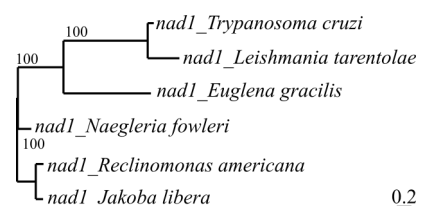
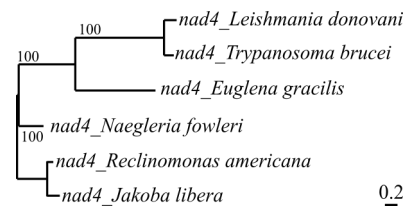
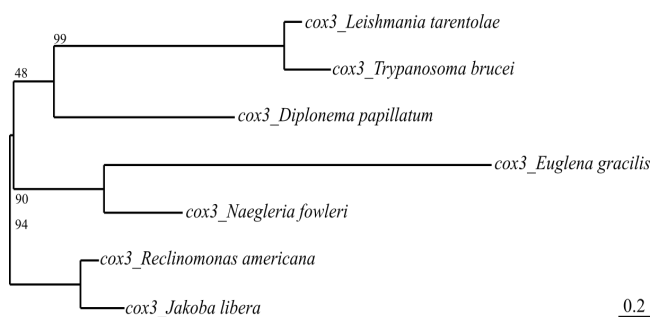
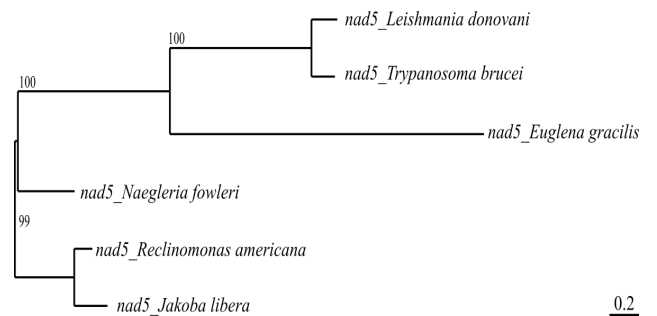
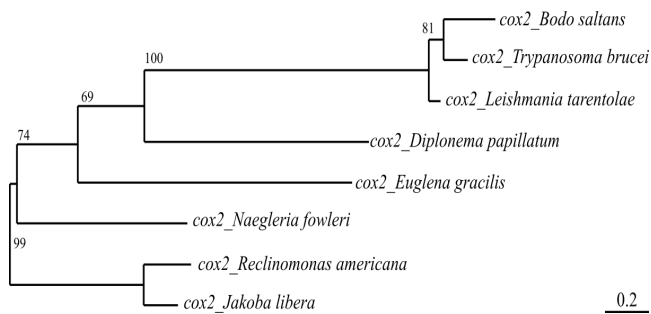
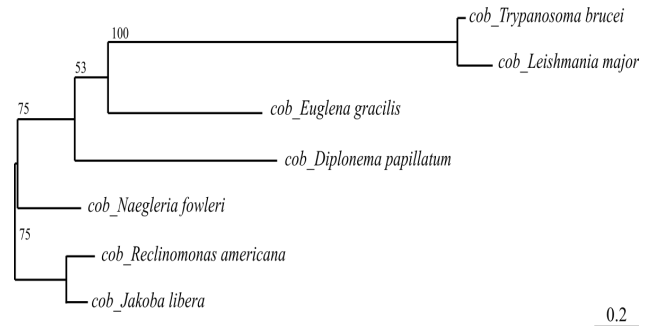
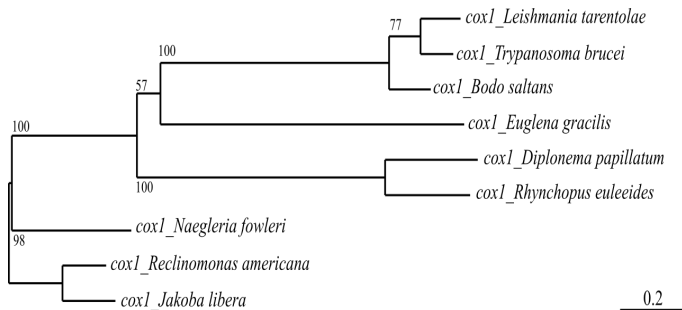


Supplementary Text 1. Maximum likelihood trees for mitochondrion-encoded proteins constructed with RAxML 8.0.0 with the LG+Γ model and 100 bootstrap replicates.



Supplementary Text 2. Accession numbers (NCBI GenBank database) of protein sequences used for alignments and phylogenetic analysis.

