

## NudC1 homologs

Angomonas\_desouzai  
Angomonas\_deanei  
Leptomonas\_costaricensis  
Crithidia\_fasciculata  
Leishmania\_braziliensis  
Leishmania\_mexicana  
Trypanosoma\_ralphi  
Trypanosoma\_sp\_TCC878  
Trypanosoma\_crüzi  
Trypanosoma\_lewisi  
Trypanosoma\_brucei  
Trypanosoma\_grayi  
Trypanosoma\_vivax  
Trypanosoma\_sp\_TCC339  
Phytonomas\_serpen  
Herpetomonas\_muscarum  
Angomonas\_deanei  
Endotrypanum\_schaudinni  
Leishmania\_major  
Bodo\_saltaensis  
Bodo\_sp  
ParaBodo\_caudatus  
XP\_008879598.1|Aphanomyces  
ETL31708.1|Phytophthora  
XP\_013233790.1|Eimeria\_tenella  
XP\_002368217.1|Toxoplasma\_gondii  
XP\_003883577.1|Neospora\_cani  
XP\_013436709.1|Eimeria\_necatrix  
XP\_726864.1|Plasmodium\_yoelii  
XP\_008815682.1|Plasmodium\_inui  
XP\_002259979.1|Plasmodium\_knowlesi  
XP\_002141127.1|Cryptosporidium\_muris  
XP\_008882748.1|Hammondia\_hammondi  
NP\_001084961.1|Xenopus\_laevis  
XP\_006270261.2|Alligator\_mississippiensis  
XP\_015264922.1|Gekko\_japonicus  
XP\_003227510.1|Anolis\_carolinensis  
XP\_005421796.1|Geospiza\_fortis  
NP\_058967.1|Rattus\_norvegicus  
NP\_001069075.1|Bos\_taurus  
XP\_006055533.1|Bubalus\_bubalis  
XP\_004478818.1|Dasypus\_novemcinctus  
XP\_013115147.1|Stomoxys\_calcitrans  
XP\_005181854.1|Musca\_domestica  
XP\_014239874.1|Cimex\_lectularius  
NP\_006591.1|Homo\_sapiens  
EFC40417.1|Naegleria\_gruberi  
P17624.1|Aspergillus\_nidulans

