

P.parasit MSTE-----EVVA-----VEEQEIPDVIERLPKPKDKAEHEAKISALDGAIK 41
G.sulph MANTT-----SQGPTTQSQAMAVEQKLLTPE--ERQEEIRKLEQKKQ 40
ScBFR1 -----MSSQQHKKFRPDVSVRDKKLDTLNVQLK 28
Endotryp -----MPGALEKPKLSEYSAKISGLVEQRR 25
Paratryp MSRSASAEAVATEPATTVVAEAPRRKPGQKPGWMSIPGGPKPEPDRQAFSAKIREFGDRKR 60
Bodo -----MAAVPAAENRPRTRPGWMMNIPGGPKPEPNDQDFRNKMQLTNTQKT 44
Blechomonas -----MSAASPKEEHQRKRLPPWMSMPGAPPKPDFSAFSGGKMAQLSAEKK 45
T.rangeli MPGK--EIMSG--TADVAVATPAPSRMPWLLTPGGPKPEPNTAEFRAKMAALAEKKR 54
T.cruzi -----MT--STEAADVVAAPSKRMPWPWSMPGGPKPEPNSAAFRAKMSALAEKKR 47
T.grayi -----MPGGPPEPNAAAFRSKMSRLAEKKR 25
T.theileri -----MSAT--PPPAAAAAPTAKKQMPGWMSIPGGPPEPNGAAFRAKMNRLVEERR 49
T.vivax -----M--TSKVQTGAVEARRPPRWMTPGDALPKPNVAEFRAKIAQLAKEKN 46
T.brucei MSK-----TE--TAPEAAPPTERRPQPRWMTAPGAPPRPDVMEHRTKMKALSQEK 50
T.congolense MGGD-----AT--EVVAPAAGPAVRRGLPKWMTGPGAMPKPDFRAFKAKMAELAEKKR 51

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P.parasit KLQARTNVIRAEMDALKTNRGGYGGQIQ-----EAKAKF---- 75
G.sulph ELIQQIVVVQQPSKDELETAVAAQRAIIESALSQKEQKRLLRQKYQKMEETKPEFLAAK 100
ScBFR1 KIDTEIGLIRKQIDQHQV-----NDT----- 49
Endotryp ALLDELKQLQSTVQNDPE-----RQK----- 46
Paratryp ALFDQLKEVQEKLHANGG-----NEA----- 81
Bodo KLFDNLKELQGRAGPRDD-----TEREA----- 67
Blechomonas KLFEEIKRLQNSIRGDTG-----NEA----- 66
T.rangeli TLLTEVRQLRASLGPREG-----REA----- 75
T.cruzi ALLNEVKQLRASLGPREG-----REE----- 68
T.grayi ALFTEVKQLRASLGPREG-----REE----- 46
T.theileri ALLAEVKTLRASLGPREG-----QEA----- 70
T.vivax TLFDKIKELRATLEPRDE----- 64
T.brucei ALIAQIKELRASLGPKSE----- 68
T.congolense SLIAQVKGLRASIGPKGD----- 69

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P.parasit -----AALRAEKDNLFQ-----QRNQITARLRQTRDEKDISTIKQQR 111
G.sulph AAYEEQVTLRLKREERKQLMGKIQETRKLMDAQQD-----NKSNNISTGNAALD 151
ScBFR1 -----TQOERKKLQDKNKEIIKI--QADLKTRRSNIHDSIKQLDAQIKRKNNQIE 97
Endotryp -----CIAERNAFGEELNEIDACRQVRELRAVQNAKIAKLRKSRTVTEKLRVSVQ 97
Paratryp -----IAVERQALRDRLGELEKERRGQRDVLTAKNEEIAALRKQREIQDKQKELS 132
Bodo -----VMGERQELRRRMNEIDANRKKERDARSTKNEEISRIRRRQSDIEGKLELS 118
Blechomonas -----LDEERKALRQRMGEIEAQRSAMRDLRVGKSEEISKFRKKRQETADKLRVLQ 117
T.rangeli -----TDNELAELRQMSDIDARRKMEQEMRFKKNEEIQRVQKLHDERQSRLRELS 126
T.cruzi -----SGKELDGLRQRMGEIDNQRKVEQEMRFKKNEEIQRIQKLHDERVSRRLRELS 119
T.grayi -----QENELGELRQRMGEIDTQRKAEQEMRFKKNEEIQKIQKVHEERLSKLELS 97
T.theileri -----VEAELSELRQRMGEIDTQRKAEQEMRFKKNEEIQKIQKIHDERLNKLHEL 121
T.vivax -----NDKEREELRERIKELDNKKKLENDLRKKKSDEIQKVKVQEEQLKKLREL 115
T.brucei -----PDKERDEIRQLKELDDKRKAEQEMRSKKSSEIIEVRRKKHDEYVKKLRL 119
T.congolense -----NGKERDELFRIKSIEEMRKAQEMRSKKSSELNEAKKHNENARKLREL 120

