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1 MUSCLE (3.8) multiple sequence alignment
2
3
4 EgracilisZ1 -----
5 Tborrelli -----MDHVD
6 Pserpens -----MSTDRQDVS
7 Lbrasiliensis -----MEKDMLSLYP
8 Ltarantolae -----MEGPRTTHTGDTSEKEMLSPCS
9 Lmexicana -----
10 Lmajor -----
11 Linfantum -----
12 Bsaltans -----MDHAD
13 Tvivax -----MDYMD
14 Tcongolense MVKGASSIIFFFRSPLLKVLFGSTAGRKKRNRHLSNTGRIAAACALLAGYARQDLMHDID
15 Tbrucei -----MDHID
16 Tbgambiense -----MDHID
17 Tcarassii -----MDHVD
18 Ttheileri -----MDHVD
19 Tgrayi -----MDHVD
20 Tcruzi -----MDHVD
21
22
23 EgracilisZ1 -----
24 Tborrelli LTVGSD---SEFLTAISLRMP-----
25 Pserpens LVSSVNNGEDEPSMTVSTSGPSGRMPRVISAVSSVSKEFLPGDIVSGGVGLKNLTTSSYI
26 Lbrasiliensis SHLQERRASGPPVLHVNLVCG-----
27 Ltarantolae NHIHERRSCGPPVLRVHVLRG-----
28 Lmexicana -----
29 Lmajor -----
30 Linfantum -----
31 Bsaltans IAASPELTGG-PLTQLHVRIP-----
32 Tvivax FASARETGPLLSPATISVSIP-----
33 Tcongolense ITEVRELGGEVSLKTLNISIP-----
34 Tbrucei LAEEREMNGDPIMVLNVSVP-----
35 Tbgambiense LAEEREMNGDPIMVLNVSVP-----
36 Tcarassii VVG TREMDSASVQRTLHVITIP-----
37 Ttheileri LASAREMGSSPAFTTLHVSVP-----
38 Tgrayi VAG TREMGAAASL TTHLVFIP-----
39 Tcruzi VAGTRDMGSTPSL TALQVIIP-----
40
41
42 EgracilisZ1 -----
43 Tborrelli -----AFANSKG-----
44 Pserpens VSAGDTQALGDSLHPSTSAIIPSSSQRRSLDTNITERYYPFNATRHPIRTLSTSVSLNA
45 Lbrasiliensis -----LSNEDITSSSFVA---TIGR-SSTGAGTLNRVNPTSSIPASATAFASRRAR
46 Ltarantolae -----MPKGD TTSDFSFS---TFDRTTSTGTGSPNRAGPLSSLPAS---ASRRTS
47 Lmexicana -----
48 Lmajor -----
49 Linfantum -----
50 Bsaltans -----FNAAGDGGGSSAG-----
51 Tvivax -----YTAAVSSSSSNT-----CNSSVSG
52 Tcongolense -----FTSSSPRNDSGD-----
53 Tbrucei -----YSANSSDRKSNVS-----
54 Tbgambiense -----YSANSSDRKSNVS-----
55 Tcarassii -----SSKNCSGHFPSVT-----
56 Ttheileri -----YSSNNSTYNSNSN---IYNNNNNSSHINNNSNASGSTSGVAAYGGSTSPRT
57 Tgrayi -----YSNSATNKTSNSG-----AAGVPAVSSSFTPRTA
58 Tcruzi -----YGSNSNNNNNNNN-----NNNNNFYSGGVCFTRCP
59
60
61 EgracilisZ1 -----LKPVSEWVQDDVVTHCVS--CH
62 Tborrelli -----LGGGFTALRPPRTN--DVYCMPREKWIPDARVVECMASECR
63 Pserpens MNPPQLLGLGAI FSSSVHPQNGDARSFAKPTLDPASVRWCSPDHWVPDAQVVNCPMAPDCK
64 Lbrasiliensis NGSLSPLRSFPSSSVANGTSPVQSSTLAKPVL DLSQVRCIPI DQWIPDAHVVNCPMAPDCG
65 Ltarantolae DGVQSTMGP AVNACSTGAAGIVQSSTLAKPVL DLSQVRCIPLDQWVPDAHVVNCPMAPDCS
66 Lmexicana -----MSGTGVVQSSTLAKPVL ELSQVRCIPLDQWVPDAHVVNCPMAPDCS
67 Lmajor -----MSGNGAVQSPALAKPVL DLSQVRCIPLDQWVPDAHVVNCPMAPDCS
68 Linfantum -----

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69 Bsaltans -----RYHQRTNSTNPALYSRQTIAKPTLNRTVV-LMPSSRWIADNQVACCTAPECQ
70 Tvivax NGDNDGVTSSSTCLSSSGTIAHKFTRLTKPTLDPHIRFCPPSQWVPAQIMTCMTHCECN