***cob* (apocytochrome b)**

<i>Diplonema papillatum</i>	ADP88933.1
<i>Euglena gracilis</i>	KT732262
<i>Jakoba libera</i>	AGH24175.1
<i>Leishmania major</i>	AIT97144.1
<i>Naegleria fowleri</i>	YP_007890033.1
<i>Reclinomonas americana</i>	AGH24450.1
<i>Trypanosoma brucei</i>	AAA32115.1

***cox1* (cytochrome c oxidase subunit 1)**

<i>Bodo saltans</i>	AAC38978.1
<i>Diplonema papillatum</i>	ABW73865.1
<i>Euglena gracilis</i>	KT732263
<i>Jakoba libera</i>	P_007890687.1
<i>Leishmania tarentolae</i>	P14544.1
<i>Naegleria fowleri</i>	YP_007890026.1
<i>Reclinomonas americana</i>	AGH24452.1
<i>Rhynchopus euleeides</i>	AEB96346.1
<i>Trypanosoma brucei</i>	P04371.1

***cox2* (cytochrome c oxidase subunit 2)**

<i>Bodo saltans</i>	AAC38976.1
<i>Diplonema papillatum</i>	ADP88934.1
<i>Euglena gracilis</i>	KT732264
<i>Jakoba libera</i>	YP_007890686.1
<i>Leishmania tarentolae</i>	P14545.2
<i>Naegleria fowleri</i>	YP_007890057.1
<i>Reclinomonas americana</i>	AGH24386.1
<i>Trypanosoma brucei</i>	P04372.2

cox3 (cytochrome c oxidase subunit 3)

<i>Diplonema papillatum</i>	ADP88935.1
<i>Euglena gracilis</i>	KT732264
<i>Jakoba libera</i>	YP_007890722.1
<i>Leishmania tarentolae</i>	P14546.1
<i>Naegleria fowleri</i>	YP_007890030.1
<i>Reclinomonas americana</i>	NP_044756.1
<i>Trypanosoma brucei</i>	AAA32122.1

nad1 (NADH dehydrogenase subunit 1)

<i>Euglena gracilis</i>	KT732265
<i>Jakoba libera</i>	YP_007890725.1
<i>Leishmania tarentolae</i>	P15576.1
<i>Naegleria fowleri</i>	YP_007890019.1
<i>Reclinomonas americana</i>	NP_044754.1
<i>Trypanosoma cruzi</i>	AAO47331.1

nad4 (NADH dehydrogenase subunit 4)

<i>Euglena gracilis</i>	KT732266
<i>Jakoba libera</i>	AGH24231.1
<i>Leishmania donovani</i>	ACJ47214.1
<i>Naegleria fowleri</i>	YP_007890052.1
<i>Reclinomonas americana</i>	AGH24445.1
<i>Trypanosoma brucei</i>	AAB59224.1

nad5 (NADH dehydrogenase subunit 5)

<i>Euglena gracilis</i>	KT732267
<i>Leishmania donovani</i>	ACJ47215.1
<i>Trypanosoma brucei</i>	AAB59225.1
<i>Naegleria fowleri</i>	YP_007890032.1
<i>Reclinomonas americana</i>	NP_044800.1
<i>Jakoba libera</i>	YP_007890739.1

