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Name	Accession	Region	Author	Reference
BABOON.TZ.2010G	U10899	GAG	Jin, MJ	<i>J Virol</i> 68 (12):8454–8460 (1994)
BABOON.TZ.BAB2010E	U10897	ENV	Jin, MJ	<i>J Virol</i> 68 (12):8454–8460 (1994)
COLOBUS.CM.COL1216	AF301155	POL	Courgnaud, V	<i>J Virol</i> 75 (2):857–866 (2001)
COLOBUS.CM.COL163	AF301154	POL	Courgnaud, V	<i>J Virol</i> 75 (2):857–866 (2001)
COLOBUS.CM.COLCGU1	AF301156	ENV GAG NEF POL REV TAT TAT VIF VPR	Courgnaud, V	<i>J Virol</i> 75 (2):857–866 (2001)
DRILL.-.SIVDRLGAG	AJ310481	GAG POL	Clewley, JP	Unpublished
GRIVET.-.GRI2E	U03995	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
GRIVET.-.GRI2L	U04007	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
GRIVET.-.GRI3E	U03994	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
GRIVET.-.GRI3L	U04006	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
GRIVET.ET.GRI-677	M66437	ENV GAG NEF POL REV TAT VIF VPR VPX	Fomsgaard, A	<i>Virology</i> 182 (1):397–402 (1991)
LHOEST.CD. SIVlhoest447	AF188114	ENV GAG NEF POL REV TAT VIF VPR	Beer, BE	<i>J Virol</i> 74 (8):3892–3898 (2000)
LHOEST.CD. SIVlhoest485	AF188115	ENV GAG NEF POL REV TAT VIF VPR	Beer, BE	<i>J Virol</i> 74 (8):3892–3898 (2000)
LHOEST.CD. SIVlhoest524	AF188116	ENV GAG NEF POL REV TAT VIF VPR	Beer, BE	<i>J Virol</i> 74 (8):3892–3898 (2000)
LHOEST.KE.SIVlhoest	AF075269	ENV GAG NEF POL REV TAT VIF VPR	Hirsch, VM	<i>J Virol</i> 73 (2):1036–1045 (1999)
MANDRIL-1.GA.MNDGB1	M27470	ENV GAG NEF POL REV TAT VIF VPR	Tsujimoto, H	<i>Nature</i> 341:539–541 (1989)
PATAS.SN.PAMG31NEF	U26299	NEF	Bibollet-Ruche, F	<i>J Gen Virol</i> 77(Pt 4):773–781 (1996)
RCM.NG.RCMNG409	AF349681	GAG POL VIF	Beer, BE	<i>J Virol</i> 75 (28):12014–12027(2001)
RCM.NG.RCMNG411	AF349680	ENV GAG NEF POL REV TAT VPR VPX	Beer, BE	<i>J Virol</i> 75 (28):12014–12027(2001)
SABAEUS.-.AGMSD42	U20813	NEF	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.-.SAB2L16	U04010	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.-.SAB3E	U03997	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.-.SAB3L18	U04012	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.-.SAB4E	U03998	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.-.SAB4L10	U04014	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.-.SABD37P	U04018	POL	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SABAEUS.SN.AGMSD30	U20812	TAT	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD30	U20965	VPX	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD30	U20966	REV	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD30	U21093	NEF	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD42	U20814	TAT	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD42	U20967	VPX	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSD42	U20968	REV	Jubier-Maurin, V	<i>J Virol</i> 69 (11):7349–7353 (1995)
SABAEUS.SN.AGMSP055	U26297	NEF	Bibollet-Ruche, F	<i>J Gen Virol</i> 77(Pt 4):773–781 (1996)
SABAEUS.SN.P056	U26298	NEF	Bibollet-Ruche, F	<i>J Gen Virol</i> 77(Pt 4):773–781 (1996)
SABAEUS.SN.SAB1C	U04005	ENV GAG NEF POL REV TAT VIF VPX	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
SUN.GA.SIVSUN	AF131870	ENV GAG NEF POL REV TAT VIF VPR	Beer, BE	<i>J Virol</i> 73 (9):7734–7744 (1999)
SYKES.KE.SYK173	L06042	ENV GAG NEF POL REV TAT VIF VPR	Hirsch, VM	<i>J Virol</i> 67 (3):1517–1528 (1993)

TANTALUS.-.AGMT17	L19250	GAG	Hirsch, VM	<i>Virology</i> 197 :426–430 (1993)
TANTALUS.-.AGMT27	L19251	GAG	Hirsch, VM	<i>Virology</i> 197 :426–430 (1993)
TANTALUS.-.AGMT40	L19252	GAG	Hirsch, VM	<i>Virology</i> 197 :426–430 (1993)
TANTALUS.-.AGMT49	L19253	GAG	Hirsch, VM	<i>Virology</i> 197 :426–430 (1993)
TANTALUS.-.AGMT9	L19254	GAG	Hirsch, VM	<i>Virology</i> 197 :426–430 (1993)
TANTALUS.-.TAN17E	U04000	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
TANTALUS.-.TAN40E	U04001	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
TANTALUS.-.TAN49E	U04002	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
TANTALUS.CF.AGMB05	M81070	ENV	Muller, M	<i>J Virol</i> 67 :1227–1235 (1993)
TANTALUS.CF.AGMTB14	M80208	ENV	Nerrienet, E	Unpublished (1992)
TANTALUS.UG.TAN1	U58991	ENV GAG NEF POL REV TAT VIF VPR VPX	Stivahtis, GL	<i>Virology</i> 228 :394–399 (1997)
VERVET.-.VER1E	U04003	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
VERVET.-.VER2E	U04004	ENV	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
VERVET.-.VER2L	U04017	NEF	Jin, MJ	<i>EMBO J</i> 13 (12):2935–2947 (1994)
VERVET.DE.AGM3	M30931	ENV GAG NEF POL REV TAT VIF VPR VPX	Baier, M	<i>Virology</i> 176 (1):216–221 (1990)
VERVET.ET.AGM691	M33719	NEF	Johnson, PR	<i>J Virol</i> 64 (3):1086–92 (1990)
VERVET.ET. AGM_VER-692	M29974	GAG	Johnson, PR	<i>J Virol</i> 64 (3):1086–92 (1990)
VERVET.ET.VER385E	U10898	ENV	Jin, MJ	<i>J Virol</i> 68 (12):8454–8460 (1994)
VERVET.KE.AGM155	M29975	ENV GAG NEF POL REV TAT VIF VPR VPX	Johnson, PR	<i>J Virol</i> 64 (3):1086–1092 (1990)
VERVET.KE.AGMTYO	X07805	ENV GAG NEF POL REV TAT VIF VPR VPX	Fukasawa, M	<i>Nature</i> 333 :457–461 (1988)
VERVET.KE. AGM_VER-9063	L40990	ENV GAG NEF POL REV TAT VIF VPR VPX	Hirsch, VM	<i>J Virol</i> 69 (2):955–967 (1995)
VERVET.KE.VER266E	U10896	ENV	Jin, MJ	<i>J Virol</i> 68 (12):8454–8460 (1994)

GRIVET_FT.AGM_GRI-677	MGGHSA.LSGRSLDTFEKIRLRPNPKGKKYQIKHLIHWAGKMERFGLHKLLETKEGCQKIIEVILPTLPLETSGSEGLKALFNLCVVICIHAHQVKVDTEAVVTKVQHYHLVDKNEKA.....TAT	117
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CONSENSUS TAN	MGaGHSa.LsGRNLDtFEkIRLrPNgKkKYqIKhLIHWAGKeMERFGLhPKLLEtKtEGCQKIIEVILaPlePtSGSEGLKsLfnLccvVICiHAEHQVKVDTEAVVtKvQhYHLvDKNEKa.....aap	119
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TANTALUS -- AGMT49	-----V-----A-----R-----K-----E-----D-----	120
TANTALUS -- AGMT9	-----T-----S-----S-----S-----S-----	120
TANTALUS -- UG.TANI	-----V-----V-----Y-----A-----Q-----S-----R-----	120
CONSENSUS VER	MGaatSA.LnrRqLDtFqFhIRLRpNgKkKYqIKhLIHWAGKeMeRFGlHrLEtBeGCKKIIEVILyPLePtSGSEGLKsLfnLvcvLYc?Hpe?kVKVDTEAVAva?vr?QcCHLveKeknA.....ERNtTe?	119
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VERVET_KE.AGM_VER-9063	-----KG-----K-----K-----D-----D-----D-----	120
CONSENSUS LHO	MGSGNSV.LSRQIE?FcS?RLRpGSKkTYQKRHvWAThELDRFGLGahLLEtA?GCKKILlGvCmPlySvTgSKNlKAlVgTvcV?CCCHLGI?2adTqEA?cK?KIePte?rGkKQO.....	108
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BABOON_TZ.2010G	MGNSGA.LLGTDLDFEKIRLRKGGKCYRLKHLCKWCKGELDRFGLSDKLELTOQGCEKILISVCWPLYDQGSNlKAlVgTvcVvACiHAGIEIKStODAlKkLkVITrKBEKQeDESK.....AET	20
MANDRIL_1.GA.MNDGB1	MGNEQGL.LGKkTLLEDlQkVRLkKGGkCYkIKhVrWmCtEvsRcVLIpELlKsATgVAQILkEktVPlVDTGSSEVLSLYG.CSVcYcLHRkWNIEDtQEAkKvEAYkKQAMIEASKEEE.....	119
COLOBUS_CM.COLCGUI	MGRASV.LSGKLDaWEöVRLpPgKkYkMLkHLvWAcReLrFGLSDtLLeNAEGIQKIIGVILPlVPTGSSEGLKsLfnLccvLWCvHkVVKVDTEAVAhVKKöCHLVDNNEABE.....	121
RCW_NG.RCMG409	MGRASV.LSGKLDaWEöVRLpPgKkYkMLkHLvWAcReLrFGLSDtLLeNAEGIQKIIGVILPlVPTGSSEGLKsLfnLccvLWCvHkVVKVDTEAVAhVKKöCHLVDNNEABE.....	119
RCW_NG.RCMG411	MGRASV.LSGKLDaWEöVRLpPgKkYkMLkHLvWAcReLrFGLSDtLLeNAEGIQKIIGVILPlVPTGSSEGLKsLfnLccvLWCvHkVVKVDTEAVAhVKKöCHLVDNNEABE.....	119
SUN_GA.SIVSUN	MGAGNST.VDREvVSRFvAlKpGkKTYQARhVvWAGkELDRFGLnKELlRtVegQKILlSVCWpLYASGSNlKAlVgTvcVlACcHOGIPVkdTöRAlKvLEAKNFEAQASö.....	118
SYKES_KE.SYK173	MGAAGSAILTGTRELDryEKIRLRPKGKKRYLVRHLVWAKKELDRFGLSDQLESKGECKEILITVLLPLeANSENLsLFGIISVWAhVhKkEVEDTEGAKQVKvEAcNWkRDDPAtSGGSNSQNM.....	130
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SABAEUS_SN.SABIC	SSGöTKELöAQkKNEPTVTPSGSRNYPiVSV.NNöQVHöQPISPRtLNAWKvEeKkFGAEIVPMFQALSEGClSYDvNöMlNvIgdHöGALöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	248
CONSENSUS TAN	SgGöQ.....?NyntaAppgghGNYPVVOQ.NNöQVHöTPISPRtLNAWKtVBEKkFGAEiVPMFQALSEGClSYDINöMlNvIgdHöGAMöIQIvKEINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	240
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TANTALUS -- UG.TANI	-----O-----L-----D-----O-----YV-M-----C-----M-----	243
CONSENSUS VER	ssGq.....AkkndkgttappgSQNFPAöQö.gNawHvPIsPRtLNAWKvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGALöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	243
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CONSENSUS LHOpKsgNyPLiRE.NöRwVHöTPIsPRtIQTWKvIvEDRGWkPEtVAMFSALTEKALpDdLNvMLNAIgdHöGAMöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	216
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MANDRIL_1.GA.MNDGB1NFPVöRDAAGöQYöTPIsPRtIQTWKvIvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGAMöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	224
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COLOBUS_CM.COLCGUIKEKGATATSSGöRGNYPIVTI.NöPEHöPIsPRtLNAWKvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGALöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	232
RCW_NG.RCMG409öEQGATVTSöGöRGNYPIVTI.NöPEHöPIsPRtLNAWKvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGALöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	236
RCW_NG.RCMG411NFPVöRE.GöNYHöPIsPRtVöTöTWKvIvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGAMöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	236
SUN_GA.SIVSUNNFPVöRE.GöNYHöPIsPRtVöTöTWKvIvEeKkFGAEIVPMFQALSEGCTPYDINöMlNvIgdHöGAMöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	222
SYKES_KE.SYK173	ASETSöGöKVöQöEQKöKAATPPöRöGNYPöLLEöNFöQöNöIHöTöGöVöPöRöLkTWöEAVNSöKkFDASiVöPöLöFöQALöTEöGöIPöYDöINGöMLNAIgdHöGAMöIQIvKEIINEFAEAöWDRtHRPPAPLPAGöLRDPTGSD	260