71 Tcongolense -----GTNGDSKITGLSTSATTW--LTKPVLDPWRICLCPKRWVWVDMQVTCMAHECN
72 Tbrucei -----SPLLSKCASKQTSQVMW--LTKPTLDPSCIRLCPLRRWVWVDMQVTCMAHECN
73 Tbgambiense -----SPLLSKCASKQTSQVMW--LTKPTLDPSCIRLCPLRRWVWVDMQVTCMAHECN
74 Tcarassii -----NLSPPQSSSLQRTLAKPTLDPSCIRFCPLDRWVWVDMQVTCMAHECN
75 Ttheileri PHVHSLAGSMAASSVMNPTSNTSRSLAKPTLDTSHIRLCSEECWMPDAQVMTMAHECN
76 Tgrayi TSAGTAVASSAALNGGGTTASSRWM-LAKPTLDPSCIRFCPETCWVWVDMQVTCMAHECN
77 Tcruzi SLTANVTRSLSVSCGGDSSFSNVWSLAKPTLDPHIRFCPEGCWVWVDMQVTCMAHECN
78
79
80 EgracilisZ1 AAFSIFNRKHHRCVCGHIFCHFCSAKTLP-----
81 Tborrelli QQFTFFTRRHRCVCGRIYCAKCSSESIHR-----YVDTNFTQRSDVNYVQLSA
82 Pserpens MPFSIFTRKEHCKLCGRVFCYSCCSNEVEILTDGSPCSSHSRNASGNIKGSEMLSSNGFP
83 Lbrasiliensis NSFSLFNRKHHRCMGRVFCSSCCNLLVYIPAAVAQNAASSSTDMAMGCTATSYPVS
84 Ltarantolae NSFSLFNRKHHRCMGRVFCSSCCNHLVSIPAVVSRANGSPEG-MAVGGYVATSNASII
85 Lmexicana NSFSLFNRKHHRCMGRVFCSSCCNLLVYIPAAVNRANSSTEGPAAV-SYVATANTSMS
86 Lmajor NSFSLFNRKHHRCMCGHVFCSSCCNLLVYIPAAVNKRANSSTEGAAAAGSYSAMTNTSLS
87 Linfantum -----
88 Bsaltans LPFTIFNRKHHRCVCGNIFCANCSSHTLPA-----
89 Tvivax VFFSFFNRRHHCHICGRVFCACCRRMVNL-----GDYPRMSSPNS
90 Tcongolense VAFTMFNRRHHRCRCGRIFCFACCSNTVRV-----PSGPLHAASHYAGAD
91 Tbrucei VAFSMFNRRHHRCVCGRVFCACCSETVNA-----LVQSALEVQSNPIE
92 Tbgambiense VAFSMFNRRHHRCVCGRVFCACCSETVNA-----LVQSALEVQSNPIE
93 Tcarassii VFSFLNRRHHRCICGHLFCAACSSHTVTV-----PSTASVAMSGRSS
94 Ttheileri VFSFLNRRHHRCVCGRIFCAACCSHFITL----RGDNHTGTTGSLVTSFLDGVESPTA
95 Tgrayi VFSFLNRRHHRCVCGRIFCAACCSHIITA--LNYHNNDSYYSQNRQLQNSSYTNSMA
96 Tcruzi VFSFLNRRHHRCRCGRIFCAACCSHVITI-----RSTRGGLSASCALSG
97
98
99 EgracilisZ1 -----
100 Tborrelli EDDHHQHLAADT----ETAPNGGPLVSSSSTTVRSIADNNINSNNI----NSNNRKT
101 Pserpens HPRSHSQIANET----GSNPVTGSSSYPKRSESTGFSNVTTVHTAMGNAVAISTATS
102 Lbrasiliensis SAITSELQQFHRACARDGSAPSNGMRRGSQSPITSAPDLFPATSMTHHGSLVVCGEENG
103 Ltarantolae PAATSEPQSLNRASAGEGSASSTGMRRGPQAQVAQGESEFFASSATLLSGTLPVSSDNG
104 Lmexicana SAATPEPQQFNACASDGSASSNGMRRGSQAHAQAQADVSSASSTLFPGPLHVCNDNG
105 Lmajor SVVTPPEPQQFNACASDGSALPNGMRRGPQAPAAQLDVSSASSALLPGPLPVCSDNG
106 Linfantum -----
107 Bsaltans -VGAEDA AVNK-----SIAAAQ
108 Tvivax RSDGMNGVHLNA----VAPQSSVRTSVASSIFSPR-----YAPQREFQ
109 Tcongolense NARGVDRMPLPN----GEAVAREAGRDDSD-----LDQNKQN
110 Tbrucei ACGGVDKTSLPS----GRVSGTDIANGEDN-----ISQQQQQG
111 Tbgambiense ACGGVDKTSLPS----GRVSGTDIANGEDN-----ISQQQQQG
112 Tcarassii PCHGPPKNLSRR----NTAPGTLPAQPTASPVQTSTASS-----MSCISAAT
113 Ttheileri SSTTPHRIGDKVHGQRNSILSSTRPLQSSPSQSLQQIGSS-----YHQRPQSQ
114 Tgrayi QCTVSCGDALDSF----GSPSTVQSHRGDGSPLGACST-----PSSARLHQ
115 Tcruzi AEGQETATSLPA----ILGATDDNSAGGASSNPNSFFYPSQA-----QLVQQQQH
