## Supplementary Figures

	20		40	60	80	
Cd rein Plus	MS TTHPP - ERGLVALIKG	TIGNVPALQPDVLEL	YAELKGAYEAQERAAP -	REYAGDQDEDVE	QACKQASLLEVARVL	76
Cd rein Minus	MS TTHPP - ERGLVALIKG	TIGNVPALQPDVLEL	YAELKGAYEAQERAAP -	REYAGDQDEDV	QACKQASLLEVARVL	76
Cd alob	MS TTHPP - ERGLVALIKG	TVGNVPALQPDVLDL	YAELKEAYEAQERAAPTI	DRQTEFAGDQDEDV	QACKQASLLFVARVL	80
Gn pect Plus	MSAE-AERFTALLKS	SLGNTPAAQEGLQRL	FAELQECYEEQERVSP -	PEFVGEQDEELF	NACRQASILFVARVL	73
Gn_pect_Minus	MSAE-AERFTALLKS	SLGNTPAAQEGLQRL	FAELQECYEEQERVSP -	PEFVGEQDEELF	NACRQASILFVARVL	73
Ym_unic_Plus/Minus	MDVALGGGIAP - IDRV\$\$LLKG	KVGSTPAVQEGVLQL	YAELKDCYEAQERAAP -	AEYAGEQDEDV	QACKQASLLFVARVL	80
Eu_spMale	MA-AFSGGVAPLLDRLSSLLKD	EKLDSASA - HAGITKV	YDELKECYEAQERASPS	SEYSVEQDEELF	RQACTQASLLFVARVL	80
Eu_spFemale	MA - AFSGGVAPLLDRLSSLLKD	EKLDSASA - HAGITKV	YDELKECYEAQERASPS	SEYSVEQDEELF	RQACTQASLLFVARVL	80
Pl_star_Male/Female						-
Vx_afri_Male	MD - AFSSGVTP - VDRLSSLFND	KIDDVTA-HEGLLKL	FEELKECYEAQEPAAP -	TEYMGEQDEELM	QICTQASLLFVARVM	78
Vx_afri_Female	MD - AFSSGVAP - VDRLSSLFND	KIDDVTA-HEGLLKL	FEELKECYEAQEPAAP -	TEYMGEQDEEL	QICTQASLLFVARVM	78
Vx_obve_Male	???????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	???????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,	******	-
Vx_car_naga_Male	MD RMNTGGPPVERL\$\$LLKG	TLN-DDVAREKLFML	FDELKECYEAQERATP -	AEFTGEQDEEL	(HLCTEASLLFVARVL	78
Vx_car_naga_Female	MD TLNRNGPLNDRISFLLKE	/NFG-DAISQEGFLQL	YRELRASYECQENASP -	ASDYAGEQDEEVE	(HLCTQASLLFVARVL	79
Vx_car_kawa_Male	MD TINSGGPPVEWLSSLLKG	KLE-DDTSREKLLKL	FRDLKESYEAQERATP -	AEYTGEQDEEL	(HLCTEA\$LLFVARVL	78
Vx_car_kawa_Female	MD ALNSSSPLVEKISFLLKE	KYG-DAIAQEGFLQL	YRELRDNYECQESASS -	ASDYAGEQDEEVH	(YLCTQASLLFVARVL	79
Vx_car_weis_Male	7777777777777777777777777777777	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	*****	,,,,,,,,,,,,,,,,,,,,,,	*****	-
Vx_car_weis_Female	******		******	,,,,,,,,,,,,,,,,,,,,,,	*******	-
	100	120	140		160	
Cd rein Plus	SAAQKKEKDGSETQPSNLGLSI	RIVAVAGINLLDFFR	EVHVVVSELSAYFESRG	SSSKQFSQQALLKEN	SETVVVMGLLAKKYK	161
Cd rein Minus	SAAQKKEKDGSETQPSNLGLSI	RIVAVAGINLLDFFR	EVHVVVSELSAYFESRG	SSSKQFSQQALLKEN	SETVVVMGLLAKKYK	161
Cd_glob	SAAQKKEKDGSEAKRTNLGLSI	RIVAVAGINLLDFIR	EVQVIVSKLSAYFESRG	SSSNQFSQQALLQET	SETIVVMGLLAKKYK	165
Gn_pect_Plus	FFQDKPD AHAS GCSI	STIVSAAGINLLDFFR	EVNVVVSKLSAYFEAHG	SSSKLFCQAAHLKEN	SEMVVVLGLLAKKFK	151
Gn_pect_Minus	FFQDKPD AHAS GCSI	STIVSAAGINLLDFFR	EVNVVVSKLSAYFEAHG	SSSKLFCQAAHLKEN	SEMVVVLGLLAKKFK	151
Ym_unic_Plus/Minus	FAAQKQD GDPQPANLGCS I	SRIVAAAGINLLDFFR	EVNVVVSKLSAYFEARG	GSSKLFTQQAQLKEN	ISETVVVMGLLAKKYK	162
Eu_spMale	FAKQSPG TAGCPSNMGCPI	SKIVAVAGINLLDFFR	EVNLVVSKLSAYFEARG	SSSRFFTQQAQLKEN	ISETVVVLGLLAKKYK	162
Eu_spFemale	FAKQSPG TAGCPSNMGCPI	SKIVAVAGINLLDFFR	EVNLVVSKLSAYFEARG	SSSRFFTQQAQLKEN	ISETVVVLGLLAKKYK	162
Pl_star_Male/Female					MVVVMGLLAKKYK	13
Vx_afri_Male	FAAQ\$RD CKIMPANLGCPI	SRIVAAAGINLLDFFR	EVNVVVSKLSTFFESRG	GSARLFTQQAQLKEN	SETVVVMGLLAKKYK	160
Vx_afri_Female	FAAQSRD CKIMPANLGCPI	SRIVAAAGINLLDFFR	EVNVVVSKLSTFFESRG	GSARLFTQQAQLKEN	ISETVVVMGLLAKKYK	160
Vx_obve_Male		???????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	?????????????????	******	-
Vx_car_naga_Male	FVAQSGV GRNAPGHIGCPI	SRIVAAAGINLLDFFR	EVHVVVSKLSAYFEARG	GSSRIFTQQAQLKEN	SETVVVMGLLAKKYK	160
Vx_car_naga_Female	FAAQAQG GRTVSNFGCPI	SRIVAAAGINLLDFFR	EVNVVVSKLSSYFEARG	GSSRLFAQQAQLKEN	SETVVVMGLLAKKYK	160
vx_car_kawa_Male	FVAQSGI GRNAPAHIGCPI	SRIVIAAGINLLDFFR	EVYVVVSKLSAYFEARG	GSSRIFIQQAQLKEN	SEIVVVMGLLAKKYK	160
vx_car_kawa_remale	FAAKAQGGEKVPNLGCPV	SRIVAAAGINLLDFFR	EVNVVVSKLSSYFEARG	GSSRLFAQQAQLKEN	SEIVVVMGLLAKKYK	160
vx_car_weis_male						-
vx_car_weis_remaie						-
	180	2000	7171/2			
	1	200	220	24		
Cd_rein_Plus	DNFNTFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILAS	HAPRLPDCLTHITRE	DRGKFLLKSMADTCK	246
Cd_rein_Plus Cd_rein_Minus	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILAS	HAPRLPDCLTHITRE HAPRLPDCLTHITRE	DRGKFLLKSMADTCK ENRGKFLLKSMADTCK	246 246
Cd_rein_Plus Cd_rein_Minus Cd_glob	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD GAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLTHITRE	DRGKFLLKSMADTCK ENRGKFLLKSMADTCK ENRGKFLLKSMADTCK	246 246 250
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD GAFLVLRVKLLSAFPD LAFLVLRVKLLGPFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI VVSCVELLPCVFAVLVSI	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLAHITRE HAPRLPDCLARITRE	<sup>10</sup> EDRGKFLLKSMADTCK ENRGKFLLKSMADTCK EDREKLLLKSMADVCK EQ-RSDLLRRMAEMCK	246 246 250 235
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLSAFPD AFLVLRVKLLGPFPD AFLVLRVKLLGPFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI VVSCMELLPCIFAILASI VVSCVELLPCVFAVLVSI	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLAHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE	DRGKFLLKSMADTCK ENRGKFLLKSMADTCK EDREKLLLKSMADVCK G. RSDLLRRMAEMCK EQ.RSDLLRRMAEMCK	246 246 250 235 235
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD GAFLVLRVKLLSAFPD GAFLVLRVKLLGPFPD GAFLVLRVKLLGPFPD	ZZO VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI	HAPRLPDCLTH I TRE HAPRLPDCLTH I TRE HAPRLPDCLAH I TRE HAPRLPDCLKR I TRE HAPRLPDCLKR I TRE HAPRLPDCLSH I SRE	DRGKFLLKSMADTCK ENRGKFLLKSMADTCK EDREKLLLKSMADTCK G. RSDLLRRMAEMCK EQ. RSDLLRRMAEMCK ENRANLLLKTMSEMCK	246 246 250 235 235 247
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD GAFLVLRVKLLSAFPD AFLVLRVKLLGPFPD LAFLVLRVKLLGPFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	ZZO VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLAHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHISRE HAPRLPDCLSHLTRE	URGKFLLKSMADTCK ENRGKFLLKSMADTCK DREKLLLKSMADVCK G-RSDLLRRMAEMCK EQ-RSDLLRRMAEMCK ENRANLLKTMSEMCK EDNKTALLKAMSEMCK	246 246 250 235 235 247 247
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Eu_sp_Gemale Eu_sp_Gemale	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLSAFPD AFLVLRVKLLGPFPD FAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCMELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLAHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHISRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADVCK G.RSDLRRMAEMCK G.RSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DNKTALLKAMSEMCK	246 250 235 235 247 247 247
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Pl_star_Male/Female	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILSI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI	A HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKHISRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADVCK Q - RSDLLRRMAEMCK NRANLLKRMAEMCK DNKTALLKAMSEMCK JONKTALLKAMSEMCK JONKTALLKAMSEMCK	246 250 235 235 247 247 247 98
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Eu_sp_Female Pl_star_Male/Female Vx_afri_Male	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLGPFPD AFLVLRVKLLGPFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE	U ENRGKFLLKSMADTCK ENRGKFLLKSMADTCK EREKLLKSMADVCK EREKLLKSMADVCK EREKLERMAEMCK EREKLKRMSEMCK ENRTALLKAMSEMCK EDNKTALLKAMSEMCK EGEKPALLKAISEMCK EGERPALLKTMSEMCK	246 250 235 235 247 247 247 98 245
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Vs_afri_Male Vx_afri_Female Vx_afri_Female	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDYKQVVLRLGW DNFHIFLHQLELYKQWVLKLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLGPFPD AFLVLRVKLLGPFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLACI VVSCMELLPCVFAVLACI VVSCMELLPCVFAVLACI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSAC	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK CREKLLKSMADVCK G.RSDLLRRMAEMCK G.RSDLLRRMAEMCK EDNKTALLKAMSEMCK GEKPALLKAMSEMCK GEKPALLKANSEMCK DGRPALLATMSEMCK	246 250 235 247 247 247 247 98 245 245
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_female Pl_star_Male/Female Vx_afri_Male Vx_afri_Female Vx_obve_Male Vx_cobve_Male	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLKLGW DNFHIFLHQLELYKQMVLKLGW 2727272727272727272727272	AFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD DAFLVLRVKLLSAFPD AFLVLRVKLLSAFPD AFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLACI VVSCMELLPCVFAVLACI VVSCMELLPCVFAVLACI VVSCMELLPCVFAVLACI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLSHISRE HAPRLPDCLSHISRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE 7?????????????	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADVCK Q-RSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DOKTALLKAMSEMCK DOKTALLKANSEMCK DORTALLKAISEMCK DGRPALLKTMSEMCK 27272727272727272	246 250 235 247 247 247 98 245 245 - 243
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus/Minus Eu_sp_Female Pl_star_Male/Female Vx_afri_Female Vx_afri_Female Vx_car_naga_Male Vx_car_naga_Male	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLEYKQWVLRLGW DNFNHFLHQLELYKQWVLKLGW DNFHIFLHQLELYKQWVLKLGW DNFHIFLHQLELYKQWVLKLGW DNFNLFLHQLDFFKQVVLRLGW	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLGPFPD AFLVLRVKLLGPFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAULASI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHVSGE	U ENRGKFLLKSMADTCK NRGKFLLKSMADTCK EDREKLLKSMADTCK CORSDLRRMAEMCK CORSDLRRMAEMCK NRANLLKTMSEMCK EDNKTALLKAMSEMCK EDNKTALLKAMSEMCK EDGRPALLKTMSEMCK EDGRPALLGTMSEMCK 27272727272???? SS - KLLKALSDMCK	246 250 235 235 247 247 247 98 245 - 245 - 243 245