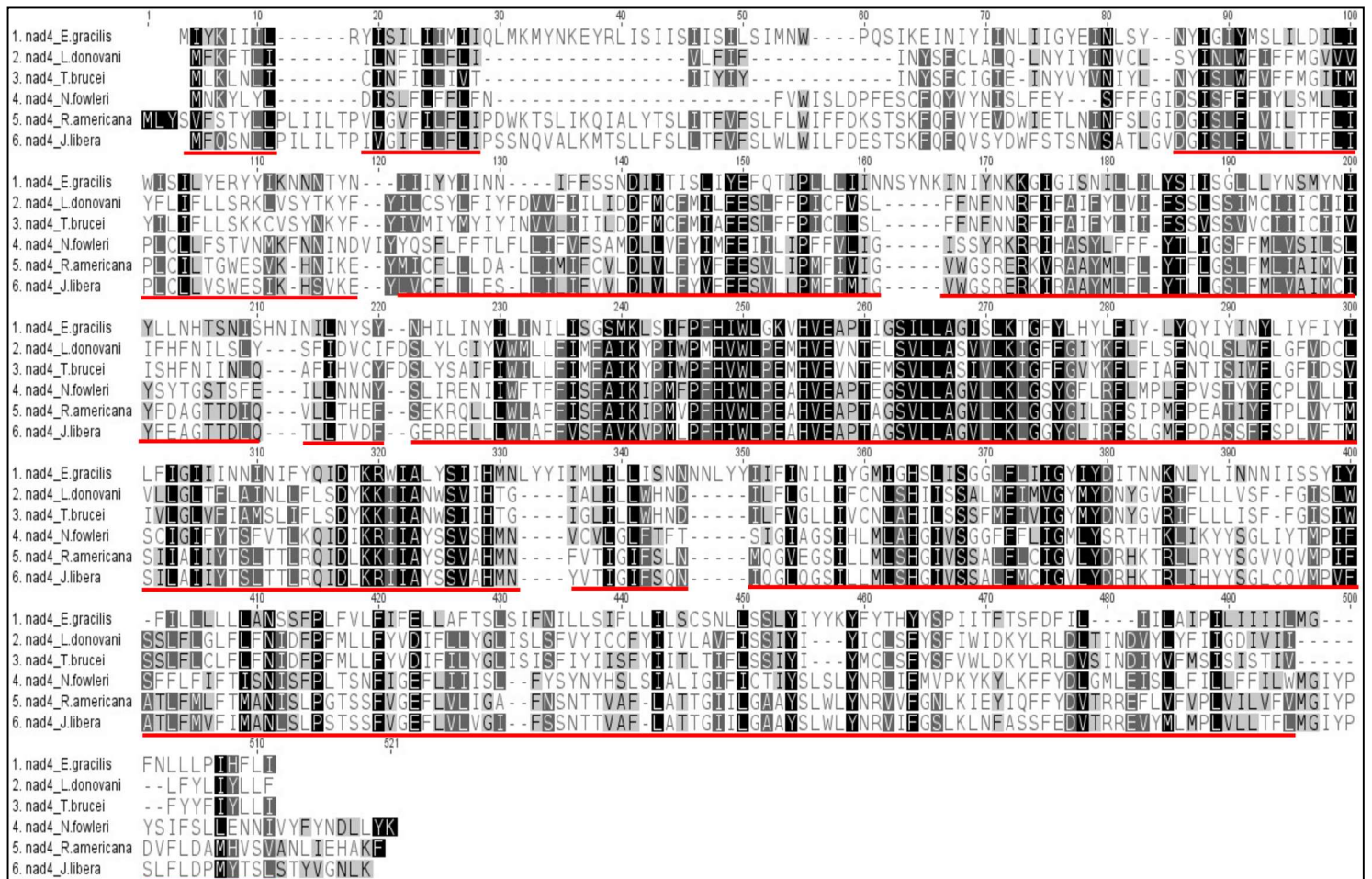
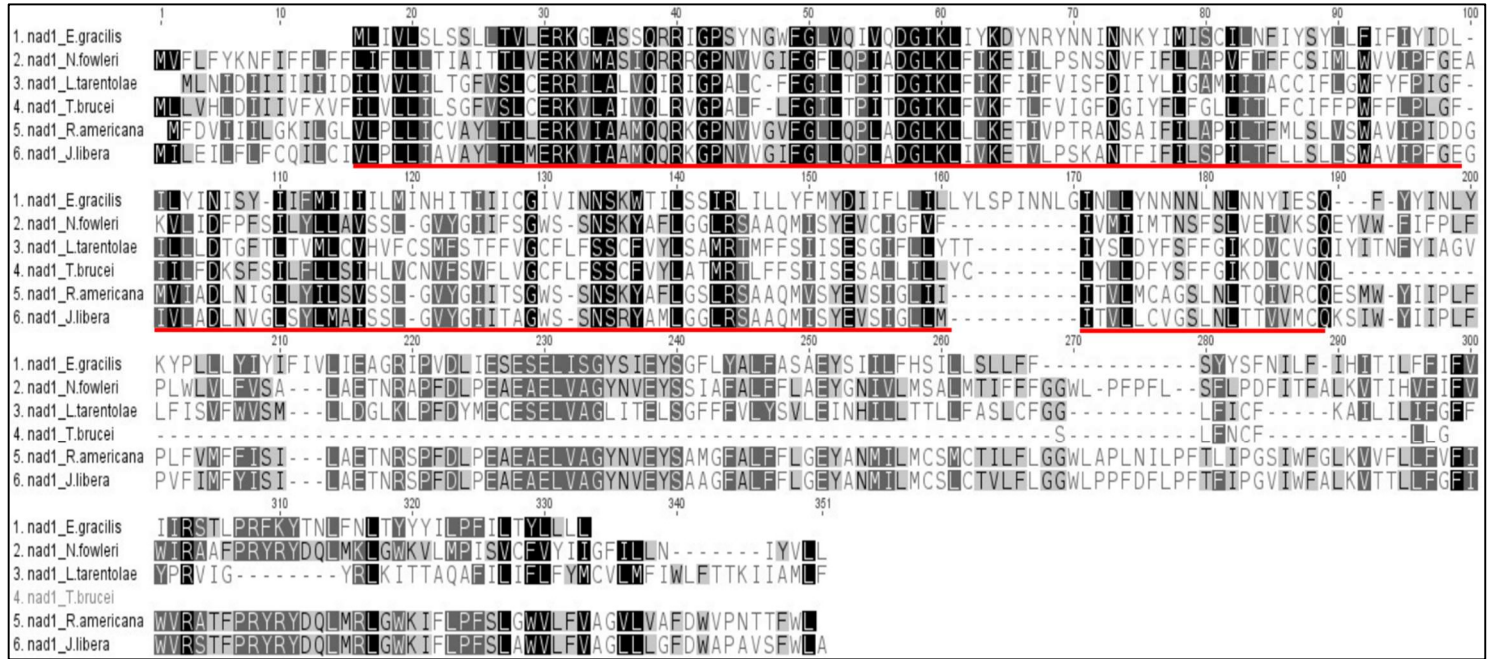
***rnsR* (small ribosomal subunit)**

