S3 Figure

```
              1         10        20        30        40        50        60        70        80        90        100       110       120       130
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    MPFLASTTKPPTAVSGAVTGNFLGDGEKLVLLSRLNIVSLFRADDHSFEHVADFSLFASLRFVESLPLFDNRGCGRHVYFFLSVKQEVSVYAFERRNNGLIGMVTLFHGDVETYFHQGKINDASLCCSG
HsDDB1    MSYNYVYVTAQKPTAVNGCVTGHFTSAEDLNLLIAKNTRLEIYVVTAEGLRPVKEVGMYGKIAVME---LFRPKGESKDLLFILTAKYNACILEYKQSGES-IDIITRAHGNVQDRIGRPSETGIIGIIDP
SpDDB1     MTYVTYLHKPSSIRNAVFCKFVNASSWNVIVAKVNCLEVYSYENNRLCLITSANIFAKIVNVK---AFKPVSSPTDHIIVATDSFRYFTLFWDANDNT-VSNGIKIQ-DCSERSLRESQSGPLLLVDP
Consensus ....gv.t..kPta!.gaVtg.F..a...nvl.ak.n.le.%.......l..!.....%aki..ve...lF.p.g...d..f.lt.k.......l......#..!...t...hg#v..r..r.s..g..l..dp

              131       140       150       160       170       180       190       200       210       220       230       240       250       260
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    VYRSTTGNLLPIVIFSIYRGGVIGFDVAAAISGYSRDSKTAAAALNALFPSDYVQGVLKKTKRRSNFAHGNFAAAEIDVRSIALDHRDGIDGAVSLLVLYADLTGKTHVSEYLVNFWRNADQRRVPKTQG
HsDDB1    ECR--------MIGLRLYDG-------LFKVIPLDRDNKELKA----------F----------------NIRLEELHVIDVKFLYGCQ---APTICFVYQDPQGR-HVKTYEVSLREKEFNKGPWKQEN
SpDDB1    FQR--------VICLHVYQG-------LLTIIPIFKSKKRFMTSHNNPSLHDNF---------------SVRIQELNVVYDIAMLYNSS---RPSLAVLYKDSKSIVHLSTYKINVREQEIDEDDVYCHD
Consensus .R.......!.l..Y.G.......l..!ip..rd.K..a..n....d.f.......n.r..El.V.d!a.ly......apsl.vlY.D..g..HvstY.!n.re.e.#...k...

              261       270       280       290       300       310       320       330       340       350       360       370       380       390
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    RSRIPEALNILPGGDIIQRKGLLSTSVETNACLLHVYPDGFFILGPQLLNFCSWKSSGVQSGSSKNVTTLEYPRLGAYYEPVCCATLPGGELLILFEDGSYLKVSVRDDCEGLNSGKSMLSQSSGAPLRT
HsDDB1    VEAEASMVIAVPE----PFGGAIIIGQESITYHNGD---KYLAIAPPIIKQSTIVCHN-RVDPNGSRYLLGDMEGRLFMLLLEKE---------EQMDGTVTLKDLRVELLGETSIAECLTYLDNGVVFV
SpDDB1    IEEGK----LIPS----ENGGVFVFGEMYYYYISKDIQVSKLLLTYPITAFSPSISNDPETGLDSSIYIVADESGMLYKF---KA---------LFTDETVSME---LEKLGESSIASCLIALPDNHLFV
Consensus .e..........P........gG....g.e..y...d.....l.l.ppi..fs...s.....g...s.y.l.d..g.l%......ka.......lf.Dgtv.....r.#.lGe.Siascl..l....lfv

              391       400       410       420       430       440       450       460       470       480       490       500       510       520
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    IPKCVAVVGECCVVGSHMDHTLWMRWLTGESGVLVYNCGPVFDVTVAA--DGSRTSVIAGTGVGLNGGLSFVRSAVSVRQD--IRVTGLQNVRQISVSEDTIIFSLPGYSRVC--RYCVGETMVLEEIHN
HsDDB1    GSRLGDSQLVKLNVDSNEQGSYVVAMET------FTNLGPIVDMCVVDLERQGQGQLVTCSGAFKEGSLRIIRNGIGIHEHASIDLPGIKGLAPLRSDPNRETDDTLVLSFVGQTRVLMLNGEEVEETEL
SpDDB1    GSHFNNSVLLQLPSITKNNHKLEI-LQN------FVNIAPISDFIIDD--DQTGSSIITCSGAYKDGTLRIIRNSINIENVALIEMEGIKDFFSVSFRANY--DNYIFLSLICETRAIIVSPEGVFSANH
Consensus gs....svl..l.v.s..#h.l.....t......f.N.gP!.D..!.d..dq...s.!tcsGa.k#G.Lri!Rn.!.!.#.a.I...Gik.....s...#...d.....lS.!c.tR......e.vee...

