

Supplemental Figure S1. Multi-sequence alignment of the ODC amino acid

sequences.	
L.donovani	MGDHDVALCHVSRYNHANYWAFVPLPTVSDDTGCDLSLHSDSASKRIRMAPPASASKAGAA
L.major	MGDHDVALCQVSHYNHANYWDFVPLPTVDDTGCDLSLHSDSERIRMAPPPSASKAGAA
L.braziliensis	-----MMTMVPPVSVLVDVDAV
T.brucei	-----
M.musculus	-----
H.sapiens	-----
L.donovani	EERLHPYERRLLDQYQIHLQPANRNPLSRADSAGREETAQ-----T
L.major	EERLPPCERRLLDQYHIHLQPANRNPLSRADSAGRKEAAE-----T
L.braziliensis	PDRLHTCKRRLLEQYHIDRSRITLNLPLSRANTTAGRNEAAQLSDVDAQQPILPTECNKQT
T.brucei	-----
M.musculus	-----
H.sapiens	-----
L.donovani	PAQVQMVSGVAVADSTSDQHASVASSQDLVDLFFLEGSQAVDGLCFSPYPIYGWRTAEER
L.major	PAQVQMMACVAAADSTADQHPAVAATQDLVDLFFLEGSQAVDGLCFSPYPIYGWRTAEER
L.braziliensis	PEYVQEVALGAAADSTVNQHTAVAASQDIVDLFFLEGSQAVNGLCFSPYPTYGWRTAEER
T.brucei	-----
M.musculus	-----
H.sapiens	-----
L.donovani	RAAVCEVFKTYNVVTRLPASPAALAAARRRYSRRHSIAIPINKSAETREQYWRRLSNL
L.major	RAAVCEVFKAYNVVTRLPASPAALAAARRRDSRHQSIAIPINKSVETREQYWRRLSNL
L.braziliensis	RAATYAVFKKYNVATHLPASPAALATAQHSHSHHQHASIHAINKMAETREQYWRRLSNV
T.brucei	-----MDHVVDNL-----SCR
M.musculus	-----MSSFTKDEF-----DCH
H.sapiens	-----MNNFGNDEF-----DCH
L.donovani	YIQKGVKDAASADAATAATTATNGAVPAAPAYEPEDPFYIIDLGRVVEQMARWRHELMVR
L.major	YIQKGVKDAASADAATAATTATNGAVPAAPAYEPEDPFYIIDLGRVVEQMARWRHELMVR
L.braziliensis	YIEKGVKAAAATA-AATTTFTNCTISGVPRHEPEDPFYIIDLGRVVEQMARWRHELMVR
T.brucei	FL-EGFN-----TRDALCKKIS-MNTCDEGDPFFVADLGDIVRKHEWKKCLPRVT
M.musculus	ILDEGFT-----AKDILDQKINEVSSSSDDKDAFYVADLGDILKKHLRLNLKALPRVT
H.sapiens	FLDEGFT-----AKDILDQKINEVSSSSDDKDAFYVADLGDILKKHLRLNLKALPRVT
L.donovani	PYFAVKSNPQPAVLEVLGALGAGFDCASKEEIHMLVGLHQLVASPDDIIFANPCKQLGDLR
L.major	PYFAVKSNPQPAVLEVLGALGAGFDCASKEEIHMLVGLRHVLVASPDDIIFANPCKQLGDLR
L.braziliensis	PYFAVKSNPQALALEVLGALGSGFDCASKEEITVLVDNLHVLVASPDDIIFANPCKQPGDMR
T.brucei	PFYAVKCNDDWRVLGTLAALGAGFDCASNTQIRVRG--GVPFERKIYANPCKQNSHIR
M.musculus	PFYAVKCNDSRAHVTLLAALGAGFDCASRTEIQVLQGL--GVPAERVIYANPCKQVSGIK
H.sapiens	PFYAVKCNDSKATVKTLLAALGAGFDCASRTEIQVLQVSL--GVPFERVIYANPCKQVSGIK