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Raile Eu_sp_Female Vx_afri_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_car_naga_Male Vx_car_naga_Female Vx_car_naga_Female	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFNMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW ????????????????????????????????????	SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLGPFPD AFLVLRVKLLGPFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSSFPD	VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLACI VVSCMELLPCVFAVLACI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAILVSI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE APRLPDCLSHLSHE APRLPDCLSHLSHE MAPRLPDCLSHLNGG	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADTCK G-RSDLLRRMAEMCK G-RSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DNKTALLKAMSEMCK DGRPALLKTMSEMCK ??????????????? S-KLLKALSDMCK EYRSALLKSLSEICK	246 246 250 235 247 247 247 98 245 245 245 243 245 244
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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Female Pl_star_Male/Female Vx_afri_Female Vx_afri_Aale/Female Vx_car_naga_Male Vx_car_naga_Female Vx_car_kawa_Female Vx_car_kawa_Female Vx_car_weis_Male	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNHFLHQLEYKQWVLKLGW DNFNHFLHQLEYKQWVLKLGW DNFNLFLHQLDFFKQVVLRLGW DNFNLFLHQLDFFKQVVLRLGW DNFNLFLHQLDFFKQVVLRLGW DNFNLFLHQLDFFKQVVLRLGW DNFNLFLHQLDFFKQVVLRLGW DNFNLFLHQLDFFKQVVLRLGW DNFNMFLHQLDFFKQVVLRLGW	200           SAFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           AFLVLRVKLLSAFPD           AFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           SAFLVLRVKLLSFPD           SAFLVLRIKLLSFPD           SAFLVLRIKLLSFPD           SAFLVRVKLLSFPD           SAFLVRIKLLSSPD           SAFLVRIKLLSSFPD           SAFLVRIKLLSSFPD           SAFLVRIKLLSSFPD           SAFLVRIKLLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLVRIKLSSFPD           SAFLSSFPD           SAFLSSFPD           SAFLSSFPD           SAFLSSFPD           SAFLSSFPD           SAFLSSFPD <t< td=""><td>24 VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLACI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI</td><td>APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHVSGA HAPRLPDCLSHLNGG HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA</td><td>U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADTCK G.RSDLLRRMAEMCK G.RSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DDKTALLKAMSEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK VGRPALLKAISEMCK SCKPALLKASLSDMCK VEYRSALLKSLSDICK S-KPALLKASDNCK VEYRSALLKSLSDICK S-KPALLKASDNCK</td><td>246 250 235 247 247 247 247 247 245 - 243 245 - 243 245 - -</td></t<>	24 VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLACI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI VVSCVELLPCVFAILASI	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHVSGA HAPRLPDCLSHLNGG HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA HAPRLPDCLSHVSGA	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADTCK G.RSDLLRRMAEMCK G.RSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DDKTALLKAMSEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK VGRPALLKAISEMCK SCKPALLKASLSDMCK VEYRSALLKSLSDICK S-KPALLKASDNCK VEYRSALLKSLSDICK S-KPALLKASDNCK	246 250 235 247 247 247 247 247 245 - 243 245 - 243 245 - -
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect,Plus Gn_pect,Plus Ym_unic_Plus/Minus Eu_sp_Alae Eu_sp_Alae Eu_sp_Alae Vx_afri_Female Vx_afri_Female Vx_afri_Male Vx_car_naga_Female Vx_car_kawa_Male Vx_car_weis_Female Vx_car_weis_Female	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFEALLPHLDYYKQVVLRLGW DNFMFLHQLDYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW ONFNMFLHQLDFYKQVVLRLGW 77???????????????????? DNFNLFLHQLDFFKQVVLRLGW DNFHIFLHQLDFFKQVVLRLGW DNFMLHQLDFFKQVVLRLGW DNFSMFLHQLDFFKQVVLRLGW 2????????????????????????????????????	244           SAFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           AFLVLRVKLLSAFPD           AFLVLRVKLLSAFPD           SAFLVLRVKLLSAFPD           Y????????????????????           SAFLVLRVKLLSSFPD           YZ????????????????????????????????????	240 VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLACI VVSCVELLPCVFAVLACI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAVLASI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELLPCVFAILVSI VVSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI VSCVELPCVFAILVSI V	HAPRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLKHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSHE HAPRLPDCLSHLSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDCLSHVSG HAPRLPDC HAPRLPDCLSHVSG HAPRLPDC HAPRLPDC HAPRLPDC HAPRLPDC HAPRLPDC	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK CREKLLKSMADTCK GRSDLRRMAEMCK GRSDLLRRMAEMCK NRANLLKTMSEMCK DNKTALLKAMSEMCK DNKTALLKAMSEMCK DORFALLKANSEMCK 2077??????????????? 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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Female Plus/Minus Plus/Minus Vx_afri_Hemale Vx_afri_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_awas_Female Vx_car_awas_Female Cd_rein_Plus Cd_rein_Plus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Eu_sp_Female Vx_car_male/Female Vx_car_naga_Male Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female	DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFNTFLHQLDFYKQVVLRLGW DNFEALLPHLDYKQVVLRLGW DNFEALLPHLDYKQVVLRLGW DNFMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFYKQVVLRLGW DNFNMFLHQLDFKQVVLLGW DNFNHFLHQLDFKQVVLLGW DNFNHFLHQLDFKQVVLLGW DNFNHFLHQLDFKQVVLLGW DNFNLFLHQLDFKQVVLLGW DNFNLFLHQLDFKQVVLLGW DNFNKFLHQLDFKQVVLLGW DNFNKFLHQLDFKQVVLLGW DNFNKFLHQLFXQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW DNFNKFLHQLFKQVVLLGW T????????????????????????????????????	AFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD AFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD SAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVLRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVKLLSAFPD FAFLVRVRLSAFPD FAFLVRVRLSAFPD FAFLVRVRLSAFPD FAFLVRVRAFFL FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF FAFLF	240 VVSCVELLPCIFAILASI VVSCVELLPCIFAILASI VVSCVELLPCVFAVLVSI VVSCVELLPCVFAVLVSI VVSCVELLPCIFAILASI VVSCVELLPCIFAILVSI VVSCVELLPCIFAILVSI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VVSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI VSCVELLPCVFAVLASI SVLAKATAAEKCFFG SNLAKATAAEKCFFG SNLAKAAAEKCFFG	APRLPDCLTHITRE HAPRLPDCLTHITRE HAPRLPDCLAHITRE HAPRLPDCLKRITRE HAPRLPDCLKRITRE HAPRLPDCLSHITRE HAPRLPDCLSHLTRE HAPRLPDCLSHLTRE HAPRLPDCLSHLSHE Y777777777777777777777777777777777777	U DRGKFLLKSMADTCK NRGKFLLKSMADTCK DREKLLKSMADTCK CORSDLRRMAEMCK GARSDLRRMAEMCK GARSDLRRMAEMCK DRTALLKAMSEMCK DNKTALLKAMSEMCK DGRPALLKTMSEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK DGRPALLKAISEMCK DGRPALLKSLS SARA CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST CORST 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	360	380	400	420	
Cd rain Plue				PEGGPI CPGI HTA	388
Cd rein Minus	PVLEGLVTDTDPMNRVVAALERETEQH	SRGATELDEREFLSIDFIRFASF	RESPONDESTMAKERSOSMET	RECORLOPCINTA	300
Cd_rein_winus	PVLEGLVIDIDRMNRVVAALERETEGH	SKGATELDEREFLSTDFIKFASP	RESPONNES IMAKLESGSMPI	RSGGPLGPGLHTA	200
Ca_glob	PVLEGLVINMERMNRAVAALERETEQH	SRGATELDEREFLSTDFTRFASP	RESPGHMHSIMAKERSEPMPI	RSGGLLSPGLHII	300
Gn_pect_Plus	PILSGLVIDIDRMNLALAALERVYEQHI	ACSGSELDEREFLIIDFIKFASP	RYSPGQMHYVLSILRGGSIP	IRPGILLGPGAHRI	3/4
Gn_pect_Minus	PILSGLVIDIDRMNLALAALERVYEQHI	ACSGSELDEREFLIIDFIKFASP	RYSPGQMHYVLSILRGGSIP	IRPGILLGPGAHRI	374
Ym_unic_Plus/Minus	PILEGLVTDSDRMNRAVAALEVEYEQH	VRGTSELDERDFLSTDFTKFASP	RFSPGQMHSVMTKLRGGPMPI	RPGDLLGPGAHTT	393
Eu_spMale	SSLEGLVTDADRMQRALAALETEYEQH	NRGDSELDEREFLQTDFTKFASP	RLSPAHLQTAMAKVRAGPMPI	RQGALLGPGAHTT	392
Eu_spFemale	SSLEGLVTDADRMQRALAALETEYEQH	NRGDSELDEREFLQTDFTKFASP	RLSPAHLQTAMAKVRAGPMPI	RQGALLGPGAHTT	392
Pl_star_Male/Female	PVLEGLVTDADRMQRALAALEAEYEQH	TLGGTELDERQFLHTDFTKFASP	RF\$\$GHLHAAMTKLRAGPMPI	RQGGLLGPGAHTT	244
Vx_afri_Male	PVLEGLVTDADRMQRAITALEAEYERH	KHGGSELDEREFLFTDFTKFASP	RFSPRHMHSAITKLQSGPTPI	RQGALLGPGAHIT	391
Vx_afri_Female	PVLEGLVTDADRMQRAITALEAEYEQH	KHGGSELDEREFLFTDFTKFASP	RFSPRHMHSAITKLQSGPTPI	RQGALLGPGAHIT	391
Vx_obve_Male	PVLEGLVTDGIRMEQALAALEAEYEHHY	VHGGSELDEREFLYTDFAKFASP	RLSPGHIHSAMVKLRSGFLPI	RQGALLGPGAHTT	95
Vx car naga Male	PVLEGLVTDAVRMQRALDALESEYEKHY	EHGGSELDEREFLFTDFTKFASP	RFSPGHMQSAITKMRLGPMPI	RQGALLGPGAHTT	387
Vx car naga Female	RLLEGLVTDGNRMQRALSALETEYAQH	TRGGSELDEREFLFTDFTKFASP	RFSPRHMQSAVMKLRAGPLP	RQGSLLGPGAHTT	392
Vx car kawa Male	PVLEGLVTDAARMQRALDALESEYEKHY	ALGGSELDEREFLYTDFTKFASP	RFSPGHMQSAVTKLRLGPMPI	RQGALLGPGAHTT	407
Vx car kawa Female	RVLEGLVTDANRMQRALSAMELEYEQH	TRGGSELDEREFLYTDFSKFASP	RFSPGHMQSAVMKLRAGPLP	RQGEFLGPGAHTT	401
Vx car weis Male	PVLEGLVTDAVRMQRALDALESEYEKY	VHGGSELDEREFLYTDFTKFASP	RESPGHMQSAITKLRLSPMPI	RQGGLLGPGAHTT	117
Vx car weis Female	RVLEGLVTDANRMORALTALETEYEOH	TRGGSELDEREFLYTDETKEASP	RESPGHMQSAVMKLGAGPLP	RQGALLGPGAHIT	104
	440	460	480	500	
	1	1	1	1	
Cd_rein_Plus	TPAHPGPQQ LHL VPLGLHSPI	PMMHLNAGPGVPGTPISEAMGAS	AWLRGVTSNMVAEPSPTLQR	LAALPI	459
Cd rein Minus	TPAHPGPQQ LHL VPLGLHSPI	PMMHLNAGPGVPGTPISEAMGAS	AWLRGVTSNMVAEPSPTLQR	LAALPI	459
Cd glob	IPAHPGPQQ MQL - MGPAPWLHSPI	PMMHLNAGPGLQGTPISEAMGAS	AWLRGVTSSMAAEPSPALQRI	LAALPI	459