116
117
118 EgracilisZ1 -----PAPSY-----ESVRVCDNCHADHQLAIVKNDFERKVENAR
119 Tborrelli PPS---MASPLSPV-----TNEMRVCKECCYYSYQLAICRRDVATGLPRRR
120 Pserpens PSC---AASVDNVL----SMGTPLPQTSKGTLYRVCNECFYETQLVVSVRG-EDGSPRRK
121 Lbrasiliensis NLP---SSALNSVAMTTAPSPSSPSTQTSVPCRVCASCSEYEVQLVVSTRQ-ENGEPRRR
122 Ltarantolae HLS---FNSLTAPS-----SVPCRVCSCSYEIQLVVSARQ-ENGEPRRR
123 Lmexicana HLTSNALTSPSTVTAVTTLPSLLSPSTQAAVPCRVCASCSEYEVQLVVSTRQ-ENGEPRRR
124 Lmajor HPPSNALTAPS AVT---ALPSSMSPSTQAAVPCRVCASCSEYEVQLVVSTRQ-ENGEPRRR
125 Linfantum -----
126 Bsaltans QVA---ANNNSNAS-----TTVRVCAECFYEHQLVVVRRV-NEGLVRRR
127 Tvivax SQQ---LACSTVSP-----GSCRICTSCHYETQLVVSRRG-PNGGLRRK
128 Tcongolense QPQ---QVDYTTMT-----AYRICTSCHYEIQLVIPP RR-CNGEVRRK
129 Tbrucei VQV---FMNPTTVA-----AYRVCFACHYEVQLVVSRRD-RNGEVRRK
130 Tbgambiense VQV---FMNPTTVA-----AYRVCFACHYEVQLVVSRRD-RNGEVRRK
131 Tcarassii TTT---TTATAPT-----STYRICSSCNYEIQLVVARRD-ENGEVRRK
132 Ttheileri QQQ---QLQPSGSS-----SFSTTHRICACYYELQLVVSRRD-HTGEARRK
133 Tgrayi QQQ---FVTSSPTT-----TCRVCSACHYELQLVVP RR-HNGEARRK
134 Tcruzi STS---HLEPTATT-----TTHRICACYYEIQLVVP RR-QNGEVRRR
135
136

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137	EgracilisZ1	DRGALACL SREVMERVLAF L P P W L V H V A P L V S R D F Y F L A R S N A L W K P L Y E A R W R G L P V -
138	Tborrelli	CRGELKMIQRARIVDICSFLSLKDLFNVS-LVSSDFYFITRDNNLWVYFNAMRWEGYNNN
139	Pserpens	CRGQLKMFQRALLVNVLSFLSLRDLLETA-LVSSDFYFMSRDNIWYQYNTARWLKETEN
140	Lbrasiliensis	SRGELKMIQRVLLVNIMTFLTRDLANVS-LVSADFYFMSRDNIWYQYNMTRWAQESE-
141	Ltarantolae	SRGELKMIQRVLLINVMSFLTRDLANVS-LVSADFYFMSRDNIWYQYNMTRWAQEA-
142	Lmexicana	SRGELKMIQRVLLVNVMSFLTRDLANVS-LVSADFYFMSRDNIWYQYNMTRWVQEA-
143	Lmajor	SRGELKMIQRVLLVNVMSFLTRDLANVS-LVSADFYFMSRDNIWYQYNMTRWVQEA-
144	Linfantum	-----
145	Bsaltans	ARGHLKMFQWPLIVNILSYLSSELLCVS-AVSSDFYFMSRDNLWFTHNMQQWGASMA-
146	Tvivax	CRGELKMIQWSLLVRILSFLPMEDLLEVS-LVSSDFYFMSRDNIWLRHNMSRFAMEKE-
147	Tcongolense	CRGELKMLQRLLLVRIVSYLSMEDLLKVS-LVSSDFYFMSRDNIWYRYNMTRCVREEE-
148	Tbrucei	CRGELKMLQWSLLVRVLSYLTMEELLGVS-LVSSDFYFMSRDNIWYRYNMTRCLREEE-
149	Tbgambiense	CRGELKMLQWSLLVRVLSYLTMEELLGVS-LVSSDFYFMSRDNIWYRYNMTRCLREEE-
150	Tcarassii	CRGELKMLQWPLLVRMLTYLSRPDILQVS-LVSSDFYFMSRDNIWYHYNMARCKEEEL-
151	Ttheileri	CRGELKMLQWSLLVNMLTYLSMHDLLEVS-LVSSDFYFMSRDNIWYQYNLAQYQQKEK-
152	Tgrayi	CRGELKMMQWPLLVRMLS YLTMHDLLEVS-LVSSDFYFMSRDNIWYQYNMARCWQVE-
153	Tcruzi	CRGELKMFQWSLLVKVLSYLSMHDLLEAS-LVSSDYFISRDNIWYQYNMAQRQKEV-
154		
155		
156	EgracilisZ1	-----
157	Tborrelli	NGERTSKERTEEDTRSSTPTSIGSYG-----YRP-----
158	Pserpens	PYFSFTGDTNHMLTVAANSASASGGIRYWFS AHDNYYKSSSSPSASSALTIALDGSSASV