Euglena gracilis

KT732268

Supplementary Text 3. Protein alignments of *Euglena gracilis* mitochondrion-encoded genes.

All protein alignments were performed using MUSCLE 3.8.31 with default settings, and adjusted manually. The amino acid similarity is color-coded, with black indicating the highest similarity. Site selection for building phylogenetic trees was performed manually: selected sites are underlined in red. GenBank accession numbers of protein sequences used for alignments are available in Suppl. Text 2.



1. nad5_E.gracilis	1	10	20	30	40	50	60	70	80	90	100
2. nad5_L.donovani	1	10	20	30	40	50	60	70	80	90	100
3. nad5_T.brucei	1	10	20	30	40	50	60	70	80	90	100
4. nad5_N.fowleri	1	10	20	30	40	50	60	70	80	90	100
5. nad5_R.americana	1	10	20	30	40	50	60	70	80	90	100
6. nad5_J.libera	1	10	20	30	40	50	60	70	80	90	100
1. nad5_E.gracilis	110	120	130	140	150	160	170	180	190	200	
2. nad5_L.donovani	110	120	130	140	150	160	170	180	190	200	
3. nad5_T.brucei	110	120	130	140	150	160	170	180	190	200	
4. nad5_N.fowleri	110	120	130	140	150	160	170	180	190	200	
5. nad5_R.americana	110	120	130	140	150	160	170	180	190	200	
6. nad5_J.libera	110	120	130	140	150	160	170	180	190	200	
1. nad5_E.gracilis	210	220	230	240	250	260	270	280	290	300	
2. nad5_L.donovani	210	220	230	240	250	260	270	280	290	300	
3. nad5_T.brucei	210	220	230	240	250	260	270	280	290	300	
4. nad5_N.fowleri	210	220	230	240	250	260	270	280	290	300	
5. nad5_R.americana	210	220	230	240	250	260	270	280	290	300	
6. nad5_J.libera	210	220	230	240	250	260	270	280	290	300	
1. nad5_E.gracilis	310	320	330	340	350	360	370	380	390	400	
2. nad5_L.donovani	310	320	330	340	350	360	370	380	390	400	
3. nad5_T.brucei	310	320	330	340	350	360	370	380	390	400	
4. nad5_N.fowleri	310	320	330	340	350	360	370	380	390	400	
5. nad5_R.americana	310	320	330	340	350	360	370	380	390	400	
6. nad5_J.libera	310	320	330	340	350	360	370	380	390	400	
1. nad5_E.gracilis	410	420	430	440	450	460	470	480	490	500	
2. nad5_L.donovani	410	420	430	440	450	460	470	480	490	500	
3. nad5_T.brucei	410	420	430	440	450	460	470	480	490	500	
4. nad5_N.fowleri	410	420	430	440	450	460	470	480	490	500	
5. nad5_R.americana	410	420	430	440	450	460	470	480	490	500	
6. nad5_J.libera	410	420	430	440	450	460	470	480	490	500	
1. nad5_E.gracilis	510	520	530	540	550	560	570	580	590	600	
2. nad5_L.donovani	510	520	530	540	550	560	570	580	590	600	
3. nad5_T.brucei	510	520	530	540	550	560	570	580	590	600	
4. nad5_N.fowleri	510	520	530	540	550	560	570	580	590	600	
5. nad5_R.americana	510	520	530	540	550	560	570	580	590	600	
6. nad5_J.libera	510	520	530	540	550	560	570	580	590	600	
1. nad5_E.gracilis	610	620	630	640	650	660	670	680	690	700	
2. nad5_L.donovani	610	620	630	640	650	660	670	680	690	700	
3. nad5_T.brucei	610	620	630	640	650	660	670	680	690	700	
4. nad5_N.fowleri	610	620	630	640	650	660	670	680	690	700	
5. nad5_R.americana	610	620	630	640	650	660	670	680	690	700	
6. nad5_J.libera	610	620	630	640	650	660	670	680	690	700	
1. nad5_E.gracilis	710	720	730	740	750	760	762				
2. nad5_L.donovani	710	720	730	740	750	760	762				
3. nad5_T.brucei	710	720	730	740	750	760	762				
4. nad5_N.fowleri	710	720	730	740	750	760	762				
5. nad5_R.americana	710	720	730	740	750	760	762				
6. nad5_J.libera	710	720	730	740	750	760	762				

