVAEMVE
SLQSVLALGHRNSGVPFLTPLLR
NIIISLARLPLVNSYTRVPLVWKL
WSPKPGGDFGTAFPEIPVEFLQEKE
VFKEFIYRINTLGWTSRTOFEETWAT
LLGVLVTQPLVMEQEEESPPEEDTER
TQINVLAVQAITSVLVSAMTVPVAGN
PAVSCLEQQPRNKPLKALDTRFGRK
LSIIRGIVEQEIQAMVSKRENIATHHL
YQAWDPVPSLSPATTGALISHEKLLL
QINPERELGSMYSYKLGQVSIHVS
GNSITPLREEWDEEEEEADAPAP
SSPPTSPVNSRKHRAAGVDIHSQS
LLELYSRWILPSSSARRTPAILISEV
RSLLVVSDLFTERNQFELMYVTLTE
LRRVHPSDEILAQYLPATCKAAAV
LGMCKAVAEPVSRLLLESTLRS
SRVGALHGVLYVLECDLLDDTAKQLI
PVISDYLNLKGAHCVNIHSQOHV
LVMCATAFYLIENYPLDVGPEFSASII
QMCVMLSGSEESTPSIYHICALRG
LERLLSEQLSRLDAESLVKLSVDRV
NVHSPHRAMAALGLMLTCMYTGKE
KVSPGRTSDPNPAAPDSESVIVAME
RVSFLDRIRKGFPCARVVARILPQ
FLDDFFPPQDIMNKVIGEFLSNQQP
YPQFMATVVYKVFOTLHSTGQSSMV
RDWVMLSLSNFTORAPVAMATWSL
SCFFVSASTSPWVAAILPHVISRMGK
LEQVDVNLFLVATDFYRHQIEEEL
DRRAFQSVLEVVAAPGSPYHRLTTC
LRNVHKVTTTC