159	Lbrasiliensis	-----LPRLSSLKSHAEASRTQQQKGLSWYASSSGSAARSSLAED-----
160	Ltarantolae	-----LPRLSTLNSRAAASQMQRAPSWYAYSSVSGVLNSFADD-----
161	Lmexicana	-----LPRLSSLNSRAAASRMQQQRGPSWYTYSSGNVARSSLIDD-----
162	Lmajor	-----LPRLSSHNSRAAASRMQQQRGPSWCTYSSGSGPRSSLVDD-----
163	Linfantum	-----
164	Bsaltans	-----QEKT TTTTRKGSNATAAST-----AAQ-----
165	Tvivax	-----IQRTVMKTVEGTSALLKQNS-----HGR-----
166	Tcongolense	-----VQRMLTMTVESPNSTRKWRS-----TGK-----
167	Tbrucei	-----LQRMLSTTLGSRNSTRRQRL-----PQK-----
168	Tbgambiense	-----LQRMLSTTLGSRNSTRRQRL-----PQK-----
169	Tcarassii	-----QLKLPLALPSLRRLR-----SLT-----
170	Ttheileri	-----ELKIPTASNYFNPSLRHLLN-----
171	Tgrayi	-----LKIPTTRSSSSSFLRRRL-----LN-----
172	Tcruzi	-----QLRIPRRQNSSLSLRRFL-----QRQ-----
173		
174		
175	EgracilisZ1	-----NPQQTNSRETNWVYQTYQRQHLSDAVMSNSRLRM
176	Tborrelli	-----ISRDTSATGFLKGVTPSDGGE--ISNHCRYNYTQFLQYCTLLENARCGGLANFAT
177	Pserpens	VEGSIKFPRAPVLEDATVLTQGEAFKRVISLHARYNYTQFLDFARRQEMARCEGLWFSV
178	Lbrasiliensis	-----MFNSAPVIQDAAALSESEAAKRVISLHARYNYTQFLDFARRQEMARCEGLSSFSL
179	Ltarantolae	-----MFSSAPVIQDATALSESEAAKRVISLHARYNYTQFLDFARRQEMARCEGLSSFSL
180	Lmexicana	-----MFPSAPVIHDATALSESEAAKRVISLHARYNYTQFLDFARRQEMARCEGLSSFSL
181	Lmajor	-----MFSSAPVIQDATALSESEAAKRVISLHARYNYTQFLDFARRQEMAWCEGLSSFSL
182	Linfantum	-----MARCEGLSSFSL
183	Bsaltans	-----KGGKQALVVS----VAAPLSKVVISLHARYNYTQFLDFARRLEGARCQGLSSFSA
184	Tvivax	-----QRREIPFSTDIDDIVSADALKPSISLNARYNFTQFLDFTRRQETTRCKGLSCFAV
185	Tcongolense	-----ITRELSFNDFDSITSADAAPKPAISLHARYNFTQFLDFTRRRREATRCKGLSCFSV
186	Tbrucei	-----QLGELTFGTD FDSITSAGA AKPTISLNARYNFTQFLDFTRRRREATRCKGLSCFSV
187	Tbgambiense	-----QLGELTFGTD FDSITSAGA AKPTISLNARYNFTQFLDFTRRRREATRCKGLSCFSV
188	Tcarassii	-----RQNQKIVNTDLGDVAADDAKRVISLHARYNFTHFLDFARRHEMSRYKGLSSFAV
189	Ttheileri	-----RHKVRAFRTDFEDITPTDASKRVISLHARYNFTQFLDFARRQEMARCKGFLSFSV
190	Tgrayi	-----RAKPQTFLEFGDIIPDASKRVISLHARYNFTQFLDFARRRELARCKGVSSFSE
191	Tcruzi	-----KEPLRAFGEIEFDVSSSDASKRVISLHARYNFTQFLDFARRQEMARCRGLSSFSV
192		
193		
194	EgracilisZ1	RIQTLTGLSKFFLIGASGVGKTCLLHRFL-TGEYRRQPSGTVGVAV-----
195	Tborrelli	NAKLLLMKSVKVAIVGHSRVGKSMVRHFMDLYGSIRGNTRIFSPHSHHRTTSHHT
196	Pserpens	AARVLFSSSTIRVALIGPPGVGKTTSLTFL-----KKNKRGSTV-----
197	Lbrasiliensis	GARILLSSPIRVALVGPCGIGKTASVRAFL-----GEKLSQMVV-----
198	Ltarantolae	GARILLSSPIRVALVGPCGIGKTASAHTFL-----GEKPSQMVV-----
199	Lmexicana	AARILLSSPIRVALVGPCGIGKSACAHAF-----GEKPSQMVV-----
200	Lmajor	GARLLLSSPIRVALVGPCGIGKTASAHAF-----GEKPSQMVV-----
201	Linfantum	GARLLLSSPIRVALVGPCGIGKTASAHAF-----GEKPSQMVV-----
202	Bsaltans	GAKQLLSSPIKICVVGPPGIGKTFMMKRFTGEISGDPTTIASHALSI-----
203	Tvivax	GAHTLLSSPLKVALIGPCGARKTLMQHLVPFNQHNGRNAGSEHSET-----