GRIVET_ET.AGM_GRI-677	..NANPRIDVYVGRYKRVIIILGKQVYQVMNPKVLDIROGPKPEPFQDYVDRFYKALRAEQAPQVDYKNNMTQTLIIQANPDFDKLIIKGLGWNPTLEMLTACOGVGGPQHKARL	365
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MANDRILL_1_GA.MNDG81	..MOQNAVNTGIIYKSWIIILGKQVYQVMNPKVLDIROGPKPEPFKDYVDRFYKALRAEQAPQVDYKNNMTQTLIIQANPDFDKLIIKGLGWNPTLEMLTACOGVGGPQHKARL	352
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SUN_GA.SIVSUN	..RANNPFAVGNIVRNWIIILGKQVYQVMNPKVLDIROGPKPEPFKDYVDRFYKALRAEQAPQVDYKNNMTQTLIIQANPDFDKLIIKGLGWNPTLEMLTACOGVGGPQHKARL	352
SYKES_KE.SYK173	..RANNPFAVGNIVRNWIIILGKQVYQVMNPKVLDIROGPKPEPFKDYVDRFYKALRAEQAPQVDYKNNMTQTLIIQANPDFDKLIIKGLGWNPTLEMLTACOGVGGPQHKARL	387
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TANTALUS_-_AGMT17	..-O- - - - -I- -H- - - - -SK- - - - -V- - - - -V- - - - -V- - - - -V- - - - -R- - - - -G- - - - -R- - - - -A- -	455
TANTALUS_-_AGMT27	..-N- - - - -I- -P- - - - -SK- - - - -V- - - - -V- - - - -V- - - - -V- - - - -R- - - - -G- - - - -R- - - - -A- -	455
TANTALUS_-_AGMT40	..-N- - - - -I- -P- - - - -SK- - - - -V- - - - -V- - - - -V- - - - -V- - - - -R- - - - -G- - - - -R- - - - -A- -	453
TANTALUS_-_AGMT49	..-N- - - - -I- -P- - - - -SK- - - - -V- - - - -V- - - - -V- - - - -V- - - - -R- - - - -G- - - - -R- - - - -A- -	455
TANTALUS_UG.TANI	..-N- - - - -I- -P- - - - -SK- - - - -V- - - - -V- - - - -V- - - - -V- - - - -R- - - - -G- - - - -R- - - - -A- -	454
CONSENSUS_VER	..QNM.QS.QNM.VQOQ.??KR.GIGgrgr.??RPP?kCynCGKFGHMQrQcpeprkikCLKCGKPGHMLAKDCRGqVNFLLGY.RWmg.aKP	453
VERVET_DE.AGM3	..MQOPVVVVVVVVVVVVV	455
VERVET_ET.AGM_VER-692	..NO.-GV- -A.G.-V-K- -V-KN-TQKGPVV- -F-R- - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A- - - - -A	446
VERVET_KE.AGM155	..LLPPPPPPPPPPPPPPP	451
VERVET_KE.AGMTYO	..-T- -N- - -GP.Q- -LR- - -T- -L- - -L	450
VERVET_KE.AGM_VER-9063	..-T- -N- - -AA.-VR- -Q- -L- - -L	453
CONSENSUS_LHO	..LAEAMAtAmQsQmrcqnm.VQVt.PprNaQGRFVVTGGGRPRPLTCFNCGKFGHMLARECKAPRQEGCWNCGSkeHrFAQCPRKGKVNFLGY.PWr?.gPp	439
LHOEST_CD.SIVLhoest447	..-E- - - - -G- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R- - - - -R	447
LHOEST_CD.SIVLhoest485	..-G- - - - -KHL- - -O- -	447
LHOEST_CD.SIVLhoest524	..-G- - - - -KHL- - -O- -	445
LHOEST_KE.SIVLhoest	..-S- -I- -Q- -V- - -L- -	450
MANDRILL_1_GA.MNDG81	..RFQPRGRVQPR.TG.RKPI.CFNCKEGHVARFRCAPRMMQON.PPRGPRGRGPPPKO.LRCPNCGQYGHALROCTPREVTAKCFNCGQYGHALROCTPRIGGAGRGRGRGGRGFRGAPRPRPVRCFTCNQBOHMORCPNKQANFLGATRGVEL.OTA	444
DRILL_-_SIVDRILGAG.NEW	..OFOOE.RTNMIOMAOCSIMAOQ.GPRRGPPKQGGQGGPR.FLRCYNGKGTHTARCYKTNRKKGWRCGEHGHMLKDCPKRVNFLLGSA.PWKQ.GKP	246
COLOBUS_CM.COLCGUI	..OMVGSNIMAOQ.GPRKGPPKGGPR.FLRCYNGKGTHTARCYKTNRKKGWRCGEHGHMLKDCPKRVNFLLGSA.PWKQ.GKP	450
RCM_NG.RCMNG409	..OMVGSNIMAOQ.GPRKGPPKGGPR.FLRCYNGKGTHTARCYKTNRKKGWRCGEHGHMLKDCPKRVNFLLGSA.PWKQ.GKP	450
RCM_NG.RCMNG411	..OMVGSNIMAOQ.GPRKGPPKGGPR.FLRCYNGKGTHTARCYKTNRKKGWRCGEHGHMLKDCPKRVNFLLGSA.PWKQ.GKP	450
SUN_GA.SIVSUN	..VMAQOS.VNMVQ.GFSKGRSMIKCYNCGQYGHMLARECKAPRKACFCNGKGTHTARACRQPKRNQGGPFAQANFLGKMGVSR.RPP	454
SYKES_KE.SYK173	..VMAQOS.VNMVQ.GFSKGRSMIKCYNCGQYGHMLARECKAPRKACFCNGKGTHTARACRQPKRNQGGPFAQANFLGKMGVSR.RPP	476

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GRIVET_FT.AGM_GRI-677
SABAEUS_SN.SABIC
CONSENSUS TAN
TANTALUS -.AGMT17
TANTALUS -.AGMT27
TANTALUS -.AGMT40
TANTALUS -.AGMT49
TANTALUS -.AGMT9
TANTALUS_UG.TANI
CONSENSUS VER
VERVET_DE.AGM3
VERVET_FT.AGM_VER-692
VERVET_KE.AGM155
VERVET_KE.AGMTYO
VERVET_KE.AGM_VER-9063
CONSENSUS LHO
LHOEST_CD.SIVlhoest447
LHOEST_CD.SIVlhoest485
LHOEST_CD.SIVlhoest524
LHOEST_KE.SIVlhoest
MANDRIL-1_GA.MNDGB1
DRILL -.SIVDRLGAG.NEW
COLOBUS_CM.COLCGUI
RCM_NG.RCMNG409
RCM_NG.RCMNG411
SUN_GA.SIVSUN
SYKES_KE.SYK173
RNfVQYRGDIIVGLEPTAPPMME.....TAYDPAKKLLQOYAEKGGORLFREREQTRKQKEKEVEDV.SLS.SLFGGDDQ
RNfPL...T..SIRFTAPPMERDYSRPEENWYADRPPTTRGPFDDPATALLKQYAVQGRKQK.QOQNHSPQOSPFYEAAYSLSRSLFGEDQ
RNfL...EOGCaVPTAppmpaH.....gfptGppDaagAYDFAKrLLeQYakKg.....dOLrKQKEKELEdY.SLS.SLFGeDQ
-----IA-----V-----G-----R-----
-----KK-----L-----R-----E-----K-----
-----T-----V-----O-----R-----R-----
-----RL-T-----V-----S-WR-----T-----E-----
-----D-----L-----TSV-T-R-----R-----
-----S-----RK-----
rNfP...AatLgaePsAPPPPT.....N?tpYDpAkkLlqgYaeKqLReq?nppa?npdwtEgY.SLn.SLFGEDQ
K-L...EHRA-V.....H.....S-----D-----RKK--V-----
VERVET_KE.AGM155.....PGA-E-TR--EK-TQE-A-Q-RKVE.KSQAGREE-D--K.
VERVET_KE.AGMTYO.....S-----M-N-NR--N--N-----
VERVET_KE.AGM_VER-9063.....SG-----K-----M-----
--L...--H-V-----.....GKRT-PT--A-----
GNfPlm.GG?AGv?PSAPPMEr?p.....PTKAERALFTYRnLGGQLr?QOQO..vPQKCVDRPC..L?PffFPDDQ
-----N-V-----S-----R-----I-----S-----
-----N-V-----NS-----KV-----K-----N-----
-----I-A--I-----R-----I-----K-----N-----
-----Y-L--A-RI-----SA-----T-----KR-----N.SL-----
GNYP.....AQEVTTAPPPL.....EKPL..Q..KTLSTYQKLGRLGRQRMK..EEKREDFH..SLS.TLFQEDQ
RNfP...QASLTPSAPPMPGY.....AGEDFAEKMLR.Q.YMEQGQQRQOQOQO...KKGPFYDAYNSLS.SLFGSDQLQ
IFPPKM.....SKDLPPRR.....NPOYDPAEEMLKKY.LALG..FOHKQEQKKNKE..EGLYP...SLK.SLFGDDQ
RNfPL...TSLRPTAPGENAW.....NPOYDPAEEMLKKY.LALG..FOHKQEQKKNKE..RVGRAYDEALSSLN.SLFGSDL
RNfLPL...TSLRPTAPGREGW.....NPOYDPAEEMLKKY.LALG..FOHKQEQKKNKE..KVGRAVEDALSSLN.SLFGSDL
GNfPVM.....PSAPPLEDLTGNRMT.....PFSQAKERALETY.RLLG.OGLRAO..OKEKE..R.GEQC.EPC.LN.MLFPEDP
ANfPVR.....SEFSAPPLEDIEDGPWLTSQAQMSQAQAKAQNPSKPKPTNREVLSPKSSGKE..ETKSLYP.....SLS.SLFGEDQ

