

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q12888	TP53B_HUMAN	Homo sapiens	TP53-binding protein 1	21.096414	S659;T864;S1094;S1642;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	32119511;34019948;16408927;28510447;35132862;37217939;35254053;26853435;29237092;23301498;31492838;29351928;30379171	MDPTGSQLDSDFSQQDTPCLIIEDS QPESQVLEDDSGSHFMSLRHLPLNL QTHKENPVLDVVSNPEQTAGEERG DGNSGFNEHLKENKVADPVDSSNL DTCGSISQVIEQLPQPNTSSVLGMS VESAPAVEEEKGEELEQKEKEKEED TSGNTHSLGAEDTASSQLGFGVLE LSQSQDVEENTVPYEVDKEQLQSVT TNSGYTRLSDVDANTAIKHEEQSNE DIPIAEQSSKDIPVTAQPSKDVHVVK EQNPPPARSEDMPFSPKASVAAMEA KEQLSAQELMESGLQIQKSPPEVFL STQEDLFDQSNKTVSSDGCSTPSRE EGGCSLASTPATTLLHLLQLSGQRSLV QDSLSTNSSDLVAPSPDAFRSTPFIV PSSPTEQEGRQDKPMDTSVLSEEGG EPFQKKLQSGEPVELENPPLLPESTV SPQASTPISQSTPVFPFPGSLPIPSQPQ FSHDIFIPSPSLEEQSNQDGGKKGDM HSSSLTVECSKTSEIEPKNSPEDLGL SLTGDSCKLMLSTSEYSQSPKMESL SSHRIDEDGENTQIEDTEPMSPVLN SKFVPAENDSILMNPADQGEVQLSQ NDDKTKGDDTDTRDDISILATGCKG REETVAEDVCIDLTCDSGSQAVPSPA TRSEALSSVLDQEEAMEIKEHHPEE GSSGSEVEEIPETPCESQGEELKEEN MESVPLHLSLTETQSQGLCLQKEMP KKECSEAMEVETSVISIDSPQKLAIL DQELEHKEQEAWEEATSEDSVVIV DVKEPSPRVDVSCPELEGVEKCSDS QSWEDIAPEIEPCAENRLDTKEEKS EYEGDLKSGTAETEPVEQDSSQPSL PLVRADDPLRLDQELQOPQTQEKTS NSLTEDSKMANAKQLSSDAEAQKL GKPSAHASQSFCESSSETPFHFTLPK EGDIIPPLTGATPPLIGHLKLKLEPKRHS TPIGINSYPESTIATSDVMSESMVET HDPILGSGKGDGAAPDVDDKLCCLR MKLVSPETEASEESLQFNLEKPATG ERKNGSTAVAESVASPQKTMSVLSC ICEARQENEARESDPPTTPIRGNLLH FPSSQGEKEKLEGDHTIRQSQQP MKPISPVKDPVSPASQKMVIQGPSSP QGEAMVTDVLEDQKEGRSTNKENP SKALIERPSQNNIGIQTMECSLRVPE TVSAATQTIKNVCEQGTSTVDQNFQ KQDATVQTERGSGEKPVSAPGDDTE SLHSQGEFEFDMPPHGHVLRHRH MRTIREVRTLVTRVITDVYYVDGTEV ERKVTEETEPIVECQECETEVSPSQ TGGSSGDLGDISSFSSKASSLHRTSS GTSLSAMHSSGSSGKAGPLRGKTS GTEPADFALPSSRGGPGKLSRPGV SQTGTPVCEEDGDAGLGIRQGGKAP VTPRGRRRGRPPSRTTGTRETAVP GPLGIEDISPNLSPDDKSFVRVPRV PDSTRRTDVGAGALRRSDSPEIPFQA AAGPSDGLDASSPGNSFVGLRVVAK WSSNGFYFSGKITRDVGAGKYKLLF

									DDGYECDVLGKDILLCDPIPLDTEVT ALSEDEYFSAGVVKGHRKESGELY SIEKEGQRKWKYKRMVILSLEQGN LREQYGLGPYEAVTPLTKAADISLDN LVEGKRKRRSNVSSPATPTASSSST TPTRKITESPRASMGVLSGKRKLITS EEERSPAKRGRKSATVKPGAVGAGE FVSPCESGDNTGEPSALEEQRGPLP LNKTLFLGYAFLTMATTSKLASRS KLPDGPTGSSEEEEFLEIPPFNKQY TESQLRAGAGYILEDNFNEAQCNTAY QCLLIADQHCRTRKYFLCLASGIPC SHVWVHDSCHANQLQNYRNYLLPA GYSLEEQRILDWQPRENPFQNLKVL LVSDQQNFLELWSEILMTGGAASV KQHSSAHNKDIALGVFDVVVTDPS CPASVLKCAEALQLPVVSQEWWIQ LIVGERIGFKQHPKYKHDYVSH
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