1. cox1_E.gracilis MNNIMHMTIKYTLTTSKTIIGLIGYMGYIAGLIGYHSMTRMELNTQGLAVRKKVKEVTIYNWITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
2. cox1_D.papillatum MHLLEAASVWVITNKLIGVYISWSIAFGVSGLMSMTRAEGLSEQVLFSDHQL--YVNVITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
3. cox1_R.euleioides MPTISVTPATAWITNKLIGVYISWSIAFGVSGLMSMTRAEGLSEQVLFSDHQL--YVNVITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
4. cox1_B.saltans MYFLSLLCLTISKIMGYSYILAIMCGFVGVYISLFRLELLELLCGVLFSDYOF--YVNVITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
5. cox1_L.tarentolae MFMQLVCLISKIMGICYLVAILSGFVGVYISLFRLELLELLCGVLFSDYOF--YVNVITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
6. cox1_T.brucei MFFLCLVCLISKIMGICYLVAILSGFVGVYISLFRLELLELLCGVLFSDYOF--YVNVITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
7. cox1_N.fowleri MYDFLIRWVLYITNKLIGLIGYMGYIAGLIGYHSMTRMELNTQGLAVRKKVKEVTIYNWITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
8. cox1_J.libera MTLGTRWVLYITNKLIGLIGYMGYIAGLIGYHSMTRMELNTQGLAVRKKVKEVTIYNWITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI
9. cox1_R.americana MVTSEVRRWFFSTNHLKIGLIGYMGYIAGLIGYHSMTRMELNTQGLAVRKKVKEVTIYNWITITLGLMLFVFTIPVIGIFYGNYLIPMLTGTSELSPMRNIGSFNMLIVGVVIFININVMISKI

140 150 160 170 180 190 200 210 220 230 240 250 260

1. cox1_E.gracilis PISSGWTLVYPLSTRDADNIGVNDLQLVHVLGISSTIGSNVYITIKYNRHVGLTFMNIYVNESITVTSITLIGSLPTIGVAITGILLDRINISITIDYVI--SDPVLVYQHLWFEGHPEVYVITLPIV
2. cox1_D.papillatum GAGTAVTVYPLSMTASIG-GVSDVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRITGITVYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
3. cox1_R.euleioides GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
4. cox1_B.saltans GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
5. cox1_L.tarentolae GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
6. cox1_T.brucei GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
7. cox1_N.fowleri GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
8. cox1_J.libera GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV
9. cox1_R.americana GAGTAVTVYPLSMTASIG-GTSMVDFITVSLHAAQLSSTIGATNIVICCYARRTHSCVQLQSSLYPMSVAITGALLVIGITIPVWAGATITMLLDRGCTSYDYDVAAGGDVVMYEHLEWEGHPEVYVITLPIV

270 280 290 300 310 320 330 340 350 360 370 380 390

1. cox1_E.gracilis FGLVSLITLTSIHKDIFREGMMYITLISGIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
2. cox1_D.papillatum FGLVSLIRGGFLSIVYMGVYVANIHAIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
3. cox1_R.euleioides FGLVSHIIRTAVFVSIVYMGVYVANIHAIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
4. cox1_B.saltans FGLVSLITLTIIGLRCVSTWAMVYSLNLSLGLGFFVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
5. cox1_L.tarentolae FGLVSTLIVIEVIGRCVSTWAMVYSLNLSLGLGFFVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
6. cox1_T.brucei FGLVSTLIEVTSFRCVSSTWAMVYSLNLSLGLGFFVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
7. cox1_N.fowleri FGLVSHIIRTAVFVSIVYMGVYVANIHAIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
8. cox1_J.libera FGLVSHIIRTAVFVSIVYMGVYVANIHAIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL
9. cox1_R.americana FGLVSHIIRTAVFVSIVYMGVYVANIHAIVGVYVAHMHMTGLDIDSRSYESTATISITIPISIKKVESYINWAGGRGFRGNNSWSVFFSFLICFCGGFGLSSGSLDMLHDTIYVWVHEHIVL