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GRIVET_FT.AGM_GRI-677	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	104
SABAEUS_S.SABD37P	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	2
SABAEUS_SN.SABIC	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	120
CONSENSUS_VBR	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	92
VERVET_DE.AGM3	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	101
VERVET_KE.AGM155	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	104
VERVET_KE.AGM150	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	104
VERVET_KE.AGM150	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	101
CONSENSUS_LHO	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	101
LHOEST_CD.SIVLHOEST447	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	100
LHOEST_CD.SIVLHOEST485	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	100
LHOEST_CD.SIVLHOEST524	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	101
LHOEST_KE.SIVLHOEST	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	97
TANTALUS_UG.TANI	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	104
COLOBUS_CM.COLCGU1	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	68
MANDRILL_1.GA.WNDG81	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	93
DRILL_1.SIVDRILGAG.NEW	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	103
RCM_NG.RCMNG409.NEW	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	106
RCM_NG.RCMNG411	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	106
SUN_GA.SIVSUN	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	99
SYKES_KE.SYK173	FFRVW.PLGRSETKKFCAIQRHHSWSTN.SP...	114
GRIVET_FT.AGM_GRI-677	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	228
SABAEUS_S.SABD37P	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	120
SABAEUS_SN.SABIC	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	238
CONSENSUS_VBR	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	204
VERVET_DE.AGM3	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	223
VERVET_KE.AGM155	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	226
VERVET_KE.AGM150	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	226
VERVET_KE.AGM150	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	223
CONSENSUS_LHO	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	217
LHOEST_CD.SIVLHOEST447	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	222
LHOEST_CD.SIVLHOEST485	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	222
LHOEST_CD.SIVLHOEST524	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	223
LHOEST_KE.SIVLHOEST	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	219
TANTALUS_UG.TANI	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	226
COLOBUS_CM.COLCGU1	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	188
MANDRILL_1.GA.WNDG81	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	215
DRILL_1.SIVDRILGAG.NEW	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	222
RCM_NG.RCMNG409.NEW	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	224
RCM_NG.RCMNG411	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	224
SUN_GA.SIVSUN	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	221
SYKES_KE.SYK173	IOEKDLHPHPKWRKSVVGGIGGIVHKEYGVQVQLEDKIIT...	239

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GRIVET_ET.AGM_GRI-677      GENPYNTPFVFAIKKKDKTQWRMLVDFRELNKATQDFEFVQLGIPHPAGLQKQKKTIVLIDIGDAYYSIPLCKEFRKY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
SABAEUS_..SABD37P        PENPYNTPVFAIRKKDKSQRWMLMDFRELNKATQDFEQEVQLGIPHPAGLQKQREQTIVLIDADAYFSCPLDDEDFQKY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
SABAEUS_SN..SABIC       PENPYNTPVFAIRKKDKTQWRMLMDFRELNKATQDFEQEVQLGIPHPAGLQKQREQTIVLIDADAYFSCPLDDEDFQKY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
CONSENSUS_VER            GenAYNTP?FCI?HKDKsQRWMLVDFRELNKATQDFEFVQLGIPHPAGL?KMKqITvId?GDAYYSIPLDPeFRKY..TAFTTIP?VNNq?GGIRYQFNCLPQGMKGSPTIFQNTAA?ILLeIKkeLkplT
VERVET_DE.AGM3          -D-----V--K-----K--FE--TE--S--E--I--V-----I--I--V-----K--R--R-----K--R--R-----S--K-----S-----Q-----
VERVET_KE.AGM155        -I--K-----I-----K-----R-----R-----I-----V-----I-----V-----I-----V-----I-----V-----S-----K-----S-----Q-----
VERVET_KE.AGM150        -I--R-----T-----V-----V-----I-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----Q-----
VERVET_KE.AGM_VER-9063 ?GNPYNTPIFAIAKKKKDKNEWRKLLDFR?LM?LTQDFHE?QLGIPHPAGIKKCKQITVVDIGDAYYSIPLDpDrqY..TAFT?P?PS?NNTGPIRYQFNCLPQGMKGSPTIFQATVaGLLsEPRKLNpDli
LHOEST_CD.SIVlhoest447  A-----Q--A-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----V-----
LHOEST_CD.SIVlhoest485  A-----Q--A-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----L--V-----
LHOEST_CD.SIVlhoest524  P-----K--E-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----
LHOEST_KE.SIVlhoest    P-----K--E-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----
TANTALUS_UG.TANI       GENPYNTPVFCIRKKDKTQWRMLDFRELNKATQDFEFVQLGIPHPAGLQKQKKTIVLIDIGDAYYSIPLDPeFRPY..TAFTTIPVNNVGGPIRYQFNCLPQGMKGSPTIFQHTAQRVLKELGKVVODLE
COLOBUS_CM.COLGGUI     LGNPNTPIFCIRKKDKNEWRKLLDFR?LM?LTQDFHE?QLGIPHPAGIKKCKQITVVDIGDAYYSIPLDpDrqY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
MANDRIL_1.GA.MNDG51    PGNVYNTPIFAIAKKDKNEWRKLLDFR?LM?LTQDFHE?QLGIPHPAGIKKCKRITVLDIGDAYYSIPLDpDrqY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
DRILL_..SIVDRLGAG.NEW  RCM_NG.RCMNG409.NEW    PENPYNTPVFCIRKKDKTQWRMLDFRELNKATQDFEFVQLGIPHPAGLQKQKKTIVLIDIGDAYYSIPLDPeFRKY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW    RCM_NG.RCMNG409.NEW
SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN         SUN_GA.SIVSUN
SYKES_KE.SYK173      PTPNYNTPVFAIRKKDKKWRMLDFRELNKATQDFEFVQLGIPHPGGIK.RQKLTIIDLDAYYSVPLDKEFRPY..TAFTTIPSVNNTGPIRYQFNCLPQGMKGSPTIFQNTAANILLEIKRHPTPGL
GRIVET_ET.AGM_GRI-677      IVQYMDLLWLASDHDHETRHQVQVIVRKMILLEKGLTEPDKKQREPPWEMWGMYLHPNKWTINKITELPPLRGE.WTVNKIQQVGVVGLNWSAQIYVPGIKTKHTCAML.R.GKKNLLEIVWTEEAEEYKNN
SABAEUS_SN.SABIC      IVQYMDMLIASDRPKAEHLVMYQQLRDLYLETWGFKTPKPKQKQDPPYLLMGMGYELYPKKWQLQEIILPE.REE.WTVNDIQKLVGKLNWASQIYTGIKTKHLCLL.R.GARPLTEIVQWTEEAEELESEN
CONSENSUS_VER          IVQYMDLLWVGSQEdedytHdkLvequr?klqaWGLETP?KkyQk?PpyEMWGYKlWpKkKwqlslelEe.Ke?WTVNDIQKLVGKLNWAAQLYVpGlrTkniCkLrGGKNNLLeV?WT?EAEEYAEEN
VERVET_DE.AGM3        -R-----M--S--D-----D-----K-----I-----D-----E-----I-----R-----R-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----
VERVET_KE.AGM155      -EGPK--Q--OT--NR--E-----E--RE--F-----K--Q-----K--Q-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----
VERVET_KE.AGMTYO      -N--H-----T-----E--M--E-----E--R--Q-----DE-----K--R-----T-----L-----L-----L-----L-----L-----L-----L-----L-----L-----L-----
VERVET_KE.AGM_VER-9063 -V--KT-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----
CONSENSUS_LHO         IVQYMDLLfIGSDR?kkGhQAVKELReLLmTWNLLeTPKkFOaePPYHWMGYLHPDRWEIEkvkLp?iDlqkTtVnNiQKLVGLNWSAAQLY?GIRTKELCKLl.R.GVK?LeevvtWT?ALeEYeqN
LHOEST_CD.SIVlhoest447  -D-----D-----V-----K-----T-----D-----T-----D-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----
LHOEST_CD.SIVlhoest485  -L-----D-----E-----S-----I-----DK-----R-----E-----TR-----E-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----
LHOEST_CD.SIVlhoest524  -E-----E-----S-----I-----DK-----R-----E-----TR-----E-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----
LHOEST_KE.SIVlhoest  I-----ER-----ER-----I-----EM--T-----Q-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----D-----
TANTALUS_UG.TANI       IIQYMDMWIGSDLPKehdEkeVEVRKLLLRGfETpDKKQREPPYDMWGMGYKlYpShSlnKtIePE.QEH.WTVNDIQKLVGLNWSAQIYpGikTKALCKLl.R.GAQLITAVVQWTEEAEEVFRQN
COLOBUS_CM.COLGGUI     IAQYMDLLfIGSDLPLeEhrrAVQeURdAlLYGLTEPDKKQADPPYKMMGYELHPKQWKkVqIPEQD..KWTVNDIQKLVGLNWSAQIYpGikTKeISKCTk.GRKHLLLeEVQLSAEAEELQON
MANDRIL_1.GA.MNDG51    IVQYMDLLfVGSdYTAEEHKAIVeRALMTWNLLeTPKkFOepFFHWMGYELHPDKWKIEKvqLPELAE.QPTVNEIQKLVGLNWSAQIYpGikTKLCKLl.R.GGLNITEKVTMTTEARLEYEQN
DRILL_..SIVDRLGAG.NEW  IVQYMDLLfVGSdRTEYHNElIKRkHLHLLAWGfETpDKKFOENPPEWGMGYLHPKkKtVQeIKLPEKET..WTVNDIQKLVGLNWSAQIYpGikTKLCKLl.R.GAKPLDEEVEWTEARLEYEEN
RCM_NG.RCMNG409.NEW    IVQYMDLLfVGSdRTEHSHQMLKRfLHLLMFWGfETpDKKFOKPPPEWGMGYLHPDKKtVQeIKLPEKEE..WTVNDIQKLVGLNWSAQIYpGikTKLCKLl.R.GVKALDEKVVFTREAELEYEEN
RCM_NG.RCMNG411       IVQYMDLLfVGSdRTEHSHQMLKRfLHLLMFWGfETpDKKFOKPPPEWGMGYLHPDKKtVQeIKLPEKEE..WTVNDIQKLVGLNWSAQIYpGikTKLCKLl.R.GVKALDKKVVFTREAELEYEEN
SUN_GA.SIVSUN         IVQYMDLLIGSDYKkKHEEIVKQLRfLHLLMFWGfETpDKKFOKPPPEWGMGYLHPDKKtVQeIKLPEKEE.EPTVNDIQKLVGLNWSAQIYpGikTKLCKLl.R.GNKPLAEKVKWTEARLEYEEN
SYKES_KE.SYK173      LIQYMDLLIGTDSEKAHQEIvQqIVtALLKkVGFkVpKekWQDQYpMqWlGvYTLHPDKWQlQKIElENIDD.EITVnQlQKlLlGvLNWSAQIYpGikTKELCKCIR.CTKQlTEVlTLTEAAEALEEN

