

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O95071	UBR5_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase UBR5	5.263786	S94	S110;S327;S352;S578;S612;T637;S808;S928;S1018;T1115;T1135;S1227;S1308;S1355;S1375;S1481;S1549;T1736;S1741;T1746;S1780;T1969;S1990;S2026;S2028;T2030;S2076;T2213;S2241;S2289;S2469;S2484;S2486	34229054;30379171;23301498;34019948	MTSIHFVHPLPGTEDQLNDRLREV SEKLNKYNLNSHPPLNVLEQATIKQ CVVGNHAAFLLEDGRVCRIGFSVQ PDRLELGKPDNNDGSKLNSNSGAG RTSRPGRTSDSPWFLSGSETLGRLA GNTLGSRWSSGVGGSSGGSSGRSS AGARDSRRQTRVIRTGRDRGSGLLG SQPQPVIPASVIPEELISQAQVVLQK SRSVIIRELQRTNLDVNLAVNNLLSR DDEDGDDGDDTASESYLPGEDLMS LLDADIHSAHPSVIIDADAMFSEDIS YFGYPSFRRSSLSRLGSSRVLLLPLE RDESELLRERESVLRRLRERRWLDGAS FDNERGSTSKEGEPNLDKKNTPVQS PVSLGEDLQWWPKDGTGKFCIGAL YSELLAVSSKGELYQWKWSESEPYR NAQNPSLHHPRATFLGLTNEKIVLL SANSIRATVATENNKVATWVDETL SVASKLEHTAQTYSELOGERIVSLHC CALYTCAQLENSLYWVGVPFSQRK KMLEKARAKNKKPKSSAGISSMPNI TVGTQVCLRNPLYHAGAVAFSISA GIPKVGVLMEVWNMNDSCRFLR SPESLKNMEKASKTTEAKPESKQEP VKTEMGPPSPASTCSDASSIASSAS MPYKRRRSTPAPKEEEKVNEEQWSL REVVVEDVKNVPVGKVLKVDGAYV AVKFPGTSSNTNCQNSSGPDADPSS LLQDCRLLRIDELQVKTGGTPKVPD CFQRTPKKLCIPEKTEILAVNVDSKG VHAVLKTGNWVRYCIFDLATGKAEQ ENNFPSTSSIAFLGQNERNVAIFTAGQ ESPIILRDGNGTIYPMKDCMGGIRD PDWLDLPPISSLGMGVHSLINLPAN STIKKKAIVIIMAVEKQTLMOHILRC DYEACRQYLMNLEQAVVLEQNLQM LQTFISHRCDGNRNILHACVSVCFP TSNKETKEEEEAERSERNTFAERLS AVEAIANAISVVSSNGPGNRAGSSSS RSLRLREMMRRSLRAAGLGRHEAG ASSSDHQDPVSPPIAPPSWVPDPPA MDPDGDIDFILAPAVGSLTTAATGTG QGPSTSTIPGPSTEPSVVESKDRKAN AHFILKLLCDSVVLQPYLRELLSAKD ARGMTPFMSAVSGRAYPAAITILETA QKIAKAEISSSEKEEDVFMGMVCPS GTNPDDSPLYVLCCNDTCSFTWTGA EHINQDIFECRTCGLLESLCCCTECA RVCHKGHDCKLKRTSPTAYCDCWE KCKCKTLIAGQKSARLDLLYRLTAT NLVTLPNRGEHLLLFLVQTVARQT VEHCQYRPPRIEDRNRKTASPEDS DMPDHDLEPPRFAQLALERVLQDW NALKSMIMFGSQENKDPLSASSRIG

HLLPEEQVYLNQQSGTIRLDCFTHC  
LIVKCTADILLDTLLGLTVKELQNK  
YTPGRREEIAVTRFLRSVARVFVI  
LSVEMASSKKKNNFIPQPIGKCKRV  
FQALLPYAVEELCNVAESLIVPVRMG  
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VEPLPPRPSSDQSSSSSQSSSYIIRN  
PQQRISQSQPVRGRDEEQDDIVSA  
DVEEVEVVEGVAGEEDHHDEQEEH  
GEENAEAEQHDHEDHEDGSDMEL  
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DVCSLKHVAYVFQALIYWIKAMNQQ  
TTLDTPQLERKRTRELELGIDNEDS  
EHENDDDTNQSATLNDKDDDSLPA  
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FEVPLAEAIPLADQPHLLQPNARKED  
LFGRRPSQGLYSSASSGKCLMEVTV  
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LTSFRPQCSFMGMVISHDMLLGRW  
RLSLELFGRVFMEDVGAEPGSILTEL  
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DADAVFSAMDLAFAIDLCKEEGGGQ  
VELIPNGVNIPVTPQNVYEVVRKYAE  
HRMLVVAEQPLHAMRKGLLDVLPK  
NSLEDLTAEDFRLLVNGCGEVNVQ  
MLISFTSFNDESGENAEKLLQFKRW  
FWSIVEKMSMTERQDLVYFWTSSPS  
LPASEEGFQPMPSITIRPPDDQHLPT  
ANTCISRLYVPLYSSKQILKQKLLAI