204	Tcongolense	STRTLLSSPIKIALIGPSGVGKTMLMREWV--QGGRPD TDGTSYEAS-----

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205 Tbrucei      GMRDLLSSPIKIALIGPCGVGKTSLMREWG--RQRRPGDNSARFAVT-----
206 Tbgambiense GMRDLLSSPIKIALIGPCGVGKTSLMREWG--RQRRPGDNSARFAAT-----
207 Tcarassii    CARMLLSSPVKIAIIGPSGIGKTPMLQHFI-----GTIPLDGP-----
208 Ttheileri    GARMLLSSPLKIAIIGPTGIGKSSMVRCA-----GPHAAHTSWREP-----
209 Tgrayi       GARMLLSSPLKIAIIGPAGVVGKTLVQQFV--DQHE--NRRLAGRPL-----
210 Tcruzi       AARTLFSSPLKIAIIGSMGVGKTLVVRHFV--VSHE--NGGSSGGRI-----
211             . *: . . . : :* *:
212
213 EgracilisZ1  -----RTRPVQVTVGDPALSSPRCPPVSLTLGATP-AGPVTNLVFDASGDPRYEA
214 Tborrelli    AQLDKDGYR-----PTCGLVVS-HKRISITGEITLPQSGVII--YDVCGDSRYEK
215 Pserpens     -----H-----STMGFTRH-KVTLWTGGDSK-VGVNLEI--YDVS GDERYES
216 Lbrasiliensis -----R-----PTIGFERR-AVTVRLARGLS-TEAVLHI--YDLSGADRYRE
217 Ltarantolae -----R-----PTIGFERR-VTVRLARDLS-TEAVLHI--YDLSGADRYGE
218 Lmexicana    -----R-----PTIGFERR-AVTVRLARGLS-AEAVLHI--YDLSGADRYGE
219 Lmajor       -----R-----PTIGFERR-AVRVRLARGLS-AEAVLHI--YDLSGADRYGE
220 Linfantum    -----R-----PTIGFERR-AVTVRLARGLF-AEAVLHI--YDLSGADRYGE
221 Bsaltans     -----H-----PTCGFTTY-TKRASIVGGLT-TTATFTI--MDVAGDRRYEQ
222 Tvivax       -----Q-----PTASFQTY-EKAIHVTGGLT-ADARLQV--FDISGEKRFRE
223 Tcongolense -----V-----PAVPFNRF-EEVVHLSGGLT-ADARLQV--FDISGHPCFEE
224 Tbrucei      -----P-----PTVTFNQF-DKTVFLTGGTL-ARAQLRV--FDISGHPRFRE
225 Tbgambiense -----P-----PTVTFNQF-DKTVFLTGGTL-ARAQLRV--FDISGHPRFRE
226 Tcarassii    -----R-----ATMGFTRY-CKRVHLTGGLV-SDVMLHI--FDISGEPRYEE
227 Ttheileri    -----L-----PTMGFTRY-EKTVHLTGSLM-ADVMLHV--FDISGEPRFEE
228 Tgrayi       -----L-----PTMGFTLY-EKTVHIVGSLT-TDVRQLI--FDISGEPRFEE
229 Tcruzi       -----S-----PKLGFVRY-AKMVHLTGSLA-ADVMLHI--YDISGELRFEE
230             . : * . * :
231
232 EgracilisZ1  LLPLYVYGVQVACVFFDLTAPETLEVCAHWCRALQATLPPDVVIAICGLKGD-----
233 Tborrelli    LRALVCQSVHVIIILCYNASLKKSFIEAAVQMTSIESMLGPQPVV-MCGIIDQ-----
234 Pserpens     LRRFVCSHCHAIGLCYNPCRKVTLVQAADVMMGVEPALGPQPVV-VCGLIPRENGATDA
235 Lbrasiliensis LRRFVCRHCHAIGLCYDPSRKMTLVQAADIMMELEGALGPQSVV-VCGLVRQPPRASSSG
236 Ltarantolae LRRFICRHCHAIGLCYDPSRKVTLVQAADIMMGLESTLGPQPVV-VCGLVRPPHPSSSSG
237 Lmexicana    LRRFVCRHCHAIGLCYDPSRKVTLVQAADIMMGLESALGPQSVV-VCGLMRQPHTSSSG
238 Lmajor       LRRFVCRHCHAIGLCYDPSRKVTLVQAADIMMGLESALGPQPVV-VCGLMRQPHTSSSG
239 Linfantum    LRRFVCRHCHAIGLCYDPSRKVTLVQAADIMMGLESALGPQPVV-ICGLMRQPHTSSSS
240 Bsaltans     LRGLCAQSAHAVVVCYDTHSKMSLVHAANMMSLEPFLGPQPAV-VCGFVTD-----
241 Tvivax       LRLRILCHCHAIGLCYDPSRSTFMEAVDMIQDLVSALGPQPVV-LCGVLPQAST-----