400 410 420 430 440 450 460 470 480 490 500 510 520

1. cox1_E.gracilis SLAATFGLLIAHYFLPIIFSYSIFESFSFYHTLVLGALLVYPMHAGLSMARRVPEYADIFPEMTVGFHGTFLIF-----STLTF-IRSYFQLSHINHSNYL
2. cox1_D.papillatum SLGAVFGLLNGVLSCHELCSGYRASAALLRQVVLVWGTCTIFWGMHSGTLGLSRVVDADQYIGTVVSTTCGLVWLVWALLCASLEASLWDTQQL--RATRSTNPGMHNHMLSGM-----
3. cox1_R.euleioides SLGAVYGMLTGLSVHLLGGDIGAMHARMLGIMLIGTATLWMSLSSGSLGPRRMPDPTDYMQYVPTVGIYVWLVWALLHGGIGAMESVLESTHA-RNTISYVSTSGMHSSTTLPNSDARST
4. cox1_B.saltans SLGAVIGFRCGFLHFCVRLPILFYFLMYYFLWTLWLGSLNLLPRLSLGAYAFPRRISDYDISLFWSVLLCGMLFVCLLFAACLFVSLMFDYCIFFVSIYICLFCFYSFNSWLPFVMLYLLL
5. cox1_L.tarentolae SLGAVIGFRTGFIHFLAKWLPILFYFLMYYFLWTLWLGSLNLLPRLSLGAYAFPRRISDYDISLFWSVLLCGMLFVCLLFAACLFVSLMFDYCIFFVSLFVSLYCFYFSTWPCVMVLYLLL
6. cox1_T.brucei SLGAVIGVFGGFFHLMKWLPIELHTFWLFFFISTLWFGSNMVEPRLSLGAYAFPRRISDYDISLFWSAFTLGMMLLFFLWIFCCCLFVNLFWDYCLFFINLFTYSIFFYFVWVPCMAIYLLV
7. cox1_N.fowleri SMGAVAIYGGYFYMWGMKTLGSYSELGQAHFMTFIFNFTFPMHGLSAGMPRRIPDYDPAFAGWNLISTVGSYSSISULL-----WFYIVY--RTLTDGKCSNNPWANDTSTNQTNYF
8. cox1_J.libera SMGAVAFSMAAAYYWGKMTGYQYPETLAKIQFWTTFIFNLTFFPMHGLSAGMPRRIPDYDPAFAGWNLISTVGSYSSISULL-----WFYIVY--RTLTDGKCSNNPWANDTSTNQTNYF
9. cox1_R.americana SMGAVAFIYAAAYYWGKMTGYQYPETLAKIQFWTTFIFNLTFFPMHGLSAGMPRRIPDYDPAFAGWNLISTVGSYSSISULL-----WFYIVY--RTLTDGKCSNNPWANDTSTNQTNYF

530 540 550 560 570 580 590 600 610 620 630 640 654

1. cox1_E.gracilis -----SLLHATRQQLMHTCVSTSHRASHMLEE
2. cox1_D.papillatum -----AII-----VLSMVAHNGVCSATLY
3. cox1_R.euleioides -----VDFAIH-----VLDYLF-----IITISFCFIYVFFSFSVLLLL
4. cox1_B.saltans -----VDFAIH-----VLDYLF-----IITISFCFIYVFFSFSVLLLL
5. cox1_L.tarentolae -----VDFAIH-----VLDYLF-----IITISFCFIYVFFSFSVLLLL
6. cox1_T.brucei -----VDFAIH-----VLDYLF-----IITISFCFIYVFFSFSVLLLL
7. cox1_N.fowleri GVIYVYKYGVSGRSVNIKMSDFIEKWIISFNYYTNRVYISSESIKTTLWTLTSPPYCHTEVVPKDFTTGKHVYRWRVAIWNKRRKLLPLYLKGTETFNHFYITTYTYINPLVSNWIKTEGSSSFS
8. cox1_J.libera TLEWTLSSPPQVHTFEEVPPYRETITKH
9. cox1_R.americana TLEWTLSSPPLSHTEFVPPYKETTK

