

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q12888	TP53B_HUMAN	Homo sapiens	TP53-binding protein 1	19.009464	S659;T864;S1094;S1643	S25;S63;S105;S124;S166;S176;S178;S222;S265;S294;T302;S366;S380;S395;S398;S429;S452;S464;S500;S507;S518;S523;S525;T543;T548;S552;S566;S580;S630;S635;S639;S640;S692;S724;S727;S771;S809;S830;S831;S834;T855;T922;S970;S975;S1028;T1056;S1068;S1086;S1094;S1101;S1114;S1148;T1214;S1216;S1219;S1317;S1342;S1362;S1368;T1372;S1426;S1430;S1460;S1462;S1474;T1609;S1618;S1631;S1635;T1638;T1648;S1656;S1673;S1678;S1701;S1759;S1778	16408927;30379171;31492838;321195111;29351928;29237092;34019948;26853435;23301498;28510447	MDPTGSQLDSDFSQQDTPCLIIEDS QPESQVLEDDSGSHFSMLSRHLPLNL QTHKENPVLDDVSNPEQTAGEERG DGNNSGFNEHLKENKVADPVDDSNL DTCGSISQVIEQLPQPNRTSSVLGMS VESAPAVEEEKGEELEQKEKEKEED TSGNTHSLGAEDTASSQLGFGVLE LSQSQDVEENTVPYEVDKQLQSVT TNSGYTRLSDVDANTAIAKHHEEQSNE DPIAEQSSKDIPVTAQPSKDVHVVK EQNPPPARSEDMPFSPKASVAAMEA KEQLSAQELMESGLQIQKSPEPEVL STQEDLFDQSNKTVSSDGCSTPSRE EGGCSLASTPATTLLHLLQLSGQRSLV QDSLSTNSSDLVAPSPDAFRSTPFIV PSSPTEQEGRQDKPMDTSVLSEEGG EPFQKKLQSGEPVELENPPLLPESTV SPQASTPISQSTPVFPQSLPIPSQPQ FSHDIFIPSPSLEEQSNKGKDGDM HSSSLTVECSKTSEIEPKNSPEDLGL SLTGDSCKLMLSTSEYSQSPKMESE SSHRIDEDGENTQIEDTEPMSPVLN SKFVPAENDSILMNPADQGEVQLSQ NDDKTKGDDTDTRDDISILATGCKG REETVAEDVCIDLTCDSGSQAVPSPA TRSEALSSVLDQEEAMEIKEHHPEE GSSGSEVEEIPETPCESQGEELKEEN MESVPLHLSLTETQSQGLCLQKEMP KKECSEAMEVETSVISIDSPQKLAIL DQLEHKEQEAWEEATSEDSSVVIV DVKEPSPRVDVSCPELEGVEKCSDS QSWEDIAPEIEPCAENRLDTKEEKSV EYEGDLKSGTAETEPVEQDSSQPSL PLVRADDPLRLDQELQQPQTQEKTS NSLTEDSKMANAKQLSSDAEAQKL GKPSAHASQSFCESSETPFHFTLPK EGDIIPPLTGATPPLIGHLKLEPKRHS TPIGISNYPESTIATSDVMSESMVET HDPILGSGKGDGAAPDVKLCLR MKLVSPETEASEESLQFNLEKPATG ERKNGSTAVAESVASPQKTMSVLSC ICEARQENEARSEDPPPTPIRGNLLH FPSSQGEKEKEKLEGDHTIRQSQQP MKPISPVKDPVSPASQKMVIQGPSSP QGEAMVTDVLEDQKEGRSTNKENP SKALIERPSQNNIGIQTMECSLRVPE TVSAATQTIKNVCEQGTSTVDQNFQ KQDATVQTERGSGEKPV SAPGDDTE SLHSQGEFEFDMPPHGHVLRHRH MRTIREVRTLVTRVITDVYYVDGTEV ERKVTEETEPIVECECETEVSPSQ TGGSSGLGDISSFSSKASSLHRTSS GTSLSAMHSSGSSGKGAGPLRGKTS GTEPADFALPSSRGGPGKLSPRKGV SQTGTPVCEEDGDAGLGIRQGGKAP VTPRGRGRRGRPPSRTTGTRETAVP GPLGIEDISPNLSPDDKFSFRVVRV PDSTRRTDVGAGALRRSDSPEIPFQA

									AAGPSDGLDASSPGNSFVGLRVVAK WSSNGYFYSGKITRDVGAGKYKLLF DDGYECDVLGKDILLCDPIPLDTEVT ALSEDEYFSAGVVKGHRKESGELY SIEKEGQRKWKYKRMVILSLEQGNR LREQYGLGPYEAVTPLTKAADISLDN LVEGKRKRRSNVSSPATPTASSSSST TPTRKITESPRASMGVLSGKRKLITS EEERSPAKRGRKSATVKPGAVGAGE FVSPCESGDNTGEPSTALEEQRGPLP LNKTLFLGYAFLLTMATTSKLASRS KLPDGPTGSSEEEEFLEIPPFNKQY TESQLRAGAGYILEDNFNEAQCNTAY QCLIADQHCRTRKYFLCLASGIPC SHVWVHDSCHANQLQNYRNYP GYSLEEQRILDWQPRENPFQNLKVL LVSDQQNFLELWSEILMTGGAASV KQHHSSAHNKDIALGVFDVVVTDPS CPASVLKCAEALQLPVVSQEWVIQC LIVGERIGFKQHPKYKHDYVSH
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