L.donovani	EAQACGVTVTVTDNPLEMERISRLMPSAHAIIRIKTNDSKAOCSPSTKFGAPLEDVEGLL
L.major	EAQACGVTVTVTDNPLEMERISRLMPSAHVIRIKTNDSKAOCSPSTKFGAPLEDVDGLL
L.braziliensis	EAQARGVTYTVTDNLLTEKISRLMPSARAVIRIKTNDSKAKAFSPKFCVPLNDVESLL
T.brucei	YARDSGVDVMTFDCVDETEKVAETHPKAKMLVRISTDLSLARCRLSVKFGAKVEDCRFIL
M.musculus	YAAANGVQVMTTFDSEIELMKVRAHHPKAKLVLRITATDSDKAVCRLSVKFGATLRTSRLLL
H.sapiens	YAAANGVQVMTTFDSEVELMKVRAHHPKAKLVLRITATDSDKAVCRLSVKFGATLRTSRLLL
L.donovani	EAAKRFNVTVVCGVSFHVGSQNDQSAVVSAVRDAYHVFQQAQVYGFCKTLLDIGGGFPGT
L.major	KVARQLNVAVCGVSFHVGSQNDQSAVLSAVRDAYHVFQQAQVYGFCKTLLDIGGGFPGT
L.braziliensis	QAAKRFKVDVVGVSFHVGSQNDPATVVSAVRDAYHVFQQAQVYGFNCTLLDIGGFPFV
T.brucei	EOAKKLNLDVVGVSFHVGSQNDASTFAQAISDSRFVDMGTGLFNMHLLDIGGGFPGT
M.musculus	ERAKELNLDVVGVSFHVGSQNDPETFVQAISDARCVDMGAEVGFSMYLLDIGGGFPGS
H.sapiens	ERAKELNLDVVGVSFHVGSQNDPETFVQAISDARCVDMGAEVGFSMYLLDIGGGFPGS
L.donovani	EVVEGSGNTSFETARTIRPVLAEELFGG-GDVTTIIEPGRYFTAASHALLMNVFASRTLRL
L.major	EVVQSGSGNTSFETARTIRPVLAEELFGG-GDVTTIIEPGRYFTAASHALLMNVFASRTLRL
L.braziliensis	ETNTASGEATFEDTARIRPVLAEELFGG-GDVTTIIEPGRYFTAASHALLMNVFASRKLRL
T.brucei	RDA---PLKFEETAGVNNALDKHFFPDLLKTIIVAEPRGYVASAFTLAVNVIKAKTVTP
M.musculus	EDT---KLKFEETITGVNIPALDKYFPDSGSGVRIIAEPGRYVASAFTLAVNIIAKKTVW
H.sapiens	EDV---KLKFEETITGVNIPALDKYFPDSGSGVRIIAEPGRYVASAFTLAVNIIAKKIVL
L.donovani	LSDVEV-SRQAFQSVVSMDEPEEYOYYVNDGVLHSPNCILYDHAHPTLLLLNDGDGADGV
L.major	LSDVEV-SRQAFQSVVSMDEPEEYOYYVNDGVLHSPNCILYDHAHPTLLLLNDGDGADGV
L.braziliensis	MSDVEKASSQALQSVVPMDEPEEYOYYVNDGVLHSPNCILYDHAHPTLLLLNDGDGADGV
T.brucei	GVGTQDVG-----AHAESNAQSFMYVNDGVYGSFNCILYDHAHVRLPLQRE-----
M.musculus	KEQPGSD-----DEDESNEQTFMYVNDGVYGSFNCILYDHAHVRLKQKR-----
H.sapiens	KEQTQSD-----DEDESSEQTFMYVNDGVYGSFNCILYDHAHVRLKQKR-----
L.donovani	ESGTEAAAVCSEEEGETSLSGPLANDPLFMSAWDRRRSFARRPLRITITFGPTCDSDMDCI
L.major	KSGTAAAVCSEEEGGMSLGLVNDPLFVSAWDRRRSFARRPLRMTITFGPTCDSDMDCI
L.braziliensis	EGNKE-----EGETSL-----SRTRELRITITFGPTCDSLDCI
T.brucei	-----PIPNKELYPSSVWGPTCDGLDOI
M.musculus	-----PKPDEKYYSSSIWGPTCDGLDRI
H.sapiens	-----PKPDEKYYSSSIWGPTCDGLDRI
