

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion
O95714	HERC2_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase HERC2	22.7915	T995;T1851;S3475;S3487;S4182	T272;T647;S1577;S1942;T1944;S2454;S2928;S4810;S4811;S4814;T4827	37217939;29351928;30379171;40307207	MPSESFCLAAQARLDSKWLKTDIQLAFTRDGLCGLWNEVMVKDGEIVYTGTESTQNGELPPRKDDSVESGTTKEDLNDKEKKDEEETPAPIYRAKSILDSWVWGKQPDVNLKECLSVLVKEQQA LAVQSATTTLSALRLKQRLVILERYFI ALNRTVFQENVKVKWSSGISLPPV DKKSSRPAGKGVGLARVGSRAALS FAFALRRRAWRSGEDADLCSSELLQE SLDALRALPEASLFDESTVSSVWLEV VERATRFLRSVVTGDVHGTPATKGP GSIPLQDQHLALAILLELAVQRGTL S QMLSAILLLLQLWDSGAQETDNER S AQGTSAPLLPLLQRFOSIICRCKDAPH SEGDMHLLSGPLSPNESFLRYLTLP QDNELAIDLRTAVVVM AHLDRLAT PCMPPLCSSPTSHKGS LQEVIGWGLI GWKYANVIGPIQCEGLANLGV TQIA CAEKRFILSRNRGRVY TQAYNSDTLA PQLVQGLASRNIVKIAAHS DGHYHL ALAATGEVYSWCGDGGRLGHGDT VPLEEPKVISAFSGKQAGKHVVHIAC GSTYSAAITAEGELYTWGRGNYGRL GHGSSDEAIPMLVAGLKG LKVIDV ACGSGDAQTLAVTENGQVWSWGDG DYGKLGRRGSDGCKT PKLIEKLQDL DVVKVRCGSQFSIALTKDQGVYSWG KGDNRQLGHGTEEHVRYPKLLEGL QGKKVIDVAAGSTHCLALTEDSEVH SWGSNDQCQHFDL RVTKPEPAALP GLDTKHVIGIACGPAQSF AWSSCSE WSIGLRVPFVVDICSM TFEQLDLLLR QVSEGMDGSADWPP PPOEKECVAVA TLNLLRQLHAAISHOVDPEFLGLGL GSILLNSLKQTVVTLASSAGVLSTVQ SAAQAVLQSGWSVLLPTAEERARAL SALLPCAVSGNEVNISPGRRRFMIDLL VGSMLMADGGLESALHAAITAEIQDIE AKKEAQKEKEIDEQEANASTFHRSR TPLDKDLINTGICESSGKQCLPLVQLI QQLLRNIASQTVARLKDVARRISSCL DFEQHSRERSASLDLLRFORLLISK LYPGESIGQTS DISSPELMGVGSLLK KYTALLCTHIGDILPVAASIASTSWR HFAEVAVIVEGDF TGVLPELVVSVL LLSKNAGLMQEAGAVPLLG LLEHL DRFNHLAPGERDDHEELAWPGIM ESFFTGNCRNNEEVT LIRKADLEN HNKDGGFWTVIDGKVYDIKDFQTOS LTGNSILAQFAGEDPVVALEAALQFE DTRESMHAF CVGQYLEPDQEIVTIP DLGSLSSPLIDTERNLG LLLGLHASY LAMSTPLSPVEIECAKWLQSSIFSGG LQTSQIHYSYNEEKDEDHCS SPGGT PASKSRLCSHRRALGDHSQAFLQAI ADNNIQDHNVKDFLCOIERVCROC HLTPIMFPPEHPVEEVGRLLLC LL KHEDLGHVALSLVHAGALGIEQVKH RTLPKSVVDVCRVVYQAKCSLIKTHQ EQGRSYKEVCAPVIERLRFNFNLRP AVCNDLSIMSKFKLLSSLPRWRIA QKIIRERRKKRVPKPESTDDEEKIG NEESDLEEACILPHSPINVDKRPIAK SPKDKWQPLLSTVTVGHVYKWLKQ NVQGLYPQSPLLSTIAEFALKEEPVD VEKMRKCLLKQLERAERLEIGIDTIL KLASKNFLLPSVQYAMFCGWQR LIP EGIDIGEPLTDCLKDVDLIPPFNRML LEVTFGKLYAWAVQNRINVLMDASA KFKELGIQVPVPLQTITNENPSGPSLG TIPQARFLLVMLSMLTLQHGANNLD LLLNSGMLALTQTALRLIGPSCDNV EEDMNASAAQASATVLEETRKETAP VQLPVSGPELAAMMKIGTRV MRGV DWKVGDDQDGPPLGRVIGELGED GWIRVQWDTGSTNSYRMGKEGKYD LKLAELPAAAQPSAEDSDTEDDSEA EQTERNIHPTAMMFTSTINLLQTLCSAGVHAEIMQSEATKTLCGLLRML VESGTTDKTSSPNRLVYREQHRSWC	True	False	4.475	5.0	False

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LQAVLPSWDKTERARDMKCLVEKLF  
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VRPQASLTATHSSTLAEVVALLRTL  
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AVLAVIGGIDGRLRGGQVMHDEFG  
EGTVTRITPKKITVQFSDMRTCRCV  
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GGSEGCNIPQNIERLNGQVCQIEC  
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GGEOTLFAVTADCKLYATGYGAGGR  
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DGKLGHNRSPCDRPRVIESLRGIE  
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