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P.parasit -SVRANLKYGSVAEFDAAIAELKHKQETSSMSLNEEKRVIKEIEQLQAQKQQ-VSGFSDD 169
G.sulph EK--LKNFKNLEQLDKHISLERRQATESLSLTHEEKLVSEISLLKNKGRAFLNMOKL 208
ScBFR1 EKLKAKAFSSSTAEAKQRINEIEESIAGDLSLVQEKLLVKEMQSLNKLKID-LVNIEPI 156
Endotryp AE--VGGFTTLKEIDEAIDHMMRKMETS GGGLVAERRNQHLQKLEEAKMH-LQKLQPL 153
Paratryp TE--LGGFKTVQEIDEAIDYIMLKMETS GGGLSSEKKTAKRLHQLGEAKNL-LLQLQPL 188
Bodo NE--LGAFRELSDIEMAIDHIMVRMETS GGGLASEKKAIKRLSQLEEAKSL-LLQLQPL 174
Blechomonas AE--LGGFTDIAEIDTAIEFVMRKMETS GGGLAAEKRTIKRLLQLEEVKSL-LLQLQPL 173
T.rangeli ED--LGGFTTLKEIDNAIALITRKMETS GGGLAAEKRTVRQLSKLEEAKRY-LVELQPL 182
T.cruzi DD--LGGFTTIKIDDAIAFVTRRMETS GGGLGAEKRAVRQLSKLEEAKRY-LVELQPL 175
T.grayi DE--LGGFKSLKEIDGAIIDYLTRKMETS GGGLAAEKRAVRQLNKL EAKRY-LLELQPI 153
T.theileri DG--LGGFKTLKEIDEAIAYLTRKMETS GGGLAAEKRTVRQLSKLEEAKRY-LLEMQPL 177
T.vivax TE--LSGFKSVEEIDEAIAIYMTKKMETS GGGLAAEKRMRLRQLSQLEDAKRY-LQELQPV 171
T.brucei DD--LGGFKSVEEFDEAIEYMTKKMETS GGGLAAEKRMRLRQLSQLEDAKRY-LQELQPV 175
T.congolense EE--LAGFKSVEEIDRAIVYMTKKMETS GGGLAAEKRMRLRQLSQLEDAKRY-LQELQPL 176

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P.parasit QGVVEKQNE-SIKEIRALQT---KKNEEIDAIQEKLEQKQALDELYRL-----NEEENK 220
G.sulph EAERKSSQEERKKELEKLFEEKKSLETKINETSKELERLKQSKDDIRTK-----QEISIA 263
ScBFR1 RKSVD---DA-DKAKINQLKEELNGLNPKD---VSNQFEENQQKLNDIHSKTQGVYDKRQTL 210
Endotryp TEAI---KE-ITEEEVILQOQYLAICEKIGILNGEYEEKQKNAKH-----KEAQED 202
Paratryp DEAL---SE-FEERFGLQOQYREIHERIGVINKEYEVQNDVRRK-----ISDN 233
Bodo QEAI---TD-ADDREASLQOQYREIHERIGALNKDYDEQYTVKQSKD-----KEAQKT 223
Blechomonas TEAI---QE-AGDREVMLOQEHREIHERIGALNKKYEEELHTKQATE-----KNLHTT 222
T.rangeli TEAI---TE-AKHREAMLQREWQEIHDRIRSLWSEYNEQRATKQOKE-----QEIRIT 231
T.cruzi TEAI---TE-AKHREAMLQREWQEIINERIRNLRAEYNEQRATKQOKE-----QEIRSS 224
T.grayi TEAI---TE-AKHREAMLQREWQEIINERIRNLGTEYNEQRSMKQORE-----QEMHST 202
T.theileri TEAI---TE-AKHREALLOREWQEIINERVRNLKSEYNEQRMTKQOKE-----QELRKT 226
T.vivax NEAI---AE-AKHREALLOKEFDEINERIRGLTTACNEQRSTKMEKD-----QLVRGK 220
T.brucei SEAI---AE-AKHCEATLQREIQEINERIRGLNEEYKQQRSTKMEKD-----DKMRST 224
T.congolense SEAV---DE-AKHHEATLLRELQEIINERIRDLNSKYKDQRSVKMQKD-----EEIRSA 225