242 Tcongolense LCRFICARCHIVVLCYDPRRRSSFVEAQEMMAKVDSALGAQPVV-VCGISPP-----
243 Tbrucei      LTRFVCASCHAVVICYDPQRKSSLMEAKAIIADVETKLGVPVI-VCGLIPP-----
244 Tbgambiense LTRFVCASCHAVVICYDPQRKSSLMEAKAIIADVETKLGVPVI-VCGLIPP-----
245 Tcarassii    LRRFICSSCHAIGLCYDARQKVTLVQAADVMMNGVEPVLGAQPVV-VCGIVPPRREHSPPA
246 Ttheileri    LRRFICSNCHAVGICYDARRKVTLVQAADIMMGVEPALGPQPVV-VCGIMGPTNTNTNTD
247 Tgrayi       LRRLLCSNCHAIGICYDARRKVTLVQAADVMMVEPTLGPQPTV-VCGIVRPPAAAAA--
248 Tcruzi       LRRFLCSNCHAVGLCYDPRRKFTLVQAADVMMGVEPALGPQPVV-VCGILCPAEPARQD-
249             * : : : : : * : : : **
250
251 EgracilisZ1  -----
252 Tborrelli    -----
253 Pserpens     SSTVPKNIGNGLND-----TRLDLRVSQTAHQRPDTLPAVSFTTLATASSEASSRSQ
254 Lbrasiliensis SVPLDCHKADPTHLSTTM---TALHLSTLPKREGQSLQSLPVDPAVPV--STGALTGELM
255 Ltarantolae  RAPLNHHKEGSTRLPAVSSVAALKFSAPSKREDENSDSLPVVSTKPEAEAAGIVSDDWI
256 Lmexicana    SVPLNRPRVVPARLPAVVSAVTALSASPKREARSHSVLVGSVESEAGAAGGVADESM
257 Lmajor       SVPLNYHRAGPARLPAVVSAVTAVGLSAPLVRRDQSSHAVPVGSAESAAEAAGGVAGESM
258 Linfantum    SAPLHHHRAGPARFPAVVSAAATLNL SAPPKKEDECSHSMVGSAAEAE--AAGGVAGESM
259 Bsaltans     -----
260 Tvivax       -----
261 Tcongolense -----
262 Tbrucei      -----
263 Tbgambiense -----
264 Tcarassii    A-----
265 Ttheileri    EIPTTTTNTNTNSNS-----
266 Tgrayi       -----
267 Tcruzi       -----
268
269
270 EgracilisZ1  -----
271 Tborrelli    -----
272 Pserpens     GSTVASATATREATSSPLKSVHPACGAMVWGAGG-----

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273 Lbrasiliensis LATPLCGVSNNGTKTPLQSSSSSTSTARLSGVTAESNGDQSDRLQVNTATSTMALLRAV
274 Ltarantolae LAAPLFGATNGCSALHQTKRSRAGIATTLPGGGGEGVDHNNGGPLQADAAISPI-----
275 Lmexicana LAATMCGVANGCNTSLQASSCPASAAVALHGVVAENCDHESCDRLQADAAVSPV-----
276 Lmajor LAAPICGVANGCNTSPRASSSPAGTAVTLPGGMAENGAHESCDRLQADAAVSPM-----
277 Linfantum GAAPMCGAANGCNTPPQASSSPAGTAVRLPGVVAENGGHESCDGLQDDAAVSPV-----
278 Bsaltans -----
279 Tvivax -----
280 Tcongolense -----
281 Tbrucei -----
282 Tbgambiense -----
283 Tcarassii -----
284 Ttheileri -----
285 Tgrayi -----
286 Tcruzi -----
287 -----
288 -----
289 EgracilisZ1 -----AAHRKVDAHTLAQFPVVRPDVRFECALADRGVGSFFFEACV
290 Tborrelli -----TNNNNNKEVTESDASQITPRCKASIQIYSHNAK---VAFESAI
291 Pserpens -----SHSSRSEGLTPPRLSLSIEVSEEDAAGITVRDGGSLHCPIDQMH---VFYDRL
292 Lbrasiliensis PLSSTTPAPALPPFTTATSSSGSLEVSAEDAVGITVRGHSSIQCLLHPT---PFFEAVV
293 Ltarantolae -----LSPRSRPFTMASPHVSALEVSVEDAVGITVRGHSSIHCPLLHPT---PLFEALV
294 Lmexicana -----PSPAPPPFTIASPHSSALEVSVNDAVGITVRGHSSIHCPLLHPT---PLFEALV
295 Lmajor -----PSPPQPPFAVASPQSRALVSVEDAVGITVRGHSSIHCPLLHPT---PLFEALV
296 Linfantum -----PSPTPPPFTIASPQSSVLEVSVEDAVGITVRGHSSIHCPLLHPT---PLFEALV