1. cox2_E.gracilis MRYGNREIESLILFFDQTHIYTSIINALVIGITL--IIRKWNKRGKICN-----
2. cox2_D.papillatum MVLHGLAVNYTTHVALL--VNLVAIVVFAAGAMHSATVSRN-----
3. cox2_B.saltans MSAFISFWMLFIDSLVLL--SGAIFVCIWICSLFFCLIFKLDYIFCSW-----
4. cox2_L.tarentolae MSAFISFWMLFIDSLVLL--SFCVFCVWICACMLFSTVLLVSKLNNIYCTW-----
5. cox2_T.brucei MSAFISFWMLFIDSLVLL--SFSIFLSVWICACMLIATVLTVTKINNIYCTW-----
6. cox2_N.fowleri METKRAFLFSNINVELTRYFGGMPANDKMSLVLQYIETWVSL--IAVAFVVGFI--VLSWITKFNNSVNPVAYHF
7. cox2_R.americana MLLQVTVFTLIVLVYVSGTITPAFADYAEKWLDFEQDPAVPMVEGIIINHHDLWFFL--ILIAVFLVLI--LRLTYLFFDRSKNTPMS
8. cox2_J.libera MLQKLFLLTISFACTLGLACADAPEQWQDFQDAASPIIMEGIVDHHDLWFFL--VVIVVFTWL--LARVVIQFRSSVNPVPS

110 120 130 140 150 160 170 180 190 200

1. cox2_E.gracilis ---QYIYHIKTEVITLPIIFLIVIVLHVSIVYVNL--EINKGTTNKYINVIIGNQWYVIYNN-----IES
2. cox2_D.papillatum ---LYTSNLYLELVVLLTPRTAMVIVLVRVVMVQCSE--EELQ-LHGTQWVHVANQWYVYV--DA-----VSLFLYAVQ
3. cox2_B.saltans ---DFISAKFIDLYWFTLGCDFVLCILRLCLLYFS--CLNF-VCFDLCKCTIGQWYVYVFI--FGE--TTIFSNTLLE
4. cox2_L.tarentolae ---DFTASKFIDYWFITGGMFLGILRLCLLYFG--HLNF-VSFDLCKVIGQWYVYVFI--FGE--TTIFSNTLLE
5. cox2_T.brucei ---DFISSKFIDYWFVFLGMMFLLCLRLCLLYFS--CINF-VSFDLCKVIGQWYVYVFI--FGE--TTIFSNTLLE
6. cox2_N.fowleri ---SKKVEAFLDITVALLPVLISYLLPALGFTLQLEYDENFLETFNWYIIGHQWYVYVFI--FGE--TTIFSNTLLE
7. cox2_R.americana ---KVVHGTVLEIITTIAPSFILLAITPSPFALLYSM--EEST-DPAITLKAIGHQWYVYVFI--SDYTTD-SES-----LAFDSYMWPE
8. cox2_J.libera ---TTHGTTIEITTIIPAVLITLITPTFAALLYSM--DEGI-DPAITLKAIGHQWYVYVFI--SDYTS-DES-----LAFESYMWPE

210 220 230 240 250 260 270 280 290 300

1. cox2_E.gracilis RISSLG--RITLVDQPLFIKANNNTHTISSLQVTHSFAIPTLGIKVDATPGRININISINGLTQGLYVGYCSELGGSGHAFMPINLIVY
2. cox2_D.papillatum HDMHHGDLRLLCGMQSLIDSSCVLQALTSDDVTHAWALPSLGMKVDQVPRGRANTATLVSVTGTLYGOCSEVCGALHGMYPLCMTV
3. cox2_B.saltans SDYLIQDLRLLCQNHVLTLSLVYIKWLSAIVDTHSFAISLGIKVDCTIPGRCNELIFSNSSITVYOCSELGGVHGMPITVSCFI
4. cox2_L.tarentolae SDYMIQDLRLLCQNHVLTLSLVYIKWLSAIVDTHSFAISLGIKVDCTIPGRCNELIFSNSSATVYOCSELGGVHGMPITVSCFI
5. cox2_T.brucei SDYLIQDLRLLCQNHVLTLSLVYIKWLSAIVDTHSFAISLGIKVDCTIPGRCNELIFSNSSATVYOCSELGGVHGMPITVSCFI
6. cox2_N.fowleri SKKN--RLNVDKCLVPPNGNHICFYVLSAIVDTHAWAVPQLGKVDALPGRRLMRFVLYSSIEGVYOCSELGGVHGMPITVSCFI
7. cox2_R.americana ADLQPGQLRLLEVDNRVIVPVDTHYRMLVTSQDVLHSAWALPSLGIKVDAPGRLLNQVSMFKREGVYVYOCSEICGVNHFMPITVSCFI
8. cox2_J.libera EDLQPGQLRLLEVDNRVIVPVDTHYRMLVTSQDVLHSAWALPSLGIKVDAPGRLLNQVSMFKREGVYVYOCSEICGVNHFMPITVSCFI