P.parasit KDKFPALAKERKEIKEQLDEKFTAIAKTLRKEFKAEANDKYNNIRLVRKKKELERQKEEEA 280
G.sulph KISEELSEVNLDDIQKRIDAANEEIRRLRQDFNQKLNKWNKYKRSSE-----LDRLN 316
ScBFR1 FNKRAALYKRRDELYSQIRQI-----RADFDNEFKSFRAKLDKER-----LKREEEQ 257
Endotryp GAHRAEVYKCDALRVRIAIEISQTVESLRAERDRLSSEWHAWSREARTKYAQLQORREQ 262
Paratryp IVDKPKPLFERRDLIRKELDAVSVMETLRAAHRQAEAWDKWRVEAQAKYAAKIKAEERE 293
Bodo SVDRTVLIKERDDLQKITKLNEMTKLREGFNTEKESWEAWREEAIKKYGEKMEAEERKE 283
Blechomonas FQQRTSVYKQCDELREKINKLNEMDTRASHNDVQKWTWCAEAREKYTAKMETERQE 282
T.rangeli GVNRSVYKCCIEISAKINKLSEEMNRMREEHNKAMEAWNAWREEARAKYLAKMEAEERKE 291
T.cruzi GVNRAEIVYKCCIEINGKITKLSGEMDRLREEHNKAMEAWNTWREEARAKYIAKMEAEERKE 284
T.grayi GANRAEVYKCDASAKINKLNEMNTLREEHNKALEAWNAWREEARTKYAAKVEAEERKE 262
T.theileri GVNROEVYKCCIEISAKIKLSDEMNTLREEHNKAVEAWNAWREEARAKYAAKVEAEERKE 286
T.vivax GASRQEVYAKCSELHAKITGIVEKMNTLREEHNSKAMEAWNAWRFAFAKHQAKMEEIRKE 280
T.brucei GANROEVFKCCIEISAKITSITKEMNALSDFQKAMEVWKSWCDEARAKHMAKMEEVKKE 284
T.congolense GANROEVFKCCIEINANIAKIAQEMNSLSEAHQKAMEKWNAWCDEARAKHIAKMEEIQKD 285

P.parasit RKAEY--E-----AKL--ADYEKEMAKIHPYQDEMDCDALVSFLEKTYAKELKEEQDE 330
G.sulph RHLRFQYRQYQDLKRVKEKEKELAEYGTDPPEEKKAMCDNLIQ-----YLQRLSKIDVD 371
ScBFR1 RLSKLLQKDV--DMGKL--QEKLTHAKI--PAFTYEIGAIENSLVLDPTYVVKPKKNILPD 313
Endotryp RRKEYEEIRN---AHKI--AAKRERAAKRONPYVTEISACATLIQ-----YLKQKVMLEQ 313
Paratryp KLRRYLERRD---ASKL--AEKRERAMKRMNRYASEIASCITLVQ-----YLRDKRMSQR 344
Bodo RERRRNEYMN---AEKI--ARKQARATKRQNPHEQTQIGACSTLVR-----YLRDRIVMSQR 334
Blechomonas RYKRELERHT---NAKL--TEKLNRAQRRRNRYEMEISACDTLSQ-----YLIDKXHMVTR 333
T.rangeli RQRRYLERN---AAKL--EEKRARALRRQNPYEVEIEACKTLLR-----YVQDHKVMVQR 342
T.cruzi RRRRYLERKN---AAKI--AEKRARALRRQNPYEVEIEADCKTLLR-----YMQDQKVMVQR 335
T.grayi RHLRYLERKN---AAKL--EEKRARAMRRQNPYEAEVDACSLLVR-----YLRDHKMMVQR 313
T.theileri RQRRYLEYKN---AAKM--EEKRARALRRQNPYEAEADACSTLVR-----YLRDKKAMVQR 337
T.vivax RERRIHEKNN---AAKL--EEKRARALRRMNPYEVEIAACDTLIQ-----YLRQKVMVQR 331
T.brucei RHRRFLERKN---APKL--AEKRERALRRMNPYEVEIAACDTLLQ-----YLRDQKIMVQR 335
T.congolense RQRRIMERKN---AAKL--EEKRARALRRMNPYEVELAACDTLLR-----YLGEQKIMVQR 336