              521       530       540       550       560       570       580       590       600       610       620       630       640       650
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    TFFGTEETLLLEYNNERNVFLQVTTAGLRNVWPDRGEYV---IRVINNDIGHAHASEGLLVFSNPANLYVFCM--KTLTPVATLCLADAISCLLVFS-------SSSLLVGTWG-SCAVHLYELHDGMIQ
HsDDB1    MGFVDDQQTFFCGNVAHQQLIQITSASVRLVSQEPKALVSEWKEPQAKNISYASCNSSQVVVAVGRLYYLQIHPQELRQISHTEMEHEVACLDITPLGDSNGLSPLCAIGLWT-DISARILKLPSFELL
SpDDB1    DLSCEEISTIFVSTIYGNSQILQITTKEIRLFDGKK----LHSHISPMSITCGSSFADNVCVAVAGGLILFF-----EGITEVGRYQCDTEVSSLCFTE-------ENVYYVGLWSADIIMLTYCQDGISLT
Consensus ..f...#.t.f...n.....q.lQ!Tta..Rlv.......v..ui.p....ig.a.a....vvva.g..L%........lt.!.......e!scL..t........s.....!GlW..di....y.l....l.

              651       660       670       680       690       700       710       720       730       740       750       760       770       780
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    SKVILQCSATPCSMCVVFH--SGGHRLLVGLHNGYVADVPIS-GANVCGEMVETHLLTTQPV--RLFNLESHAAVLCLGEIPLILIVTNTGFQLTGIDFRDVSACAIMPKHRSPSRYIFFSKSECALILGS
HsDDB1    HKEMLGGEIIPRSILMTTF--ESSHYLLCALGDGALFYFGLNIETGLLSDRKKVTLGTQPTVLRTFRSLSTTNVFACSDRPTVIYSSNHKLVFSNVNLKEVNYMCPLNSDGYPDSLALANNS--TLTIGT
SpDDB1    HSLKLTD--IPRSIVYSQKYGDDGGTLYVSTNVYLMFNFQNGQVIEHSLRRNQLGVAPIILKHFDSKEKNAIFALGEKPQLMYYESDKLYITPLSCTEHLNISSYVNPSLGVNMLYCTNS--YISLAK
Consensus hk...L.....iPrSi........gh.Llv.l.#Gyv..f...g.........LgtqP..lr.F.s.s..a!falg#.P...y..n.klv.t.....#v...........p........nS...l.lg.

