

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q69ZR2	HECD1_MOUSE	Mus musculus	E3 ubiquitin-protein ligase HECTD1	16.194344	NaN	S632;S641;S1389;S1493;S1572;S1777;S2323	22517741	MADVDPDTLLEWLQMGQGDERDM QLIALEQLCMLLLMSDNVDRCFETC PPRTFLPALCKIFLDESAPDNVLEVT ARAITYYLDVSAECTRRIVGVDGAIKA LCNRLVVVELNNRTSRDLAEQCVKV LELICTRESGAVFEAGGLNCVLTFFIR DSGHLVHKDTLHSAMAVVSRLCGK MEPQDSSLEICVESLSLLKHEDHQ VSDGALRCFASLADRFRTRRGVDPAP LAKHGLTEELLSRMAAAGGTVSGPS SACKPGRSTTGAPSAAADSKLSNQV STIVSLLSTLCRGSPLVTHDLLRSELP DSIESALQGDERCVLDTMRLVDLLL VLLFEGRKALPKSSAGSTGRIPGLRR LDSSGERSHRQLIDCIRSKDTDALID AIDTGAAFEVNFMDVVGQTLNWA SAFGTQEMVEFLCERGADVNRGQR SSSLHYAACFGRPQVAKTLRLRHGAN PDLRDEDGKTPLDKARERGHSEVVA ILQSPGDWMCVNVKGGDDKKKDDTN KDEEECNEPRGDPEMAPLYLKRLLP VFAQTFQHTMLPSIRKASLALIRKMI HFCSEALLKEVCSDVGHNLPTTLV EITATVLDQEDDDGHLLALQIIRD VDKGGDIFLDQLARLGVISKVSALAG PSSDDENEEESKPEKEDEPQEDAKE LQQGKPYHWRDWSIIRGRDCLYIWS DAAALELSNGSNGWFRFILDGKLAT MYSSGSPEGGSDESSESRSEFLEKLO RARGQVKPSTSSQPILSAPGPTKLT GNWSLTCLKEGEIAIHNSDGQQATI LKEDLPGFVVFESNRGKHSFTAETS LGSEFVTGWTGKRGRKLKSKLEKTK QKVRTMARDLYDDHFKAVESMPRG VVVTLRNIATQLESSWELHTNRQCI EGENTWRDLMKTALENLIVLLKDEN TISPYEMCSSGLVQALLTVLNNVSIF RATKQKQNEVLVERINVFKTAFSES EDDESYSRPAVALIRKLIAVLESIERL PLHLYDTPGSTYNLQILTRRLRFRLE RAPGETSLIDRTGRMLKMEPLATVE SLEQYLLKMVAKQWYDFDRSSFV RKLREGQNFIFRHQHDFDENGIIYW IGTNAKTAYEWNPAAYGLVVVTSS EGRNLPYGRLEDILSRDNSALNCHS NDDKNAWFAIDLGVVWVIPSAYTLRH ARGYGRSALRNWVVFQVSKDGNWT SLYTHVDDCSLNEPGSTATWPLDPA KDEKQGWRHVRLKQMGKNASGQT

HYLSSGFEYGTVNGVCEDQLGKA
 AKEAEANLRRQRRLVRSQVLKYMVP
 GARVIRGLDWKWRDQDGSPQEGGT
 VTGELHNGWIDVTWDAGGSNSYRM
 GAEGKFDLKLAPGYDPTVASPKPV
 SSTVSGTTQSWSSLVKNNCPDKTSA
 AAGSSSRKSSSSVCSVASSDISLA
 STKTERRSEIVMEHSIVSGADVHEPI
 VVLSSAENVPQTEVGSSSSASTSTLT
 AETGSENAERKLGPDSSVRAPGESS
 AISMGIVSVSPDVSSVSELTNKEAA
 SQRPLSSASNRLSVSSLLAAGAPM
 SSSASVPNLSSRETSSLESFVRRVAN
 IARTNATNNMNLRSRSSSDNNTL
 GRNVMSTATSPLMGAQSFPNLTPPG
 TTSTVTMSTSSVTSSSNVATATTVLS
 VGQSLSNLTTSLTSTSSSEDGTGQEA
 EYSLYDFLDSCRASLLAELDDDEDL
 PEPDEEDDENEDDNQEDQEYEEVM
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 LPQVPSGAGSRPVGEQEEEEYETKG
 GRRRAWDDDYVLKRQFSALVPAFDP
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 EEVECTPSPRLALTLKVTGLGTTREV
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 VKSDKLRRRIWEPTYTIMYREMKDSD
 KEKENGKMGCSWIEHVEQYLGTD
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 GTNKSIRKNRNCSQLIAAYKDFCEH
 GTKSGLNQGAISLQSSDILNLTKAQ
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 FTSKKITTILQOIEEPLALASGALPD
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 FGASRAIVWLQNRREATVERTRTTS
 SVRRDDPGEFRVGRKHERVKVPRG
 ESLMEWAENVMQIHADRKSVEVE
 FLGEEGTGLGPTLEFYALVAAEFQRT
 DLGTWLCDDNFPDDESRLVLDLGGG
 LKPPGYVQRSCGLFTAPFPQDSDEL
 ERITKLFHFLGIFLAKCIQDNRLVDL
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 IYGFTAVDLKPGEDEMITMDNAEE
 YVDLMFDFCMHTGIQKQMEAFRGN
 VDGFNKVFPMEKLSSFSHEEVQMIL
 CGNQSPSWAAEDIINYTEPKLGYTR
 DSPGFLRFVRVLCGMSSDERKAFLQ

FTTGCSTLPPGGLANLHPRLTVVRK
VDATDASYPSVNTCVHYLKLPEYSSE
EIMRERLLAATMEKGFHLN