Gn pect Plus	APQQ PMR SFPVSAGTPGLHSPI	PGVHCG - DPGPPITPVSELMSAS	TWLRGLATTLTAEPSCTLQR	LAAVPVSV	447
Gn pect Minus	APQQ PMR SFPVSAGTPGLHSPI	PGVHCG - DPGPPITPVSELMSAS	TWLRGLATTLTAEPSCTLOR	LAAVPVSV	447
Ym unic Plus/Minus	APSHP - PTSHHMSMHIRMDIAPGLHSPI	PMMHLGAGAGQPGTPVSEVMGAS	AWLRGVTANLAPEPSPVLQR	LAAVNVPSGASQA	477
Eu sp. Male	APSPSSPQY I QEKMAPSPGEHSPI	PMI HI GVDI GQPNTPVSEVMGAS	AWIRGVTASIQTEPSASIME	(LEAVSVPGGVGQS	473
Fu sp. Female	APSPSSPQY I QEKMAPSPGEHSPI	PMIHIGVDIGOPNTPVSEVMGAS	AWIRGVTASIOTEPSASIME	LEAVSVPGGVGQS	473
Pl star Male/Female	ASNTSSPHPHITMSI STGMYSPI	PMIHIGMDSGOPNTPVSEVMGAS	AWIRSVIANIAPEPPPSIIO	EEAVAVPGAGPOS	324
Vy afri Male	ASSVS PHI INFTMPIPAGTHSPI	PMINIAMDVGOPTTPVSEVMSAS		LAAIDMPLSGTRS	471
Vy ofri Eemale					471
VX_all_Fellale		PHENEAMDVGQFIIFVSEVMSAS.			470
VX_ODVe_Male	APSAVSPHF LNLRIPMPAGMQSPI	PLENEGIDMGQPNIPVSEVMNAS	AWLRALIANLEAEFIFGLVR	ILSAGGAIKS	1/2
vx_car_naga_wale	APSSVSPRLNFRVPMSAGMHSPI	PVLNLSIDIGQPSIPVSEVMNIS	AWLRGRIANLAAEPSPGLIR	LAAVGGIRS	403
vx_car_naga_remale	ASTAISPSSMNPKISLLARMHSPI	PKLNLGVEIGPPVIPVSEIMSIS	AWLRGITASLAAEPSPSVMR	LAEVAVPPDGEQG	4/3
vx_car_kawa_Male	APSSVSPR LHFRVPMPAGMHSPI	PVLHLSIDIGQPSIPVSEVMNIS	AWLRGRIANLAAEPSPGLAR	LAAVGG IRS	483
Vx_car_kawa_Female	APCVISPSL MNLKTPLWAGVHSPI	PKLDLGVETGPPVTPVSEIMSAS	AWLRGVTANLAAEPSPSVMR	LATVAVPPYGEQG	482
Vx_car_weis_Male	APSSVSPR LNFRMPMPAGMHSPI	PVLNLGIDIGQPSIPVSEVMNIS	AWLRGRIANLAAEPSPGLIR	LAAVGG IRS	193
Vx_car_weis_Female	APYSISPSS TPLKTPFWAGLHSP	- KLDLGVEAGPPVTPVSEIMSAS	AWLRGVTANLAAEPSPSLMR	LAAVAVPHDGGQG	183
	500				
	520	540 560	580		
Cd rain Plue					544
Cd_rein_Plus		540 580 I AAPSLLGPFPLLNTSLGVERRIE	580 I ATKLYCHSLDTILQNEQRTNO		544
Cd_rein_Plus Cd_rein_Minus	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTGLGTPAQLMKRVRDLVASVIPD	640 560 AAPSLLGPFPLLNTSLGVERRIE.	580 ATKLYCHSLDTILQNEQRTNO ATKLYCHSLDTILQNEQRTNO ARLYCHSLDTILQNEQRTNO	GLPAALALLGSAKF GLPAALALLGSAKF	544 544
Cd_rein_Plus Cd_rein_Minus Cd_glob	SZU NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSTGLGPTPAQLLMKRVRDLVASVIPDI	500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSVLGPFPMLNTSLGAERRIE	580 ATKLYCHSLDTILQNEQRTNO ATKLYCHSLDTILQNEQRTNO AARLYCHSLETIMLNEERTNO AARLYCHSLETIMLNEERTNO	GLPAALALLGSAKF Glpaalallgsakf Glpaalallgsakf	544 544 544
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus	S20 I NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSTGLGPTPAQLLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI	540 550 HAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSVLGPFPMLNTSFGAERRIQ SSSTLLGSFP-LGPRLAAERRME	580 ATKLYCHSLDTILQNEQRTNO ATKLYCHSLDTILQNEQRTNO AARLYCHSLETIMLNEERTNO AYKLYLHSLETLLVAEEKVNO	GLPAALALLGSAKF GLPAALALLGSAKF GLPAALALLGSAKF GLAGVVALLSSSKF	544 544 544 531
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus	NSNSSGTPVQQLMKRVRDLVASVIPDI NSNSSGTPVQQLMKRVRDLVASVIPDI NSNSSGTPVQQLMKRVRDLVASVIPDI NSTGLGFTPAQLLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI	500 560 H APSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSVLGPFPMLNTSFGAERRTQ SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG	GLPAALALLGSAKF GLPAALALLGSAKF GLPAALALLGSAKF GLAGVVALLSSSKF GLAGVVALLSSSKF	544 544 544 531 531
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus	S20 NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSTGLGPTPAQLLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPPGSQSLAVQLSRRVRDMVASVIPDI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGVERRIE AAPSVLGPFPMLNTSFGAERRIE SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME NGPSVLGPFPLLQPSLAAERRME	ATKLYCHSLDT I LQNEQRTNO ATKLYCHSLDT I LQNEQRTNO ATKLYCHSLDT I LQNEQRTNO AARLYCHSLET I MLNEERTNO AYKLYLHSLETLLVAEEKVNO AYKLYLHSLETLLVAEEKVNO ATKLYYHSLET I LMSEEKASO	GLPAALALLGSAKF GLPAALALLGSAKF GLPAALALLGSAKF GLAGVVALLSSSKF GLAGVVALLSSSKF GLAGVVALLSSSKF	544 544 531 531 562
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSGPTPVQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPPGSQSLAVQLSRRVRDMVASVIPDI SGSAASAAAQQLSRRVRDLVLSIMPDI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSULGPFPLNTSLGAERRIE AAPSVLGPFPMLNTSFGAERRIG SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME RIPSVLGPFPLLQPSLAAERRME RIPALFGPFPLLQTSLAAERRME	ATKLYCHSLDT ILQNEQRTNC ATKLYCHSLDT ILQNEQRTNC AARLYCHSLDT ILQNEQRTNC AYKLYLHSLETIMLEETNNC AYKLYLHSLETILVAEEKVNC AYKLYLHSLETILVAEEKVNC ATKLYYHSLETILMSEEKASC VTKLYYHSLENILRAEEKASC	GLPAALALLGSAKF GLPAALALLGSAKF GLPAALALLGSAKF GLAGVVALLSSSKF GLAGVVALLSSSKF GLTGVTALLVATKF GIAAAIALLSAGKF	544 544 531 531 562 558
Cd_rein_Pius Cd_rein_Minus Cd_glob Gn_pect_Pius Gn_pect_Minus Ym_unic_Pius/Minus Eu_sp_Male Eu_sp_Female	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTGLGPTPAQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPPGSQSLAVQLSRRVRDMVASVIPD SGSAASAAAQQLSRRVRDLVLSIMPD	500 500 APSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE SAPSULGPFPMLNTSFGAERRIG SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME RIPALFGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE	ATKLYCHSLDTILQNEQRTN( ATKLYCHSLDTILQNEQRTN( ATKLYCHSLDTILQNEQRTN( AARLYCHSLETIMLNEERTN( AYKLYLHSLETLLVAEEKVN( ATKLYYHSLETILMSEEKAS( VTKLYYHSLENILRAEEKAS(	SLPAALALLGSAKF SLPAALALLGSAKF SLAGVVALLGSAKF SLAGVVALLSSSKF SLAGVVALLSSSKF SLTGVTALLVATKF SI AAA IALLSAGKF	544 544 531 531 562 558 558
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Female Pl_star_Male/Female	NSNSSGPT PVQQLMKRVRDLVASVI PDI NSNSSGPT PVQQLMKRVRDLVASVI PDI NSTGLGPT PAQLLMKRVRDLVASVI PDI AQAGTSLSAAEQLSRRIRELISLVI PDI SGPPGSQSLAVQLSRRVRDLVASVI PDI SGSAASAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAAQQLSRRVRELVSSVMPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGVERRIE AAPSVLGPFPMLNTSFGAERRIG SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME RGPSVLGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE KIPSLGPFPLLQTSLAAERRTE	580 ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG AYKLYLHSLETLLVAEEKVNG ATKLYYHSLETILMSEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILRAEEKASG	SIPAALALLGSAKF SIPAALALLGSAKF SIPAALALLGSAKF SLAGVVALLSSSKF SLAGVVALLSSSKF SITAVTALLVATKF SITAAIALLSAGKF SITAAIALLSAGKF SMPSAVALLSTGKF	544 544 531 531 562 558 558 409
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Fu_sp_Male Eu_sp_Male Pl_star_Male/Female Vx_afr_Male	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTGLGPTPAQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPASASAAAQQLSRRVRDLVLSIMPD SGSAASAAAAQLSRRVRDLVLSIMPD TCPTGPSAAAAQLSRRVRDLVSSVMPEI TYTSGYASAAEQLGQRVRDLVSSVMPEI	500     500       I     AAPSLLGPFPLLNTSLGVERRIE       AAPSLLGPFPLLNTSLGAERRIE     SAPSLGPFPLLNTSLGAERRIE       SSSTLLGSFP-LQPRLAAERRME     SSSTLGSFP-LQPRLAAERRME       SSSTLGSFP-LQPRLAAERRME     SSSTLGSFP-LQPRLAAERRME       RIPALFOPFPLLQTSLAAERRTE     SSTSLLGSFP-LQPRLAAERRME       ERIPALFOPFPLLQTSLAAERRTE     SSTLLGPFPLLQTSLAAERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG ATKLYHSLETILVAEEKNG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILQNEEKASG	SIPAALALLGSAKF SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SITGVTALLVATKF SIAAAIALSAGKF SIAAAIALSAGKF SMPSAVALLSTGKF SIAGVAPLLASGKF	544 544 531 531 562 558 558 409 556
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_female	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTSGLGPTPAQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPPGSQSLAVQLSRRVRDMVASVIPD SGSAASAAAQQLSRRVRDLVLSIMPD TCPTGPSAAAQQLSRRVRDLVLSIMPD TYTSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI	60     500       I     AAPSLLGPFPLLNTSLGVERRIE       AAPSLLGPFPLLNTSLGAERRIE       AAPSLLGPFPLLNTSLGAERRIE       SSSTLLGSFP-LOPRLAAERRME       SSSTLLGSFP-LOPRLAAERRME       NGPSVLGPFPLLQTSLAAERRME       RIPALFGPFPLLQTSLAAERRTE       EIPSLLGPFPLLQTSLAAERRTE       EIPSLLGPFPLLQSSLAVERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG AYKLYLHSLETLLVAEEKVNG ATKLYYHSLENILMSEEKASG VTKLYYHSLENILHXEEKASG VTKLYYHSLENILHVEEKASG ITKLYYHSLEIILQNEEKASG	SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SITGVTALLSSSKF SITGVTALLSSSKF SIAAIALLSAGKF SIAAIALLSAGKF SIAQVAPLLASGKF SIAGVAPLLASGKF	544 544 531 562 558 558 409 556 556
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male	NSNSSGTPVQLIMKRVRDLVASVIPDI NSNSSGTPVQLIMKRVRDLVASVIPDI NSNSGGTPVQLIMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPPGSQSLAVQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAQLSRRVRDLVLSIMPDI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSIMPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSULGPFPLLNTSLGAERRIE SAAPSULGPFPMLNTSFGAERRIE SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME RIPALFGPFPLLQTSLAAERRME RIPALFGPFPLLQTSLAAERRTE KIPSLLGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EAPSLLGPFPLLQSSLAVERRTE	580 ATKLYCHSLDTILQNEQRTNC ATKLYCHSLDTILQNEQRTNC AARLYCHSLETIMLEETTNC AYKLYLHSLETLLVAEEKVNC AYKLYLHSLETLLVAEEKVNC ATKLYYHSLETILMSEEKASC VTKLYYHSLENILRAEEKASC VTKLYYHSLENILHVEEKASC ITKLYYHSLENILHVEEKASC ITKLYYHSLEIILQNEEKASC VTKLYYHSLEIILQNEEKASC	SLPAALALLGSAKF SLPAALALLGSAKF SLPAALALLGSAKF SLAGVVALLSSSKF SLAGVVALLSSSKF SIAAVALLSSKF SIAAAIALLSAGKF SIAAAIALLSAGKF SLAGVAPLLASGKF SLAGVAPLLASGKF SMPGVTSLLLAGKF	544 544 531 562 558 558 409 556 556 255