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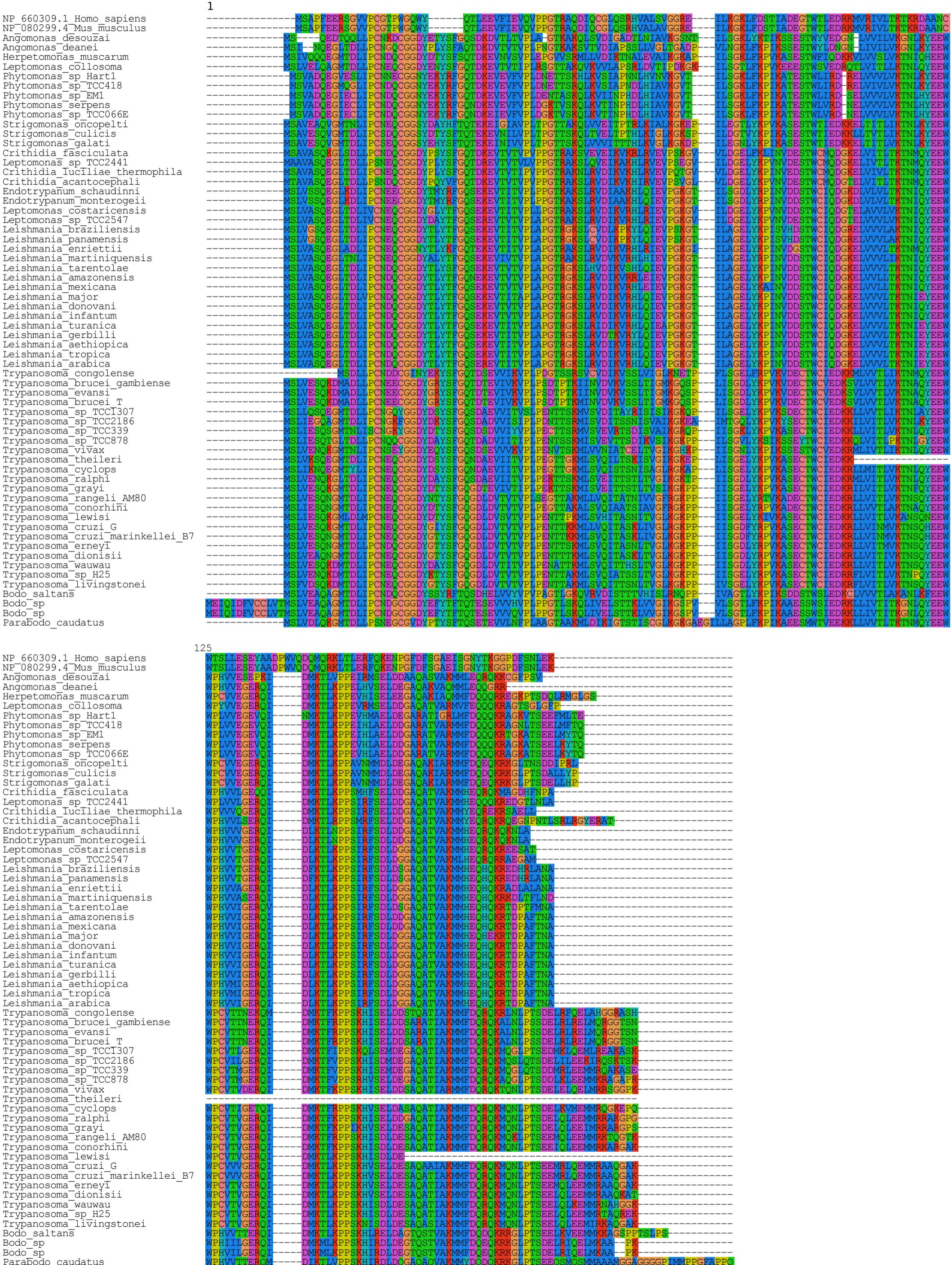
Angomonas\_desouzai  
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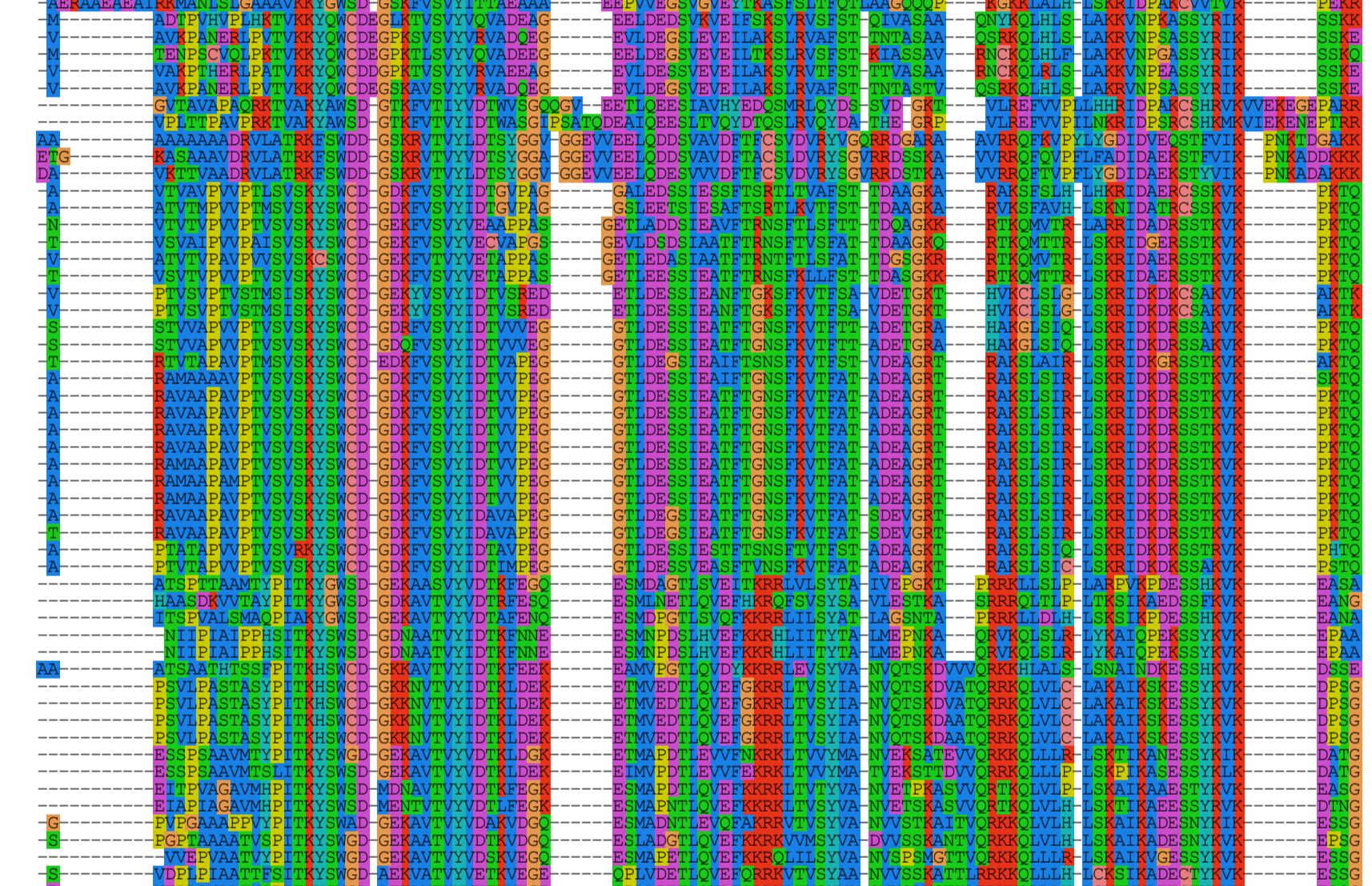
