

ESAG2p type

1 10 20 30 40 50 60 70 80 90

1 MRYEIVIAFGVFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFESLCKIYRITQAEAPQPSFKNREKEREIMSKLEEMVREVEAAGG

2 MRYKIVFTVGLFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILSKLEEMVREVEAAGG

3 MRYKIVFTVGLFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILSKLEEMVREVEAAGG

4 MRYKIVFTVGLFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILSKLEEMVREVEAAGG

5 MRYKIVIAVGVFVAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREREREIMSKLEEMVREVEAAGG

6 MRYKIVIAVGVFVAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFKNREKEREIMSKLEEMVREVEAAGG

7 MRYKIVFTVGLFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILSKLEEMVREVEAAGG

8 MRYKIVFTVGLFAAVLSPSFQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILSKLEEMVREVEAAGG

T. b. gambiense

1 MRCEIVIAVGVFVAVLSPS-----FQSDLGSFKWSTELIDWSKITDYIGDGKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILNKLEEMVRET

2 MRYEIVIAVGLFAAVLYSSSEEAVDDGCTRQARVTNGRPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

3 MRYETVFTVGLFVAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILNKLEEMVRET

4 MRCETVLTIGLFAVAVLSHCDGEYIDDECTRVARVTSDRADWETIRECVSGDYMYHNTVDFDVLCKIYRITQAEAPQPSFKNRDKGEIMNKLEEMVREV

5 MRYEIVIAVGVFVAVLSSSEEAVDDECTRDARVTNGTPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

6 MRYEIVFVVGGLFAAVLYSSSEEAVDDECTRDARVTNGTPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

7 MRCEIVFVVGGLFAAVLYSSSEEAVDDECTRDARVTNGTPDSDTITECVSGDYLYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

8 MRYEIVIAVGLFAAVLYSSSEEAVHDECTREARVTNGRPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

9 MRYEIVIAVGLFAAVLYSSSEEAVHDECSRARVTNDTPDSDTITECVSGDYLYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEREIMSKLEEMVREV

10 MRCEIVFVVGGLFAAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVRET

11 MRCEIVFVVGGLFAAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVRET

12 MRYKIVIAVGVFVAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILNKLEEMVRET

13 MRYEIVIAVGVFVAVLSSSEEAVHDECTREARVTNGRPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

14 MRYEIVFTVGLFAAVLSPS-----FQSDLRSFKWSTELIDWSKITDYIGDGKHHNAGEFETLCKIYRITQAEAPQPSFENREKEGEIMSKLEEMVREV

15 MRCEIVFVVGGLFAAVLYSSSEEAVDDECTRDARVTNGTPDSDTITECVSGDYLYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

16 MRYETVFTVGLFAAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEILNKLEEMVRET

17 MRYEIVIAVGLFAAVLYSSSEEAVDDECTRVARVTNGRPDWDITTECVSGDYMYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

T. b. brucei

T. equiperdum

1 MRYKIVIAVGVFVAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREREREIMSKLEEMVREV

2 MRYKIVFTVGLFAAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEIMNKLEEMVREV

3 MRYEIVIAVGLFAAVLSSSEEAVDDECLRDARVTNDTPDSDTITECVSGDYLYHNTGDFDVLCKIYRITQAEAPQPSFKNREKEGEIMSKLEEMVREV

4 MRYKIVFTVGLFAAVLSPS-----FQSDLGSFKWSTELIDWSKVTEYIDESYKHHNAGEFETLCKIYRITQAEAPQPSFENREKENEIMNKLEEMVREV

ESAG2p type

	100	110	120	130	140	150	160	170	180	190				
<i>T. b. gambiense</i>	1	TQGLSHSSNR	RTTAYQEIK	ILLEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDN	AGTSCGSF	GDKSVGK'	
	2	TQDLSHSSNR	RTTAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GDKLVGK'	
	3	TQDLSHSSNR	RTTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GDKLVGK'	
	4	TQDLSHSSNR	RTTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GDKLVGK'	
	5	TQDLSHSSNR	RTTAYQEIK	KLFEAKKL	KEEIEVNR	TKALNASH	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDN	AGTSCGSY	GDKSVGK'	
	6	DKGS	SKLCKR	TTAYQEIK	ILLEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEQAMRGNK	SLLFNSIDH	NMSCGSY	GDKLVGK.
	7	TQDLSHSSNR	RTTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GDKLVGK'	
	8	TQDLSHSSNR	RTTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GDKSVGK'	