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GRIVET_FT.AGM_GRI-677	RIEEAQDDHAKYHNMRSMVQEFGLPNI	VAKEIVAAACPKCQIRGERFKHGQVDAS	LETWQMDCTHLEGGKIIIVAVHVASGF	LEAEVPIPRETKETAHFLLKLLARVPK	HLHTDNGFNFTSQNVAAVCWGG	870
SABAEUS_SN.SABIC	RIEEAQEEHDKYHANRSMQOEFGLPAI	VAKEIVAAACPKCQIRGERFKHGQVDAS	PVQMDCTHLEGGKIIIVAVHVASGF	TEAEVPIPRETKETAHFLLKLLASRWP	ITQLHTDNGFNFTSQOAAAICWGG	880
CONSENSUS_VBR	?IEEAQEEH?RYH?NW?NLADT?GLP	QIVAKEIVAMCPKcqi.KGEP?HQVD	ASPGVQMDCTHLEGGKIIIVAVHVAS	GFTEAEVPIPRETKETAHFLLKII	LSRWPITqLHTDNGFNFTSQEVAA?CWGG	806
VERVET_DE.AGM3	K-----E-N-R-----Y-----	V-----V-----VI-----	-----I-----I-----	-----IG-----H-----	-----M-----	864
VERVET_KE.AGM155	R-----D-S-R-----Y-----	V-----V-----I-----	-----I-----I-----	-----IG-----H-----	-----M-----	867
VERVET_KE.AGMTYO	K-----E-N-K-----Y-----	V-----V-----K-V-----	-----T-----K-V-----	-----R-----V-----	-----I-----	866
VERVET_KE.AGM_VER-9063	R-----D-S-K-----F-----	NAK-----I-----	-----V-----I-----	-----R-----	-----I-----	864
CONSENSUS_LHO	KIEPA?EEHskFHNAKDLLEEKfh?	PPWAKQIVNsC?CQcKGEAItGQVD?	S?GIWQ?DCTH?PFGQVIINAVHvAs	GFVWAEVIEPDETKTTa?FLK	KLCSRWPV?Q?HTDNGFNFSKvQAVtWwI	830
LHOEST_CD.SIVlhoest447	Q-----Y-----I-----	N-----T-P-----I-----	M-----Q-----V-----	-----H-----	-----I-----	867
LHOEST_CD.SIVlhoest485	Q-----L-----L-----	N-----T-P-----I-----	M-----Q-----V-----	-----H-----	-----I-----	867
LHOEST_CD.SIVlhoest524	V-----G-----YGI-----	E-A-Q-----N-----	L-I-M-----K-I-----	-----L-----K-I-----	-----D-----	868
LHOEST_KE.SIVlhoest	V-----V-----NL-----	D-AN-K-----V-V-----	L-L-----L-----	-----SH-----	-----K-I-----	864
TANTALUS_UG.TANI	RMEEAQESHDKYHTNWQ?IRD	AFGIPALVAKEIVAAACPKCQIRGERP	IHGQVDASVQMDCTHLEGGKIIIVAVH	VASGFLEAEVIARETKETAHFLLKII	LSRWPITKLHTDNGFNFSQEVQITCWGG	867
CONSENSUS_COL	KIEeAE?DHOKfHSNvOYmKEqGLP	tLVAKEIWERcpeCQnFGpVHGqLD	YSYGlWQlDCTHTEEGKvIIIVAVH	VCTLFCWATI.LKREtGEETGrALIK	LASQWEVvKOVHTDNGFNFSvSOHFKA	AVWwL
COLOBUS_CM.COL1216.NEW	L-----L-----A-----	Y-----I-----L-----	KY-----S-----	D-----T-----V-----	M-----I-----G-----	R-----
COLOBUS_CM.COL163.NEW	-----A-----E-----	-----L-----V-----	-----S-----K-----	-----A-----	-----	-----R-----
COLOBUS_CM.COLCGUI	-----L-----	-----V-----	-----S-----K-----	-----A-----	-----	-----R-----
MANDRIL-1_GA.MNDGB1	NIEPAQEEHEKYHNSAQLREKPHL	PALVAKQIVQSCSKCCHGEP	IKGOTDASLGVWQIDCTHLENGQII	IVAVHVASGFMMKAEVITAE	GKKTAEFLKLAaOWPISKLHTDNGFNFTSQ	EVETMCWwL
DRILL_-SIVDRLGAG.NEW	NMEKAQEEHDLYHNMRSLAQEFLG	PVIAKQIVQCPKQVKGPEMRQVDAS	PGTMDCTHLEGGKIIIVAVHVASG	YIEAEVIEPAETGKTAFLKLAGRVP	WVHLHTDNGFNFTSEKvATvCWwA	866
RCM_NG.RCMNG409.NEW	GIEKAQEEHEKHHNMRMAAEFKI	POIvAKEIVAQCPKQVKGPEMRQVDAS	PGTMDCTHLEGGKIIIVAVHVASG	YIEAEVIEPAETGKTAFLKLAGRVP	WVHLHTDNGFNFTSAaVQvCwMA	866
RCM_NG.RCMNG411	GIEKAQEEHEKYHNSRMAAEFFQI	POIvAKEIVAQCPKQVKGPEMRQVDAS	PGTMDCTHLEGGKIIIVAVHVASG	YIEAEVIEPAETGKTAFLKLAGRVP	WVHLHTDNGFNFTSAaVQvCwMA	866
SUN_GA.SIVSUN	KIEPAVEHGGKfHNNAAALQEMF	DIPVAVAKQIVNCAQCOQKGEAIt	IGQVDASVGIWQIDCTHTEEGKvII	IVAVHVASGFVWAEVLEQKTTA	WLLKLCAMWVPKQILHTDNGFNFTSK	DEvAaCwWwL
SYKES_KE.SYK173	RIPQAQEDHERYHNSMEYLRFQ	EHLPRQvAKAIIQCPKQvNRGEP	KHQVDVDIYNVQMDCTHTEEGKvII	CVAVNTASGYIETKILKREtGETAL	FLMQIASRWP IKQILHTDNGFNFSvD	KfKAaCwWc
GRIVET_FT.AGM_GRI-677	NIEHTTGIPYNPQSQSVESMNRQL	KEIISQIRDDCERLETA	VOMATHIHNFKRGGIGG	ISSAERLIVNMLITTOLE	NLTONQIQKILNFKVYRGRDPV	WKGPARLLWKGEGAVVKEGED.LKVVPR
SABAEUS_SN.SABIC	KIEHTFGVPYNPQSQSVESMNRQL	KEIIGQIRDDAERLETA	VIMAVHIHNFKRGGIGG	YSAAERLINIHTHELETKIQOK	LSKIQNFRVYRGRDPV	WKGPAKLLWKGEGAVVIQEQGE.LKTIIPR
CONSENSUS_VBR	KiEHttGvPYNPQSQGSiESMnK	QlKEIIGKIRDDCQYTeT	vLMAChI.HNFKRGGIGG	IITQlE?Q?LQTKIQKILNFRVY	RGRDPVWKGPAqLWKGEGAVV?KeGee.LKvVvPR	
VERVET_DE.AGM3	V-----I-----L-----	A-----IL-----	Q-S-----	I-----I-----	H-----L-----	D-SD-----
VERVET_KE.AGM155	-----I-----	-----A-----	-----IL-----	-----Q-S-----	-----I-----	-----H-----
VERVET_KE.AGMTYO	-----V-----	-----V-----	-----Q-----	-----S-----	-----I-----	-----L-----
VERVET_KE.AGM_VER-9063	-----V-----	-----V-----	-----Q-----	-----S-----	-----I-----	-----L-----
CONSENSUS_LHO	GIEHTTGIPYNPQSQVVEAKN	VlKqIIErvREDAQQLKTA	vLMAVHIHNFKQRGGIGG	LsPaERfINMINAGLETOY	lQKLSKILKFKVYRGRDPQ	WKGPAQLLWKGEGAVVKEG??.IFsvPR
LHOEST_CD.SIVlhoest447	-----A-----	-----T-----	-----	-----	-----	-----DT-----
LHOEST_CD.SIVlhoest485	-----S-----	-----	-----	-----	-----	-----DT-----
LHOEST_CD.SIVlhoest524	-----S-----	-----	-----	-----	-----	-----EN-----
LHOEST_KE.SIVlhoest	-----S-----	-----	-----	-----	-----	-----EN-----
TANTALUS_UG.TANI	QVEHTTGIPYNPQSQSVESMNRQL	KEIIEKIREDCAFLETA	vLMACHIHNFKRGGIGG	MTPaERLIVNMLITTOLE	TIHQIQTQOKISNFKVYRGRDP	VWKGPAQLLWKGEGAVVKEGEE.LKVVVPR
CONSENSUS_COL	GI?HTTGT?PYNPQSQGI?VEQR	Nm?Ke?IEKMT?dQAEtL	ESKvAMAVYALNFKR?gGI	GKSPWEROVERAIIElD	TQNLTKLQNKfKFNKAYWKEHTG	EWQGPGLWKGEGAVVIRNSOGTILFVKPR
COLOBUS_CM.COL1216.NEW	-----T-----	-----I-----	-----N-----	-----RE-----	-----R-----	-----
COLOBUS_CM.COL163.NEW	-----E-----	-----L-----	-----T-----	-----S-----	-----I-----	-----E-----
COLOBUS_CM.COLCGUI	-----A-----H-----	-----V-----	-----DV-RK-K-----	-----K-----	-----L-----	-----
MANDRIL-1_GA.MNDGB1	KIEHTFGVPYNPQSQVVEAKN	VlKqIIErEDCKELKTA	vAMATFLHNFKQRGGIGG	MTAGERIVNMLINTELE	YQYQNOIISKNLNFVYRGRDOL	WKGPGULLWKGEGAVVLYQEE.IKIVPR
DRILL_-SIVDRLGAG.NEW	QIEHTFGVPYNPQSQVVEAKN	VlKqIIErEDQAEKLETA	vOMAVLHNFKRGVGECSA	ERIVNIIATLITLTKLQONV	LKIQNFRVYRGRDOLW	K
RCM_NG.RCMNG409.NEW	QIEHTFGVPYNPQSQVVEAKN	VlKqIIErEDQAEKLETA	vOMAVLHNFKRGVGECSA	GERIIDIIASDLQINLQON	LSKIQNFRVYRGRDQW	KGPakLLWKGEGAVVLEDDQD.LKVVPR
RCM_NG.RCMNG411	QIEHTFGVPYNPQSQVVEAKN	VlKqIIErEDQAEKLETA	vOMAVLHNFKRGVGECSA	GERIIDIIASDLQITTKLQON	LSKIQNFRVYRGRDQW	KGPakLLWKGEGAVVLEDDQD.LKVVPR
SUN_GA.SIVSUN	GIQHTTGIPYNPQSQVVEAKN	VlKqIIErEDQAEKLETA	vMALHINNFKQRGGIGG	MTAERfINMINADLETOY	lQKINSKILKFKVYRGRDP	WKGPAKLLWKGEGAVVIKQGEN.ILVVPR
SYKES_KE.SYK173	GIEHTTGIPYNPQSQVVEAKN	VlKqIIErEDDVT	HLQTA	vAMATFLNFKRGGIGG	IISpGERYINMLYTELQ	LQ.QNTTSPKFSNFRVYRQKNE.WKGPakLLWKGEGAVVQTEEGDIFAVPR