297 Bsaltans -----SQRKRETVSGAEGITVRCRASIQT--NHAD---EIFEAVL
298 Tvivax -----MVGRHDVPPLEVGESQDVGGEWQSGSLRCPYDRGD---LLFQRIV
299 Tcongolense -----VSRNRGAVEFEVTKEEARAASRERGSVQCSWAKSE---VLFESVV
300 Tbrucei -----ADAGRGSVAEVSAAEEATEISSRERGSLLCAWHEGK---ILFEHVV
301 Tbgambiense -----ADAGRGSVAEVSAAEEATEISSRERGSLLCAWHEGK---ILFEHVV
302 Tcarassii -----HHRSPDALEAPEEGLPVREVKEVHAEGITVRGRGSVQCAWNRSE---RVFQTLV
303 Ttheileri -----NTNSTATTMATPIAVSEPAVQEIHAMGITVRGRASLQCQWNNSE---PLFQSL
304 Tgrayi -----QEIGEKGAPLEVSEVHARDITVRGRGSLQCAWDKGE---MLFQKLV
305 Tcruzi -----LHEAGTQELEVTEVDASGITVRGRGSLQCAWDNSE---CLFQQLV
306 -----* . . . : :
307 -----
308 EgracilisZ1 TACVQKIVQSP-----SAAVP--
309 Tborrelli QVLDRLMIGG-----
310 Pserpens CSLIDRLSLAAMANRTSIANLTDAEE-----SESNKFSGVSATNSSRT-F
311 Lbrasiliensis QSVLDRLVEATVASTSTISEISAVLAMQSGGSGRRNSSTCSAGSLSAGSAPRSTIQAS-S
312 Ltarantolae QSVLDVLEATVAST-----DLTMHGNGNSSQSFPTCHPSSLNNGRASTAMRVT-S
313 Lmexicana QSVLDLLVEATVASTSTISDIAELTMHGSASGAQSFPTSCPSSLSAGSPASAMRVA-S
314 Lmajor QSVLDLLVEATVASTSTISEISAELETHGSGSGPQSFPTCCPSSLSAGSAPANATRVA-S
315 Linfantum QSVLDLLVEATVASTSTISEISAGLETHGSGSGPQSFPTCCPSSLSAGSAPANATRVA-S
316 Bsaltans QTLLDRLVLTAT-----ATAAAASPASKLGA--
317 Tvivax QCLLDRIALAT-----SVVSFNPSNSSCIP-N
318 Tcongolense QCLLDRIALGT-----SALPFSPSVRSSGEY-V
319 Tbrucei QCLLDICIALGT-----SAISFTAPVSPLGVP-V
320 Tbgambiense QCLLDICIALGT-----SAISFTAPVSPLGVP-V
321 Tcarassii QCLLDRLSLAT-----STAAGVRVST-----E
322 Ttheileri QSLLDRLAMAT-----ATSSVVAASNGRAKI
323 Tgrayi QCLLDRLALAT-----TTSSVIATTTPTGRVRR
324 Tcruzi QSLLDRLAMAT-----ATSSVVAASNTALLA-G
325 : : .
326 -----
327 EgracilisZ1 -----PPPNSTPVD--
328 Tborrelli -----RQSHELISLTTNPSVFDLLID--
329 Pserpens AKRDPKVDKVI AEELLKLTMQPSTLNILLDR-
330 Lbrasiliensis VRRRPHASRAIVQDLLNLTMQPCALDILLDRK
331 Ltarantolae ARRRPHASRAIMEDLLNLTMQPCSLDILLDRK
332 Lmexicana TRRRPKASRAIMEDLLNLTMQPCALDILLDRK
333 Lmajor TRRRPHASRAIMEDLRNLTMQPCALDILLDRK
334 Linfantum TRRRPHASRAIMEDLLNLTMQPCALDILLDRK
335 Bsaltans -----AAARTAAQELLEISSNPSVMDVLLDGK
336 Tvivax EGAFSVTNHTAAHELLKISTTPSPIDVLIN--
337 Tcongolense THEEPLANRTVAQELLQITVCPSAIDILLN--
338 Tbrucei DSEEFVNRSTAQELLRITMCPSAIDVLLD--
339 Tbgambiense DSEEFVNRSTAQELLRITMCPSAIDVLLD--
340 Tcarassii DEKERVANRTAAELQLTLNPSAIDVLLD--

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341	Ttheileri	DEKESATNLAVAQELLRITLNPSALDILLE--
342	Tgrayi	DERETSMNLNVAQELLQITMQPSPLDVLL---
343	Tcruzi	DEKEATVNCNIAQELLRITLDPSPLDVLMSDN
344		* . :

Table S1: Synthetic oligonucleotides used in this study. All sequences are written with the 5' end left-most, and where relevant restriction endonuclease sites are underlined.

