

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9ULT8	HECD1_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase HECTD1	19.134842	T891;T1342;S1345;S1350;S1351;T1352;T1356;T1357;T1372;S1373;S1393;S1509;S1510;S1530;S1531;S1569;S1570;S1571;T1932;S2114	S631;S640;S1384;S1488;S1567;T1760;S1772;S2318	31492838;32119511;29351928;34725712;34019948;29237092;30620550;35254053;35132862;35138101;30059200;23301498;28604694;31637018;30379171;33214551	MADVDPDTLLEWLQMGQGDERDM QLIALEQLCMLLLMSDNVDRCFETC PPRTFLPALCKIFLDESAPDNVLEV ARAIYYLDVSAECTRRIVGVDGAIKA LCNRLVVVELNNRTRDLAEQCQVKV LELICTRESGAVFEAGGLNLCVLT DSGHLVHKDTLHSAMAVVSRLCGK MEPQDSSLEICVESLSSLLKHEDHQ VSDGALRCFASLADRFRTRRGVDPAP LAKHGLTEELSRMAAAGGTVSGPS SACKPGRSTTGAPSTTADSKLSNQV STIVSLLSTLCRGSVVTHDLLRSEL PDSIESALQGDERCVLDTMRLVDLL LVLLFEGRKALPKSSAGSTGRIPGLR RLDSSGERSHRQLIDCIRSKDTDALI DAIDTGAFEVNFMDDVVGQTLNWA SAFGTQEMVEFLCERGADVNRGQR SSSLHYAACFGRPQVAKTLLRHGAN PDLRDEDGKTPLDKARERGHSEVVA ILQSPGDWMCVNVKGGDKKKKDTN KDEEECNPKGDPPEMAYIYKRLLP VFAQTFQQTMLPSIRKASLALIRKMI HFCSEALLKEVCDSVGHNLPTILV EITATVLDQEDDDGHLLALQIIRDL VDKGGDIFLDQLARLGVISKVSTLAG PSSDDENEEESKPEKEDEPQEDAKE LQQGKPYHWRDWSIIRGRDCLYIWS DAAALELSNGSNGWFRFILDGKLAT MYSSGSPGGSDSSESSEFLEKLQ RARGQVKPSTSSQPILSAPGPTKLT GNWSLTCLKEGEIAIHNSDGGQATI LKEDLPGFVFESNRGTKHSFTAETS LGSEFVTGWTGKRGRKLSKLEKTK QKVRTMARDLYDDHFKAVESMPRG VVVTLRNIATQLESSWELHTNRQCI ESENTWRDLMKTALENLIVLLKDEN TISPYEMCSSGLVQALLTVLNNSMD LDMKQDCSQLVERINVFKTAFSENE DDESRAVALIRKLIAVLESIERLPLH LYDTPGSTYNLQILTRRLRFRLERAP GETALIDRTGRMLKMEPLATVESLE QYLLKMVAKQWYDFDRSSFVVRKL REGQNFIFRHQHDFDENGHIYWIGT NAKTAYEWNPAAYGLVVVTSSEGR NLPYGRLEDILSRDNSALNCHSNDD KNAWFAIDLGLWVIPSAYTLRHARG YGRSALRNWVVFQVSKDGNWTSY THVDDCSLNEPGSTATWPLDPPKDE KQGWRHVRKQMGKNASGQTHYLS LSGFELYGTVNGVCEQLGKAAKEA EANLRRQRRLVRSQVLKYMVPGARV IRGLDWKWRDQDGSPPQEGTGTGE LHNGWIDVTWDAGGSNSYRMGAEG KFDLKLAPGYDPDTVASPKVSSSTVS GTTQSWSSLVKNNCPDKTSAAGSS SRKGSSSVCSVASSDISLGSTKTE RRSEIVMEHSIVSGADVHEPIVVLSS AENVPQTEVGSSSASTSTLTAETGS ENAERKLGPDSSVRTPGESSAISMGI VSVSSPDVSSVELTNKEAASQRPLS SSASNRLSVSSLLAAGAPMSSSASVP NLSSRETSSLESFVRRVANIARTNAT NNMNLRSRSSDNNNTLGRNVMS

TATSPLMGAQSFNLTTPGTTSTVT  
MSTSSVTSSSNVATATTVLSVGQSL  
NLTSTSLTSTSSSDTGQEAESLYD  
FLDSCRASTLLAELDDDEDLPEPDE  
EDDENEDDNQEDQEYEEVMILRRP  
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WDDDYVLKRQFSALVPAFDRPGR  
NVQOTTDLIPPPPTPHSELLEVEEC  
TPSPRLALTLKVTGLGTTREVELPLT  
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DLITYLQKNADAAFLRHWKLTGTNK  
SIRKRNRCSQLIAAYKDFCEHGTS  
GLNQGAISTLQSSDILNLKEQPQAK  
AGNGQNSCGVEDVLQLLRILYIVASD  
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KITTKILQIEEPLALASGALPDWCE  
QLTSKCPFLIPFETRQLYFTCTAFGA  
SRAIVWLQNRREATVERTTRTSSVR  
RDDPGEFRVGRKHERVKVPRGESL  
MEWAENVMQIHADRKSVELEFLG  
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GAWLCDDNFPDDESRHVDLGGGLK  
PPGYVQRSCGLFTAPFPQDSDELE  
RITKLFHFLGIFLAKCIQDNRLVDLP  
SKPFFKLMCMGDIKSNMSKLIYESR  
GDRDLHCTESQSEASTEEGHDSLSV  
GSFEEDSKSEFILDPPKPKPPAWFN  
GILTWEDFELVNPHRARFLKEIKDLA  
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KNPSGSGPPLSIEDLGLNFQFCPSSR  
IYGFTAVIDLKPSGEDEMITMDNAEE  
YVDLMFDFCMHTGIQKQMEAFRDG  
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FLRFVRVLCGMSSDERKAFQFTTG  
CSTLPPGGLANLHPRLTVVRKVDAT  
DASYPSVNTCVHYLKLPEYSSEEIMR  
ERLLAATMEKGFHLN