A

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                                   PDIb
Tb   MVFS-THGIRVVYNTAN----VDRSLYAVVHCSDGKYAEVSKDHLNRLKFIEKSSEEEDI 55
Tc   MASF-TSCARILYNTTN----VDRTMHTIVHCSDGKYVEVPKAVADKCPFIEKVKEEMIP 55
Lm   MADEGAIDIRLVLKGPNGEFKVDRDLYIIVHCDDGKYIEVSKNYIKQCPFIEEA-EGEIP 59

Tb   EFDYPEAVLESLAQWTLKYGMDGVAVSSTVRPCIYRNVQHVLKDDWEREFFTTRLMNDLN 115
Tc   EFEYPAAVLENLVCWTEHYGIDGFAESEIVRPCIYRNILHVLKNKWDNGFFVSRLTSELN 115
Lm   EFGYPAAVLEHLIRWAVHYGVDGHAASQLTRPCIYRDFSYVVTDKWDNDFFNQRLCSPLN 119

Tb   IMHYLQTINAAEKYEMKGFHDFLCVCLSCKLRNEEDTELVHKIMGLEDFVEIGPSDLDEA 175
Tc   IGHYLQTVNAAEKFNMKGLHCFLCVGLSCKFRSEDDAELIHKIMGLPSNVQPNQEDIENV 175
Lm   QKHYLLTMTAAEQFGMQGLLDFMCIGLGCKLRGKDDNGIIHEVMGLDKEMEITSEDLAEV 179

Tb   ACRYTWLDQAIKPTVRR 192
Tc   TTRYPWLNEAIEPVVRK 192
Lm   SRDYPWFDDAVKATTKK 196
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B

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Tc   --MSYRAYG----GGYRGRGGRGGRGGQHWQQTACEEDTF-RDPSN-----FNSGSP--- 45
Tb   --MYHRGYG----GHYRGGRG-GGRGHSHWHNNAPMERGG-HMPSNNEGAAISSGSTG-- 50
Lm   MSSYYRGGSTRGRGHYRGGGEGGFRRGRGSYADAVSDGNMNRNEEQQRGERYRSQSSGDD 60

Tc   ----------------------YAELRNYFNSVEGVNYGELKSLTNASFALS-------E 76
Tb   ----------------------FSPLMDFFHSVEGRNYGELRSLTNETYQIS-------E 81
Lm   ESERGSGGFGGNPQCHAGPPLPLVALESFLRDVDGSNYSQLKQLTGRTYSLTRQMKPDPA 120

Tc   SVRCTFLAIQSDPFAPGSQVRMSCPCPFQLQKILQCSELSS---------------CVPC 121
Tb   NVRCTFLSIQSDPFAPGSQVRLVCPCTFSLEKVLQTTDLAA---------------ANPC 126
Lm   SVSIRFVRIQPDPFAPGSQVCVSVPAPFATHALLHSAHSTPPGVTAAALGNLLSPEDVAC 180

Tc   RRIAAEDYILRSFHDGHRRGVARHHSGALHVMRPSQHVLERSTVVLVNG---DRERGG-- 176
Tb   RRVAAEDFILRSFHAGYRNGIPRRTSGAVQVLRPSQHVLERSTVGLVKA---HQQKSGMQ 183
Lm   RRVAAEDFILRCVKGGFAAG--RNTSGAVQTIHQSQHVIARSAVRLLDASEAHDSDGTSD 238