L.donovani	LKKQFFPENKLGDWLLVDPDMGSYTTAAAGFFNFGPATRRLEWVSSVDLCARPRPV-----
L.major	LKKQFFPENKLGDWLLVDPDMGSYTTAAAGFFNFGPATRRREWVSSVNLICARPRPV-----
L.braziliensis	LRKQFFPENKLGDWLLVDPDMGSYTTAAAGFFNFGPATRRFEWVSSIAL-----
T.brucei	VERXYLPEMVGWLLFEDMGAYTVVGTSSFFNGFQSPRTIYYVSGLPDHVVRRLKQSKGS-
M.musculus	VERCNLPEMVGWMLLFENMGAYTVAAASTFNCFORPNIIYYVSGPWLQMLKQIQSGGFP
H.sapiens	VERCDLPEMVGWMLLFENMGAYTVAAASTFNCFORPTIYYVSGPAWQLMQQFQNPDPF
L.donovani	---YTREGN---TLRCVSE-----
L.major	---YTREGN---TLRCMSE-----
L.braziliensis	---
T.brucei	---
M.musculus	PEVEEQDGTLPSCAQESGMDRHPAACASARINV
H.sapiens	PEVEEQDASTLPVSCAWESEGMKRHRACASASINV

Sequences from *L. donovani* BPK282A1 LdBPK_120105.1, *L. major* Friedlin LmjF.12.0280, *L. braziliensis* MHOM/BR/75/M2904 LbrM.12.0300, *T. brucei* brucei TREU927 Tb927.11.13730, *Mus musculus* NP_038642.2, *Homo sapiens* P11926 were aligned using Clustal Omega. Boxshade was utilized to illustrate identical (black), conserved (grey) and divergent residues (white).

Supplemental Figure S2. Multi-sequence alignment of the ADOMETEDC amino acid sequences.

L. donovani	MNVCSNNTKDPPLTLAMAMWGS	MKGYNPEQGF	SFEGPEKRLEVL	RLCTLETH	---VDGLRSL	
L. major	MNVCSNNTKDPPLTLAMAMWGS	MKGYNPEQGF	SFEGPEKRLEVL	RLSTLETH	---VDGLRSL	
L. braziliensis	MNVSLNNTKDPPLTLAMAMWGS	MKRYNPEQGF	SFEGPEKRLEVL	RLCTLETH	---VDGLRSL	
T. brucei	----MSSCKDSL	SLAMAMWGS	IARFDPKHER	SFEGPEKRLEVL	MRVVDGTH---VSGLLAH	
T. cruzi	----MLSNKDP	PLSLAMAMWGS	VKGYPD	NQAS	SFEGPEKRLEVL	MRITDETH---SEGLHAL
M. musculus	-----	MSAAH	FFECTEK	LLEVV	FSRQSD	ASQSGDLRTI
H. sapiens	-----	MSAAH	FFECTEK	LLEVV	FSRQSD	PANQSGDLRTI
L. donovani	DDSVWSGVVGSLNAQIVS	RESNECINYSVLT	ESSLFV	MKNRIL	ILITCGTTTLLNSIPNII	
L. major	DDSVWSGVVGSLNAQIVS	RESNEYINSYLT	ESSLFV	MKNRIL	ILITCGTTTLLNSIPNII	
L. braziliensis	DDSVWTRVVGSLNAQIVS	REANEYINSYLT	ESSLFV	MKNRIL	ILITCGTTTLLNSIPNII	
T. brucei	DDDVWQKVIDAICAHIVSR	NEFYIRSYVLS	ESSLFV	MKDRIL	ILITCGTTTLLNCVPLIC	
T. cruzi	GDGVWKGVVGSLNAQIVS	REANEYIRSYVLT	ESSLFV	MKDRIL	ILITCGTTTLLNAVEFVL	
M. musculus	PRSEWDVLLKDVQCS	IISVTKTDKQEA	YVLS	ESSMFVSKRR	FILKTCGTTLLKALVPLL	
