```
                        10        20        30        40        50        60
P53_HUMAN  ...MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSP...LPSQAMDDLMLSPDDIEQWFTEDPGPDEAPRMPEA    69
P53_MOUSE  MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILP.....SPHCMDDLLLL.PQDVEEFFE...GPSEALRVSGA    66
P53_RAT    ...MEDSQSDMSIELPLSQETFSCLWKLLPPDDILPTTATGSPNSMEDLFL.PQDVAELLE...GPEEALQVS.A    67
consensus  ...MEesQSD.S.ElPLSQETFS.LWKLLPp.diLp.....sp...MdDL.L.PqDvee.fe...GP.EAlrvs.A

                 70        80        90       100       110       120       130       140
P53_HUMAN  APPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQ   144
P53_MOUSE  PAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQ   141
P53_RAT    PAAQEPGTEAPAPVAPASATPWPLSSSVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQ   142
consensus  paaq.P.teaP.PvAPApatpWPLSSsVPSQKTYQGnYGFhLGFLqSGTAKSVmCTYSp.LNKlFCQLAKTCPVQ

                150       160       170       180       190       200       210
P53_HUMAN  LWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVP   219
P53_MOUSE  LWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVP   216
P53_RAT    LWVTSTPPPGTRVRAMAIYKKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNPYAEYLDDRQTFRHSVVVP   217
consensus  LWV.sTPPpGtRVRAMAIYKkSQHMTEVVRRCPHHERCSDgDGLAPPQHLIRVEGNly.EYLdDRqTFRHSVVVP

                220       230       240       250       260       270       280       290
P53_HUMAN  YEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGE   294
P53_MOUSE  YEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEV   291
P53_RAT    YEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEE   292
consensus  YEPPEvGSdyTTIHYkYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRdSFEVRVCACPGRDRRTEEENfRKKee

                300       310       320       330       340       350       360
P53_HUMAN  PHHELPPGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRAHSSHL   369
P53_MOUSE  LCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKDAHATEESGDSRAHSSYL   366
P53_RAT    HCPELPPGSAKRALPTSTSSSPQQKKKPLDGEYFTLKIRGRERFEMFRELNEALELKDARAEESGDSRAHSSYP   367
consensus  .cpELPPGSaKRALPt.TSsSPqqKKKPLDGEYFTLkIRGRеRFEMFRELNEALELKDA.A.eEsGdSRAHSSyl

                370       380       390
P53_HUMAN  KSKKGQSTSRHKKLMFKTEGPDSD   393
P53_MOUSE  KTKKGQSTSRHKKTMVKKVGPDSD   390
P53_RAT    KTKKGQSTSRHKKPMIKKVGPDSD   391
consensus  KtKKGQSTSRHKK.M.KkvGPDSD
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X non-conserved
X ≥ 50% conserved
X all match