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_spFemale Pl_star_Male/Female Vx_afri_Female Vx_afri_Female Vx_obve_Male Vx_car_naga_Male	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSGGTPVQQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPPGSQSLAAQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAAQQLSRRVRDLVLSIMPDI TCYTGSASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSIMPEI ANGSATAHQLGQRVRDLVSSIPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSLLGPFPLLNTSLGAERRIE SASTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME NGPSVLGPFPLLQTSLAAERRME RIPALFGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE EXAPSLVGAFPLLQSSLAVERRTE KIPSLVGAFPLLQSSLAAERRSE KIPSLVGAFPLLQSSLAVERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG ATKLYYHSLETILMSEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILRAEEKASG ITKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKASG	SIPAALALLGSAKF SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVTALLSSSKF SIAAIALLSSGKF SIAAIALLSAGKF SIAAAIALLSAGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SMAGVTSLLAGKF	544 544 531 562 558 558 409 556 556 255 548
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Eu_sp_Male Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Female Vx_cor_nga_Male Vx_car_nga_Female	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTGLGPTPAQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPAGSQSLAVQLSRRVRDMVASVIPD SGSAASAAAQQLSRRVRDLVLSIMPD TCPTGPSAAAQQLSRRVRDLVLSIMPD TYSGYASAAEQLGQRVRDLVSSVMPE TYKSGYASAAEQLGQRVRDLVSSVMPE - ANGSATAVHQLGQRVRDLVSSIMPE EVYTGSASTAHQLGQRVRDLVSSIMPE EVYTGSASTAHQLGQRVRDLVSSIMPE	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE SAPSULGPFPLLNTSFGAERRIE SSSTLLGSFP-LQPRLAAERRME NGPSVLGPFPLLQTSLAAERRME RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE KIPSLVGPFPLFQSSLAAERRSE KIPSLVGFPLFQSSLAVERRTE KIPSLVGFPLLQPSLTAERREE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETLLVAEEKVNG AYKLYLHSLETILMSEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQAEEKNGG	SLPAALALLGSAKF SLPAALALLGSAKF SLAGVVALLSSSKF SLAGVVALLSSSKF SLAGVVALLSSSKF SITGVTALLSSSKF SIAAIALLSSAKF SMPSAVALLSAGKF SLAGVAPLLASGKF SLAGVAPLLASGKF SMAGVTSLLSAGKF	544 544 531 558 558 409 556 556 255 548 556 255 548 558
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Fm_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_ar_Male Vx_car_naga_Male Vx_car_naga_Male	NSNSSGT PVQQLMKRVRDLVASVIPD NSNSSGT PVQQLMKRVRDLVASVIPD NSNSGGT PVQQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGSAASAAAQQLSRRVRDLVLSIMPD SGSAASAAAQQLSRRVRDLVLSIMPD TCPTGPSAAAQQLSRRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI - ANGSATAVHQLGQRVRDLVSSIMPEI EYVTGSASTAHQLGQRVRDLISSIIPEI ACVTVLSAAEQLDQRVRDLISSIIPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE SAPSULGPFPLLNTSLGAERRIE SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME SSSTLGSFP-LQPRLAAERRME RIPALFOFFPLLGTSLAAERRTE ENPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE EXAPSLVGAFPLLQPSLAAERRE KIPSLVGAFPLLQPSLAAERRE KIPSLVGAFPLLQPSLAAERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG AARLYCHSLETILLVAEEKVNG AYKLYLHSLETILVAEEKVNG ATKLYYHSLETILVAEEKNG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILQNEEKASG ITKLYYHSLENILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLDSILQNEEKASG VTKLYYHSLDSILQNEEKASG VTKLYYHSLDSILQTEEKVSG VTKLYYHSLDRILTTEEKVGG	SLPAALALLGSAKF SLPAALALLGSAKF SLAGVVALLSSSKF SLAGVVALLSSSKF SLAGVVALLSSSKF SLAGVALLSSSKF SLAGVALLSSGKF SIAAAIALSSAGKF SMPSAVALLSSGKF SMAGVAPLLASGKF SMAGVTSLLSAGKF SVAGVTSLLSAGKF	544 544 531 558 558 558 558 556 556 556 556 556 558 558
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Female Pl_star_Male/Female Vx_afr_Female Vx_afr_Female Vx_car_naga_Male Vx_car_naga_Female Vx_car_kawa_Female	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSTSGLGPTPAQLLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPASASAAQLSRRIRELISLVIPD SGSAASAAAQQLSRRVRDLVLSIMPD TCPTGPSAAAQQLSRRVRDLVLSIMPD TCPTGPSAAAQQLSRRVRDLVSSVMPE TYSGYASAAEQLGQRVRDLVSSVMPE TYKSGYASAAEQLGQRVRDLVSSVMPE C-ANGSATAVHQLGQRVRDLVSSVMPE CVTGSASAHQLQQRVRDLVSSIMPE CVTGSASAHQLQQRVRDLVSSIMPE CVTGSASAHQLQQRVRDLVSSIMPE CVTGSASAAQLNQRVRDLVSIMPE	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSLLGPFPLLNTSLGAERRIE SAPSLLGPFPLLNTSLGAERRIE SSSTLLGSFP-LQPRLAAERRME RIPALFGPFPLLQTSLAAERRME RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE KIPSLVGAFPLLQPSLAAERRTE KIPSLVGAFPLLQPSLTAERRE KIPSLUGSFPLLQPSLAAERRTE KIPSLUGSFPLLQPSLAAERRTE KIPSLUGSFPLLQPSLAAERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETILNEERTNG AYKLYLHSLETLLVAEEKVNG AYKLYLHSLETILMSEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILNEEKASG VTKLYYHSLENILNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKSG VTKLYYHSLDNILHTEEKVGG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDSILHTEEKVSG	SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVALLSSSKF SIAGVALLSSSKF SIAGAAIALLSAGKF SIAAAIALLSAGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSSGKF	544 544 531 558 558 558 558 556 255 556 255 548 558 568 568 568
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Fu_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_ari_nga_Female Vx_car_naga_Male Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSGGPTPAQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPPGSQLAVQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CANGSATAVHQLGQRVRDLVSSIMPEI EYVTGSASTAHQLGQRVRDLISSIIPEI ECVTGSASAAQLSRRVRLISSIIPEI ACVTV1-SAAEQLAQRVRDLISSIIPEI CATGSATAAHQLGQRVRDLISSIIPEI CATGSATAAHQLQQRVRDLISSIIPEI CATGSATAAHQLQQRVRDLISSIIPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE SAPSULGPFPLLNTSLGAERRIE SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE EIPSLLGPFPLLQSSLAVERRTE KIPSLVGAFPLLQPSLAAERRE KIPSLVGAFPLLQPSLAAERRTE KIPSLVGAFPLLQPSLAAERRTE KIPSLUGAFPLLQPSLAAERRTE	TKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETIMLNEERTNG AARLYCHSLETIMLNEERTNG AYKLYLHSLETILVAEEKVNG AYKLYLHSLETILMSEEKASG VTKLYYHSLENILMSEEKASG VTKLYYHSLENILNEEKSG VTKLYYHSLEIILQNEEKSG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDSILHTEEKSG VTKLYYHSLDSILHTEEKSG	SLPAALALLGSAKF SLPAALALLGSAKF SLAGVVALLSSKF SLAGVVALLSSKF SLAGVVALLSSKF SLAGVALLSSKF SLAGVALLSAGKF SIAAAIALLSAGKF SLAGVAPLLASGKF SLAGVAPLLASGKF SMAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF	544 544 531 558 558 558 556 255 548 558 558 558 558 558 558 558 558 5
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Female Vx_car_naga_Male Vx_car_naga_Male Vx_car_ar_maga_Hale Vx_car_waw_Female Vx_car_kawa_Female Vx_car_wais_Female	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGPASASLSAAEQLSRRIRELISLVIPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAAAQQLSRRVRDLVLSIMPDI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CYTGSASTAVHQLGQRVRDLVSSIMPEI CYTGSASAAQQLSRRVRDLVSSVMPEI CYTGSASAAQQLQQRVRDLSSIPEI CYTGSASAAQQLQQRVRDLSSIPEI CYTVSASAAQLQQRVRDLSSIPEI ACVTVT.SAAEQLQQRVRDLSSIPEI ACVTV-SAAEQLQQRVRDLSSIPEI ACVTVSAAAQLQRVRDLSSIPEI ACVTVSAAAQQLSRVRDLYSCIMPEI CYTGSASAAHQLQQRVRDLSSIPEI ACVTV-SAAEQLNQRVRDLSSVPEI CYTGSASAAHQLQQRVRDLSSIPEI ACVTVSAAKQLTQRVRDLVSCIMPEI	500 500 AAPSLLGPFPLLNTSLGVERRIE AAPSLLGPFPLLNTSLGAERRIE AAPSLLGPFPLLNTSLGAERRIE SASTLLGSFP-LQPRLAAERRME SSSTLLGSFP-LQPRLAAERRME NGPSVLGPFPLLQPSLAAERRME RIPALFGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQSSLAVERRTE EAPSLVGPFPLLQSSLAVERRTE KIPSLVGAFPLLQPSLTAERRE KIPSLVGAFPLLQPSLTAERRE KIPSLUGSFPLLQPSLTAERRE KIPSLUGFFPLQPSLAAERRTE KIPSLUGFFPLQPSLAAERRTE KIPSLUGFFPLLQPSLAAERRTE KIPSLUGFFPLLQPSLAAERRTE KIPSLUGFFPLLQPSLAAERRTE KIPSLUGFFPLLQPSLAAERRTE	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETILVAEEKVNG AYKLYLHSLETLLVAEEKVNG AYKLYHSLETILMSEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLEIILQNEEKASG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYLSLSRILQAEEKNSG	SIPAALALLGSAKF SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVALLSSSKF SIAAAALLSAGKF SIAAAAIALLSAGKF SIAAAAIALLSAGKF SIAGVAPLLASGKF SMAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF	544 544 531 558 558 558 409 556 556 556 556 558 558 558 558 558 568 56
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Male Eu_sp_Male Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale Vx_afri_Aale	NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSSGPTPVQQLMKRVRDLVASVIPD NSNSGGPTPAQLMKRVRDLVASVIPD AQAGTSLSAAEQLSRRIRELISLVIPD SGPPGSQSLAVQLSRRVRDLVLSIMPD SGSAASAAAQQLSRRVRDLVLSIMPD SGSAASAAAQQLSRRVRDLVLSIMPD TCPTGPSAAQQLSRRVRDLVSSVMPEI TYTSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CYTGSASAAQLSRRVRLVSSVMPEI CYTGSASAAQLSRRVRDLVSSVMPEI SGSAASAAAQQLSRRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CYTGSASAAQLGQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQLQQRVRDLVSSVMPEI CYTGSASAAQQLGQRVRDLVSSVMPEI CYTGSASAAQQUQRVRDLVSCMPEI CYTGSASAAQQUQRVRDLVSCMPEI CYTGSASAAQQUQRVRDLVSCMPEI		580 ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLETILMLNEERTNG AYKLYLHSLETLLVAEEKVNG AYKLYLHSLETILMSEEKASG VTKLYYHSLENILRAEEKASG VTKLYYHSLENILAEEKASG VTKLYYHSLENILQNEEKASG VTKLYYHSLEILQNEEKASG VTKLYYHSLEILQNEEKASG VTKLYYHSLENILAEEKASG VTKLYYHSLENILAEEKASG VTKLYYHSLENILAEEKASG VTKLYYHSLENILQAEEKSG VTKLYYHSLDNILHTEEKVGG VTKLYYHSLDNILHTEEKVGG VTKLYYHSLDNILHTEEKVGG VTKLYYHSLDSILHTEEKVGG VTKLYYHSLDSILHTEEKVGG	SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAAAIALLSAGKF SIAAAIALLSAGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SVAGVTSLLSAGKF SVAGVTSLLSAGKF SVAGVTSLLSSGKF SVGVTSLLSSGKF	544 544 531 558 558 558 556 556 556 556 556 556 556
