

```

Sc      MGSINNNFNTNNNSNTDLDRDWKTALNIPKKDTRPQTDDVLNTKGNTFEDFYLKRELLMG 60
Tb      -----MVTDDDWREGLKAPTkdvrkkTEDVESRRNVTFEEYGLRRELQMG 45
              * *: .*: *.**.* :*:** . .: ***: :*:*** **

              Q                               I
Sc      IFEAGFEKPSPIQEEAIPVAITGRDILARAKNGTGKTAAFVIPTLEKVKPKLNKIQALIM 120
Tb      IFEKGFERPSPVQEEAIPVALQGDVLAARAKNGTGKTASFVIPVLEKVDTQLPHIQALLM 105
              *** ***:***:*****: *:*:***:*****:*****.***.:. * :****:*

              Ia                               Ib
Sc      VPTRELALQTSQVVRTLgkHC-GISCMVTTGGTNLRDDILRLNETVHILVGTpGRVLDLA 179
Tb      VPTRELALQTAQVTkELGKHITGLEVMVTTGGTTLRDDILRLQSVVHVLVATpGRAVDLA 165
              *****:*. .: ***** *:. *****.*****:..**:*.*.***.:.***

              II                               III
Sc      SRKVADLSDCSLFIMDEADKMLSRDFKTIIEQILSFLPPTHQSLLFSATFPLTVKEFMVK 239
Tb      SKGTAKLDHCRIIVLDEADKLLSQEFTSLMRDLYGFLPKGRQSLLFSATFPVTVKDFADK 225
              *: .*.**.* :*:*:***:***:*:*. .: .: .*** :*****:***:* *

              IV
Sc      HLHKPYEINLMEELTLKGITQYYAFVEERQKLHCLNTLFSKLQINQAIIFCNSTNRVELL 299
Tb      YLRNPYEINLMEELTLRGVTQYYAFVEERQKIHCLNTLfnRLQINQSIFCNSVNRVELL 285
              .*:*****:*.*****:*****.*****:*****.*****

              V
Sc      AKKITDLGYSCYYSHARMKQqERNKVFHEFRQgKVRTLVCSDLLTRGIDIQAVNVVINFD 359
Tb      AKKITQLGYSCYYIHARMQqHRNRVfhDFREGHCRNLVCSDLITRGIDIQAVNVVINFD 345
              *****:***** *****:*.**.*:***:***:*.*****:***:*****

              VI
Sc      FPKTAETYLHRIGRSGRFGHGLGLAINLINWnDRFNLYKIEQELGTEIAAIPATIDKSLYV 419
Tb      FPKYAETYLHRIGRSGRFGHGLGLAINFVTYEDRHNVYRIEQELDTEIKPIPAEVDPELYT 405
              *** *****:.....:*.**.*:***:***.*** .*** :* .**

Sc      AENDETVPVPFPIEQQSYHQQAIPQQQLPSQQQFAIPQqHHPqFMVPPSHQQQQAYPPP 479
Tb      A----- 406
              *

Sc      QMPSQQGYPPQqEHFMAMPPGQSQPQY 506
Tb      -----

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Figure S1. Alignment of *S. cerevisiae* Dhh1 and *T. brucei* DHH1 prepared using Clustal W. The conserved motifs of DEAD box helicases are highlighted in red. The amino acids mutated in this work are framed in blue.