              781       790       800       810       820       830       840       850       860       870       880       890       900       910
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    ITSVQKLNTDYVGLKATATCVKYMPWWNVLVLSIRRIEKD-----------QVVSTHGHEVS------------------NLSVLLDEPNSFELLENERCAFIDCVALGQANEWGSCGEVASDAGVVLIGT
HsDDB1    IDEIQKLHIRTVPLYESPRKICYQEVSQCFGVLSSRIEVQDTSGGTTALRPSASTQALSSSVSSSKLFSSSTAPHETSFGEEVEVHNLLIIDQHTFEVLHAHQFLQNEYALSLVSCKLGKDPNTYFIVGT
SpDDB1    MSEIRSLNVQTVSVKGFPRRICSN--SLFYFVLCHQLE------------ESIGTQ-------------------------EQRLLSFLRVYEKNTLSEIAHHKF--NEY--EMVESIILHNDDKRVVVGT
Consensus i.e!qkLn..tV.lk..pr.!cy...s....vl..riE...........s.sTq....s..............e.vll..l..#..t.e..a.h.f..neya.e.vsc.....d....v.!GT

              911       920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    TFVFPDEQLSRSSRFWHCTVEVAKLRTEKTLLRLQGSKDVEGALQCCCIVPNYAGRVALGIGGCVVLYSWNNAADATFVAEETIQIGTLIVRLIPVHQKEVSYIVASDARHSCFFVRIDTIQGSLNIVARD
HsDDB1    AHVYPEEAREPKQGRIV-----VFQY-SDGKL-QTYAEKEVKGAYVSMVE---FNGKLLASINSTVRLYEHTT-EKELRTECNHYNNIMALYL----KTKGDFILVGDLMRSVLLLAYKPHEGNFEEIARD
SpDDB1    GFNFPDQDAPDSGRLH-----VFEHTSDNNI-EMQAEHKVQGSVNTLVL---YKHLIVAGINASVCIFEYE--HGTMHVRNSIRTPTYTIDI----SVNQDEIIAADLMKSITVLQF--IDDQLIEVARD
Consensus .fv%P##..p.sgR.n.....Vf...s#..l...qaek.V.Gav...v....%.g...agIn..V.l%ew.....t...e..i..t....l........d.I.a.Dlm.S...l....i#g.l.e!ARD

              1041      1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    PELRGVMDCAILQYESRHDVCLGDDLFNFFCVSHVEPLANSSGVSAPAMPTKKLQTTAQYHMGDLITVMHQGSFAPCSVLNDVVPIPATLVRGVCGPQIVYGTSHGAFGAITPISSETFILLKGLEVSVA
HsDDB1    FNPNWMSAVEIL---DDDNFLGAENAFNLF--------VCQKDSAATTDEERQHLQEVGLFHLGEFVNVFCHGSLVMQNLGETSTPTQG---------SVLFGTVNGHIGLVTSLSESHAYNLLLDMQNRLN
SpDDB1    YHPLWATSVEIL---SERKYFVTEADGNAV-------ILLRDNVSPQLSDRKKLRHYKKFYLGELINKTRHCTFIEPQDKSLYTP-----------QLLCATVDGSLMIVGDAGHSNTPLLLQLQDNIR
Consensus ..p.w...veIL...s......#..fN.f.......d.vs....rkkLq....%h$G#l!nv..hgsf.......vtP..........q..l.gTv.G..g.!t..s.s...LL1.$#....

              1171      1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
              |---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
TbDDB1    SVVPPLGGFTHASFREVLRVGQERGASRNASFQVTNPQATELFNRRRRRCVPRGYCCGDVVEMFLTLSGGDQLRVVQEANQHYRRWFAYAWPTLEEYAMSDLDDFSSNQGDELAPDRIVDAEINSLLLRQ
HsDDB1    KVIKSVGKIEHSFWRSFH--TERKTEPATGFIDGDLIESFLDISRPKHQEVVANLQYDDGSGHKREATADDLIKVVEELTRIH
SpDDB1    KVIPSFGGLSHKEWKEYR--GENETSPSD-LIDGSLIESILGLREPILNEIVNG----GHEGTKLDISVQDLKSIIENLEKLHP
Consensus kV!ps.Gg..H..wre....g#..t.p....i#g.li#s.l...rp...e!v.g...d..gmkl..s..Dl..!!##l...h......................

              1301  1310      1320 1323
              |---------+--------+---|
TbDDB1    ALPTLSLTVEAVTAFIQTIQRIH
HsDDB1
SpDDB1
Consensus ......................
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