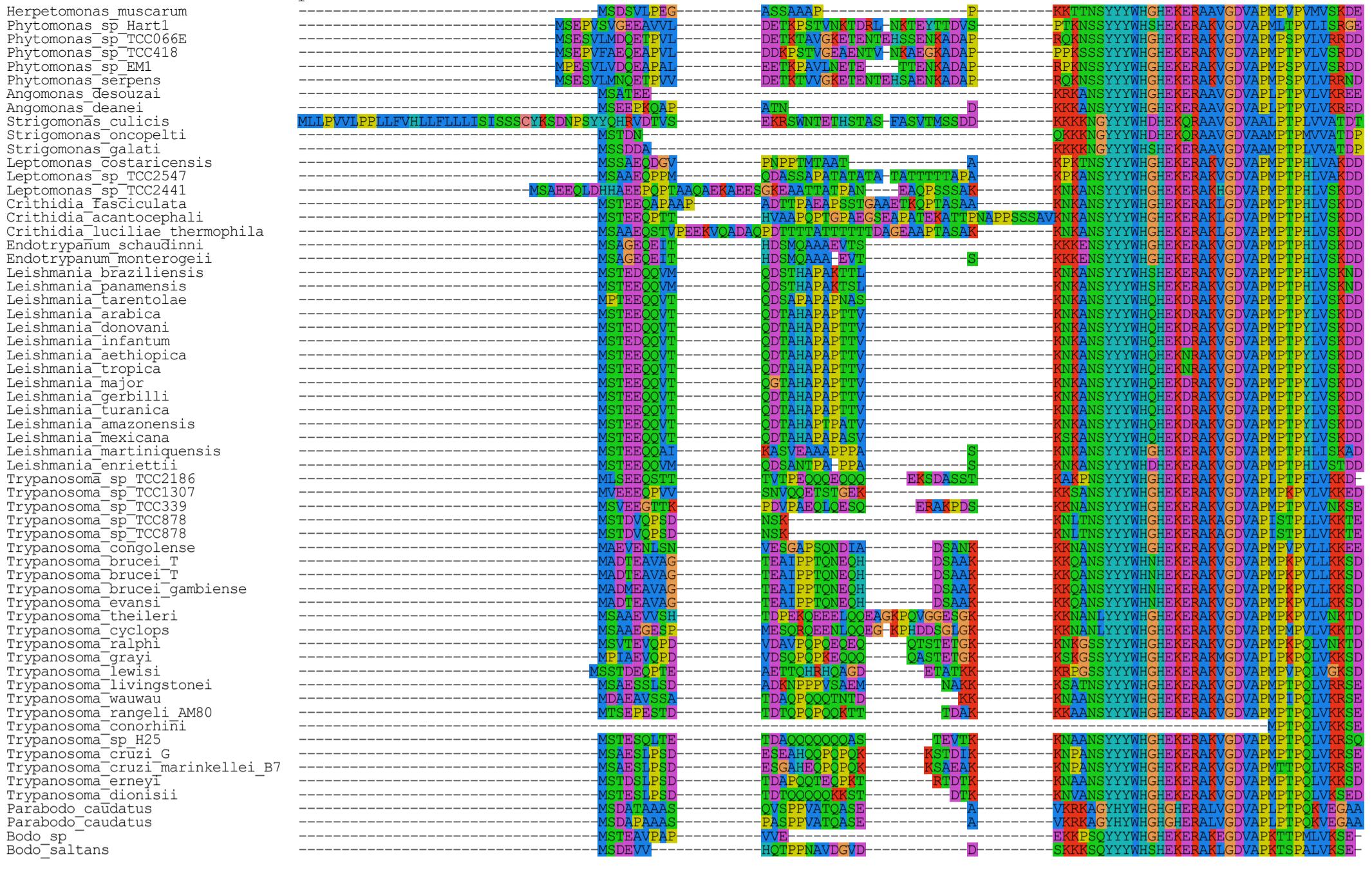
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NP\_006591.1|Homo\_sapiens  
EFC40417.1|Naegleria\_gruberi  
P17624.1|Aspergillus\_nidulans