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GRIVET_FT.AGM_GRI-677      RKAKIIKDYGERKTMDSSEGSMEGVREANKQMEGSDLDQDE      1040
SABAEUS_SN.SABIC          RKAKIIKDYG..KALDSQAPLEGNRTRAGEVD                1039

CONSENSUS_VER             RKAKIIKDYEPPrkrmgdEgnlEGa?GsDn
VERVET_DE.AGM3            -----S-----G-A--
VERVET_KE.AGM155          -----TL--TH--G--HQMAGDS
VERVET_KE.AGMTYO          -----KQ-V-N--DY--TR-----
VERVET_KE.AGM_VER-9063    -----M--LR-P--QMARNSQLIDD

CONSENSUS_LHO             RKAKLVKDYEGEPKDsE?slDnN
LHOEST_CD.SIVlhoest447    -----GG-H--
LHOEST_CD.SIVlhoest485    -----G-----
LHOEST_CD.SIVlhoest524    -----Qs-M--Q
LHOEST_KE.SIVlhoest      -----S-----

TANTALIUS_UG.TANI        RKAKIIKEYGERKTVGDKTNMEG
COLORBUS_CM.COLCGUI       RKVKITRLOYGEDYGSSENLI.SNGQKEAET
MANDRIL_1.GA.MNDGF1       RKCKIIKDYGFSGKNSQVNLSEV
RCM_NG.RCMNG409.NEW       RKCKIIKDYGRKDYDSETSMEGRQEN
RCM_NG.RCMNG411          RKAKLVKDYGGESSSEVWGX
SUN_GA.SIVSUN            RKAKLITDHG.ERMDS.GSHVENDPKTD
SYKES_KE.SYK173

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GRIVET_FT.AGM_GRI-677	MEREKQIVRVYWRVSRQISRWRGIYVYKIR.NKQLP.....WEYRHHWQVQWFQWYSQFIIPLSKDDYIEVNIYHNLTPERWGLSSHGVLGY.....YHOKGYKTEVDPDGTADRM	109
SABAEUS_SN.SABIC	M..EKHWIPLRWKVTGGQOQERWTSLVKXHMVHSKQCCH.....WRYTPHTKIRNWNWYSQEWVPLKDGALIKVTNYWHLTPEKGMLETYATGIGY.....SKGEWFTLDPWTADHII	108
CONSENSUS_VBR	MnqekewMVRvTMKvP??LITKQGIYrYmR.kRnLuk.....wY?rWHYQItwAYTMsRvYvP?gPhGgIhVdLIYWHLTPEqGWLSTVAVGIQY...vsn??pkyRTELDPaTaDsmI	102
VERVET_DE.AGM3	EE--T-K-D.....L-O-S.....L-RDPW--L	111
VERVET_KE.AGM155	S--H-L--QEEV--N.....LPGS--I--A-K--L-LVND--N	111
VERVET_KE.AGMTYO	PN--GD--O.....N-Y--I-K-C--L--LES--I	111
VERVET_KE.AGM_VER-9063	SGD--K-T.....Q-M--N--C-I-I-LE--QI-C--R.....LGAVGNF-----G--	110
CONSENSUS_LHO	MERD_QRIVRVawITtRSL?EKFLDIRabke.t?nd.....WVLSHGTVGWBFYTYnk?vIPLetGTLIVR?.YAHLaAGRGIISQWAVSIEW.....iYgnYQTEIDPIIAdOmI	101
LHOEST_CD.SIVlhoest447	Y--V--Q.....N--C.....	105
LHOEST_CD.SIVlhoest485	N-I--QV--I--C.....	105
LHOEST_CD.SIVlhoest524	N-V--K-N-S--SK--I--D--I.....	105
LHOEST_KE.SIVlhoest	I--V-LNT--AKEN.....G--H-L--S--I.....V-RD-----	105
TANTALUS_UG.TANI	MEREKLWVTRLTWRVSGEHIDKWKIVKYYHMR.NR.IOD.....WTYLMHYOCGWAMYTCRSRFLIPLGEGKIVVDYCYWHLTPEQGLSTVAVAISeF.....ENWONTYKTEVTPDVADHMI	110
MANDRIL_I.GA.MNDG81	ME.RYERIVRlTmKvSSQRTEKWHLVRVQRMAWATANNEEGC.....WMLYPHFMAYNEMWTCSKVVIINRDIRLIVRSVWHLQIEVGLSTVAVSIEAVVPPPEKEKEWCTEITPEVADHLI	118
COLOBUS_CM.COLG01	MG.KRkPKPLREW.....IKKQPEPC.....OYYLlGKTESPEWTEGKIEFLGSAIKLSLIYLGITLTPDRYHRGPPVSVEL...QIKKwETDLsMOQAVGYM	90
RCM_NG.RCMAG409_NEW	MA.EKMWIvrvvWvDRkIeOWHTLIS.IERkKPKNGMvPI.....KKVPGWSHSEVHIPLGNNTKIKVTYWNLTVEKGLTYGVLAVIDSRCDPcYFSEIDTLADKLRQY	115
SUN_GA.SIVSUN	MEERPPQWRWDEREDRQYKI.YRIvWLDIrlAVeKFLDLRRMhRETKDDWvSMYGTGTGvWbWYTKLIIIPvTYGVVAVI.YGHlTPEKGLINQWCSMEW.....IYNSYQTEIDPIVADOMI	122
SYKES_KE.SYK173	M..EKEMVIVFTRMTPRQIDRLQHLIKTHYKSEKEKATYK.....HHYQIEWQNYTYCQWTVPGDGLIWIIF.YHNLAPERWGLHMQGIKIQY.....QWQWNTDILLPvADRLI	107
GRIVET_FT.AGM_GRI-677	HLYYFNC.FTDRAIQQAIRGEKYT.WCTFKEGHGQVQSLQLLAL..VAYT.NGIRKRSKRTFTRMAGNLGSRQAM...GRMATRHAQ.....GSKRRSOKALWNEHANFpSMELLCRGGKET	219
SABAEUS_SN.SABIC	HWSYFPC.FTDRAVQQAIRGEKYL.WCKHQVGHQPTGOVPSLQYLALRVYT.NGLRRVAPT..SRRGSSQSPQESORSORDDTRMARNNGFaQRAVRRMRAPRHVTGPQFRGFVPLPKESFPFSLVEYCGRTS	233
CONSENSUS_VBR	H?HYFtC.FteRAIq?AlrG?RFv.FCOFPeGHK?TGqVPSLQYLALLAHQ.NGIReRSqRjktrr?RnlGskOgav...GrMakr?vr.....RsOsgsq?afW?R?PvPsmELLSGGr?tg?shdg	209
VERVET_DE.AGM3	T-----RK-L-Q-T.....O-S--GGT--M-FE-----HA-----Y-----D--A-A-----G-KESH--AR	229
VERVET_KE.AGM155	-D--O--N-I--G-L-----K-E-T--O-----N-OR--T--P-I-----GE-KT-S	229
VERVET_KE.AGMTYO	G-N--K--O--H-----S-----K--Y-T-----Q--Y-T-----P-GEA--E-T-----K-WY--	229
VERVET_KE.AGM_VER-9063	L--S-----K-I-E-----T-K-----I-----KQA--S-D-----RTM.....GH-----IT--Q-A-L-L-----E--SPN--	228
CONSENSUS_LHO	HcKvPhC.fsCRDIr?AlwGekIma?CamPtGHK..GCVLISLQfICLRlQ.HVQ?KaakesRktsRGLW?tkzAMGSmasRHhGmKngg.....GqTFFPRsnFGPSLgILCOQYVRrggsLHE	213
LHOEST_CD.SIVlhoest447	-----K-----F-----N-----A--G-----R-----	221
LHOEST_CD.SIVlhoest485	-----K-----I-----S-----T-----V-----H-----	221
LHOEST_CD.SIVlhoest524	-V--D--WH--VR-IR--LHS-K-----Y-----T-AQP--AP--SS-----N--Q-R-----K-----	221
LHOEST_KE.SIVlhoest	-Y-----IQ--R-L-R-TMC--O-L-----I-----A-----	156
TANTALUS_UG.TANI	HCHYFPC.FTDRAIQQAIRGESFL.WCTYKEGhVAENHWQVRSLOfLAlTYvTDFLRNGRKRKfQgKkTRMVRNLGSQOg...RTQSGSTTTPFWERTPLPSMELLSGRRGKEWGTNDR	235
MANDRIL_I.GA.MNDG81	HLHFYDC.FMDSAVMKAIRGEVILKVCRFPAHGK.AQGVLSLQfLCLRViYGPERR	172
COLOBUS_CM.COLG01	HLIRGKCVRIEeARkAIRGLPNP.CDFOVHL..GVLKQLCLALREKERTHOKMRVlKGTSHGCRTR	159
RCM_NG.RCMAG409_NEW	FPcFTDRAlQAlIGEKVLYGFORGHRAQVTLQVLAIOAWAKDOOKEYGRKSARGPbHWRSRVCFLANQANANGQPRSQI	198
SUN_GA.SIVSUN	HFkYfDC.WTSRCIERRAMLGEKLIHECRNQVAHK..GLVLSLQfLCLRVl...HGQOE	174
SYKES_KE.SYK173	HNfYfPC.FTARAVNQAVRgELLfTSHCWTP..Hl..DQVPSLQYLALQVYLKDDGGfLQSLPACARNTMVLHskKCRVDPKRDOCHCKGR.....TGSDRSTIQAFYSSRNlWSLESILKRRGRD	221
CONSENSUS_VBR	kg1	212
VERVET_DE.AGM3	---	232
VERVET_KE.AGM155	---	232
VERVET_KE.AGMTYO	---	232
VERVET_KE.AGM_VER-9063	E--	231
CONSENSUS_LHO	IHyhSK	219
LHOEST_CD.SIVlhoest447	-----	227
LHOEST_CD.SIVlhoest485	-----	227
LHOEST_CD.SIVlhoest524	--HF--	226
SABAEUS_SN.SABIC	H	234
TANTALUS_UG.TANI	KGL	238