T. b. brucei

	1	EAVG	AGGNKGS	SNKSAKST	TAYQEIR	KLFEKAKAL	KEEIEVNR	TRSLNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDN	AGTSCGSY	
	2	EAAGS	--TQDL	SHSSNR	TTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASH	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY	
	3	EAVG	--GDK	SNKSANST	TAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEKAMRENK	SLLFNSVDN	AGTSCGSY	
	4	EAAAG	--TQDL	SHSSIRT	TAYQEIK	KLFEKAKKL	QIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	ALLFNSVDH	NMSCGSY	
	5	EAAGG	--TQDL	SHSSNR	P	TAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDH	NMSCGSY
	6	EAAGG	--TQDL	SHSSNR	TTAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY	
	7	EAAGG	--TQDL	SHSSNR	TTAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY	
	8	EAAGS	--TQDL	SHSSNR	TTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASH	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY	
	9	EAAGG	--TQDL	SHSSNR	P	TAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDH	NMSCGSY
	10	EAVGGGG	NKGSNKSANST	TAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNAGR	SAEENMLRA	VYGD	AVDVARNEN	KTLEKAMRGNK	SLLFNSVDN	AGTSCGSY		
	11	EAVGGGG	NKGSNKSANST	TAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNVDN	AGTSCGSY		
	12	EAVGGGG	NKGSNKSANST	TAYEIR	KLFEKAKAL	KEEIEVNR	TKALNASR	YAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY		
	13	EAAGG	--TQDL	SHSSNR	TTAYQEIK	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDN	AGTSCGSF	
	14	EAAG	--GTQDL	SHSSNR	TTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	ALLFNSVDN	AGTSCGSY	
	15	EAAGG	--TQDL	SHSSNR	TTAYQEIK	KLFEKAKAL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	ITLEEAMRGNK	SLLFNSVDH	NMSCGSY	
	16	EAVG	--GDK	SNKSANST	TAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEQAMRGNK	SLLFNVDN	AGTSCGSY	
	17	EAAGG	--TQDL	SHSSNR	P	TAYQEIK	KLFEKAKKM	KEEIEVNR	TKALNASR	SAKDNMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	ALLFNSVDH	NMSCGSY

T. equiperdum

	1	EAAGGTQDL	SHSSNR	TTAYQEIK	KLFEAKKL	KEEIEVNR	TKALNASH	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDN	AGTSCGSY	GD
	2	EAAGGTQDL	SHSSNR	TTAYQEIK	KLFEAKKL	KEEIEVNR	TKALNASH	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSIDN	AGTSCGSY	GD
	3	EAAGGTQDL	SHSSNR	TTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	TAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDH	NMSCGSY	GD
	4	EAAGGTQDL	SHSSNR	TTAYQEIR	KLFEKAKKL	KEEIEVNR	TKALNASR	SAQENMLRA	VYGD	AVDVARNEN	KTLEEAMRGNK	SLLFNSVDD	AGTSCGSY	GD

ESAG2p type

200 210 220 230 240 250 260 270 280 290

1 TLINDFFLCLVGEPIVITTEEEK-----RKKNLEGDGDNNNIYNGFNCPCRDEIRRPENGNWTTMAAESCEGDSQGYCDPAKIKYNHTEAWDVISKACVYK

2 TLINDFFLCLVGEAINVTEDMR--QKKEKEEKEKEGKYSDSVYNGFNCPCRDAIRRPESGWTMAAEYCEGNSS-PCNPDNIKINYTDAWDVISKACVYK

3 TLINDFFLCLVGETINVTGEI IKEEKKKEEKEKEEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSS-PCNPDNIKINYTDAWDVISKACVYK

4 TLINDFFLCLVGEAINVTGEI IKEEKKKEEKEKEEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSS-PCNPDNIKINYTDAWDVISKACVYK

5 TLINDFFLCLVGEAINVTGEI IKEEKKKEEKEKEEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSS-PCYPEEDIKINYTEAWDVI SEACVYK