TrySGT1

Sequence logo showing the conservation of amino acids at each position of the protein sequence. The x-axis represents positions 125 to 200. The y-axis lists 20 organisms. Colored bars indicate the frequency of each amino acid at each position.

Organisms listed on the y-axis:

- NP\_192865.1 *Arabidopsis thaliana*
- Herpetomonas muscarum
- Phytomonas sp TCC418
- Phytomonas sp Hart1
- Phytomonas sp EMI
- Phytomonas serpens
- Phytomonas sp TCC066E
- Angomonas desouzai
- Angomonas deanei
- Strigomonas culicis
- Strigomonas oncopelti
- Strigomonas galati
- Leptomonas costaricensis
- Leptomonas sp TCC2547
- Crithidia fasciculata
- Leptomonas sp TCC2441
- Crithidia luciliae thermophila
- Crithidia acantocephali
- Endotrypanum schaudinni
- Endotrypanum monterogei
- Leishmania tarentolae
- Leishmania braziliensis
- Leishmania panamensis
- Leishmania enriettii
- Leishmania martiniquensis
- Leishmania amazonensis
- Leishmania mexicana
- Leishmania donovani
- Leishmania infantum
- Leishmania gerbilli
- Leishmania arabica
- Leishmania turanica
- Leishmania major
- Leishmania aethiopica
- Leishmania tropica
- Trypanosoma vivax
- Trypanosoma serpentis
- Trypanosoma congolense
- Trypanosoma brucei gambiense
- Trypanosoma brucei T
- Trypanosoma evansi
- Trypanosoma cyclops
- Trypanosoma theileri
- Trypanosoma sp TCC1307
- Trypanosoma sp TCC878
- Trypanosoma sp TCC878
- Trypanosoma ralphi
- Trypanosoma grayi
- Trypanosoma sp TCC2186
- Trypanosoma sp TCC339
- Trypanosoma lewisi
- Trypanosoma livingstonei
- Trypanosoma wauwau
- Trypanosoma sp H25
- Trypanosoma cruzi G
- Trypanosoma cruzi marinkellei B7
- Trypanosoma erneyi
- Trypanosoma dionisii
- Trypanosoma rangeli AM80
- Trypanosoma conorhini
- Bodo sp
- Bodo saltans
- Parabodo caudatus