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GRIVET_ET.AGM_GRI-677 MASGRDPRPPLPG...WLEIWDIDREPDPWDLQDMLRDINEEARRHFQNMMLIRVMNYCV.EEGR...HNTFPWNEIGYKYYRIYVQSMFVH.FRCGCRRRGPFSPYEERRNQGGGAPP...PPGLA 118
CONSENSUS_VER MASGRDPRPPLPG...e?EIWDLsREPDPDeWLRDMLed?NGEAKlHFGRELLfOVWNYCQ.EE.GE...R?gtPm?ERAYKYYrLVQKALFVH.FRCGCRRRQPFPEYEERRdQGGGGrA?rv.PPGld 114
VERVET_DE.AGM3 ---L---L---NR---L---K---G--- 119
VERVET_KE.AGM155 ---E---GL---V-EI-N---Y---O-R-IA---N---PG--- 119
VERVET_KE.AGM150 ---V---K---Q-L---R---H---M---N---N---E--- 119
VERVET_KE.AGM_VER-9063 ---G-N---V---N---L---R---R---R---N-A.--- 119
CONSENSUS_LHO MSRGQRSPER...PPEDFGPPRPWGQWLADTWEIKEEARRHFFPaIlaQVSeYCV.sSTGS...EeAcM?FIT?VNRAlf?H..LpTcPsvAAaRaGTAHTPTEAAPtPterDIQRGry 111
LHOEST_CD.SIVlhoest447 ---T---K---I---K---I---I---I---I---K--- 114
LHOEST_CD.SIVlhoest485 ---A---A---A---A---A---A---A---A---K--- 114
LHOEST_CD.SIVlhoest524 ---A---A---A---A---A---A---A---A---K--- 114
LHOEST_KE.SIVlhoest ---A---A---A---A---A---A---A---A---K--- 114
TANTALUS_UG.TANI MAEGRSRERRPG...WLEIWDISREPDPDELRDMVAELNQAQRHFGRELLfOVWNPfCQ.EE.GE...RNGAPMIERAYRYRVLVQKALFVH.FRCGCRRRTPPEYEERRNGVGGGRDGPPEPPGLA 119
MANDRIL_I.GA.MNDGB1 MGOKRDEOVSEDQ...GPPRPYNOWLADTWEIKFEARKHFLPILINAVSEYCV.ONTGS...EeEAcKfTlMNRAlfVH.lAOGCD...GTFRRRRPQlPPSGFRPR.GDRL 104
COLOBUS_CM.COLCGUL MSSG.PKRR...EDPPEsPERDFTWLQDOVENITREARKHFLPILHISVIMWGCT.RRH...GRPWTAGL.AYVRIMECALYLHVHAGOCRFPSSTONP 92
RCM_NG.RCMNG411 MEML...PEDEPPEPYPDeWLRDMLIEIOEAKKHFTPELLTOEGNYI.EOHGDS...LEGVKAMITLlNKALFLH.FRHGCGESRlGGARGGNPLRSILHSRNIL 100
SUN_GA.SIVSUN MASRE...PVeO...PEDEGPPPEFAQWLADTWEITRDEEERHFFPAAIvAQLQYCA.DSTGS...EKEGCMRAITLlNRALFTH.LPMCPsYIRIRSGSGVNPPrPTrPRPGQGDlRRGLQD 116
SYKES_KE.SYK173 MAEAFNPSQRHVQGTfPWFfIPRNVeLlTPNVlNVTvKAELVvTEAsKHFTPQELIYGVWvNQSLNEEAGTDSPTWAWERTMlDMVRAlNlMLFEH.FAAGCPQRTRYARHRGYPHS 115

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GRIVET_FT.AGM_GRI-677      M.....DKEEE..PPLLQDL.....HRPLOPCTNKCYCKCCYHCBELCFLQKGLGVRVHVSRRKRRTSTQD..NQDPIRQOISITV.....NGQTT...EEGKTEVEKAAAAA 94
CONSENSUS_SAB             M.....dQ??EGARPOVWEELQEEL?RPLQACANTCYCK?CCFHC?LCP??KALGICYYVPR?RR?sKKIqn.NKvpyvHN.
SABAEUS_SN.SABIC         H-----H-----I--HK--R--P-A--SH.-Q-SL--
SABAEUS_SN.AGMSD30       O-----O-----P-K-Y-S-TR--K-RA-----
SABAEUS_SN.AGMSD42       -VR-----R-----N--V--NQ-----T-H-----
CONSENSUS_VER            M.....DK.GBEEg?vsHODLlieqykpPL?tCtNKCFCKCCYHCQLCFLqKGLGvTYHApRrRRKiasl?.r?P?g?QSIstr.....WGR.....D?Q?T...gesQ?KVBT?a?t?2?1 90
VERVET_DE.AGM3           D-D-GAY-----L-A-KR-----Y-C-----P-D..-F-B-K-----S-----KG-E---S-R-AFS- 102
VERVET_KE.AGM155        R-----R-----E-----F-----R-----I-----AD..-I-VFQ-----I-----S-----K---EQ-KANLRI 102
VERVET_KE.AGM_VER-9063  -RT-L-----R-----T-R-----SVQPN..LSQ-D-----G-A-----K---REFT-AQI- 102
VERVET_KE.AGMTYO       -A-I-----S-D-Q-Q-K-----R-N..LA-L-H-----K-----G-----PT--E---T-GSN 100
CONSENSUS_LHO           MQQ?..EQEQlt?.QKQHqdpLke?YkEAVTkpL?acqMkCCKCCPFHCILCFQKGLGirYYVHRrRrVtqvfedqdpbrtk.....NSQTKKKRKRQ???.KTSTST 96
LHOEST_CD.SIVlhoest447  -O-----R-----T-----S-N-----K-A-----
LHOEST_CD.SIVlhoest485  -O-----R-----N-----I-----SV-D--R-----O-----
LHOEST_CD.SIVlhoest524  -P-----H-O-----L-O-E-I-----I-D--OS--H-V-----A-----YIL-TE--A-----RQTE-----
LHOEST_KE.SIVlhoest    --P-----PIQ-----LM--T-N-----A-Q-----T-----LH-----K-----XITSGRKK-----E-----IQRL..... 100
MANDRIL_GA.GBI          MEPSKEDHNCPPQDSGSEILDYKOLLBEVYQPLQACENKCKKCCFHCMLCFQKGLGIRVHVYKRVPGT.NKKIP.GSGEAIIRAIDLSPHRTASRYTANGQTT.....E.KKKATA 115
MANDRIL_GA.L4CG        MDA.GKAELD.....KKEANITLPEDFQRTTFC.NKCYKCCCHCOCCFLQKALGHHVHYTRR..T.RKLLGKISQDSEAAV.....GR 79
COL_CM.CGUI            MS.....LSYAKPLFACNDKCMKACCFHCQCFLQKGLGIRY.....KKNKSATQ?QVAKTGSg.....NSOTT.....QKKYTESKKTAAD 75
RCM_NG.NG411           MD.....VKGAGLEEREIEILLDFPRTESC.NSVCYKRCVYHCQCFLQKALGINYASRRRRGRPNKKKNQINFPDTSQSLs..AIGR.....NSQSK...KE.KKEAVEKAVDNTIT 106
SUN_GA.SIVSUN          M.....ST.QGHQ.QDQDQ..KGTLEAYKTNLEACDNKWCRCRCCFHCQCFLQKGLGHHYVYGRQHQ.QXIGS.RKPAP.....NPQTKKKR.ORKK..ESTST 92
SYKES_KE.SYK173       MS.....STDQICQ.TQRVPPFLGFTFL.KGPTFC.NKCFKNCYHCQCFLQKGLGHTYARPKRAARSISED..SAPTLPLPRA.....GR...TOANPQTK...KK...AVETEKDSTSLP 105
TANTALUS_UG.TAM1      M.....ESEGDMAESLLIQDLH...RPLTPTCNKCFKRCYHCQVCFLQKGLGITYHVSIRRRPKKNHSN.HQNLVSQSISA.....WGG.....NSQTT...QBEKTKIPAAAAETSRRPQ 101
CONSENSUS_VER          gRkNL????r?ayGA??
VERVET_DE.AGM3         S-----AQOGR-T--SD
VERVET_KE.AGM155      S-----GDET-CP--GN
VERVET_KE.AGM_VER-9063  ---D-ERDK-E-----NA
COL_CM.CGUI           FGD
RCM_NG.NG411          TGRDIFIS
SYKES_KE.SYK173      SAENL