P.parasit K-----AAETTAAPLE-LDGMKPLQKKEEDFMMLGGGKKGK--KGRNGK----- 371
G.sulph ENKKTKKDVQNI-----LNGAKLIGKNASFFEAEPNTNVSKG----- 409
ScBFR1 LS-----SN-ALETKPARKVVADDLVLVTPKKDDFVNVPASKSKKYK--KNQOKN----- 361
Endotryp EEQERKKREAAAHFDPSQTA-PAGCVVLNDSKWADNKTPYKSTTKLPKQKQKQEKIPQA 372
Paratryp EEEERVKCEAAAKFDPARAA-PSGFVMLGEDKWSSPHSAPKKGK----KQSAKA--PSA 397
Bodo DEEERKRRVAMASFDPASA-PSGFALAAPIELPKKSKAA----- 374
Blechomonas EEEERVKREAAATFDPAKAV-PAGCVVLNDEKKGW--NAKPAPKAS----KKQOQT-NTAP 386
T.rangeli EEAEELARKQAAAFDPSKFL-PEGAVLLNDGKKFSDSRKGGAGGK----HKAQOT----Q 393
T.cruzi EEVELARKRAAATFDPTNFL-PEGAVLLNDGKKFSEPHKAAPGGK----SKTKQN----Q 386
T.grayi EEEELARKNAAATFDPTKFL-PEGAVLLNDGKKWTEPHKAAVGGK----KNKQQQKQQQQ 368
T.theileri EEEELARQEAATFDPTKFL-PEGAVLLNDGKKRTDANKGGALGK----KNKQQQ----Q 388
T.vivax EEEERIKKEAVANFDPAKFA-PSGAVILNDGKNWGDHAKGAVGGK----NKQR-----P 380
T.brucei ENEERARREAAANFDPAEFA-PEGAVLLNDGMSHQNG---GDSKK----QKQQ-----A 381
T.congolense ENEERAKREAAAFDPTKFA-PEGAVLLNDGKGAGEG---KSQKS----QH-T-----K 381

P.parasit	-----KTKKASKLVLP-----AQMFAFSTIGLLPPASAAAVSESLAAVKTKKV	415
G.sulph	RKTTRKGAADSTFSKAVDSEKLPPHNMEYFLAFQKLNVPPVYVKDILGTIELLKERKS	469
ScBFR1	----TENEQPASIFNKVDGKFTLEP---TLIATLAELDVTVPINSDDVKITVEQLKKKHE	414
Endotryp	KAGTTLSDQKERPLHHTDEK-----IRLFRIIEIEPTRSRVAIDSTISEIESAKK	422
Paratryp	KTTEAPVATKDRVLQHSEEK-----QQMFQAVRVDPPALSAIDAAIKAIEERRK	447
Bodo	---PKAEDKTERTVTHNDEK-----KRLFASVGISAPATLSEVEKTIEQLKKKQA	421
Blechomonas	PVTAARKVDSTRMLQHPEEK-----MKLFHLIDLEPPITITAFDSTIQAIKAKRK	436
T.rangeli	KQKPEK-APKNRVLQHPEDK-----IRLFQLVNEELPVALAAIDETMERLRKQK	442
T.cruzi	KQKSESAPPKNRVLQHPEDK-----IRLFQLINEEPPVALSAIDGAMETIRSKQK	436
T.grayi	QQKQKTEPKNRVLQHGE EK-----IRLFQLIGEEPPLALAAIDDAVKRISAKQK	418
T.theileri	QQKPKAGTAKNRVLQHSEDK-----IRLFQLINEEPPALAAIDASVERIRAKQV	438
T.vivax	TSKKESGASKAVSIKHGE EK-----VELFTLIGEEPVKVDDIDTLLTKITEKRK	430
T.brucei	NKAKRDSAPKPRVIKHSE EK-----LELFKLVDEQPPRFLEDIGGIMENIRAKLK	431
T.congolense	KVNGTESAAKSGVIKHSDEK-----VKLFKLVSEEPQSVGDIDGVMESLRTKQQ	431

