

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P70399	TP53B_MOUSE	Mus musculus	TP53-binding protein 1	13.660112	NaN	S30;S68;S73;S109;S169;S179;S181;S267;S268;S297;T305;S368;S382;S397;S429;S452;S464;S507;S518;S523;S525;T543;T548;S552;S579;S622;S627;S631;S632;S684;S716;S719;S763;S822;T912;S965;S1018;S1075;S1096;S1115;T1211;S1213;S1216;S1314;S1339;S1359;S1365;S1423;S1427;S1457;S1459;S1470;S1471;T1606;S1615;S1628;S1632;T1635;T1645;S1653;S1670;S1675;S1698;S1756	24788674;28528544	MPGEQMDPTGSQLDSDFSQQDTPC LIEDSQPESQVLEEDAGSHFVLSR HLPNLQMHKENPVLDIVSNPEQSAV EQGDSNSSFNEHLKKEKASDPVESS HLGTSGISQVIERLPQPNTSSALA VTVEAASLPPEEKEEEEELEEEKEGV GANAPGADSLAAEDSASSQLGFGVL ELSQSQDVEEHTVPYDVNQEHLQLV TTNSGSSPLSDVDASTAIKCEEQTE DIAMIEQPSKDIPVTVQPGKGIHVVE EQNLPLVRSEDRPSSPQVSVAAVET KEQVPARELLEEGPQVQPSSEPEVS STQEDLFDQSSKTASDGCSTPSREE GGCSPVSTPATTLLQLLSGQKPLVQ ESLSTNSSDLVAPSPDAFRSTPFIVP SSPTEQGGRKDEPMDMSVIPVGGEP FQKLHDDEAMETEKPLLPSQPAVSP QASTPVSRSTPVFTPGSLPIPSQPEFS HDIFIPSPSLEEPSDDVKKGGGLHSS SLTVECSKTSESEPKNFTDDLGLSM TGDSCKLMLSTSEYSQSSKMESLGS PRTEEDRENTQIDDTEPLSPVSNSKL PADSENLVTPSQDDQVEMSQNV KAKEDETEDRGDCKGREDAVAEDV CIDLTCDSGSQAVPSPATRSEALSSV LDQEEAMDTKEHHPEEGFSGSEVE EVPETPCGSHREEPKKEPMESIPLH LSLTETQSEALCLQKEAPKEECPEA MEVETSVISIDSPQKLQVLDQELEHK DPDTWEEATSEDSVVIVDVKEPSR ADVSCPLEEVEKCSDSQSWEGVAP EEEPKAENRLDTPEEKRIECDGDSK AETTEKDAVTEDSPQPPLPSVRDEPV RPDQETOQPQVQEKESPVTVDAEVA DDKQLGPEGACQQLEKAPACASQSF CESSSETPFHFTLPKEGDIIPPLTGAT PPLIGHLKLEPKRHSTPIGISNYPEST IATSDVTSESMVEINDPLLGNKGD ESAPEMDGKLSLKMMLVSPETEASE ESLQFSLEKPTTAERKNGSTAIAPV ASLQKPVVFGCIYEAQQEKEAQSEA PPSAPDRANLLHFPSAQEEDKERPD VTPKLRQSEQPVKPVGPMDDAAPE DSASPVSQQRASQEQRASQEPFSPA EDVMETDLLEGLAANQDRPSKMLM DRPTQSNIGIQTVDHSLCAPETVSAA TQTVKSVCEQGTSTAEQNSGKQDAT VQTERGSGEKPASAPVDDTESLHSQ GEEEFEMPQPPHGHVLRHMRTIR

EVRTLVTTRVITDVYYYVDGTEVERKVT  
EETEEPIVECQECETEVSPTSQTGGSS  
GDLGDISSFSSKASSSHHTSSGTSLS  
AIHSSGSSGRGAGPLK GKASGTEAA  
DFALPSSRGGPGKLSRKGISQTGAP  
VCEEDGDAGLGIRQGGKAPVTPRGR  
GRRGRPPSRTTGRETVVSGPLGVE  
DISPSMSPDDKSFTRIMPRVPDSTKR  
TDASSSTLRRSDSPEIPFQAATGSSD  
GLDSSSSGNSFVGLRVVAKWSSNGY  
FYSGKITRDVGAGKYKLLFDDGYEC  
DVLGKDILLCDPIPLDTEVTALSEDE  
YFSAGVVKGHRKESGELYYSIEKEGQ  
RKWYKRMVILSLEQGNRLREQYGL  
GPYEAVTPLTKAADISLDNLVEGKRK  
RRSNISSPVTPTAASSSSTTPTRKATE  
SPRASTGVPSGKRKLPTSEEERSPAK  
RGRKSATVKPGTVGAAEFVSPCETG  
DNIGEPSVLEEPRGPLPLNKTLFLGY  
AFLTMATTSDKLASRSKLLDGPTGS  
SEEEEFLEIPPFNKQYTECQLRAGA  
GYILEDNFNEAQCNTAYQCLLIADQH  
CRTRKYFLCLASGIPCVSHVWVHDS  
CHANQLQNYRNYLLPAGYSLEEQRI  
LDWQPRENPFQNLKVLVSDQQQN  
FLELWSEILMTGGAASVKQHHSSAH  
NKDIALGVFDVVVTDPSCPASVLKCA  
EALQLPVVSQEWVIQCLIVGERIGFK  
QHPKYKH DYVSH