Designation	Sequence	Purpose
qRT For:	GCCAAACCGACAATTTCACT	qRT-PCR
qRT Rev:	CTCCCGCATTAAATGACGTTT	qRT-PCR
β -tubulin For:	CAAGATGGCTGTCACCTTCA	qRT-PCR
β -tubulin Rev:	GCCAGTGTACCAGTGCAAGA	qRT-PCR
TbFRP-RNAi-A For:	GAGCGGGAGATGGGTAATGG	qRT-PCR
TbFRP-RNAi-A Rev:	TGAACTCCGAGTTTCGTCTC	qRT-PCR
TbFRP-RNAi-B For:	GAAGAGCGGGAGATGGGTAAT	qRT-PCR
TbFRP-RNAi-B Rev:	TGTGGGGTTCATAAACTGGA	qRT-PCR
TbFRP For:	GCCAAAGCTTATGGATCATATTGATCTTGC	Ectopic expression of TbFRP
TbFRP Rev:	GCTAGGGCCCGTCCAATAGCACGTCAATAGC	Ectopic expression of TbFRP
TbFRP-FYVE Rev:	GCGGGCCCCACAACAAGCTGTACTTCATAG	Ectopic expression of FYVE domain
TbFRP-FYVE-Fbox Rev:	GCGGGCCC GGCAGCACCTGCGGATG	Ectopic expression of FYVE domain
TbFRP Tag For:	GTTCTCCGTCAACCGCTCAACAGCGCAGGAGCTATTGCGAATT ACGATGTGCCCATCGGCTATTGACGTGCTATTGGACGGTACCG GGCCCCCCTCGAG	Genomic tagging of TbFRP
TbFRP Tag Rev:	CACAAACCCAGCTGGCAAATAGTAAAACGGTACTTGTCCA CACAACAAATTACCTCATTCCAACCATGTATGGCGGCCGCTCT AGAACTAGTGGAT	Genomic tagging of TbFRP

Table S2: Number of amino acid residues between RrHHCR + 10 and RVC motifs in FYVE Domains

Gene ID	Tb09.160.3480	Tb09.211.1970	Tb02.211.2990	Tb10.05.0240	Tb927.7.1840	Tb927.7.1880	Tb11.01.6980	Tb11.01.7720
Species								
<i>T. brucei</i>	16	16	16	13	16	16	23	21
<i>T. b. gambiense</i>	16	16	16	13	16	16	23	21
<i>T. cruzi</i>	00	16	16	14	16	16	23	21
<i>T. vivax</i>	16	-	16	14	16	16	23	-
<i>T. congolense</i>	16	16	16	13	16	16	-	21
<i>L. major</i>	16	16	-	14	-	-	23	-
<i>L. mexicana</i>	16	16	16	14	-	-	23	-
<i>L. braziliensis</i>	16	16	16	14	-	-	23	-
<i>L. infantum</i>	16	16	-	14	-	-	23	-

Gene ID	Tb10.61.0730	Tb11.47.0002	Tb927.7.690	Tb927.7.3790	Tb937.7.530
Species					
<i>T. brucei</i>	118	29	59	68	17
<i>T. b. gambiense</i>	-	29	63	68	17
<i>T. cruzi</i>	107	29	65	83	17
<i>T. vivax</i>	107	29	78	71	17
<i>T. congolense</i>	107	29	-	68	17
<i>L. major</i>	119	70	-	127	36
<i>L. mexicana</i>	119	70	-	129	36
<i>L. braziliensis</i>	119	71	-	127	36
<i>L. infantum</i>	118	70	-	-	36

Species	Rn	Bt	Hs	Mm	Am	Cb	Ce	Dm	Bf	Pi
Protein										
Rabenosyn-5	59	59	59	59	59	92	98	32	62	-
PIK-D	-	-	-	-	-	-	-	-	-	129

Key: Rn (*Rattus norvegicus*), Bt (*Bos taurus*), Hs (*Homo sapiens*), Mm (*Mus musculus*), Am (*Ailuropoda melanoleuca*), Cb (*Caenorhabditis briggsae*), Ce (*Caenorhabditis elegance*), Dm (*Drosophila melanogaster*) Bf (*Branchiostoma floridae*), Rn (*Rattus norvegicus*) and Pi (*Pichia pastoris*).