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Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus Cd_rein_Plus 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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Male Eu_sp_Male P_star_Male/Female Vx_afri_Male Vx_afri_Male Vx_ar_naga_Male Vx_ar_was_Female Vx_car_kawa_Male Vx_car_was_Female Vx_car_was_Female Vx_car_was_Female Cd_rein_Minus Cd_rein_Minus Ym_unic_PlusMinus Eu_sp_Male Eu_sp_Male Vx_afri_female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male Vx_abrematic_Male	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSGFTPVQQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRIRELISLVIPDI SGPASASAAQUSRRVRDLVASVIPDI SGSAASAAAQUSRRVRDLVLSIMPDI SGSAASAAAQQLSRVRDLVLSIMPDI TCPTGPSAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAAQQLSRRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI EVYGSASTAHQLGQRVRDLVSSVMPEI CVTGSASAAQUSRRVRDLVSSVMPEI CVTGSASAAQUGRVRDLVSSVMPEI CVTGSASAAQUGRVRDLVSSVMPEI CVTGSASAAQUGQRVRDLVSSVMPEI CVTGSASAAQUGQRVRDLVSSVMPEI CVTGSASAAQUGQRVRDLVSSVMPEI CCVTGSASAAQUGQRVRDLVSSVMPEI QRUTVSAAAQUGRVRDLVSSVMPEI CCVTGSASAAQUGQRVRDLVSSVMPEI CCVTGSASAAQUGQRVRDLVSSVMPEI CCVTGSASAAQUGQRVRDLVSSVMPEI CCTGSASAAQUGRVRDLVSSVMPEI CCTGSASAAQUGRVRDLVSSVMPEI CCTGSASAAQUGRVRDLVSSVPEI QRGLACCIEVVACCRNSCAFPNVLI QRGLIACCIEVVACYRMVSCAFPNVLI QRGLIACCIEVVACYRMVSCAFPNVLI RGLVACCVEVVACYRMSCAFPKVLI HRALVACCVEVVACYRMSCAFPKVLI HRALVACCVEVVACCYRMSCAFPKVLI HRALVACCIEVVAACYRMVSCAFPKVLI HRALVACCIEVVAACYRMVSCAFPKVLI HRALVACCIEVVAACYRMVSCAFPKVLI HRALVACCIEVVAACYRMVSCAFPKVLI HRALVACCIEVVAACYRMVSCAFPKVLI HRALVACCAFFVVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI HRALVACCIEVVAACYRMVSCAFFVLI		ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG AARLYCHSLDTILWEEKNG AYKLYLHSLETLLVAEEKVNG AYKLYHSLETILWAEKKNG VTKLYYHSLENILRAEKASG VTKLYYHSLENILRAEKASG VTKLYYHSLENILRAEKASG VTKLYYHSLENILRAEKASG VTKLYYHSLENILANEEKASG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDNILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYHSLDSILHTEEKVSG VTKLYYLSLERILQAEEKNNG PRELKRHLFLIEEKILESLAW PRELKRHHFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW	SIPAALALLGSAKF SIPAALALLGSAKF SIPAALALLGSAKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVVALLSSSKF SIAGVALLSSSKF SIAAAIALLSAGKF SIAAAIALLSAGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SIAGVAPLLASGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGVTSLLSAGKF SVPGSSLVHLINVV VEPGSSLVHLINVV VEPGSSLVHLINVF VEPGSSLVHLINVF VEPGSSLVHIINF VEPGSSLVHIINF VEPGSSLVHIINF VEPGSSLVHIINF VEPGSSLVHITSI VEPGSSLVHITSI	544 544 531 5562 558 558 558 558 558 558 558 558 558 55
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CYTGSASTAHQLGQRVRDLSSIMPEI CXTTSAAEQLQQRVRDLSSIMPEI CXTTSAAEQLQQRVRDLSSIMPEI CXTTSAAEQLQQRVRDLSSIMPEI CXTTSAAEQLQQRVRDLSSIMPEI CATGSATAAHQLGQRVRDLISSIPEI CATGSATAAHQLQQRVRDLISSIPEI CATGSATAAHQLQQRVRDLISSIPEI CATGSATAAHQLQQRVRDLSSVIPEI CATGSATAAHQLQQRVRDLSSVIPEI CATGSATAAHQLQQRVRDLSSVIPI CQ0 QCGLIACCIEVVAACYRMVSCAFPNVLI QRGLIACCIEVVAACYRMVSCAFPNVLI RGLVACTVEIVAACYRMVSCAFPKVUI HRGLVACCVEVVAACYRMSCAFPKVUI HRALVACCVEVVAACYRMVSCAFPKVII HRALVACCVEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCYEVVAACYRMVSCAFPKVII HRALVACCYEVVAACYRMVSCAFPKVII HRALVACCYEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII HRALVACCIEVAACYRMVSCAFPKVII 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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Fm_unic_Plus/Minus Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_ar_naga_Male Vx_car_naga_Female Vx_car_naga_Female Vx_car_kawa_Male Vx_car_kawa_Male Vx_car_kawa_Female Cd_rein_Plus Cd_rein_Plus Cd_rein_Minus Cd_rein_Minus Cd_glob Gn_pect_Minus Gn_pect_Minus Fm_unic_Plus/Minus Eu_sp_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_afri_Male	NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSSGSTPVQQLMKRVRDLVASVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI AQAGTSLSAAEQLSRRIRELISLVIPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI TCPTGPSAAAQQLSRRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CVTGSASTAVHQLGQRVRDLVSSVMPEI 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KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSFPLLQSSLAVERRTE KIPSLGSSSLGSFFFFFLLQSSLAVERRTE KIPSLGSFFFLLQSSLAVERRTE KIPSLGSFFF	ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG AARLYCHSLETILVAEEKVNG AYKLYHSLETILVAEEKVNG AYKLYHSLETILVAEEKNG YTKLYYHSLENILRAEEKASG YTKLYYHSLENILRAEEKASG YTKLYYHSLENILQNEEKASG YTKLYYHSLENILQNEEKASG YTKLYYHSLENILQNEEKASG YTKLYYHSLDSILQNEEKASG YTKLYYHSLDSILGAEEKNG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKVGG YTKLYYHSLDSILHTEEKSG YTKLYYHSLSSILHTEEKSG YTKLYYHSLDSILHTEEKVGG PRELKRHLFLIEEKILECLAW PRELKRHFLIEEKILESLAW PRELKRHFLIEEKILESLAW PRELKRHFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW PRELKRHLFLIEEKILESLAW 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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_Male Eu_sp_Male Eu_sp_Male Plstar_Male/Female Vx_afri_Male Vx_afri_Male Vx_afri_Male Vx_ar_naga_Male Vx_car_was_Female Vx_car_kawa_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_weis_Male Vx_car_kawa_Male Vx_car_kawa_Male Vx_car_kawa_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male Vx_car_was_Male	SGO NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSSGPTPVQQLMKRVRDLVASVIPDI NSNSGGPTPAQLMKRVRDLVASVIPDI QAGTSLSAAEQLSRIRELISLVIPDI SGPPGSQSLAVQLSRRVRDLVLSIVPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVLSIMPDI SGSAASAAAQQLSRRVRDLVSSVMPEI TYTSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI TYKSGYASAAEQLGQRVRDLVSSVMPEI CYTGSASAAQLSRRVRLVSSVMPEI EYTGSASAAQLSRRVRLVSSVMPEI CYTGSASAAQLGQRVRDLVSSVMPEI 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AAPSLLGPFPLLNTSLGVERRIE AAPSLGPFPLLNTSLGAERRIE SAPSLLGPFPLLQTSLAAERRME SSSTLLGSFP-LQPRLAAERRME RIPALFGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE RIPALFGPFPLLQTSLAAERRTE EIPSLLGPFPLLQTSLAAERRTE EXPSLVGPFPLLQTSLAAERRTE KIPSLVGAFPLLQPSLAAERRTE KIPSLVGAFPLLQPSLAAERRTE KIPSLUGSFPLLQPSLAAERRE KIPSLUGSFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLUGAFPLLQPSLAERRE KIPSLVGAFPLLQPSLAERRE KIPSLVGAFPLLQPSLAERRE KIPSLGPSLGPSLZ KIPSLGPF KIPSLGPF KIPSLGPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSLZ KIPSLGPSL	500 ATKLYCHSLDTILQNEQRTNG ATKLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG AARLYCHSLDTILQNEQRTNG 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VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSSLVNNILAF VEPGSLVNNILAF VEPGSSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILAF VEPGSLVNNILA	544 544 541 531 558 558 558 558 558 558 558 558 558 55

	700	720	740	760
Cd rein Plus	HTENEAAAAAAAAAAA EAAATAA	CS - AASGDDSQHDGA - GSRAGLS	SSSGGAGAAAAAE G	GAGGGTEQPGASSSHN 703
Cd_rein_Minus	HTENEAAAAAAAAAAAQ EAAATAA	CS - AASGDDSQHDGA - GSRAGLS	SSSGGAGAAAAAE G	GADGGTEQPGASSSHN 703
Cd_glob	HAENEAAATAAALTMQ EAAATAA	CS-AASGDDSQHDGA-GSRAGPS	STSGGAGAAAAAEGGADG	GADGGAEQPGASSSHN 707
Gn_pect_Plus	QSESISNGEQQGASA		G	TASGGTPA 640
Ym unic Plus/Minus	NSENEAAAAAQEAAAQAT	CSAAASGDDSQHDGS-GSKAGPS	\$\$\$AGAG GAE	AAEGGEPAP - ASSSHE 713
Eu_spMale	TGHNEAVVPTPAVDVI SAEVV	LQHA EKAS - GTTPLPY	ARVDSAGPEPPAEARAHG	QEEE\$ 702
Eu_spFemale	TGHNEAVVPTPAVDVI SAEVV	LQHA EKAS - GTTPLPY	ARGDSAGPEPPAEARAHG	QEEE\$ 702
Pl_star_Male/Female	VNRDEGVPLSTAPTLPLPTAATEDT	SQRA GDCGAASSQLAC	QSSGGAVSQAASNCGGTGGK	TAAPNEPAV 565
Vx_arri_Male		VVMSVGSSPASAC		693
Vx obve Male	SNDDSPTRRNSTLETSTLHLMLDDG	FQHAY GPQLSS AC	IRVGGAGVNVLND	
Vx_car_naga_Male	SVNHQDITLNHNALH - VAEDALQHA	YAPLA SPA C	KADCGDGVEELNET	
Vx_car_naga_Female	VAQDELLEECATFEDDTTDKTMQAP	KS		670
Vx_car_kawa_Male	SASHQDINLHHDALHDVVEDALQNA	YGPLA SPA C	NGDCGAGVEELNET	222222222222222222222222222222222222222
Vx_car_weis_Male	SVSHQDIAFDHNALHDVT - DALQHA	YGPLA SPA C	NRDCGASIEELDET	
Vx_car_weis_Female	VVQDEQSEGIATHEDDTSDKAMQAP	NSK????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	???????????????????????????????????????
	780	800	820	840
Cd_rein_Plus	TEQSGGAPPMETAEGGAPGAATSAP	PSTTSAAPAEPAPPAAASPAAPA	ASHA PPPSPKRSQGVAFS	MMSPAKKARGTDGGAH 786
Cd_rein_Minus	TEQSGGAPPMETAEGGAPGAATSAP	PSTTPAAPAEPAPPAAASPAAPA	ASHA PPPSPKRSQGVAFS(	SMMSPAKKARGTDGGAH 786
Cd_glob	TDHSGGAAPTETAEAGAGGVATSAP	PSAAPSAPAEPAPPAAASNAMPA	ASHA PPPSPKRSQVVAFS(	MMSPAKKGRGTDGGAY 790
Gn_pect_Plus		APASTTPGGISA	AGP SGLPPL SPKR SR S I SV	WMSPAKKARGMDGAPC 687
Ym unic Plus/Minus	VNK - SGAAPMETVDGSAAGAT	P	LAGA PPPSPKRSQASVFS(	LMSPAKKARGVDGTPH 780
Eu_spMale	VCQRGG IDFVEEGI	ARTSCAQSSIA A	VQPN VPPSPKRPQEASVSV	VPMSPAKKARGGDWSPQ 763
Eu_spFemale	VCQRGGIDFVEEGI	ARTSCAQSSIAA	VQPN VPPSPKRPQEASVSV	VPMSPAKKARGGDWSPQ 763
Vx afri Male	GGTIEMGVTHYSKKNVSTS		VAPA PSPSPKKPKACPVPC	IMSPAKKARGGNGSPQ 010
Vx_afri_Female	GGTIFMGLTHSSKKNVSTS		VAVG HQLSPKRHHGSAAL	LMSPAKKARGVQGSPQ 759
Vx_obve_Male	GGTIDTALLEGCAVPADKS	SPGPSMLLVHA	VSAPSPKRTQGSIMAC	GLASPAKKVRVDDGSPQ 453
Vx_car_naga_Male	NGTRH\$AP\$EEIR	F	STPLCAPPPSPKRSQGCIM-C	SMSPAKKVRGVDGSPQ 741
Vx_car_naga_remale	NGTRRGAPSEEIR	PTRTTIIIPSSF	SAPI CAPPPSPKRPQDSINI (	S PAKKVRGVDGSPQ 761
Vx_car_kawa_Female	???????????????????????????????????????	777777777777777777777777777	???????????????????????????????????????	???????????????????