6 ALINDFFLCLVGEAHKVQTQS-----APDGDYNLTIIEIYNRLNCPCKDAIRRPESGWTMAAEYCEGNSS-PCNPDNIKINYTDAWDVISKACVYK

7 TLINDFFLCLVGEAINVTGEI IKEEKKKGEKEKEKEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSS-PCNPDNIKINYTDAWDVISKACVYK

8 TLINDFFLCLVGEAINVTEDMR--QKKEKEEKEKEGKYSDSVYNGFNCPCRDAIRRPESGWTMAAEYCEGNSS-PCYPEEDIKINYTEAWDVI SEACVYK

T. b. gambiense

1 GEKLVGMTLINDFFLCLVGEA INVTEDMRQ-----KKEEKEEKEEGKYSDSVYNGFNCPCRDEIRRP

2 GDKLVGKTLINDFFLCLVGEAD-----KVQTQSATDGDYKLTLEIYNRLNCPCKDAIRRP

3 GDKLVGKTLINDFFLCLVGEA INVTEDMK-----QKKEEKKKEEGKYSDSVYNGFNCPCRDGIIRRP

4 GDKLVGKTLINDFFLCLVGEA INVTGEI IKEEKKKKEEKKKE-----EKEKEEKEKEEGVLKIGPNATDGDYNLTMIEIYNRLNCPCKDAIRRP

5 GDKLVGKTLINDFFLCLVGEA HKVQTG-----QSATDGDNLTLIEIYNRLNCPCKDAIRRP

6 GDKLVGKTLINDFFLCLVGEA ISVTGEI IKEEKKKKEEKEKEVKEEEVKEEEEEKEEKKKEVEEVQSVQSATDGDYNLTIIEIYNRLNCPCKDAIRRP

7 GDKLVGKTLINDFFLCLVGEA H-----KVQTQSGTDGDYNLTIIEIYNRLNCPCKDAIRRP

8 GDKLVGKTLINDFFLCLVGEA ISVTGDMKEEKEE-----EKKEEKEKEEVEQSVQSATAGDYKLTLEIYNRLNCPCKDAIRRP

9 GDKLVGKTLINDFFLCLVGEA HKVQTG-----QSATDGDNLTLIEIYNRLNCPCKDAIRRP

10 GDKLVGKTLINDFFLCLVGEA INVTEDMGQ-----KKKEEQRRKEGKYSDSVYNGFNCPCRDAIRRP

11 GDKLVGKTLINDFFLCLVGEA INVT EEMK-----KKKEEKEGGKYSDSVYNGFNCPCRDEIRRP

12 GDKLVGKTLINDFFLCLVGEA ISVTGEI IKEEKKKKEE-----E-----EVKEEEVQSVQSATDGDYNLTMIEIYNRLNCPCKDAIRRP

13 GDKLVGKTLINDFFLCLVGEA H-----KVQTQSAADGDYKLTMIIEIYNRLNCPCKDAIRRP

14 GDKSVGKTLINDFFLCLVGEA INVTEDMRQ-----KKEEKEEKEEGKYSDSVYNGFNCPCRDAIRRP

15 GDKLVGKTLINDFFLCLVGEA H-----KVQTQSGTDGDYNLTIIEIYNRLNCPCKDAIRRP

16 KEKLVGKTLINDFFLCLVGEA INVTGEI IKE-----EKKKEEKEEKEGKYSDSVYNGYNCPCRDAIRRP

17 GDKLVGKTLINDFFLCLVGEA IDIVKKEERRKEE-----KEEEVQSVQSATAGDYNLTMIEIYNRLNCPCKDAIRRP

T. b. brucei

T. equiperdum

1 KSVGKTLINDFFLCLVGEA INVTEDMR--QKKEKEEKEKEGKYSDSVYNGFNCPCRDAIRRPESGWTMAAEYCEGNSSPCYPEEDIKINYTEAWDVI SEAE

2 KSVGKTLINDFFLCLVGEA INVTGEI IKEEKKKKEEKEKEEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSSPCNPDNIKINYTEAWDVI SEAE