H. sapiens	PRSEWDILLKDVQCS	IISVTKTDKQEA	YVLS	ESSMFVSKRR	FILKTCGTTLLKALVPLL	
L. donovani	EAISAVRGELEWV	---SPMHKNYSFP	WQKGPHTSLADE	FATLKQHF	FPCKPPIFGPVDS	
L. major	EAISAVRGELEWV	---SPMHKNYSFP	WQKGPHTSLADE	FATLKQHF	FPCKPPIFGPVDS	
L. braziliensis	EAISAVRGELEWV	---SPMHKNYSFP	WQKGPHTSLADE	CAATLKQHF	FPCKPPIFGPVDS	
T. brucei	EAVSTVCGEVEWV	---SPMHKNYSFP	WQKGPHTSLADE	FATLKQHF	FPCKPPIFGPIDSD	
T. cruzi	EAVSDVRGEVEWV	---SPMHKNYSFP	WQKGPHTSLADE	FATLKQHF	FPCKPPIFGPIDSD	
M. musculus	KLARDYSGFDSIQSF	FYSRKNFMKPS	HQGYPHRN	FQEEIEFL	NAIFNCAAYCMCRMNSD	
H. sapiens	KLARDYSGFDSIQSF	FYSRKNFMKPS	HQGYPHRN	FQEEIEFL	NAIFNCAAYCMCRMNSD	
L. donovani	HYFLFCYDDIIRPC	SEDDTQLSMTMYGLD	KEQTKHW	FSDRFIST	SAETAAIRAATHLDR	
L. major	HYFLFCYDDIIRPC	SEDDTQLSMTMYGLD	KEQTKHW	FSDRFIST	SAETAAIRAATHLDR	
L. braziliensis	HYFLFCYDDIIRPC	SEDDTQLSMTMYGLD	KEQTKHW	FSDRSIST	NAETAIRATHLDR	
T. brucei	HYFLFYDSDVVP	SCSDAQLSMTMYGLD	RNQRKH	WSDRMLPT	GTAVIREATGLSE	
T. cruzi	HYFLFYDSDVVP	SCSDAQLSMTMYGLD	RNQRKH	WSDRMLPT	GTAVIREATGLSE	
M. musculus	CWYLYTLDFPESR	VISOPDQTEIL	MSELDPAVMDQ	FYMKD---	GVTAKDVTRESGIRD	
H. sapiens	CWYLYTLDFPESR	VISOPDQTEIL	MSELDPAVMDQ	FYMKD---	GVTAKDVTRESGIRD	
L. donovani	VVDGVTWLHDLOF	PCGYSINAIR	DEEYQTMHIT	PEDEHCSF	ASYETNSRAANYSDRMKK	
L. major	VVDGVTWLHDLOF	PCGYSINAIR	DEEYQTMHIT	PEDEHCSF	ASYETNSRAANYSDRMKK	
L. braziliensis	VVDNSWTLHDLOF	PCGYSINAIR	DEEYQTMHIT	PEDEHCSF	ASYETNSRAANYSDRMKK	
T. brucei	VVDSDWTLHDLOF	PCGYSINAIR	GSEYQTMHIT	PEDEHCSF	ASYETNTCALNYSKCICG	
T. cruzi	VADDSWTLHDLOF	PCGYSINAIR	GSEYQTMHIT	PEDEHCSF	ASYETNTPAVNYSERINT	
M. musculus	LIPGSVIDATL	FNPCGYSMNGMKS	DGYVWTHIT	PEPEFS	SVSFETNLSQTSYVDLIRK	
H. sapiens	LIPGSVIDATL	FNPCGYSMNGMKS	DGYVWTHIT	PEPEFS	SVSFETNLSQTSYVDLIRK	
L. donovani	VLGVFRPQRF	TVIVFLDP	ESPVGKAYNECK	GIG----	VEPEYYPEYNLLHRTTNEFAP	
L. major	VLGVFRPQRF	TVIVFLDP	ESPVGKAYNECK	GIG----	VEPEYYPEYSLHRTTNEFAP	
L. braziliensis	VLGVFRPQRF	TVIVFLDP	ESPVGKAYNECK	GIG----	VEPEYYPEYRVLHRTTNEFAP	
T. brucei	VLRVFDPERF	SVIVFLDP	DSAVGKSYHSG	CTIG----	VEPEYYPYEAHQHRTVNEFAP	