Tc   VEVHLFARVKLPGHGRRIDGHGAIRIFYDELLPIMERCVVGLDEEALYQHVTCVHDQEHL 236
Tb   AEIEIFARVKLPGHGRRIDGHGAIDIFYNELVPLLEQCVVGLNEEDLHQHVICVHDQEVL 243
Lm   GWIHVYFRVKLPGHGRRIDGRRIQQILFSEVLPVFQENVLRCDHHALWAHVTCVHDQEWL 298
                                                  A-loop
Tc   RGELRAAGCVAFVANGSVLPRESGNSDRPLG-KGAVPFVSPASLERTFHLPHSGATVTGM 295
Tb   RSNLLGAGYVAFVANGAILPRDAGNSDKPLR-DNAVPFQSPKSLECSFTLPHSGKTITGM 302
Lm   RAQLREWGFAAFIADGAILPRATGNSDKPLSGPSVVAFSPPDTLRHTFQLPYSGRAISGA 358
                Walker A
Tc   GLPHGLILIAGGGFHGKSTLLRALEVGIYNHVPDDGRVYVTVDPTAVKIRAEDRRSINGV 355
Tb   GLPPGLTLIAGGGFHGKSTLLRALEVGIYNHVPDDGRTYVVVDPTAVKIRAEDRRSVHGV 362
Lm   GLPHGLTLIAGGGFHGKSTLLRALELGVYNHVPDDGRTFVVVDPTAVKIRAEDRRAVHGT 418
                     Q loop motif C        Walker B   D loop
Tc   DISPFINNLPFQKTTTSFVTSDASGSTSQAANIMEALELGSRLLLLDEDTCATNLMYRDD 415
Tb   DISPFINNLPFGKTTNFFVTADASGSTSQAANIMEALELGSQLLLLDEDTCATNLMYRDA 422
Lm   DISPFITNLPYRDNTTAFVTADASGSTSQAANIMEALELGSTTLLLDEDTSATNFMYRDP 478
                                H
Tc   LMQQLVPREQEPITPFVDRVTDLIQNHGVSSIMVIGGSGQYFPHATVTLVMNAYKAFDCS 475
Tb   LMQMLVPRAQEPITPFVERVADLSQNHGVSSIMVIGGSGQYFPQARVVLVMNAYQISDCT 482
Lm   LMEQLVPRTQEPITCFVHRVRDLMYHHGVSVIMVVGGSGQYFPMADVVLLLNAYKVTDAT 538

Tc   ERAKEISR--------TFMSSVQPPKKAISAFVSPMQRQFDGSGTFSTVHCRRGHD---- 523
Tb   KEAKEIASN-------SSLPALNPPGDTASVFIPDVNRCFDPDGSFTTVRRRRGRE---- 531
Lm   AQAKAIAAQSVGRGGVGLVESAAPP--ATSAFRLPPRRSFVYADTFGRLGSQSQQQQYHH 596

Tc   -----------SIKVSGVGVDSIRFAEETIDLSLVEQIVEEGQVNAIAQCLAMLYDGEEN 572
Tb   -----------GTKVSGIGTESIRFSEETIDLSMVEQIVEEGQVNAIAQCLALLYDGEPR 580
Lm   HHGYGYGGSGRGIKISGSGIEHIRIADEDINVTLLEQLVEEGQLNAIAQCLAMLYDSGSA 656

Tc   GIRTILAKGK-------SLKLLYSPSGGSEP-RNVPFYSEFAALIEGCDAALRDARLEAR 624
Tb   IVPEMTTKGG-------ALTQLPSPGGVCEI-QRGKFNSNFSSMIAGCCSHQHDKRLELR 632
Lm   AAAEWQREEAPRSRYPPSLSKALSVDAAAAAGAPASSLSDFGRLVYNCEGRLRQARLELQ 716
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Tc   TPSCYLPRGFTSAARRFEIGAALNRLRTLRTLTAAMK 661
Tb   TPSCYLPRGFTSATRHIEIGAALNRLRTLRTVTAKR- 668
Lm   TASCYLPVGFTALPRVFEIGAALNRLRTLVTSCK--- 750
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C

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                                SAM 2
Tb   MS--SAVDSLLVRLKIPDLIPKFREMNVDRIISLRKLSEEELRTAVPDDDQRNRIIEAIK 58
Tc   MN--SAVDSLLMRLKLSDLIPKFKEMKLDRIVNLRKLSEEELREAVPDDEQRNLIIHAIS 58
Lm   MSQQNAVEALLARLQMGDTIPAFQSMGVDRIVSLRKMSEEALSQAVPDPEQRQALMDAIE 60