Position 125: MAEEVAAAKSLFADAKYAECKAYIDTAISSISSENDAASILKEIKLIVMSEIVVNAKOLFAAAANYAOCKSVVEAGIADAST--DAASILKLKLL

Position 200: MMLLSSIMYLLEFSI

The figure displays a multiple sequence alignment of protein sequences from various organisms. The alignment is color-coded to highlight specific motifs and domains. A vertical scale bar on the left indicates positions 1-249, and a horizontal scale bar at the bottom indicates positions M-1000. The sequences are grouped into several color-coded blocks, likely representing different domains or families. The top block is highly conserved, while the bottom block shows more variation.

This figure displays a multiple sequence alignment of protein sequences from various trypanosome and phytomonad species. The sequences are color-coded by residue type, with each column representing a specific position in the amino acid sequence. Conserved regions are highlighted by colored boxes. The alignment shows significant conservation of certain motifs across the different species.

**Trypanosome Species:**

- Trypanosoma congoense
- Trypanosoma brucei gambiense
- Trypanosoma brucei T
- Trypanosoma evansi
- Trypanosoma cyclops
- Trypanosoma theileri
- Trypanosoma sp TCC1307
- Trypanosoma sp TCC878
- Trypanosoma sp TCC878
- Trypanosoma ralphi
- Trypanosoma grayi
- Trypanosoma sp TCC2186
- Trypanosoma sp TCC339
- Trypanosoma lewisi
- Trypanosoma livingstonei
- Trypanosoma wauwau
- Trypanosoma sp H25
- Trypanosoma cruzi G
- Trypanosoma cruzi marinkellei B7
- Trypanosoma erneyi
- Trypanosoma dionisii
- Trypanosoma rangeli AM80
- Trypanosoma conorhini
- Bodo sp
- Bodo saltans
- Parabodo caudatus

