

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q7Z6Z7	HUWE1_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase HUWE1	23.627949	S853;S854;S2922;S2936;S3116;S3117;T3118;S3122;S3159;S3160;S3662;S3794	S648;S649;S740;S1084;S1368;S1370;S1382;S1395;T1722;S1907;T2035;S2266;S2362;S2365;S2391;S2527;S2532;S2535;T2554;S2584;S2595;S2619;T2751;S2826;S2833;S2835;S2861;S2887;S2888;T2889;S2918;S3116;S3117;S3122;S3127;S3135;S3555;S3662;S3752;S3757;S3759;S3760;S3808;S3816;S3827;T3830;S3906;S3919;T3924;T3927;T4271	23301498;30379171;29237092;35254053;28657654;29351928;34931806;33214551;27655845;30059200;35132862;34725712;34229054;32119511;35138101;34019948;30620550	MKVDRTKTKKTPTEAPADCRALIDK LKVCNDEQLLLELQKQKWTGNKCE LYHWVDLLDRFDGILADAGQTVEN MSWMLVCDRPEREQLKMLLLAVLN FTALLIEYSFSRHLYSIEHLTTLLAS SDMQVVLAVLNLVYVFSKRSNYITRL GSDKRTPLLTRLOHLAESWGGKEN GFGLAECCRDLMHMKYPPSATTLLH FEFYADPGAEVKIEKRTTNTLHYIHI EQLDKISESPSEIMESLTKMYSIPKD KQMLLFTHIRLAHGFSNHRKRLQAV QARLHAISILVYSNALQESANSILYN GLIEELVDVLQITDKQLMEIKAASLR TLTIVHLERTPKLSSIIDCTGTASYH GFLPVLVRNCIQAMIDPSMDPYPHQ FATALFSFLYHLASYDAGGEALVSCG MMEALLKVIKFLGDEQDQITFVTRA VRVVDLITNLDMAAFQSHSGLSIFY RLEHEVDLCRKECPFVIKPKIQRPNT TOEGEEMETDMDGVQCIPQRAALL KSMLNFKKAIQDPAFSDGIRHVMD GSLPTSLKHIISNAEYYPGSLFLLATE VVTVFVFQEPSSLSSLDNGLTDVMD LHALLIKDVPATREVLGSLPNVFSAL CLNARGLQSFVQCQPFRERLFKVLDS PDYLPAMRRRRSSDPLGDTASNLGS AVDELMRHQPTLKTDTATTAIKLLEE ICNLGRDPKYICQKPSIQKADGTATA PPPRSNHAAEEASSEDEEEVEEQAM QSFNSTQQNETEPNQVVGTEERIP IPLMDYILNVMKFVESILSNNTTDD HCQEFVNQKGLLPLVTILGLPNLPID FPTSAACQAVAGVCKSILTLSHEPKV LQEGLLQLDSILSSLEPLHRPIESPG GSVLLRELACAGNVADATLSAQATP LLHALTAAHAYIMMFVHTCRVGQSE IRSISVNQWGSQGLSVLSKLSQLYC SLVWESTVLLSLCTPNLPSGCEFG QADMQKLVPKDEKAGTTQGGKRSD GEQDGAAGSMDASTOGLLEGIGLDG DTLAPMETDEPTASDSKGKSKITPA MAARIKQIKPLLASSRLGRALAEFL GLLVKLCVGGSPVRQRRSHHAATTT APTPAARSTASALTKLLTKGLSWQPP PYTPTPRFRLTFFICSVGFTSPMLFD ERKYPYHMLMLQKFLCSGGHNALFET FNWALSMGGKVPVSEGLEHSDLPD GTGEFLDAWMLLVEKMNPTTVLE SPHSLPAKLPGGVQNFQFSALRFL VVTQKAAFTCIKNLWNRKPLKVYGG RMAESMLAILCHILRGEVIRERLSK EKEGSRGEEDTGQEEGSRREPQV NQQQLQQLMDMGFTREHAMEALL NTSTMEQATEYLLTHPPPIMGGVVR DLSMSEEDQMMRAIAMS LGQDIPM DQRAESPEEVACRKEEERKAREKQ EEEEA KCLEKFDADPLEQDELHTF TDTMLPGCFHLLDELPTVYRVDL IMTAIKRNGADYRDMILKQVNVQVW EAADVLIKAALPLTTS DTKTVSEWIS QMATLPQASNLATRILLTLLFEELK LPCA WVESSGILNVLIKLEVVQPC LQAAKEQKEVQTPKWITPVLLIDFY

EKTAISSKRRMQTKYLQSNNSNNW
RWFDDRSGRWCSYSASNNSTIDSA
WKSGETSVRFTAGRRRYTVQFTTMV
QVNEETGNRRPVMLTLLRVPRLNK
NSKNSNGQELEKTEESKEMDIKRK
ENKGNDTPLALESTNTEKETSLEET
KIGEILIQGLTEDMVTVLIRACVSML
GVPVDPDLHATLRLCLRLTRDHKY
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FTPLVTLLLRHIEDPCTLRHTMEKV
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RIALPAPRGSGTASDDEFENLRKGP
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TPPALGEVPQELQSPAGEGGSSTQLL
MPVEPEELGPTRPSGEAETTMELS
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EGSPMDTSSLASCTLEEAVGDTSA
GSSEQPRAGSSTPGDAPPAVAEVOG
RSDGSGESAQPPEDSSPPASSESSST
RDSAVAISGADSRGILEEPLPSTSSEE
EDPLAGISLPEGVDPSFLAALPDDIR
REVLQNQLGIRPPTRTAPSTNSSAPA
VVGNGVTEVSPEFLAALPPAIQEEV
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PVTFIQTLPSDLRRSVLEDMEDSVLA
VMPPDIAAEAQALRREQEARQRQLM
HERLFGHSSTSALSAILRSPAFTSRL
SGNRGVQYTRLAVQRGGTFQMGGS
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EALSCLLVLLFVDEPKLNTSRLHRVL
RNLCYHAQTRHWVIRSLLSILORSSE
SELCIETPKLTTSEEKGGKSSKSCGS

SSHENRPLDLLHKMESKSSNQLSW
LSVSM DAALGCRTNIFQIQRS GGRK
HTEKHASGGSTVHIHPQAAPVVCRH
VLDTLIQLAKVFP SHFTQQR TKETNC
ESDRERGNKACSPCSSQSSSGICT
DFWDLLVKLDNMNVS RKGNVSKS
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ALPENKVSEAQANS GSGASSTTTAT
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DYHFYQGLVYLLENDVSTLGYDLTF
STEVQEFVCEVRDLKPNGANILVT
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QWFWRALRSFDQADRAKFLQFVTG
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