Tb   NRGSSE-KRTQAPAASINPPRSTD-DGGRGGMSYPRG--APRGGGPVRGRGRGGTGSAGE 114
Tc   NRGTHE-KRQQSQAANINPPRNAD-DGGRVGMSFPRG--STRGG-MGRGVSRGGRGGGST 113
Lm   SRGHLQSRRAGPPAGQPHPPRSADADFARGGMDEGRGGYAPRGD-RGGRIARGGRGGG-- 117
                                ZF
Tb   GGFHGSGSNNANMFPSRQRVCNHFLNGD-CRYGDSCRYSHN----KALCQ-EAAESVPRR 168
Tc   N--NNSNSETNTSFPGRQRACNHFFSGE-CKFGDRCRYSHD----KEIYDREMAENGPRR 166
Lm   ---RGAGAPNG---DGAARVCRHVFTPEGCKYGDKCRYSHDENDRRRAQEVPTGSGMAQR 171
                                KH
Tb   NHDATSLSEDFSETCIIPTHRIKYLLANRADRLRSIHSKNRTHNKSFQHIDPTIEKFELV 228
Tc   PNDSVSKPKDYSEVCEIPTHRIKFLLAKKAERLKQIHIQNHTHNEPFKRVDSNVEKFELV 226
Lm   SLERPPPNFKFSIEVEIPTERIKYLLGSQGNNMKFINETCGTYNERFDHVDEKEETFTIR 231

Tb   IYGADQQSVQESKKMILACIGVTREEEQKNRVQYTMNELSSNQRAAKFLAACNMKNEGTV 288
Tc   VYGPDPQSVLQSKKMILSYVGVTKQEEQKSRLQYTINELSSNQHAAKLLAACNIKNEGTA 286
Lm   ILGGSEEAINKAKEMLLLSAGVKREEEKKDRFQYAVNELDANTHAARLFAACNTKNKDTT 291

Tb   RELSEASLRNIISFFRFEKQQDIRHFWVNTN-SEHSKLDIIANIVAQLQGVQAIMFCDQK 347
Tc   RELSEETLKSIISFFRFEKQQDVRHFYLNVN-HDRVKLDKVAKIVAQLRGVQAIMFSDQK 345
Lm   RHLSDSIMRNIVSSFHFVRPQEVRHFYMYTSSSDKDKLEMVSKIVSQLKGVQAILFCDQK 351
                                Helicase
Tb   RVVDMSKVASKITRYFNGVSPLFLHRAIPKEERMKMLQTFKDGKPNENGIRERLLVTNED 407
Tc   RVMEMSKVASKIARFFNGVTPLFLHREIPKEERMRILQEFKDGEENESGIRERLLITNED 405
Lm   RVEEMCKGSQRIARHFNGVEPQFVYRQLSKEDRMMALERFKKGVENENGVRQRLLVTNED 411

Tb   YAKLARKTIVPYVNLVINYSVPRSEEYYLLQSLVAGRSDTVGVSIVCVFPHEQSLFQELQ 467
Tc   YAKLARKTLIPYVNLVINYVVPRTEEYYLLQSLVAGRSDTVGVSILCVSPYDQSTFHELQ 465
Lm   YAKLARKTIIPYVNLVINFSVPRAEEYYVLQSQVAGRQGTIGASFLCVSNYEEALFRELE 471

Tb   RNIPFEELEEEGNFKDAAVKLVYDTVDEPLTGEDADPPSNWHEQLKPKTL-------- 517
Tc   QKIVFTAIEEESDFMETAVQLVYDTTANPLTDEDADPPRDWKEKLEPKNASA------ 517
Lm   KNIQFERFEDENHFRTTAVELSYDTTAQPLTPEDADPPADWREHLNPKKPRQNFGKRR 529
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S2 Fig. Sequence alignments were performed using ClustalW multiple sequence alignment program (http://www.genome.jp/tools/clustalw/). The alignment with the trypanosomatid species; *Trypanosoma brucei* (Tb), *Trypanosoma cruzi (*Tc), and *Leishmanina major* (Lm), are presented. Residues shown in red, blue and green represent identity, similarity and weak similarity, respectively. The sequences were obtained from GeneDB. **(A)** Sequence alignment of *T. brucei* p22 (Tb927.7.7460) with its homologues. The PDIb (protein disulfide isomerase) is indicated. **(B)** Sequence alignment of *T. brucei* p72 ATPase (Tb927.3.1590) with its homologues. **(C)** Sequence alignment of *T. brucei* ZC3H41 (Tb927.11.1980) with its homologues. The different domains are indicated; SAM, sterile alpha motif; ZF, zinc finger; KH, K homology domain.