Vx_car_weis_Male	NGTKRGAPSEEIR	F	SASPSAPP KRPQGCIVLO	SSLSPAKKVRGVDGSPQ 469
Vx_car_weis_Female	***************************************	???????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	???????????????????????????????????????
		000	000	000
	I	860 I	900	920
Cd_rein_Plus	STQSYIESLPNAVGFPPAAGA - AQG	QAGLLFEFLRKVLKLTSFRLALL	900 CENFDFSPLEGPEVNSKVYEA	920 IEHALYKQTHLFYNRH 870
Cd_rein_Plus Cd_rein_Minus Cd_rein_Minus	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESIPISVGEPPAAGA - AHG	QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL	900 CENFDFSPLEGPEVNSKVYEA CENFDFSPLEGPEVNSKVYEA CENVDEGPLERPEVSSKVYEA	920 I AIEHALYKQTHLFYNRH 870 AIEHALYKQTHLFYNRH 870 I FHALYKQTHLFYNRH 874
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGA - AHG ATPVLDGPLPTCIGSP ASSN	QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL	900 CENFDFSPLEGPEVNSKVYEA CENFDFSPLEGPEVNSKVYEA CENVDFGPLERPEVSSKVYET CEKFDFSPLGRAEVNSKVYET	920   AIEHALYKQTHLFYNRH 870 AIEHALYKQTHLFYNRH 870 FIEHALYKQTHLFYNRH 874 IEHALYHHTQMFYNRH 767
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN	QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL VAGPLQEFCRKVLKLIAYRLALL	900 I CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYEI CEKFDFSPLGRAEVNSKVYEI CEKFDFSPLGRAEVNSKVYEI	920   NIEHALYKQTHLFYNRH 870 NIEHALYKQTHLFYNRH 870 FIEHALYKUTHLFYNRH 874 FIEHALYHHTQMFYNRH 767
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG	AGU QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLASFRLALM	00 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYET CEKFDFSPLGRAEVNSKVYET CNNFDFAPLDRAEVNSKVYET CNNFDFAPLDRAEVSSKVYET	920 I EHALYKQTHLFYNRH 870 NIEHALYKQTHLFYNRH 870 I EHALYKQTHLFYNRH 874 I EHALYHHTQMFYNRH 787 I EHALYHHTQMFYNRH 787 I EHALYNCTHLFYNRH 865 I EFALYRQTHLFYNRH 865
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_spMale Fu_spFemale	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG	QAGLIFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLASFRLALM SAGALYDFCRKVLKLAAFRLSLM	900 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENFDFSPLGRAEVNSKVYET CEKFDFSPLGRAEVNSKVYET CNNFDFSPLGRAEVNSKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET	920 I HALYKQTHLFYNRH 870 I HALYKQTHLFYNRH 870 I HALYKQTHLFYNRH 874 I HALYHHTQMFYNRH 767 I HALYHHTQMFYNRH 767 I HALYRQTHLFYNRH 865 I HALYFQTHLFYNRH 848 I HALYFQTHLFYNRH 848
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Female Pl_star_Male/Female	STQSY I ES LPNAVGFPPAAGA - AQG STQSY I ES LPNAVGFPPAAGA - AQG ATQAYVES LP I SVGFPPAAGT - AHG ATPVLDGPLPTC I GSP ASSN ATPVLDGPLPTC I GSP ASSN STQTFTGQLPQC I GVPAGI VPPGG PAKSSLEKLPQS I GWNLAALAPSTG PAKSSLEKLPQS I GWNLAALAPSTG ATQLTTEKLPHSI GVELPGAAKLGG	QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLASFRLALM SAGALYDFCRKVLKLAAFRLSLM SSGALYNFCHKVLKLAAFRLSLM	900 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYE1 CEKFDFSPLGRAEVNSKVYE1 CNNFDFAPLDKVEVSSKVYE1 CDNFDFMPLDRGEVNAKVYE1 CDNFDFMPLDRGEVNAKVYE1 CDNFNFSPLDRVEVSKVYE1	920 I HALYKQTHLFYNRH 870 NIEHALYKQTHLFYNRH 870 II EHALYKQTHLFYNRH 870 II EHALYHHTQMFYNRH 767 II EHALYHHTQMFYNRH 767 II EYALYRQTHLFYNRH 848 II EHALYFQTHLFYNRH 848 II EHALYFQTHLFYNRH 848
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Eu_sp_Temale Eu_sp_maile Pl_star_Maile/Female Vx_afr_Maile	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG ATQLTTEKLPHSIGVELPGAAKLGG PVIAIAGRLPKFIQKVWGVAGTGG	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLSLM SSGALYNFCHKVLKLAAFRLALM	000 CENFDFSPLEGPEVNSKVYE/ CENVDFSPLEGPEVNSKVYE/ CENVDFSPLGRAEVNSKVYEI CEKFDFSPLGRAEVNSKVYEI CNFDFSPLDRAEVNSKVYEI CDNFDFMPLDRGEVNAKVYEI CDNFDFMPLDRGEVNAKVYEI CDNFSPLDRVEVSKVYEI CDNFSPLDRAEVNAKVYEI	S20 I ALYKQTHLFYNRH 870 N EHALYKQTHLFYNRH 870 I EHALYKQTHLFYNRH 874 I EHALYHHTQMFYNRH 767 I EHALYHHTQMFYNRH 767 I EYALYRQTHLFYNRH 845 I EHALYFQTHLFYNRH 848 I EHALYFQTHLFYNRH 848 I EYALYCQTHLFYNRH 701 I EHALYYQTHLFYNRH 844
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Ym_unic_Plus/Minus Ym_unic_Plus/Minus Plus/Minus Eu_sp_Male Eu_sp_Female V_s_afri_Male Vx_afri_Female	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG ATQLTTEKLPHSIGVELPGAAKLGG PVIAIAGRLPKFIGQKVVGVAGTGG PVIAIAGRLPKFIGQKVVGVAGTGG	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLASFRLALM SAGALYDFCRKVLKLASFRLSLM SAGALYDFCRKVLKLASFRLALM SAGALPGFCRKVLKLASFRLALM SAGALRDFCRKVLKLASFRLALM	000 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYET CEKFDFSPLGRAEVNSKVYET CONFDFAPLDRAEVNSKVYET CDNFDFAPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFNFSPLDRAEVNKVYET CDNFDFTPLNRAEVNKVYET	920 I EHALYKQTHLFYNRH 870 N EHALYKQTHLFYNRH 870 I EHALYKQTHLFYNRH 874 I EHALYHHTQMFYNRH 767 I EHALYHHTQMFYNRH 767 I EYALYRQTHLFYNRH 848 I EHALYFQTHLFYNRH 848 I EHALYFQTHLFYNRH 844 I EHALYQTHLFYNRH 844
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Male Eu_sp_Fomale Pl_star_Male/Female Vx_afri_Female Vx_afri_Female Vx_obve_Male Vx car naga Male	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG ATQLTTEKLPHSIGVELPGAAKLGG PVIAIAGRLPKFIGQKVWGVAGTGG PVIAIAGRLPKFIGQKVWGVAGTGG PVQVIAERLPRCIGFIDCGVAGSNG	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLIAYRLALL SVGALYDFCRKVLKLAAFRLALM SAGALYDFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM NGGALHDFCRKVLKLAAFRLALM	000 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYE CEKFDFSPLGRAEVNSKVYET CNFDFSPLGRAEVNSKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFTPLNRAEVNKVYET CDNFDFTPLNRAEVNKVYET CDNFDFTPLNRAEVNKVYET	420 I ALYKQTHLFYNRH 870 NIEHALYKQTHLFYNRH 870 IIEHALYKQTHLFYNRH 874 IIEHALYHHTQMFYNRH 767 IIEHALYHHTQMFYNRH 767 IIEHALYRQTHLFYNRH 865 IIEHALYFQTHLFYNRH 848 IIEYALYCQTHLFYNRH 844 IIEHALYYQTHLFYNRH 844 IIEHALYYQTHLFYNRH 844 IIEHALYYQTHLFYNRH 838 IIEYALYYQTHLFYNRH 838
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Minus Ym_unic_Plus/Minus Eu_sp_Femate PlusfMinuale/Femate Vx_afri_Mate Vx_afri_Femate Vx_obve_Mate Vx_car_naga_Femate	STQSY IESLPNAVGFPPAAGA - AQG STQSY IESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG PVKSLEKLPQSIGWNLAALAPSTG PVIAIAGRLPKFIGQKVWGVAGTGG PVIAIAGRLPKFIGQKVWGVAGTGG PVQVIAERLPRCIGPIDCGVAGSNG PVQVIAERLPRCIGPIDCGVAGSNG PVQVITAKLPLLIGAKVVCGAAGASG AVHRYLRKLPPCIGAKFVESAHTDG	QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLSLM SAGALRDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM NGGALHDFCRKVLKLAAFRLALM SAGALHDFCRKVLKLAAFRLALM SAGALHDFCRKVLKLAAFRLALM	000 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENFDFSPLGRAEVNSKVYET CEKFDFSPLGRAEVNSKVYET CNNFDFAPLDRGEVNSKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFTPLNRAEVNAKVYET CDNFDFFPLNRAEVNKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLQRLDVNKVYGT	S20   ALEHALYKQTHLFYNRH 870 ALEHALYKQTHLFYNRH 870 FIEHALYKQTHLFYNRH 874 FIEHALYHTQMFYNRH 767 FIEHALYRQTHLFYNRH 865 FIEHALYFQTHLFYNRH 848 FIEYALYCQTHLFYNRH 848 FIEYALYCQTHLFYNRH 844 FIEHALYYQTHLFYNRH 844 FIEHALYYQTHLFYNRH 844 FIEHALYYQTHLFYNRH 844 FIEHALYYQTHLFYNRH 844 FIEHALFYQTHLFYNRH 846 FIEYALYNGTHLFYNRH 846 FIEYALYNGTHLFYNRH 826 FIEHALFFQTHLFYNRH 84 FIEHALFFQTHLFYNRH 84
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_female Eu_sp_female Eu_sp_female Vx_afri_Aale Vx_afri_Female Vx_car_naga_Male Vx_car_naga_female Vx_car_naga_female	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGA - AQG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG PVISLEKLPQSIGWNLAALAPSTG PVIAIAGRLPKFIGQKVWGVAGTGG PVIAIAGRLPKFIGQKVWGVAGTGG PVQVIAFLPRCIGPIDCGVAGSNG PVQVITGKLPLLIGAKVCGAAGASG PVQVIAGKLPLCIGAKVCGAAGASG	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM SAGALHDFCRKVLKLAAFRLALM SAGALHDFCRKVLKLAAFRLALM	CENFDFSPLEGPEVNSKVYEA CENFDFSPLEGPEVNSKVYEA CENVDFGPLEGPEVNSKVYEA CENVDFGPLGRAEVNSKVYET CEKFDFSPLGRAEVNSKVYET CONFDFMPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFFPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET	S20 I HALYKQTHLFYNRH 870 N EHALYKQTHLFYNRH 870 I EHALYKQTHLFYNRH 874 I EHALYHHTQMFYNRH 767 I EHALYHHTQMFYNRH 767 I EHALYFGTHLFYNRH 845 I EHALYFGTHLFYNRH 848 I EHALYFGTHLFYNRH 844 I EHALYYQTHLFYNRH 844 I EHALYYQTHLFYNRH 844 I EHALYYQTHLFYNRH 844 I EHALYYGTHMFYNRH 846 I EHALFFGTHLFYNRH 826 I EHALFGTHLFYNRH 846 I EHALFGTHLFYNRH 846