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GRIVET_ET.AGM_GRI-677 MS.LGKEE..KQALKIIKTL.....YGSNPFYQF.SGTARQRRRARQRWRKQQQIQIDKIAGRVLNFTFDQQLVAQLQELQENKDLVL...QHL.....PDPPIHIH 89
CONSENSUS_SAB MS.LG?Ee?LRRF_RIIKYL.....YTTNYPYPPG.QGTARQRRRARQWAKQRQOIiHLAERI1.....qTtpVSOID?LAQEFDQLVLDNLOQP.....Pplppghpses 91
SABAEUS_SN.AGMSD30 ---K-E---L---L---N---L---A---NLESSA 99
SABAEUS_SN.AGMSD42 ---P-DI---H---C---S---S---EDQAVO-S- 92
SABAEUS_SN.SABIC ---Q-L---F---V---E---H---S---T-NQTANSSS 99
CONSENSUS_VER MP.LqPEE..RrllrLiafL.....?rtNYPevEGTARQRRRRRrgrQ?o?raLaEriW?r?E?qIvqaidQl2ldqOHLai...QqJ.....PDPFes? 80
VERVET_KE.AGM155 ---S---S---KN-K-IY---GT-Q-D---V-I---VI.....QA 89
VERVET_DE.AGM3 ---S---S---NKN---A-E-L---HS-V-E---V-Q---H-A 84
VERVET_KE.AGMTYO ---FV---WL---YS---Q-D-I-V-V-L...QEQ-Y-V-R-ADEA.....H-A 89
VERVET_KE.AGM_VER-9063 ---KVFS---Y---N---E-R-L-F---NETK-R-E-TL---A-V.....-H---N-S
CONSENSUS_LHO MS.TGge?E1PryLk?S?IL.....WTGXTGLQVGERREFPRTARQRRRRReRrKkHLHQLR?VQERIF??TVERGLERAFT?LcVcDSPEV?gG?N?sPqcVAvPf?ArpfsDPPFLPtWATS 106
LHOEST_CD.SIVLhoest447 ---K-S---I-K---T---HS---R---D-LW-S---V- 105
LHOEST_CD.SIVLhoest485 ---E-E---I-K---T---HS---R---D-LW-S---V- 105
LHOEST_CD.SIVLhoest524 ---P-G---T---L-R---A---QA---G---AE-VG-TA-H-R-I-HL-GTY---P--- 105
LHOEST_KE.SIVLhoest ---NGD---RL-R---A---QA---R-A-S---A-RG-TP-ITS-E-QL-VA-V---K---P 118
TANTALUS_UG_TANI MS.LGSEDL_RLIIOIRIL.....YHSNOYPPG.EGTARQRRRRRROFOOOROVAALSERIIFAQORRDPGGE.SIAAAFDQILVDN.COLVLETLPDPPEHDSSTA 103
MANDRIL_GA.MNDGB1 MLVQEMLLSIVALLSKEGFRNKVPCLOETWLSICLFTGLPABEIP..GTARQRRRRKQQLRRAQRLREGLKQI...LDRGPDQICOGVTINLALAKESSEN 101
COLOBUS_CM.COLCGU1 MTNAGRVFAFTVSYAFQK...GWESAIRRIIWLHKKHWPFCV..GTARQRRRTORARKQQOQLAIDGRVVEQLVASL.QQMDYFCASANNLROEEELADSSVSIQTQSKRPSDS 116
RCM_NG.ROMNG411 MLLGEEEDAQEIRRIIRLI.....HLHLSNYPYQSG.GTANQRRRRRQRRRWTOIQAERIPLYDPPDRPLQEALSNLQQLTLDLPEPPVNFPSFSSFAVDRS 107
SUN_GA.SIVSUN MS.TGDDSI.NOYLRIKRL.....YEGTGLAPGNLFPQTHRQRRRRDRKKNLHQLRAVQRIIFATLDSRLGRFRLSVSDSSQVAEESLGNSSPSTKHLPPAKFIVAFPTYDFLPSWAPP 114
SYKES_KE.SYK173 MPDQGSQQL.AVFLRMIAHL.....QEFYFQPE.GPRQTRRRRRQRRTQRLYLQORIFEAIFGSRSTALEDLSLQQLQISD 77
CONSENSUS_LHO l?sgQqmdGGkrSbdceLe?eqQKEO?rhIssSC
LHOEST_CD.SIVLhoest447 SE-l--TG-----l-----K-----KKPOTGKEMEIOIQKRWVSO
LHOEST_CD.SIVLhoest485 -E--R-----A--l-----K-----ERHQGKEMEIQIQREKRWVSO
LHOEST_CD.SIVLhoest524 -ANP--IP--EC--N--DO--E---R-A-KN
LHOEST_KE.SIVLhoest -AD-----S--AQEM-----RTV-EH
SUN_GA.SIVSUN LADPQLAGFAPYSGYEQQDQERVONQOGESIIVSEGKK 152

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CONSENSUS_VERQkYnTrLRQAWChFgGnWrgAwkEvkqeIvkLpK.....dYrGTNGTektI?LqRq?GDPEaaNLWFNCqGGEFFYCKMDWfLNyIINNLt.....vdadH...Nqc?n				406
VERVET_V_VER1EK--K-D--R-I-K-E--E-Q-KO-F-W--H--S--M-I--N--N--N--				201
VERVET_V_VER2EE-IR-T-P--HK--F-F--F--H--S--				201
VERVET_DE_AGM3R--N--N--O--E-Y-LF--R--P--P--				431
VERVET_ET_VER385EH-I--I--O-Y-T-W--S--K--WN--D--				202
VERVET_KE_AGM155K--K--OE--E-O--N-F--E--H--K--				427
VERVET_KE_AGM155E--R-E--E-I--K--N-H-Y--W--S--W--Y--F--SS				426
VERVET_KE_AGM_VER_9063K--K--E--E--I--T--H--H--				432
VERVET_KE_VER266EL--K--E--E--I--T--H--H--				202
CONSENSUS_GRIQkYnTrLRQAWChfQGDwKAwkEvrEevkK?.....knlFEV?ienIhRRqWGDPEaaNWFNCqGGEFFYCKMDWfLnyIINNfT.....vDAdGtN??CD.				406
GRIVET_V_GRI2EH--H--KQ--A--..TDD-K--I--E--NK--				194
GRIVET_V_GRI3EK--S-N-L--K-I-EE--K--H--Q--KS--				197
GRIVET_ET_AGM_GRI-677K--K--K--V--S--I--S--R--E-E-RT--				413
CONSENSUS_SABQkYnTrLRQAWCWFgGnWRGAWGvKvketIV?LpP.....?rYsgTkdTnkIFLQRWGDPEaEFFFNCqGGEFFYCKMDWfLnyLNNgs.....VDPdH..N?C.				415
SABAEUS_V_SAB3ER--K--A--A--A--A--A--D-O--N-SQ--G--T--P--				199
SABAEUS_V_SAB4FR--K--A--E--K--S--E--N--SQ--G--T--N--T--				199
SABAEUS_SN_SAB1CK--K--R--R--R--S--K--N--S--K--N--N--N--				420
CONSENSUS_TANQkYnTrLRQAWChFgDwKAwkEvrETvklPk.....eKYGtNmTkgIwlrRQWGDPEaaNIWfNCqGGEFFYCTPDWfVn?LNNESaAgrn?dVEG..N?Csn				388
TANTALUS_V_TAN17ER--K--E--R--D--K--R--D--K--Y--D--RR-KE--D--				204
TANTALUS_V_TAN40EH--H--H--K--TE--N--W--D--KSVN--T--				206
TANTALUS_V_TAN49EQ--T--T--DR-S--N--W--G-NYT--P--				143
TANTALUS_CF_AGM805Q--T--T--H--D--K--S--L--Y--N--T--L--K-PD				385
TANTALUS_CF_AGMTB14Q--R--K--E--R--R--S--L--L--Y--SE-SFT--R--				428
TANTALUS_UG_TAN1Q--R--K--E--R--R--S--L--L--Y--SE-SFT--R--				428
CONSENSUS_LHO	G...LEHGSRLRLAOCKfEGOWGRMFNlGkMLkLNatAmNyteGn.....GTG??kpkpGGRGLKGLPIANWTR+G?dIATeMlMhTCGEEmFFCNVTRIfOEWNNKN..SDKWYP.				434
LHOEST_CD_SIVlhoest447H--N--R--H--IDNT--GN--				445
LHOEST_CD_SIVlhoest485R--Q--N--Q--PEG-Q--H--EG--I--L--				444
LHOEST_CD_SIVlhoest524R--E--E--K--T--STPG--V--				447
LHOEST_KE_SIVlhoestE--E--T--Dsk-TT--K--H-A--				442
MANDRIL_1_GA_MNDG51	G...LEPGkNlKGMCTfKGRWGLALWSLAKELNKLNdSikVnQTCkNFTStGEENkQNTDkQEFaKCIkTLKIDNYtTSgDRaEMMMWTCQEMfFCNvTRImRwNDPn..EKKWYP.				465
BABOON_TZ_BAB2010EQkYnTrLRQAWChfngnWRGAWEvKREIVkLpK.....DRyQgTNDaQKIYlQRQFDPEaANLWFNCqGGEFFYCKMDWfLNyIINNfT.....VdANHhTNRcNk				159
COLOBUS_CM_COLCGUI	E...LIpYskIyGRCoFVPMtGONKknKTQFAIEIkkNLtAwL.....ERISRNkTITPRNGNRTSDPEaTFtFVIChRlFFyCn.....ASllKKHdSP				403
RCW_NG_ROMG411LRVOKRPkGAWCRfDGDwKAwkEvaInkTKyKgTrOP.....ENTIRSVyGgDDEAKCfWlNGDEGFLyckMnWfLNyLNNkT..EgNkNEARQAM...				416
SUN_GA_SIVSUN	G...LEPGSKLRLaOCKfVGOWGRAFATlGkLkRQvEPLANNsNGCTFD....NIITkTrFTngTDFkMikfKpWekKgADAAteMlMhTCGEEmfFCNlTRlFKVWnDfT..SNkWyP.				448
SYKES_KE_SYK173	IqGkLkTGRDakraFCrVtGnWtEtfFkQvHEqAtKW.....KNvTnTTWrsQpGGDLvRThWfQcGGEFFYCNVSKLfanITngN.ASKNnyASnLr.....				405

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^^ * * * * *
?t?k?krapGCVQRTYVaGHIRSVINDwYtiSkKtYappREGH...LqCtStVTGmtVELM.YnmknRT...NVTLSPOIe?IWaaELgRYKLVkEITPIGFAPTeVRRYTGg...herqKR.
S-OG...KR...G...G...G...A...I...A...S...P...S-E-
VERVET...VER1E
VERVET...VER2E
VERVET...VER2E
VERVET DE AGM3
VERVET ET VEr385E
VERVET KE AGM155
VERVET KE AGM155
VERVET KE AGM155
VERVET KE AGM155
VERVET KE AGM155
VERVET KE AGM155
VERVET KE VER266E

* * * * *
CONSENSUS_VER
VERVET...VER1E
VERVET...VER2E
VERVET DE AGM3
VERVET ET VEr385E
VERVET KE AGM155
VERVET KE AGM155
VERVET KE AGM155
VERVET KE VER266E

* * * * *
??k?kqPQ.GPGpCvqrTVVACHIRQVNDWYTLlEkKtYappREGh...LECNsSVtAlYVeIn.YNnkSGP...INVTLSpQvRSiWAElgDYKLVkEITPIGFAPTDVRRYTGp...treKR.
NKP-G...R...Q...
TSH-G...AKK...T...S...
...KG...VS-V...A-D...
...?k?sdk?CWORTYvPCHIROVNDWYTLlSKKtYappREGH...LECNStATAlYVELM.YNSKNRT...NVTLSPOIeSIWANElgDYKLVkEIKPIGFAPT?VRRYTGp...EROKR.
...N-T-K-N-A...
...TPK--R...
...A-NNT-P...