T. cruzi	VLGVFAPRFR	SVIVFLDP	DSVGRLYQK	CNVG----	VEPEYYPKYLEQNRVTNEFAP	
M. musculus	VVEVFRPCKF	VTTFLVNQSS	SKCRTVLS	SPQKIDG	FKRLDCOSAMFNDYNFVFTS	
H. sapiens	VVEVFRPCKF	VTTFLVNQSS	SKCRTVLS	SPQKIDG	FKRLDCOSAMFNDYNFVFTS	
L. donovani	GYVAMKIN	YVRTAAVEETD	TAUVGGAEP	GAEGGPD		
L. major	GYVAMKIN	YVRTAAVEETD	AAVGAEP	GAKSGPD		
L. braziliensis	GYVAMKIN	YIKTTALQ	EANA	AAV		
T. brucei	GHWLVK	VNVKRAVGT	VTGS	SAASGAKE		
T. cruzi	GYVVMK	MYAMRAE	VAEKD	STD	PVEE	
M. musculus	-----	FAKKQ	QQQQS	-----		
H. sapiens	-----	FAKKQ	QQQQS	-----		

Sequences from *L. donovani* BPK282A1 LdBPK_303150.1, *L. major* Friedlin LmjF.30.3110, *L. braziliensis* MHOM/BR/75/M2903 LBRM2903_300037800, *T. brucei* brucei TREU927 Tb927.6.4410, *T. cruzi* CL TcCL_ESM01038, *Mus musculus* NP_033795.1, *Homo sapiens* NP_001625.2 were aligned using Clustal Omega. Boxshade was utilized to illustrate identical (black), conserved (grey) and divergent residues (white).

Supplemental Figure S3. Multi-sequence alignment of the prozyme amino acid sequences.

L. donovani	-----MSLWGGFNSNPTYSDSGLEKRLEFDFAAAVDVRTFTVEEL
L. major	MPTNSWASSRDVFPESVURALMSLWGGFNSNPTSYSDSGLEKRLEFDFAAAVDVQTFAVEEL
T. brucei	-MSVTRINQQTCEPSSVHDLVSCWGGCTQSKSTDSGLEKRFELNFAQPDIGTGTVKQL
T. cruzi	MLESTWAAAREEVPESVHALMAMWGGFDGPRNANDCGTEKRLELDFRGVIVPSEVSVLDL
L. donovani	EEVLAAAGQRLQEHSSADGLLSLEMTQCIILTPCKLVVTSASEVMLHQVITPTIALLLTS
L. major	EDVLAAGQKRLQEHFSAEGLLSLEMTQCIILTPCKLVVTSASEVMLHQVITPTIALLLTS
T. brucei	ASVMERAGESLRQNSAELGIHTLKFDRLVFTAKQIVVRSSVSVMLHEAVHPMLELMRS
T. cruzi	ESVMSHAGELLERHSAEKGILISLVFGNSLMQLTORHVIIVTSSSSSVLLHEILGPLLDLLRS
L. donovani	KGVRVEWASYLRKNITSPWCAESEMSDIMAQEAELKAAPFAGKSF LTGPVDGHHCFNFV
L. major	KGVRVEWASYLRKNITSPWCAESEMSDIMAQEAELKAAPFAGKSF LTGPVDGHHCFNFV
T. brucei	HNIIVDWASFMRVNYGSPWDMTSETSDIMAHEYAE LKSAFP TGH PYLA GPVDRDHCFYFV
T. cruzi	HGIDIEWASFMRMNTSPWSSLC E M S E I M A Q E Y A Q L K S V F P S G H P Y L T G P L D S D H F F Y F V
L. donovani	YDNVERM--AGRKEEDVQVNVFLYDVAAGL----EEVDKTTORFHALQS GEYEV MR TFA-
L. major	YDNVERI--AGRKEEDVQVNVFLNDVAAGL----EEVNKTTORFHALQS GEYEV MR TFA-