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Ym_unic_Plus/Minus Eu_sp_Female Eu_sp_female Vx_afri_Female Vx_afri_Male Vx_afri_Male Vx_afri_emale Vx_car_naga_Female Vx_car_naga_Female Vx_car_kawa_Male Vx_car_kawa_Male	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGA - AQG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG PYIAIAGRLPKFIGQKVGVAGTGG PVIAIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKFIGQKVGAAGTGG PVQVIAGRLPKFIGAKVCGAAGASG AVHRYLRKLPPCIGAKYCGAAGTSG ????RKLPPSIGTKFVESAHTDG ????	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL VAGPLQEFCRKVLKLAYRLALL SVGALHEFCRKVLKLAAFRLALM SAGALYDFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM SAGALRDFCRKVLKLAAFRLALM SAGALHDFCRKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM	POD CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYEI CEKFDFSPLGRAEVNSKVYEI CENFDFSPLGRAEVNSKVYEI CONFDFMPLDRGEVNAKVYEI CDNFDFMPLDRGEVNAKVYEI CDNFDFFPLNRAEVNAKVYEI CDNFDFFPLNRAEVNKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI	920           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I           I
Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Fus_Minus Plus/Minus Eu_sp_Male Eu_sp_Male Eu_sp_Female Vx_afri_Female Vx_afri_Female Vx_car_naga_Female Vx_car_awa_Male Vx_car_weis_Female Vx_car_weis Female	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG ATQLTTEKLPHSIGVELPGAAKLGG PVIAIAGRLPKFIGQKVCGVAGTGG PVQVIAERLPRCIGPIDCGVAGTGG PVQVIAERLPRCIGPIDCGVAGTGG QVQVIAERLPRCIGAKVCGAAGTSG 2?????RKLPPSIGTKFVESAHTDG PVQIIAGKLPLSIGAKVCGAAGTSG 2???????	QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL QAGLIFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLIAYRLALL SVGALHEFCRKVLKLAYFRLALL SVGALHEFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLSLM SAGALPDFCRKVLKLAAFRLALM SAGALPDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM	000 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYET CEKFDFSPLGRAEVNSKVYET CEKFDFSPLGRAEVNSKVYET CONFDFMPLDRGEVNAKVYET CDNFDFMPLDRGEVNAKVYET CDNFDFTPLNRAEVNKVYET CDNFDFTPLNRAEVNKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNAKVYET CDNFDFSPLDRVEVNKVYET CDNFDFSPLDRVEVNKVYET CDNFDFSPLDRVEVNKVYET	920   
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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_spFemale Plus/Minus Vx_afri_Male Vx_afri_Female Vx_abve_Male Vx_car_naga_Male Vx_car_naga_Female Vx_car_kawa_Male Vx_car_weis_Female Cd_rein_Plus Cd_rein_Plus Gn_pect_Minus Eu_sp_Female Plustar_Male/Female Plustar_Male/Female Cd_rein_Plus	STQSY IESLPNAVGFPPAAGA - AGG STQSY IESLPNAVGFPPAAGA - AGG ATQAYVESLPISVGFPPAAGA - AGG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN ATQKTGQLPQCIGVPAGIVPGG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG PVKSLEKLPQSIGWNLAALAPSTG PVAKSLEKLPQSIGWNLAALAPSTG PVQVIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKFIGQKVGVAGTGG PVQVIAGRLPKCIGPIDCGVAGSNG PVQVIAGRLPKCIGAKVCGAAGTSG ??????RLPSSIGKVCGAAGTSG ???????????????????????????????????	$B^{80}$ $QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLASFRLALL SVGALHEFCRKVLKLASFRLALM SAGALYDFCRKVLKLASFRLALM SAGALYDFCRKVLKLAAFRLSLM SAGALPGFCRKVLKLAAFRLALM SAGALPGFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM CAAALNHFCCKVLKLAAFRLALM CAAALNFCCKVLKLAAFRLALM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAAFRLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLKLAFFLAM CAAALNFCCKVLK CAAALNFCCKVLK CAAALNFCCKVLK CAAALNFCCKVLK CAAQQSIFRSVI ILAYKQP - QAQQSIFRSVI ILAYKQP - QAQQAFFRSVI ILAYKQP - QAQQAFFR$	000 CENFDFSPLEGPEVNSKVYE/ CENFDFSPLEGPEVNSKVYE/ CENVDFGPLERPEVSSKVYEI CENFDFSPLGRAEVNSKVYEI CEKFDFSPLGRAEVNSKVYEI CONFDFNPLDRGEVNSKVYEI CONFDFNPLDRGEVNAKVYEI CDNFDFNPLDRGEVNAKVYEI CDNFDFTPLNRAEVNKVYEI CDNFDFTPLNRAEVNKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNAKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKYEI CDNFDFSPLDRVEVNKVEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVYEI CDNFDFSPLDRVEVNKVEI CDNFDFSPLDRVENKVEI CDNFDFSPLDRVENKVEI CDNFDFSPLDRVEINKVEI CDNFDFSPLDRVEINKVEI CDNFDFSPLDRVEINKVEI CDNFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRIENKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEI CONFDFSPLDRVEINKVEINKVEI CONFDFSPLDRVEINKVEINKVEI CONFDFSPLDRVEINKVEINKVEINKVEINKVEINKVEINKVEINKVEINK	920 1 1 1 1 1 1 1 1 1 1 1 1 1
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846           I EHALYFQTHLFYNRH 847           I EHALYYQTHLFYNRH 848           I EHALYYQTHLFYNRH 844           I EHALYYQTHLFYNRH 846           I EHALYYQTHLFYNRH 846           I EHALYYQTHLFYNRH 846           I EHALYYQTHLFYNRH 846           I EHALFFQTHLFYNRH 846           I EYALYYQTHLFYNRH 856           I EYALYYQTHLFYN
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Cd_rein_Plus Cd_rein_Minus Cd_glob Gn_pect_Plus Gn_pect_Plus Eu_sp_fman Plus/Minus Eu_sp_fmale Plus/Minus Plus/Minus Vx_afr_Male Vx_afr_Male Vx_afr_Aale Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_ads_Female Vx_car_ads_Female Vx_car_ads_Female Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Cd_rein_Minus Eu_sp_female Plus/Minus Eu_sp_female Vx_car_naga_Male Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female Vx_car_naga_Female	STQSYIESLPNAVGFPPAAGA - AQG STQSYIESLPNAVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGA - AQG ATQAYVESLPISVGFPPAAGT - AHG ATPVLDGPLPTCIGSP ASSN ATPVLDGPLPTCIGSP ASSN STQTFTGQLPQCIGVPPAGIVPPG PAKSSLEKLPQSIGWNLAALAPSTG PAKSSLEKLPQSIGWNLAALAPSTG PVGVIAGRLPKFIGQKVGCVAGTGG PVQVIAGRLPKFIGQKVGCVAGTGG PVQVIAGRLPKFIGQKVGCVAGTGG PVQVIAGRLPKFIGAKVCGAAGASG QVQVIGKLPLLIGAKVCGAAGASG QVQVIAGKLPLCIGAKVCGAAGASG QYQTAGKLPLCIGAKVCGAAGTSG ?????RKLPPSIGTKFVESAHTDG PVQVIAGKLPLCIGAKVCGAAGTSG ?????RKLPPSIGTKVESAHTDG PVQIAGKLPLCIGAKVCGASGTSG ?????RKLPPSIGTKVESAHTDG PVQIIAGKLPLSIGAKVCGASGTSG ?????RKLPPSIGTKVESAHTDG PUQIIASLYGYCKVHKLSQVSFRE IDQIMLSTLYGYCKVHKLSQVSFRE IDQIMLSTLYGYCKVHKLSQVSFRE IDQIMLSTLYGYCKVHKLSQVSFRE IDQIMLSALYGYCKVHKLSQVSFRE IDQILSALYGYCKVHKLSQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILLSALYGYCKVHKLQVSFRE IDQILSALYGYCKVHKLQVSFRE IDQILSALYGYCKVHKLQVSFRE IDQILSALYGYCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE IDQILSALYGCKVHKLQVSFRE	AGALIFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL QAGLLFEFLRKVLKLTSFRLALL VAGPLQEFCRKVLKLAYFRLALL VAGPLQEFCRKVLKLAYFRLALL SVGALPFCRKVLKLAAFRLSLM SAGALYDFCRKVLKLAAFRLALM SAGALYDFCRKVLKLAAFRLALM SAGALPFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM SAGALDFCRKVLKLAAFRLALM CAAALNFCCKVLKLAAFRLALM CAAALNFCCKVLKLAAFRLALM CAAALNFCCKVLKLAAFRLALM 2727272727272727272727272727 B→ 900 IAQYRKQP QAQQSIFRSVII IAQYRKQP QAQQSIFRSVII IAQYRKQP QAQQSIFRSVII IAQYRKQP QAQQSIFRSVII IAYRKQP QAQQCIFRSVII IAHYRKQP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP QAQQCIFRSVII IAHYRCP	B00         CENFDFSPLEGPEVNSKVYEJ         CENFDFSPLGREVNSKVYEJ         CENFDFSPLGREVNSKVYEJ         CEKFDFSPLGRAEVNSKVYEJ         CEKFDFSPLGRAEVNSKVYEJ         CENFDFRPLDRGEVNSKVYEJ         CONFDFMPLDRGEVNAKVYEJ         CDNFDFMPLDRGEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFFPLNRAEVNKVYEJ         CDNFDFSPLDRVEVNKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLDRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNAKVYEJ         CDNFDFSPLQRVEVNKVYEJ         CDNFDFSPLQRVEVNKVYEJ         CDNFDFSPLQRVEVNKVYEJ         CDNFDFSPLQRVEVNKVYEJ         CDNFDFSPLQRVEVNKVYEJ         CDNFDFSPLQNERADIJSFJNO         EQSNPGLQVTRADIJSFJNO         EQSNPGLQVVTRADIJAFYNO         EQSNPGLQVVTRADIJAFYNO         EQSNPGLQVVTRADIJAFYNO         EQSNPGLQVVTRADIJAFYNO         EQSNPGLQVVTRADIJAFYNO	920           I E HALYKQTHLFYNRH 870           N E HALYKQTHLFYNRH 871           I E HALYKQTHLFYNRH 874           I E HALYKQTHLFYNRH 874           I E HALYKQTHLFYNRH 874           I E HALYHTQMFYNRH 767           I E HALYHTQMFYNRH 767           I E HALYKQTHLFYNRH 874           I E HALYFQTHLFYNRH 865           I E HALYFQTHLFYNRH 848           I E HALYFQTHLFYNRH 848           I E HALYYQTHLFYNRH 844           I E HALYYQTHLFYNRH 844           I E HALYYQTHLFYNRH 846           I E HALYYQTHLFYNRH 846           I E HALYYQTHLFYNRH 846           I E HALFFQTHLFYNRH 846           I E HALFFQTHLFYNRH 846           I E HALFFQTHLFYNRH 846           I E HALFFQTHLFYNRH 856           I E HALFFQTHLFYNRH 856           I E YALYYQTHLFYNRH 856           I E YALYYQTHLFYNRH 856           I E YALYYQTHLFYNRH 856           I F YPAMKSFLLKSESN 953           I F YPAMKSFLLKSESN 953           I F YPAMKSFLLKSESN 953           I F YPAMKSFLLKSESN 953           I F YPAMKSFLLKSEQ 931           I F YPAMKSFLLKSEQ 931           I F YPSMKSFLLKSEQ 931           I F YPSMKSFLLKGEN 909           I F YPSMKSFLLKGEN 909           I F YPSMKSFLLKGET 9093      <