P.parasit	WFNEQTSRPK-----AGKVVEPAEEAAP-----AKVVSPPKKSSKNNKFN	455
G.sulph	YYENAPE-----KVDLEATEEEDLS-----TLLPKSDSDNVI	501
ScBFR1	ELLSKQEEQTKQNI ESVEKEIEKLNLDYSNKEQQV--KKELEE-KRLKE-----QEE S	464
Endotryp	KYESHIQ-----TGELVLSSGDEEEDDEENTVNDDEVPSELAPADAQGVV	467
Paratryp	VMETHIV-----TGEPVLSDDENEENAEETNSPVA-----NGDE	483
Bodo	EYESHIK-----TGDLVLSDDDEEEEEKEEAAPADE-----	451
Blechomonas	EYESHIT-----TGDIVLSSSESDGEGETHPEDSNLAEPDAAPA-----	474
T.rangeli	EYESHIK-----VGELELSSDDEEDEEAQEEEG--AAEATEE---E-AP	480
T.cruzi	EYESHIK-----TGELELSSDDEEEEEEQPQEEETAAAATE---E-VQ	476
T.grayi	EYESHIK-----TGDLLELSSDDEEEEEQEEPPQPQEEKGEEQEV--VDGAK	461
T.theileri	EYESHKK-----TGELELSSDDDEEEEEENVEQEQKEEQNQGDDEEQED	483
T.vivax	EYASHIK-----VGELELSSDDDEQEHQPQEEFEAEVEDAVESSKEKGEK	475
T.brucei	EYSSHIK-----TGPELSSDDEEDEEKKEQEGEEAVA-----KEDE	469
T.congolense	EYASHIK-----TGPELSSDDEEEQEQEQEQEQEQEQEN-----EGAA	469

P.parasit	ASDKDAFP SLGVAALPSWGPMPAPAVAEPAVAEEFAEAD---VVTESE-	502
G.sulph	VEDREDFPDG-----LPIVSN GYS-YRAQQGSKPSFAEVMQHS SLTDSVD	545
ScBFR1	EKDK-----EN-----	470
Endotryp	VDDA-----KKDIAE-----	477
Paratryp	KEEA---EEA-----APVLA AA-----	497
Bodo	-----	451
Blechomonas	EHNE---EP-----VPEVTAE-----	487
T.rangeli	KEAD---DV-----EE-VTAGAAEAVTQSGQEEATV-----	507
T.cruzi	KKKD---EV-----EKEVTADKIGLVTQ---NEETVEA-----	503
T.grayi	TESQ---LE-----ESEVKADE-----	475
T.theileri	KE-----	485
T.vivax	EE EK---EG-----EEKKDEERAE-----	491
T.brucei	TNEG---EG-----EDFA-----	479
T.congolense	EEEG---DT-----N-----	476

Abbreviation

Species

Gene ID

P.parasit	<i>Phytophthora parasitica</i>	ETI45734
G.sulph	<i>Galderia sulphararia</i>	XP_005709255
ScBFR1	<i>Saccharomyces cerevisiae</i>	BFR1
Endotryp	<i>Endotrypanum moterogeii</i>	EMOLV88_320005100
Paratryp	<i>Paratrypanosoma confusum</i>	PCON_0018750
Bodo	<i>Bodo saltans</i>	BSAL_12610
Blechomonas	<i>Blechomonas ayalai</i>	rna_Baya_154_0090
T.rangeli	<i>Trypanosoma rangeli</i>	TRSC58_05341
T.cruzi	<i>Trypanosoma cruzi</i>	TcCLB.506525.10
T.grayi	<i>Trypanosoma grayi</i>	DQ04_02291030
T.theileri	<i>Trypanosoma theileri</i>	TM35_000033410
T.vivax	<i>Trypanosoma vivax</i>	TvY486_1013600
T.brucei	<i>Trypanosoma brucei</i>	Tb927.10.14150
T.congolense	<i>Trypanosoma congolense</i>	TcIL3000_10_12030