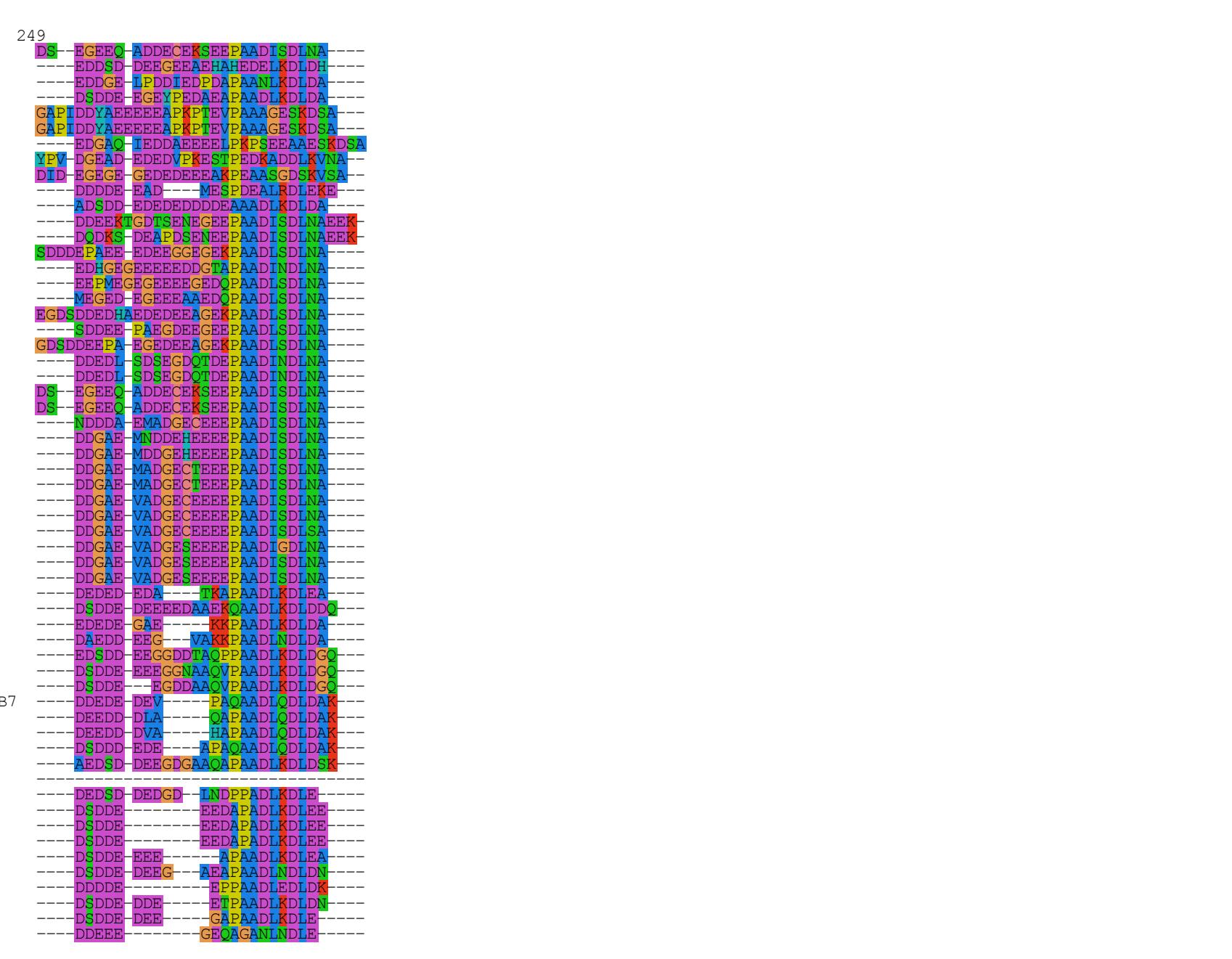
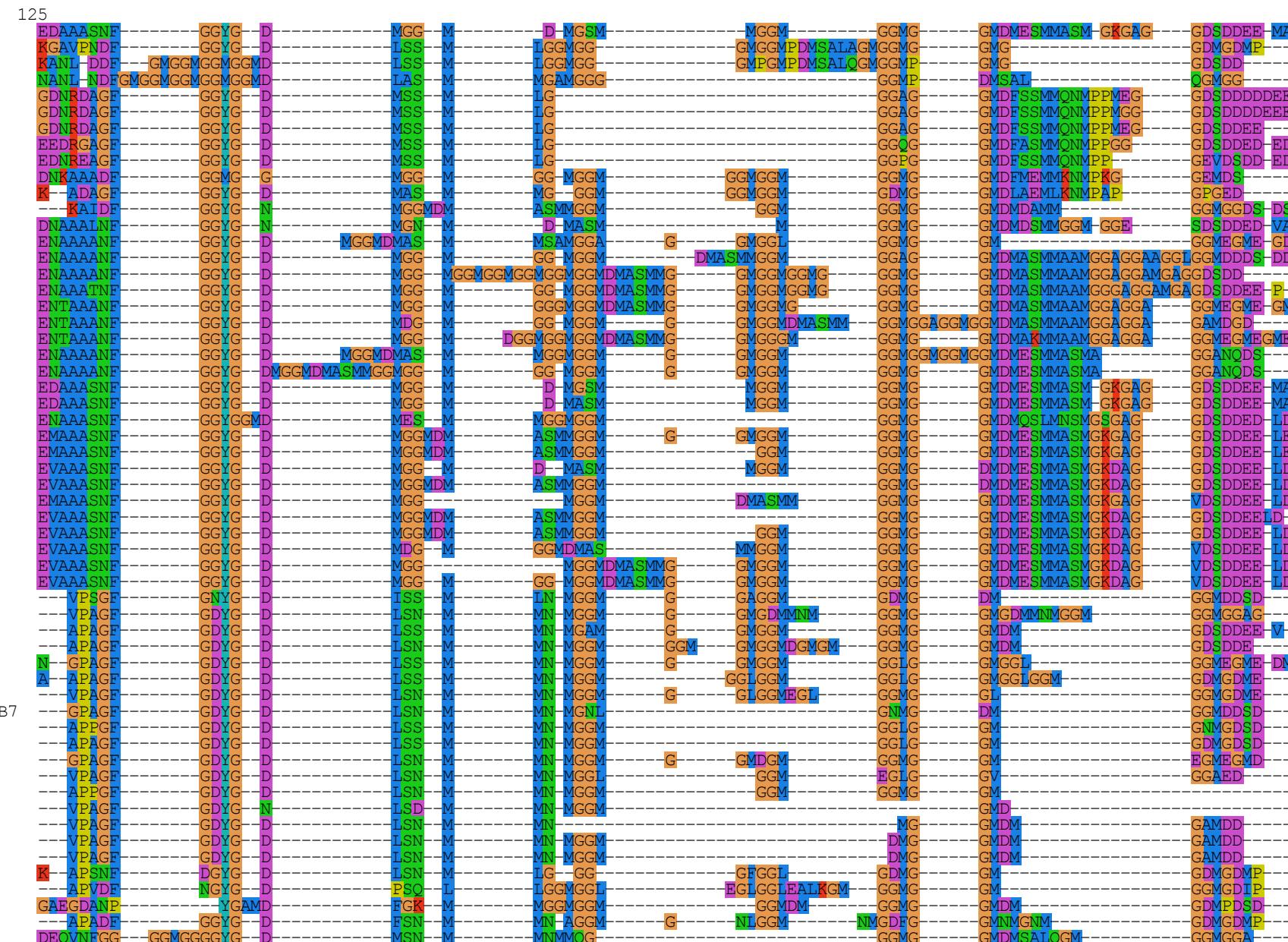
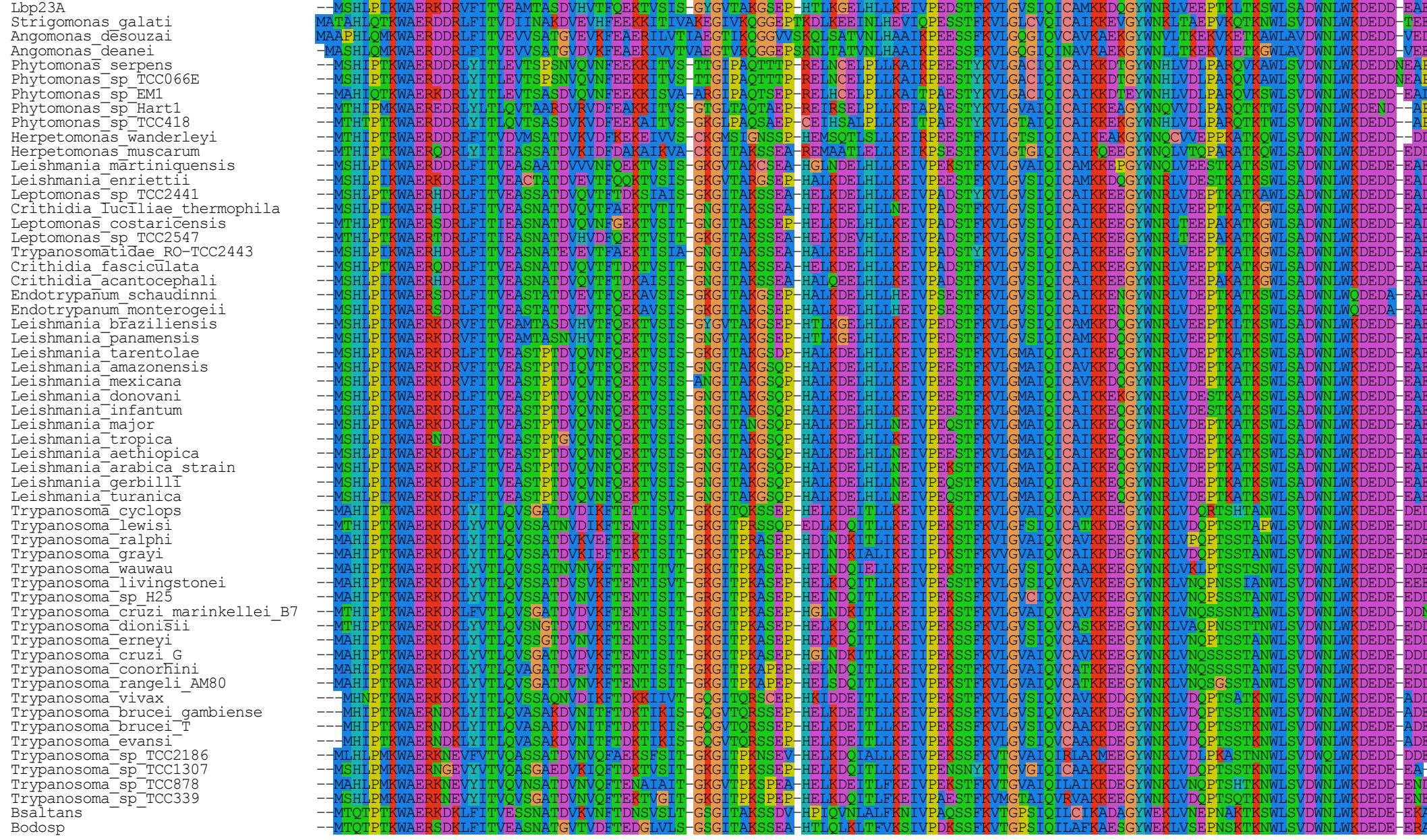
**Phytomonad Species:**