3 KLVGKTLINDFFLCLVGEA HKVQTQS-----ATDGDNLTMIEIYNRLNCPCKDAIRRPESGWTMAAEHCDGGERICDPENVTYGHTAEAWDVI SEAE

4 KLVGKTLINDFFLCLVGEA INVTGEI IKEEKKKKEEKEKEEGKYSDSVYNGYNCPCRDAIRRPESGWTMAAEYCEGNSSPCNPDNIKINYTDAWDVI SKA

ESAG2p type

	300	310	320	330	340	350	360	370	380	390									
<i>T. b. gambiense</i>	1	NIGSNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSYKH	TL	ENGGIP	PWYNHL	TNATE	QLQEM	TKYAKE	ADSHL	HELEEY
	2	NVASNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	HELEEY
	3	NVASNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	HELEEY
	4	NVASNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	HELEEY
	5	NIASNVKT	LKSALA	QFDSL	LVNLEQ	DKYQV	RGIFGY	VKTEHN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNHL	TNATE	QLQEM	DKYAKE	ADSHL	HELEEY
	6	NVASNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DMYAKE	ADSHL	HELEEY
	7	NVASNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	YVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	HELEEY
	8	NIASNVKT	LKSALA	QFDSL	LVNLEQ	DKYQV	RGIFGY	VKTEHN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	HELEEY

T. b. brucei

1	KNGSWT	MMAEY	CEGNSS	PCNPED	IKYNH	TEAWDV	ISKACV	YKSVAS	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	RGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
2	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISKACV	YKNVAS	SNVKT	LKSALA	QFDAL	VNLEQ	DEYQV	KGVLGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
3	KNGSWT	MMAEY	CEGNSS	PCNPED	IKYNH	TEAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
4	KSGSWT	MMAEY	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISEACV	YKNIG	SNVKT	LKSALA	QFDAL	VNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
5	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISEACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGIFGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
6	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
7	KSGSWT	MMAEY	CKGGED	ICNPEN	VTYGHT	EAWDV	ISEACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
8	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISKACV	YKNVAS	SNVKT	LKSALA	QFDAL	VNLEQ	DEYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
9	KSGSWT	MMAEH	CDGVER	ICDPEN	VTYGHT	EAWDV	ISKACV	YKNVAS	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
10	KNGSWT	MMAEY	CEGNSS	PCNPED	IKYNY	TEAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
11	KNGSWT	MMAEY	CEGNSS	PCNPED	IKYNY	TEAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
12	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISKACV	YKNVAS	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	SHTAGFT	CVSY	
13	KSGSWT	MMAEH	CDGDGR	LCDPEN	VTYGHT	EAWDV	ISKACV	YKNVAS	SNVKT	LKSALA	QFDAL	VNLEQ	DEYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
14	KNGSWT	MMAEY	CEGNSS	PCNPED	IKYNY	TEAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
15	KSGSWT	MMAEY	CKGGED	ICNPEN	VTYGHT	EAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSY	
16	RSGSWT	MMAEY	CEGNSS	PCNPED	IKYNY	TEAWDV	ISKACV	YKNVAS	SNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSY	
17	KSGSWT	MMAEH	CDGDGR	MCDPEN	VTYGHT	EAWDV	ISKACV	YKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRS	DHNKNH	ACT	GHTAGFT	CVSY

T. equiperdum

1	CVYKNIA	SNVKT	LKSALA	QFDSL	LVNLEQ	DKYQV	RGIFGY	VKTEHN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNHL	TNATE	QLQEM	DKYAKE	ADSHL	LHE
2	CVYKNIA	SNVKT	LKSALA	QFDSL	LVNLEQ	DKYQV	RGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNHL	TNATE	QLQEM	DKYAKE	ADSHL	LHE
3	CVYKNIG	SNVKT	LKSALA	EFDDL	LVNLEQ	DKYQV	KGILGY	VRTDHN	KNHACT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNRL	SNATE	QLQEM	DKYAKE	ADSHL	LHE
4	CVYKNVA	SNVKT	LKS	VLAQFN	ALVNLE	QDKYQV	KGIFGY	VKTENN	DNRTCT	GHTAGFT	CVSYSY	TL	ENGGIP	PWYNHL	TNATE	QLQEM	DKYAKE	ADSHL	LHE