T. brucei	YDGI DRDPSSCRFENDVQINVYMYNVQADDEYDLDGNTKEQQLLVSHCAGEYETLRVSTY
T. cruzi	YDAIERNVLGAPPEDDVQINVYMYNVKTDGSGDDDDALKSVQOVVPLSET EY EMLRVST
L. donovani	--GVPCISFETNAKAAVAS-PTRVQKLLDTFQPAHFTVAALQDRDA DGLALRRNFNSFTP
L. major	--GVPCISFETNAKAAVAS-PTRVQKLLDTFQPTHFTVAALQDRDADESALRCNFNAFTP
T. brucei	GSTHPFASFETNAVSAASDITKIVNGLLKKFYPERVLLVLLQDRDAQGTACGVMDRLEG
T. cruzi	NMAHPFAAFETNSMIAATKKRELVRGLLEKFCPDRFTMVVLQDRCSPLAQKGSIFDEMEG
L. donovani	YTLQNRITVNLFGEGYAFHQLLFARSAD
L. major	YTLQNRITVNLFGEGYAFHQLLFARSAD
T. brucei	FTVVERGANHFHFGG GYVFHQATYARSA-
T. cruzi	YTIMNRATNHFHFGG GYAFHQTSYIRAE-

Sequences from *L. donovani* BPK282A1 LdBPK_303160.1, *L. major* Friedlin LmjF.30.3120, *T. brucei* Lister strain 427 Tb427.06.4470, *T. cruzi* CL Brener Esmeraldo-like TcCLB.509167.110 were aligned using Clustal Omega. Boxshade was utilized to illustrate identical (black), conserved (grey) and divergent residues (white).

Supplemental Figure S4. Multi-sequence alignment of the SPDSYN amino acid

sequences.	
L.donovani	-----MPGGCLLPDGWFREESTMWPGQAQGLKVEKVLVDQPTFQHLTVFESDPFG
L.major	-----MPGGCLLPDGWFREESTMWPGQAQGLKVEKVLVDQPTFQHLTVFESDPFG
L.braziliensis	-----MPGGCLLPDGWFREKSSMWPGQAQGLKVEKVLVDQPTFQHLTVFESDPKG
T.brucei	-----MPGGLLADGWFREENGQWPGQAMSFKEVLELDTPTKFOHLSIFEIDPKG
T.cruzi	-----MPGSELISGGWFRENDQWPGQMSLKEVVKLVLDAPTKEOHLTIFESDPKG
M.musculus	MEFGPDGPAAGGPAAIRGWFRETCSLWPGQALSLQVEQLLHRRRSRYQDILVERSK--
H.sapiens	MEFGPDGPAASGPAIREGWFRETCSLWPGQALSLQVEQLLHRRRSRYQDILVERSK---
L.donovani	PWGTVMTLDGVIQLTDYDEFVYHEMLANLSITCHHKPERVLIIIGGGDGGVVRVLRHKSE
L.major	PWGTVMTLDGAIQLTDYDEFVYHEMLANLSITACHHKPERVLVIIGGGDGGVVRVLRHKSE
L.braziliensis	PWGTVMTLDGAIQLTDYDEFVYHEMLANLSITCHHKPERVLVIIGGGDGGVVRVLRHKSE
T.brucei	PWGTVMLDGCIQLTDYDEFVYHEMLSHTPLCAHPEDVDVLIIGGGDGGVVRVLRHG--
T.cruzi	PWGTVMALDGCIVTDYDEFVYHEVLGHTSLCSHPKPERVLIIGGGDGGVVRVLRHG--
M.musculus	TGYNVLVDGVIQCTERDEFVYQEMTANLPLCSHPNPKRVLIIGGGDGGVVRVLRVHKP--
H.sapiens	TGYNVLVDGVIQCTERDEFVYQEMTANLPLCSHPNPKRVLIIGGGDGGVVRVLRVHKP--