310 320 325

1. cox2_E.gracilis
2. cox2_D.papillatum
3. cox2_B.saltans
4. cox2_L.tarentolae
5. cox2_T.brucei
6. cox2_N.fowleri SLDVHLVSRNLLSSISINDSSSIFIK
7. cox2_R.americana QTEM
8. cox2_J.libera ELET

		10	20	30	40	50	60	70	80	90	100																																																																															
1. cox3_E.gracilis		W	I	L	N	T	N	I	Y	G	G	R	N	S	R	L	C	Y	L	I	P	L	---																																																																			
2. cox3_D.papillatum		W	Y	H	T	L	R	S	T	V	Q	---																																																																														
3. cox3_L.tarentolae		K	R	R	G	F	D	---																																																																																		
4. cox3_T.brucei		M	F	L	F	R	C	I	F	V	G	V	S	-																																																																												
5. cox3_N.fowleri		I	L	N	Y	W	E	K	Y	K	Y	D	V	R	T	S	S	R	R	L	H	Y	F	N	D	I	T	Y	T	P	W	P	F	H	I	S	M	I	V	F	L	S	L	F	F	C	V	Y	L	H	H	F	A	W	A	G	K	A	L	T	F	F	I	W	---																									
6. cox3_R.americana		M	S	Q	T	F	V	K	---																																																																																	
7. cox3_J.libera		W	S	S	L	S	L	K	---																																																																																	
		110	120	130	140	150	160	170	180	190	200																																																																															
1. cox3_E.gracilis		L	Y	N	I	A	T	F	I	F	L	L	I	L	I	G	F	Y	N	L	Y	I	---																																																																			
2. cox3_D.papillatum		L	A	G	V	L	L	W	L	S	E	V	A	L	F	V	S	V	I	W	A	L	V	-																																																																		
3. cox3_L.tarentolae		I	Q	C	F	V	W	F	I	S	E	L	L	F	L	S	L	F	V	V	F	S	L	V	L	F	V	S	V	E	F	A	F	V	F	I	P	M	F	S	C	L	I	C	D	F	G	F	V	Y	Y	I	D	I	F	N	L	I	N	T	F	L	F	V	S	G	L	F	V	N	F	V	L	F	L	F	W	F	R	F	F	L	C	V	L	F	M	W	W	V
4. cox3_T.brucei		I	Q	C	F	V	W	F	I	S	E	L	L	F	L	S	L	F	V	V	F	S	L	V	L	F	V	S	V	E	F	A	F	V	F	I	P	M	F	S	C	L	I	C	D	F	G	F	V	Y	Y	I	D	I	F	N	L	I	N	T	F	L	F	V	S	G	L	F	V	N	F	V	L	F	L	F	W	F	R	F	F	L	C	V	L	F	M	W	W	V
5. cox3_N.fowleri		M	V	G	F	L	L	I	S	E	A	A	V	F	A	S	F	I	M	A	Y	F	---																																																																			
6. cox3_R.americana		R	I	G	M	L	F	I	S	E	V	M	F	V	S	F	F	A	F	---																																																																						
7. cox3_J.libera		K	L	G	M	L	F	I	S	E	V	M	F	V	S	F	F	A	F	---																																																																						
		210	220	230	240	250	260	270	280	290	300																																																																															
1. cox3_E.gracilis		H	N	L	L	---																																																																																				
2. cox3_D.papillatum		V	W	C	L	G	G	C	F	-																																																																																
3. cox3_L.tarentolae		G	L	F	G	F	L	-																																																																																		
4. cox3_T.brucei		S	L	F	G	F	L	-																																																																																		
5. cox3_N.fowleri		G	T	A	L	G	V	I	V	L	F	I	Q	L	S	E	Y	V	S	T	N	T	L	S	I	S	D	S	M	V	G	S	C	Y	L	I	T	G	F	H	L	F	V	C	T	G	L	I	F	S	L	A	T	A	Q	L	D	N	Y	S	---																													
6. cox3_R.americana		T	I	L	A	V	T	E	-																																																																																	
7. cox3_J.libera		T	V	L	A	S	A	F	-																																																																																	
		310	318																																																																																							
1. cox3_E.gracilis		W	G	Q	L	V	M	---																																																																																		
2. cox3_D.papillatum		D	V	L	S	V	V	Y	Y	A	---																																																																															
3. cox3_L.tarentolae		D	V	L	S	V	M	Y	C	V	---																																																																															
4. cox3_T.brucei		I	N	G	N	I	M	Y	D	W	N	L	I	N	S	Y	W	K	---																																																																							
5. cox3_N.fowleri		W	G	G	N	---																																																																																				
6. cox3_R.americana		W	G	G	N	---																																																																																				
7. cox3_J.libera		W	G	G	A	---																																																																																				