ESAG2p type

400 410 420 430 440 450 460 470 480 490 503

T. b. gambiense

1 EDEAEEIFLEAKLGGDAELWKSSQGKGYSGGDDTVVNDGLTHLNMETGGFTLLVLSLICTL
 2 EDEAEEIFLEAKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGGFTLLVLSLICTL
 3 EDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGGFTLLVLSLICTL
 4 EDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGGFTLLVLSLICTL
 5 EDEAEEIFLEAKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGGFTLLVLSLICTL
 6 EDEAEEIFLEVKLGGDAELWKSSQGK----GDNTVVDNDGLTHLNIATGGFTLLVLSLICTL
 7 EDEAEEIFLEVKLGGDAELWKSSQGKGYSEGDGDDSRVDNDGLTHLNIATGGFTLLVLSLICTL
 8 EDEAEEIFLEAKLGGDAELWKSSQGKGDGEGDDARVDNDGLTHLNIATGGFTLLVLSLICTL

T. b. brucei

1 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHLHELEEYDEAEEIFLEVKLGGDELWKSSQGK----GDDARVDNDGLTHLNIATGVAMLLIISLFCCTL
 2 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARLDNDGLTHLNIATGVAMLLIISLICTL
 3 NYTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDNTVVDNDGLTHLNIATGVAMLLVLSLFCML
 4 KHTLENGGIPWYNRLSNATEQLQEMDKYAKEADSHIHELEDYQHEAEEIFLEVKLGGDELWKNRGRDDVEGAGTDVNDGLTHLNIATGVAMLLIIPLFCCTL
 5 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARVDNDGLTHLNIATGGFTLLVLSLICTL
 6 KHTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARVDNDGLTHLNIATGVAMLLIISLICTL
 7 KHTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDNTVVDNDGLTHLNIATGVAMLLIISLICTL
 8 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGVVMLLVLSLFCCTL
 9 SYTLENGGIPWYNRLSNATEQLQEMDKYAKEADSHLHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDNTVVDNDGLTHLNIATGGFTLLVLSLICTL
 10 NYTLENGGIPWYNHLTNATAQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARVDNDGLTHLNIATGVAMLLIISLICTL
 11 NHTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEAKLGGDAELWKSSQGKGYSGGDDTVVNDGLTHLNIATGVAMLLIISLICTL
 12 KHTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFFEVKLGDAELWKSSQGK----GDDARVDNDGLTHLNIATGVAMLLIISLICTL
 13 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDNTVVDNDGLTHLNIATGVAMLLIISLICTL
 14 NYTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEAKLGGDAELWKSSQGKGYSGGDDTVVNDGLTHLNIATGVAMLLIISLICTL
 15 KHTLENGGIPWYNHLTNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARVDNDGLTHLNIATGVAMLLIISLICTL
 16 SYTLENGGIPWYNRLSNATEQLQEMDKYAKEADSHLHELEEYDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDDSRVDNDGLTHLNIATGVAMLLIISLICTL
 17 KHTLENGGIPWYNRLSNATEQLQEMDMYAKEADSHIHELEEYDEAEEIFLEVKLGGDAELWKSSQGK----GDDARVDNDGLTHLNIATGVVMLLVLSLFCCTL

T. equiperdum

1 LEEYEDEAEEIFLEAKLGGDAELWKSSQGKGDGEGDDARVDNDGLTHLNIATGGFTLLVLSLICTL
 2 LEEYEDEAEEIFLEVKLGGDAELWKSSQGKGDGEGDDARVDNDGLTHLNIATGGFTLLVLSLICTL
 3 LEEYEDEAEEIFLEVKLGGDAELWKSSQGK----GDNTVVDNDGLTHLNIATGGFTLLVLSLICTF
 4 LEEYEDEAEEIFLEAKLGGDAELWKSSQGKGDGEGDDARVDNDGLTHLNIATGGFTLLVLSLICTL