	1,040	1,060	1,080	1,100	
Cd rein Plus	GSGAS GPGLGG DSKH	AAAGNSGNAVGAAAGAAPAQGV	GATSAMPPGLPPLPPRA-S	QSPRGPKLPL LGA AAAPR	1027
Cd rein Minus	GSGAS GPGLGG DSKH	AAAGNSGNAVGAAAGAAPAQGV	GATSAMPPGLPPLPPRA - S	QSPRGPKLPL LGAIAAAPR	1027
Cd_glob	GSGAS GPGLGG DSKH	AAAGNSGNAVGAAAGAAPALGA	GATSAMPPGLPPLPPRA - S	QSPRGPKLPLPPLGAIAPAPR	1033
Gn_pect_Plus	GQYVP GPDMG\$VGGPDGKF	QAAHQS	QGVEHASSGSLS	P \$ K	890
Gn_pect_Minus	GQYVP GPDMGSVGGPDGKF	QAAHQS	QGVEHASSGSLS	P\$K	890
Ym_unic_Plus/Minus	SGTSG AGLGGGLGGADSKP	AAGNSGNA - DDTMAASTAAGG	GTSSGLHPGLPPLPPRSSS	QSPRAAKLPV LSGGGAPVR	1026
Eu_spmale	CPAINAPAVGA	- QPAPGGNIVKDSLAAQVSI	VAAARVMGLPLLSSSSII	RSPWAAKGL AMPSLER	995
Pi star Male/Female	VAGAGEHCIASTASGVGAISKKD	APAARA	- FOGDRISMI PMOALHERG	RSPSVHAISS I ATSSEG	990 850
Vx afri Male	CAVTS GDGVDKMAG	DGNSIKTGPAACT	- AAGGSQEALQSLSFHSTS	RLPKLASLP ATASPVR	988
Vx afri Female	CAVTS GDGVDKMAG	DGNSIKTGPAACT	AAAGSQEALQSLSFHSTS	RLPKLASLP ATSSPVR	988
Vx_obve_Male	\$VGTI		- VQ RNENRGMDYKWNL	KEHDGYNREGNRNSVPIYYSN	662
Vx_car_naga_Male	CASTC GQGLDGEPGTVISI	SETNSASAC	- VTGGSRNTLPLLTLHNTA	RLSRPVQLVS MSANSSPT	973
Vx_car_naga_Female	EYPGT IGPTIG\$PDNVTGEL	(GD   S   SCG	APAMEGELSAAHDSAG	KMTQIMKQLG LEALRSPGT	940
Vx_car_kawa_Male		KGGILLSC	TADAMEGADSSCHOSAG	RESERVQLVSLSANSSPI	993
Vx car weis Male	SVSTC GOGMDSEPGTVISN	SDTNSAGVYAAGAY	- ATGESRSTIPMITIHNTA	RVSRPVKIVSISANSSPT	706
Vx car weis Female	7777777777777777777777777777	???????????????????????????????????????	???????????????????????????????????????	77777777777777777777777	381
	1,120	1,140	1,160	1,180	
Cd rain Plue				GEGUPTPTGPVPVEPEENGG	1002
Cd rein Minus	MIGRSAS GNARGGGERELGMP	HPLIPTGS STGG	GAL SPTK	GSGHPTPTGPVPVSRSSNGG-	1092
Cd glob	MLGRSAS GNAR DREPGVP	L LLPQGPAGS STGG	GALSPTK GGE	CSGQPTLVGSVPVSRSNNGG -	1095
Gn_pect_Plus			RSTGSGSNGGALVHVT	EKGIASSA PLQSSEG	921
Gn_pect_Minus			RSTGSGSNGGALVHVT	EKGIASSA PLQSSEG	921
Ym_unic_Plus/Minus	MAGRSAS LLGRDGADKSTGRK	VEESQTYPLGPAGS STAV	TTVSSSKCEGSMPLLAGLG	SRHLPSAA ASQTTSVAQS -	1102
Eu_spMale		ADSESICNAFGADIPLLGR	GYK		1059
Pl star Male/Female	GIDRIRSKTEAASEVAKYVGGEP		EPTRASOADTGTRVIATIS	LEGVEQSSOMEVRSGSFQGGG	922
Vx afri Male	GLSRQAPKGDTVADAS	-QDLELCSVVSAGS	FLVVT	DAAGPQCS PVLSHSATCG -	1040
Vx_afri_Female	GLSRQAPKGDAVADAS	HDLELCSVVSAGS	FLVVT	DAAGPQCS PVLSHSATCG -	1040
Vx_obve_Male	NSSLPN		VPA	DEENGAQVVAAEIETVGKIFS	692
Vx_car_naga_Male	AVSRSYSVKDSVATQGGN	- FMDKSCGPICAGS	AVMG	ESAQTFNSHSHVVQHICNHG-	1028
vx_car_naga_remale	EHQRSHAGNRGVLMRFG	PMDPsyAcsA	VHVML	SAQNCAALLISAHEMEVRAG-	1037
Vx car kawa Female	TDRSRIHAGSAVGVSSDR	- LVDGVQEMES		AQNYAALQITSAHEVAVRAGM	867
Vx_car_weis_Male	AAPRSYSVKDVVDKSCG		S T	SATSVAVGDSAAILNSHSPRG	746
Vx_car_weis_Female	???????????????????????????????????????	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	???????????????????????????????????????	381
	1,200	1,220	1,240	1,260	
Cd rein Plus	RG - GSGGRGGGRGS - AEHKIP	EGLAALLQALDSQKAAEENTAE	EEEEEEVDADEE - QPQAR	VTRSGRTARDR	1162
Cd_rein_Minus	RG - G\$GGRGGGRG\$ - AEHKIP	EGLAALLQALDSQKAAEENGAE	EEEEEEVDADEE - QPQAR	VTRSGRTARDR	1162
Cd_glob	RG\$G\$GGRGGGRGT - VEHIIP	DGLAALLQALDSQQGVEENG-K	EEEEAEADADEDTQPQAR	VTRSGRAARDR	1166
Gn_pect_Plus	TKPAAQRSRAS-AERRIP	DGLAALLQALDSQSAPDGMDMG	GSSPSGEGPHAPL - CDVP -	SGSGVAPS	985
Gn_pect_Minus	IKPAAQRSRAS-AERRIPI		GSSPSGEGPHAPL-CDVP-	VTRECRAAAMACAVVECKCR	985
Fu sp. Male	ALVR-KDSARSRSTST-VDHQLP	OGLAALLOALDSQAGAEGFHSG		VIRSORAAAAMASAVVESKSF	1121
Eu sp. Female	ALVR - KDSARSRSTST - VDHQIPI	GLAALLQALDSQQGVSMQGGE	DDMSDQELPGDGT	MEDKSP	1121
Pl_star_Male/Female	AR - GAGACTRPAGTLAEHQIP	GLAALLQALDSQQGGVQDG - K	SAHEEEALGSGR AI	DSQSGDLV	986
Vx_afri_Male	LQ-SGSSSGKQTKS-TMVEIP	DGLAALLQALDSQQGLQGNRVE	DHQCSEVRLHGGT - GRII -	GGDD	1102
Vx_afri_Female	LQ - SGSSSGKQTKS - TMVEIP	DGLAALLQALDSQQGLQGNRVE	DHQCSEIRLHGGT - GRII -	GGDD	1102
Vx_obve_Male	APIVADASSNITAPIVISDHQIPI	DGLAALLQALDSQQNFQEQ			734
Vx_car_naga_wale	UNTCTPGKRT FHQIPI		ESOCICEVOSELNAGPOWY	I RPVGL DGGPK	1058
Vx car kawa Male	VVEPICDHGVRSVSVAVSEHQIP	GLAALLQALDSQQSLQDRGGV	DLDSLCRDASPTD		1095
Vx_car_kawa_Female	NTCKRVKPA EHQIPI	GLAALLQALDSQQVGAQECET	ESQEYIQVGSKFKAGSGWE	LRPVGLGGSPK	933
Vx_car_weis_Male	VVQPTCSHGVRSVSVAISEHQIP	DGLAALLQALDSQQGLQDRVGM	GSDSLCGAASPTD		804
Vx_car_weis_Female	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	*********	381
	1,280	1,300 1,32	2		
Cd_rein_Plus	STGRERRG - RHT - EARD	DMDEASMDA EFSQQ TV	VTGR RQRTPNRRYGAD	1209	
Cd_rein_Minus	STGRERRG - RHT - EARDI	MDEASMDA EFSQQ TV	VTGR RQRTPNRRYGAD	1209	
Gn nect Plus	PTGD AAGK			1028	
Gn pect Minus	PTGDAAGK	OVATSAGNS LPISP AL	TTGRQAGRQRTPIRRYGAN	1028	
Ym unic Plus/Minus	SRVIGISAGRERRSTRQA - ERKDI	DGMDADGPAAMETSEQAQLAAI	WSGR RQRTPNRRYGSD	1241	
Eu_spMale	RD R\$ANERRAARRFTERRE	AVKEDSAGT - VENLDLMQ SR	SQGR RQRTPNRKYGV -	1174	
Eu_spFemale	RD RSANERRAARRFTERRE	AVKEDSAGT-VENLDLMQSR	SQGR RQRTPNRKYGV -	1174	
Pl_star_Male/Female	QRRSAFRL-ERRE	ATTDGDA VEDSGNAQSPKS	LAGR RQRTPNRRYGTD	1033	
vx_atri_Male	TNVR		RCQR	1124	
Vx obve Male				734	
Vx_car_naga_Male				1113	
Vx_car_naga_Female	CTERR\$\$RRLR	DMEDATSLGANQETHQ SC		1110	
	CTERR\$\$RRLR	GQAACAGLDVFDDADTYDCSQF	QKTCR RQRTPNRKHGSD	1107	
Vx_car_kawa_Male	CTERRSSRRLR	DMEDATSLGANQETHQ SC GQAACAGLDVFDDADTYDCSQF LRDTKEDAMSLGADLAGIRHSC	QKTCR RQRTPNRKHGSD LAVR RQK	1107 1135	
Vx_car_kawa_Male Vx_car_kawa_Female	CTERRSSRRLR 	DMEDATSLGANQETHQSC GQAACAGLDVFDDADTYDCSQF LRDTKEDAMSLGADLAGIRHSC RQTVCVALDSSGDAEFHDWPQR QDP-FAAMSIGANIGGNUBS	QKTCR RQRTPNRKHGSD LAVR RQK I I TGR RQRTPNRKHGSE LAGK RQRTPNRKHGSE	1107 1135 982 843	
Vx_car_kawa_Male Vx_car_kawa_Female Vx_car_weis_Male Vx car weis Female	CTERRSSRLAR 	JMEDATSLGANQEIHQSC GQAACAGLDVFDDADTYDCSQF LRDTKEDAMSLGADLAGIRHSC RQTVCVALDSSGDAEFHDWPQR LQDP - EAAMSLGANLEGMHHSC 23322323232323232323232323232323	AGK RQK	1107 1135 982 843 381	

## Figure S1

Alignment of full-length MAT3 proteins from isogametic mating type *plus* and *minus* or male and female from six species of the colonial Volvocales, *Chlamydomonas reinhardtii* and *C. globosa* (previously misidentified as *C. incerta* [S1]), plus partial MAT3 proteins from *V. obversus* (male), *V. carteri* f. *weismannia* (male and female) and *V. carteri* f. *kawasakiensis* (male and female) (supplementary table S1, Supplementary Material online). MAT3/RB-specific regions (boxes, Domains A and B)

are shown for *V. carteri* f. *nagariensis*. Positions 341-427, 447-503, 518-678, 874-969, 972-1016 and 1210-1227 (464 amino acids) were used for phylogenetic analysis (fig. 3).



B Eudorina sp. MAT3 (coding sequence: 3,525 bp)









## Figure S2

Semi-quantitative RT-PCR analyses of MAT3 from different colonial Volvocales. (A, B) Schematic representations of Gonium pectorale (A) and Eudorina sp. (B) MAT3 coding sequences. Numbers in the open boxes indicate the exon numbers. The regions corresponding to the two conserved domains A and B are shown. The positions of the bases different between each sex are also indicated. The primer sets (supplementary information, Supplementary Material online) used in the RT-PCR experiments and their resulting product sizes are given. A partial structure of the Eudorina sp. MAT3 splicing variant identified by sequencing of the PCR product (D, upper band amplified with the primer set EuMAT3 F23 and EuMAT3 R9 [supplementary information, Supplementary Material online]) is also shown (B). (C-E) Results of semi-quantitative RT-PCR analyses of MAT3 genes from G. pectorale (C), Eudorina sp. (D), and Volvox *africanus* (*E*). Poly(A)<sup>+</sup> mRNA from each sample was isolated and subjected to RT-PCR analysis using primer sets indicated. Loading volume for each lane was normalized to the amount of the EF-like gene (internal control) product. Note that no significant differences in expression level and splicing pattern were detected between the two sexes. For V. africanus (E), a primer set which amplifies a 3,462-bp fragment including the full-length coding sequence of female and male MAT3 (Vol Africa male F8 and Vol Africa CDS R1 [supplementary information, Supplementary Material online]) was used for the analysis.

## **Supplementary Reference**

S1. Nakada T, Shinkawa H, Ito T, Tomita M. 2010. Recharacterization of *Chlamydomonas reinhardtii* and its relatives with new isolates from Japan. J Plant Res. 123: 67–78.