L.donovani	KDGIQVSVELVDIDGAVIQQSKKHFPQIACCFANPCVTATVGDGAAFVKRAPDSVYDVII
L.major	KDGIQVSVELVDIDGAVIQQSKKHFPQVACCFANPCVTATVGDGAAFVRNVPSVYDVII
L.braziliensis	KGIQVSVELVDIDGAVIEQSKRHFPQIACCLANPCVTAMVGDDGVAFGVGNAPDNVDVVI
T.brucei	---TVKRCVLDVIDGQDVIEASKKYPQIISCSFSDPRADVVRGQGVAFVREAASESFVVI
T.cruzi	---TVEHCDLVDIDGVEQSKQHFPQISCSLTDPRATVRVGQGLAFVRQTPDNTYDVVI
M.musculus	---SVESVQCEIDEDVIEVSKKFLPGMAVCFSSSKLTLHVGDGFEMKQNG--DAFDVVI
H.sapiens	---SVESVQCEIDEDVIVSKKFLPGMATCYSSSKLTLHVGDGFEMKQNG--DAFDVVI
L.donovani	IDTTDPKGPASELFGADFYTNVLRILRPGGVVVCNQGESSVWLRHPLIEKMMGFLKKDIGFA
L.major	IDTTDPKGPASELFGADFYTNVLRILRPGGVVVCNQGESSVWLRHPLIEKMMGFLKKDIGFA
L.braziliensis	IDTTDPKGPASELFGAEFYKNVRLILRPGGVVVCNQGESIWLHRPLIEKMMFLKKDIGFT
T.brucei	IDTTDPDGPAAELFGEKFYRDVLRILKPRGICCNQGESVWLNRLNLIQWADFINKVGFA
T.cruzi	IDTTDPAGPASELFGAEFYKDVLRILKPDGICCNQGESIWLDLDLIEKMSRFIR--ETGFA
M.musculus	TDSSDPMGPAESLFKESYQLMKTKALKEDGVLCCQGEQWNLHLDLIEKMRHFCNS--LFP
H.sapiens	TDSSDPMGPAESLFKESYQLMKTKALKEDGVLCCQGEQWNLHLDLIEKMRHFCNS--LFP
L.donovani	TVKXYAMIYIPTPYCGSIGTLVCAKSADTDVTVPMRPVESLG--FADOLKYYISDMHKAAFV
L.major	TVKXYAMIYIPTPYCGSIGTLVCAKSADTDVTVPMRPVESLG--FADOLKYYISDMHKAAFV
L.braziliensis	TVKXYAMIYTPMPYCGSIGTLVCAKSVDTDITVPPRRPVESLG--FADELKYYISDMHRAAFV
T.brucei	TVKXYAMITPTPYCGSIGSLICSKVAGVDVTPQVRRPVESMP--FAGELKYYISDVHKAAFV
T.cruzi	SVQYALMHVPTPYCGSIGTLVCSKKAGVDVTKPLRPVEDMP--FAKDLKYYISDMHKAFA
M.musculus	VVDYAYCSITPTYESGQIGFMFLCSKNPSTNFPQVQOLTQAOVEQOMOLKYYISDMHRAAFV
H.sapiens	VVDYAYCTIPTYESGQIGFMFLCSKNPSTNFPQVQOLTQAOVQOMOLKYYISDVHRAAFV
L.donovani	LPRFAAHLNE---
L.major	LPRFAAHLNE---
L.braziliensis	LPRFAAYLNE---
T.brucei	LPRFAHLNQNSY
T.cruzi	LPRFAHINNSE-
M.musculus	LPFETKALNDIS
H.sapiens	LPFETAKALNDVS

Sequences from *L. donovani* BPK282A1 LdBPK_040570, *L. major* Friedlin LmjF.04.0580, *L. braziliensis* MHOM/BR/75/M2904 LbrM.04.0630, *T. cruzi* Dm28c 2017 BCY84_20019, *Mus musculus* NP_033298.1, *Homo sapiens* NP_003123.2. were aligned using Clustal Omega. Boxshade was utilized to illustrate identical (black), conserved (grey) and divergent residues (white).