- NP\_001124384.1 Homo sapiens
- NP\_192865.1 Arabidopsis thaliana
- Leptomonas muscarum
- Phytomonas sp TCC418
- Phytomonas sp Hartl
- Phytomonas sp EML
- Phytomonas serpens
- Phytomonas sp TCC066E
- Angomonas desouzai
- Angomonas deanei
- Strigomonas culicis
- Strigomonas oncopelti
- Strigomonas galatii
- Leptomonas costaricensis
- Leptomonas sp TCC2547
- Crithidia fasciculata
- Leptomonas sp TCC2441
- Crithidia luciliae thermophila
- Crithidia acantocephali
- Endotrypanum schaudinni
- Endotrypanum monterogei
- Leishmania tarentolae
- Leishmania braziliensis

The alignment shows a high degree of conservation in several regions, particularly around the N-terminus and in the middle of the sequence, which likely correspond to functional domains. The color coding (green for hydrophobic, blue for polar, red for acidic, yellow for basic) allows for a quick visual assessment of residue types at each position.

Leishmania_infantum	DVKKKKVEAQPPKGMEAKTISE
Leishmania_gerbilli	DVKKKKVEAQPPKGMEAKTISE
Leishmania_arabica	DVKKKKVEAQPPKGMEAKTISE
Leishmania_turanica	DVKKKKVEAQPPKGMEAKTISE
Leishmania_major	DVKKKKVEAQPPKGMEAKTISE
Leishmania_aethiopica	DVKKKKVEAQPPKGMEAKTISE
Leishmania_tropica	DVKKKKVEAQPPKGMEAKTISE
Trypanosoma_vivax	DVGSHYVKTTEPPSGTEAKKMQD
Trypanosoma_serpentis	DVGAREVIMEPPTGMEPRYYTR
Trypanosoma_congolense	DVGKHOVAEPPPSGMEAKKYEG
Trypanosoma_brucei_gambiense	DVGNRHVTTEPPTGMEEKKYEG
Trypanosoma_brucei_T	DVGNRHVTTEPPTGMEEKKYEG
Trypanosoma_evansi	DVGNRHVTTEPPTGMEEKKYEG
Trypanosoma_cyclops	DVGKREVVKMEPPPTGTEPKPYGG
Trypanosoma_theileri	DVGKREVVKMEPPPTGMEPKPYTS
Trypanosoma_sp_TCC1307	DVGKREVVKTEPPKGMEAKGY--
Trypanosoma_sp_TCC878	DVGKREVVKTEAPKGMEPKPYSA
Trypanosoma_sp_TCC878	DVGKREVVKTEAPKGMEPKPYSA
Trypanosoma_ralphi	DVGKREVVKTEPPTGMEAKPYTL
Trypanosoma_grayi	DVGRRREVTAEPPTGMEAKPYID
Trypanosoma_sp_TCC2186	DVGKREVKAEPPTGMEAKPYSE
Trypanosoma_sp_TCC339	DVGKREVVKAEPPPTGMEAKTYTN
Trypanosoma_lewisi	DVGKREVKAEPPTGMEAKPYNM
Trypanosoma_livingstonei	DVGKREVVKTEPPTGMEAKPYGNK
Trypanosoma_wauwau	DVGKREVVKTEPPTGMEAKPYNE
Trypanosoma_sp_H25	DVGKREVVKTEPPTGMEAKPYSD
Trypanosoma_crüzi_G	DVGKREVVKTEPPTGMVAKPYNE
Trypanosoma_cruzi_marinkellei_B7	DVGKREVVKTEPPTGMVAKSYNE
Trypanosoma_erneyi	DVGSRREVVKTEPPTGMVAKPYNE
Trypanosoma_dionisi	DVGKREVVKTEPPTGMVAKPYND
Trypanosoma_rangeli_AM80	DVGKREVVKAEPPPTGMEAKPYN-
Trypanosoma_conorhini	DVGSRREVKAEPPTGMEAKPYN-
Bodo_sp	EVGSKKVEGQPPKGMEAKPYI-
Bodo_saltans	EVGSKKVVGAEAPKGMEAKKYAP
Parabodo_caudatus	DVGKREVVKGEPPKGMEEKWNE

# Tryp23A



Lbp23B  
*Trypanosoma conorhini*  
*Phytomonas\_sp\_EM1*  
*Phytomonas\_serpens*  
*Phytomonas\_sp\_TCC066E*  
*Phytomonas\_sp\_Hart1*  
*Phytomonas\_sp\_TCC418*  
*Herpetomonas\_muscarum*  
*Herpetomonas\_wanderleyi*  
*Endotrypanum\_schaudinii*  
*Endotrypanum\_monterogei*  
*Leishmania\_tarentolae*  
*Leishmania\_braziliensis*  
*Leishmania\_panamensis*  
*Leishmania\_amazonensis*  
*Leishmania\_mexicana*  
*Leishmania\_donovani*  
*Leishmania\_infantum*  
*Leishmania\_major*  
*Leishmania\_arabica*  
*Leishmania\_gerbilli*  
*Leishmania\_turonica*  
*Leishmania\_tropica*  
*Leishmania\_aethiopica*  
*Leishmania\_enriettii*  
*Leishmania\_martiniquensis*  
*Crithidia\_luciliae thermophila*  
*Leptomonas\_costaricensis*  
*Leptomonas\_sp\_TCC2547*  
*Leptomonas\_sp\_TCC2441*  
*Crithidia\_fasciculata*  
*Crithidia\_acantocephali*  
*Strigomonas\_culicis*  
*Strigomonas\_oncopelti*  
*Strigomonas\_galatii*  
*Angomonas\_deanei*  
*Angomonas\_desouzai*  
*Trypanosoma\_sp\_TCC1307*  
*Trypanosoma\_theileri*  
*Trypanosoma\_theileri*  
*Trypanosoma\_cyclops*  
*Trypanosoma\_sp\_TCC878*  
*Trypanosoma\_vivax*  
*Trypanosoma\_congolense*  
*Trypanosoma\_brucei\_T*  
*Trypanosoma\_brucei\_gambiense*  
*Trypanosoma\_evansi*  
*Trypanosoma\_sp\_TCC2186*  
*Trypanosoma\_sp\_TCC339*  
*Trypanosoma\_ralphi*  
*Trypanosoma\_grayi*  
*Trypanosoma\_lewisi*  
*Trypanosoma\_wauwau*  
*Trypanosoma\_livingstonei*  
*Trypanosoma\_sp\_H25*  
*Trypanosoma\_erneyi*  
*Trypanosoma\_dionisiae*  
*Trypanosoma\_cruzi\_G*  
*Trypanosoma\_cruzi\_marinkellei\_B*  
*Trypanosoma\_rangei\_AM80*  
*P.caudatus*  
*Bsaltans*  
*Bodosp*  
*Bodosp*

This figure displays a multiple sequence alignment of protein sequences from various species. The sequences are color-coded by residue type: blue for hydrophobic, red for polar, and green for aromatic amino acids. The alignment highlights conserved regions and variations between species. A vertical scale bar on the left indicates sequence length, and a horizontal scale bar at the bottom indicates evolutionary distance.

