

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondri
Q9ULT8	HECD1_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase HECTD1	17.873885	T891;T1342;S1345;S1350;S1351;T1352;S1354;T1356;T1357;T1372;S1373;S1393;S1430;S1509;S1510;S1530;S1531;T1558;S1569;S1570;S1571;T1932;S2114	S631;S640;S1384;S1488;S1567;T1760;S1772;S2318	31637018;35132862;35254053;28604694;34725712;23301498;32119511;34019948;29237092;30059200;30379171;38665916;30620550;29351928;38253038;39531497;33214551;31492838;35138101	MADVDPDTLLEWLQMGQGDERDMQLIALLEQLCMLLLMSDNVDRFCFETC PRTFLPALCKIFLDESAPDNVLEVT ARAITYYLDVSAECTRRIRVGDGAIKA LCNRLVVVELNRRSRLDLAEQCCKV LELICTRESGAVFEAGGLNCVLTFFIR DSGHLVHKDTLHSAAMAVVSRLCGK MEPODSSLEICVESLSSLLKHEDHQ VSDGALRCFASLADRFRRGVDPAP LAKHGLTEELLSRMAAAGGTVSGPS SACKPGRSTTGAPSTTADSKLSNQV STIVSLLSTLCRGSPPVTHDLRSEL PDSIESALQGDERCVLDTMRLVDLL LVLLFEGRKALPKSSAGSTGRIPGLR RLDSSGERSHRQLDLCIRSKDOTALI DAIDTGAFEVNFMDVVGQTLNWA SAFGTQEMVEFLCERGADVNRGQR SSSLHYAACFGRPQVAKTLRRHGAN PDLRDEDGKTPDKARERGHSEVVA ILQSPGDWMCVNVKGGDKKKKDTN KDEEECNPEKGDPEMAPIYLRLLP VFAQTFQOTMLPSIRKASLALIRKMI HFCSEALLKEVCDSDVGHNLPTILV EITATVLDQEDDDGHLLALQIHRDL VDKGGDIFLDQLARLGVISKVSTLAG PSSDDENEEESKEPEDEPOEADAKE LQQGKPYHWRDWSIIRGRDCLYIWS DAAALELNSGNSGWFRFILDGKLT MYSSGSEPEGSDSSESRSEFLEKLO RARGQVKPSTSSQPILSAPGPTKLT GNWSLTCLEGEIAIHNSDGGQATI LKEIDLPGFVFESNRGTKHSFTAETS LGSEFVTGWTKRGRKLSKLEKTK QKVRTMARDLYDDHFKAVESMPRG VVVTLRNIATQLESSWELHTNROCI ESENTWRDLMKTALENLIVLLKDEN TISPYEMCSSLVQALLTVLNNSMD LDMKQDCSQLVERINVFKTAFAENE DDESRAVALIRKLIIVLESIERLPLH LYDTPGSTYNLQILTRRLFRLERAP GETALIDRTGRMLKMEPLATVESLE QYLLKMVAQWYDFDRSSFVVRKL REGQNFIFRHQHDFDENGIYWIGT NAKTAYEWNPAAYGLVVVTSSEGR NLPYGRLEDILSRDNSALNCHSNDD KNAWFAIDLGLWVIPSAYTLRHARG YGRSALRNWVQVSKDGQNWTSY THVDDCSLNEPGSTATWPLDPPKDE KQGWRHVRIKQMGKNASGQTHYLS LSGFELYGTVNGVCEQDLGAAKEA EANLRRQRRLVRSQVLKYMVPGARV IRGLDWKWRDQDQSPQEGEVTGTE LHNGWIDVTWDAGGSNSYRMGAEG KFDLKLAPGYDPTVASPKVSSSTVS GTTQSWSSSLVKNNCPDKTSAAGSS SRKGSSSVCSVASSSDISLGSTKTE RRSEIVMEHSIVSGADVHEPIVVLSS AENVPQTEVGSSSASTSTLTAETGS ENAERKLGPDSSVRTPGESSAISMI VSVSSPDVSSVSELTNKEAASORPLS SSASNRLSVSLLAAGAPMSSASVP NLSRETSSLESFVRRVANIARTNAT NNMNLRSSSDNNTNLGRNVMS TATSPLMGAQSPNLTTPGTTSTVT MSTSSVTSSSNVATATTVLSVGQSL NTLTTSTSTSESSTGQEAESLYD FLDSCRASTLLAELDDDEDLPEPDE EDDENEDDQEDQEYEEVMILRRP SLQRRAGRSRSDVTHAVTSQLPQVP AGAGSRPIGEQEEEEYETKGGRRRT WDDDYVLRQFSAFVPAFDRPGRGT NVQQTDLLEIPPGTTPHSELLEVEEC TPSPRLALTLKVTGLGTTREVELPLT NFRSTIFYVQKLLQLSCNGNVKSD KLRRIVEPTYTIMYREMKDSDKEKE NGKMGCSWIEHVEQYLGDELPKN DLITYLQKNADAFLRHWKLGTGNTK SIRKNRNCQLIAAYKDFCEHGKTS GLNQGAISTLQSSDILNLTKEQPQAK AGNGQNSCGVEDVLQLLRILYIVASD	False	False	2.802	3.73	0.847

PYSRISQEDGDEQPQFTPPPDEFTSK  
KITTKILQQIEEPLALASGALPDWCE  
QLTSKCPFLIPFETRQLYFTCTAFGA  
SRAIVWLQNRREATVERTRTTSSVR  
RDDPGEFVRGRLKHERVKVPRGESL  
MEWAENVMOIHADRKSIVLEVEFLG  
EEGTGLGPTLEFYALVAAEFQRTDL  
GAWLDDNFPDDESRHVDLGGGLK  
PPGYVQRSCGLFTAPFPQDSDELE  
RITKLFHFLGIFLAKCIQDNRLVDLPI  
SKPFFKLMCMGDIKSNMSKLIYESR  
GDRDLHCTESQSEASTEEGHDSLSV  
GSFEEDSKSEFILDPPKPKPPAWFN  
GILTWEDEFELVNPHRARFLKEIKDLA  
IKRRQILSNKGLSEDEKNTKLQELVL  
KNPSGSGPPLSIEDLGLNFQFCPSSR  
IYGFTAVDLKPSGEDEMITMDNAEE  
YVDLMFDFCMHTGIQKQMEAFRDG  
FNKVFPMEKLSSFSHEEVQMILCGN  
QSPSWAAEDIINYTEPKLGYTRDSPG  
FLRFVRVLCGMSSDERKAFQFTTG  
CSTLPPGGLANLHPRLTVVVRKVDAT  
DASYPSVNTCVHYLKLPEYSSEEIMR  
ERLLAATMEKGFHLN