*Trypanosoma conorhini*  
*Phytomonas* sp EM1  
*Phytomonas* *serpens*  
*Phytomonas* sp TCC066E  
*Phytomonas* sp Hartl  
*Phytomonas* sp TCC418  
*Herpetomonas* *muscarum*  
*Herpetomonas* *wanderleyi*  
*Endotrypanum* *schaudinni*  
*Endotrypanum* *monterogoevii*  
*Leishmania* *tarentolae*  
*Leishmania* *braziliensis*  
*Leishmania* *panamensis*  
*Leishmania* *amazonensis*  
*Leishmania* *mexicana*  
*Leishmania* *dovonani*  
*Leishmania* *infantum*  
*Leishmania* *major*  
*Leishmania* *arabica*  
*Leishmania* *gerbilli*  
*Leishmania* *turanica*  
*Leishmania* *tropica*  
*Leishmania* *aethiopica*  
*Leishmania* *enriettii*  
*Leishmania* *martinicensis*  
*Crithidia* *Tuciliae* *thermophila*  
*Leptomonas* *costaricensis*  
*Leptomonas* sp TCC2547  
*Leptomonas* sp TCC2441  
*Crithidia* *Fasciculata*  
*Crithidia* *acantoccephali*  
*Strigomonas* *culicis*  
*Strigomonas* *oncopelti*  
*Strigomonas* *galati*  
*Angomonas* *deanei*  
*Angomonas* *desouzai*  
*Trypanosoma* sp TCC1307  
*Trypanosoma* *theileri*  
*Trypanosoma* *theileri*  
*Trypanosoma* *cyclops*  
*Trypanosoma* sp TCC878  
*Trypanosoma* *vivax*  
*Trypanosoma* *congolense*  
*Trypanosoma* *brucei* T  
*Trypanosoma* *brucei* *gambiense*  
*Trypanosoma* *evansi*  
*Trypanosoma* sp TCC2186  
*Trypanosoma* sp TCC339  
*Trypanosoma* *ralphi*  
*Trypanosoma* *grayi*  
*Trypanosoma* *lewisii*  
*Trypanosoma* *wauwau*  
*Trypanosoma* *livingstonei*  
*Trypanosoma* sp H25

The figure displays a sequence logo for a protein sequence, likely generated by a bioinformatics tool like WebLogo. The x-axis represents the position of the amino acid residue, and the y-axis represents the frequency of each amino acid at that position. The colors used in the logo correspond to the standard genetic code: A (green), C (blue), D (red), E (orange), F (purple), G (yellow), H (pink), I (light blue), K (dark blue), L (light green), M (light orange), N (light pink), P (light yellow), Q (light red), R (dark red), S (light blue-green), T (light pink), V (light green), W (dark purple), and Y (dark pink).

**Legend:**

- A: Green
- C: Blue
- D: Red
- E: Orange
- F: Purple
- G: Yellow
- H: Pink
- I: Light Blue
- K: Dark Blue
- L: Light Green
- M: Light Orange
- N: Light Pink
- P: Light Yellow
- Q: Light Red
- R: Dark Red
- S: Light Blue-Green
- T: Light Pink
- V: Light Green
- W: Dark Purple
- Y: Dark Pink

Lbp23B  
*Trypanosoma conorhini*  
*Phytomonas* sp EMI  
*Phytomonas* serpens  
*Phytomonas* sp TCC066E  
*Phytomonas* sp Hart1  
*Phytomonas* sp TCC418  
*Herpetomonas* muscarum  
*Herpetomonas* wanderleyi  
*Endotrypanum* schaudinni  
*Endotrypanum* monterogei  
*Leishmania* tarentolae  
*Leishmania* braziliensis  
*Leishmania* panamensis  
*Leishmania* amazonensis  
*Leishmania* mexicana  
*Leishmania* donovani  
*Leishmania* infantum  
*Leishmania* major  
*Leishmania* arabica  
*Leishmania* gerbilli  
*Leishmania* turanica  
*Leishmania* tropica  
*Leishmania* aethiopica  
*Leishmania* enriettii  
*Leishmania* martinicensis  
*Critchidia* luciliae thermophila  
*Leptomonas* costaricensis  
*Leptomonas* sp TCC2547  
*Leptomonas* sp TCC2441  
*Critchidia* fasciculata  
*Critchidia* acantoccephali  
*Strigomonas* culicis  
*Strigomonas* oncopelti  
*Strigomonas* galatii  
*Angomonas* deanei  
*Angomonas* desouzai  
*Trypanosoma* sp TCC1307  
*Trypanosoma* theileri  
*Trypanosoma* theileri  
*Trypanosoma* cyclops  
*Trypanosoma* sp TCC878  
*Trypanosoma* vivax  
*Trypanosoma* congolense  
*Trypanosoma* brucei T  
*Trypanosoma* brucei gambiense  
*Trypanosoma* evansi  
*Trypanosoma* sp TCC2186  
*Trypanosoma* sp TCC339  
*Trypanosoma* ralphi  
*Trypanosoma* grayi  
*Trypanosoma* lewisi  
*Trypanosoma* wauwau  
*Trypanosoma* livingstonei  
*Trypanosoma* sp H25  
*Trypanosoma* erneyi  
*Trypanosoma* dionisi  
*Trypanosoma* cruzi G  
*Trypanosoma* cruzi marinkellei  
*Trypanosoma* rangei AM80  
*P. caudatus*  
Bsaltans  
Bodosp  
Bodosp