* * * * *
?T...sgg?tGs?rkClKRRtYV?ehIRSVNDWYtLlSkKtYappREGH...LECTStVTSmmvSLD.YnsKnmT...NVTLTANlENiWAElgRYKlIeIkPIGFAPTeVRYVGP...TREKR.
...KD.P-F-S-P...VN...D...
...TPEKD...-L-K-A...I...-LY...
S...K-M...G...S...
R...L...A...
I...L-T...GL...LQ-R...-L-D...-ER...-E...
...-KDKP-Y...P...I...-E...
...WANCHIKS?IDDDWAtVgKKIyVlpTSGFNRRIRcthrVTEWwFemEKwEP?e?LGnLS.??FLPpSWEtNQFvAtGahyKLIrLrPIGFAPTDeHrY.AP...??O?RA
...V...S...Q-F-E-N...VR...A-Q...SSK-K-
...Y...I...L...-E-N...H...IK...RGR-T-
...I...I...-I...-F...H-D...-E-SK--K-N...RGR-T-

* * * * *
YASCOIRQVDDWwQVRKIYlPpTSGFNNHIRcthrVtEMVpEMQ.KIDSNETKwQ...IKFLPPSEtSNOFvAYGAHYKLVkIMPiGiAPTDRRHtLP...EHhKEKR.
TG...KtS...APGpCAQRtYVACHIRSVNDWYtVskLTVappREGH...LECRStVGTmVtELN.YNNQsRT...NVTLSPOIeSIWAElgRYKLVkEITPIGFAPTeVRRYTGg...OEROKR.
...VMNCtIRKLvNswYTHARlLYgPPpGGH...LQCNwEKQFvIAFMGTIEGDNDNGC...AYPAApNFKHALStELGRYKLVKMRtTYVPDIKRsvNvNwHHGRQR.
...FVPcITkMvNDwTYSRkVYTPRPDA...LRCNATvYLLADID.YTDNMT...INVTLSAEVgDWIWAELGRYKLVkEITPIGFAPTeVRRYtE...KQKR.
...WANCHIKSVIDDDWASVGKkYlPpTSGFNRRIRCAvRTEAMfTLERVEDwKvGNSISvVAFOpTTLNOfYtSGAHYKLVIRiRiGiAPTDeHRY.AP...RKEKRA
...LSCAIRQIINDWRyVRKLIYlPpTtagH...IKCtSNvTAVLTDIE.YYpGS...NFTTPTANVEDvWRADLlFNyKLIQIKPIGFAPTQRREYELP...NtREKRA
...SYKES_KE_SyK173

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516
310
310
313
543
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536
543
317
515
305
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522
518
306
306
527
496
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234
488
533
531
551
550
553
548
569
270
507
509
554
501

CONSENSUS_GRI
GRIVET...GRI2E
GRIVET...GRI3E
GRIVET ET AGM_GRI-677

CONSENSUS_SAB
SABAEUS...SAB3E
SABAEUS...SAB4F
SABAEUS_SN.SAB1C

CONSENSUS_TAN
TANTALUS...TAN17E
TANTALUS...TAN40E
TANTALUS...TAN49E
TANTALUS_CF.AGM805
TANTALUS_CF.AGMTB14
TANTALUS_UG.TAN1

CONSENSUS_LHO
LHOEST_CD_SIVlhoest447
LHOEST_CD_SIVlhoest485
LHOEST_CD_SIVlhoest524
LHOEST_KE_SIVlhoest

MANDRIL-1_GA.MNDGB1
BABOON_TZ.BAB2010E
COLOBUS_CM.COLCGUI
RCM_NG.ROMNG411
SUN_GA.SIVSUN
SYKES_KE.SyK173

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CONSENSUS_VBR
VERVET_ .VER1E
VERVET_ .VER2E
VERVET_DE.AGM3
VERVET_ET.VER385E
VERVET_KE.AGM155
VERVET_KE.AGM1YO
VERVET_KE.AGM_VBR-9063
VERVET_KE.VER266E

CONSENSUS_GRI
GRIVET_ .GRI2E
GRIVET_ .GRI3E
GRIVET_ET.AGM_GRI-677

CONSENSUS_SAB
SABAEUS_ .SAB3E
SABAEUS_ .SAB4E
SABAEUS_SN.SAB1C

CONSENSUS_TAN
TANTALUS_ .TAN17E
TANTALUS_ .TAN40E
TANTALUS_ .TAN49E
TANTALUS_UG.TAN1

CONSENSUS_LHO
LHOEST_CD.SIVlhoest447
LHOEST_CD.SIVlhoest485
LHOEST_CD.SIVlhoest524
LHOEST_KE.SIVlhoest

MANDRIL-1_GA.WNDG81
BABOON_TZ.BAB2010E
COLOBUS_CM.COLCGUI
RCM_NG.RCMNG411
SUN_GA.SIVSUN
SYKES_KE.SYK173

VPFVIGFLGLGAAAGTAMGAAaAtaLTVQSGHLLAGILQQOKNLL.AAVEAQOQMLKLTITWGVKNLNARVVTALEKYLEDQARLNAGCAWKQVCHHTTVPW.....qw?Nt?TPdW?NMTWLEWEr?QI??L
-----O-----T-----
I-----G-----A-----S-----E-----P-----T-----N-----E-----N-----N-----N-----N-----SY-
-----SS-----R-----M-----
VPFVIGFLGLGAAAGTAMGAAaAtaLTVQSRHLLAGILQQOKNLL.aAVEQOQMLKLTITWGVK
-----R-----
V-----
-----T-----
VPFVIGFLGLGAAAGTAMGAAaAtaLTVQSOQLLAGILQQOKNLL.AAVEQOQMLKLTITWGVK
-----
-----
-----NLNARVTALEKYLEDQARLNAGCAFRQVCHHTTVPW.....KYNNTPDWENMTWQEWEROIEKY
-----NLNARVTALEKYLEDQARLNAGCAFRQVCHHTTVPW.....
-----NLNARVTALEKYLEDQARLNAGCAFRQVCHHTTVPW.....TFNNTPDWENMTWQEWESQITAL
APLALGALLSAAAGTAMGLVSTILTIVQAOVVIQGILOQOKOLL.VLVEKQOELLRLTITWGVKNLQARLTAI.EEYLKdOaLLASWGCOWKQVCHTNVew.....nYNItpNWT?rDTWiEW?rGvGvL
-----E-----T-----
-----I-----
-----P-----
-----V-----
-----T-----
-----K-----R-----ESK-ALY
-----A-----L-----
GAVILGILLSLAGSAMGSVVALTVQSOQLVTGIVEQOKOLL.KLIEQOSELKLTITWGVKNLQTRLTSLENYIKDQALLSQMGCSWdQVCHTSVEW.....TNTSITPNWTSETWKEMETRTDYL
VPFVIGFLGLGAAAGTAMGAAaAtaLTVQSOQL
GIFAFSIIALLSAGAAAGTAMGAAaAtaLTVQSRHLLAGILQQOKLL.DIVFQOQELLKLTITWGVKNLQARVTAI.EEYLFQAKLASIGCANWQICRTIVPW.....NKTWGEEDPQWNTWQEWEROIEK
VPFVIGFLGLSAAAGTAMGAAaAtaLTVQSRHLLAGILQQOKLL.DIVFQOQELLRLTITWGVKNLQARLTAI.EEYLVQDQSLINFFGCAWKQVCHHTVPEW.....IYSQTPWNKQTLWEWERNISRL
APVALGALLSAAAGTAMGLVSTILTIVQAOVVIQGILOQOKOLL.VLVEKQOELLRLTITWGVKNLQARLTAI.EEYLVQDQSLINFFGCAWKQVCHHTVPEW.....NYNItpNWT?rDTWiEW?rGvGvL
APLALGILLSLAGSAMGAATALTIVQSOQLLAGILQQOKLL.EAVEAQOHLGLTITWGVKNLNARLTALLETYLRDQALLSNWGCFAFKQICHTAVTWEKACGNNSNFCPKPQWKNMTWHRWEQEVNDL

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CONSENSUS_VBR	EGNIT?QL?KARQEEKNLDAYQKLP?SWSQFWSWDFSKWLNILKIGFL...vvvGIIGLRLTYVYSCIARVROGYS...PLSPQIHIHwGKG?PdNAgep?EGGD?k?k??ses.....WOK?Sg	740
VERVET_DE.AGM3	---T-EE-A-----S-----D-L-I-----O-EG-G---KR-NS-P-----E--	780
VERVET_KE.AGM155	---K-EQ-----SD-S-----A-I-V-----L-T-----O-E---RTG-SK-TH	768
VERVET_KE.AGM_VER-9063	---S-G-V-----T-----I-----M-----V-----OV-R-G---D---NRKIL- -D-K	773
GRIVET_FT.AGM_GRI-677	---E-V-----R-T-N-----I-----G-----R-G---E---ERDND-S- -G--	780
SABAEUS_SN.SABL1C	EGNITQLLEEAQEQSKNLDLYQKLDWDSQFWSWFLSTWLGXVIGLFL...VIVILGLRPAWVWICIRNIRQGYN...PL.PQIHH.S.SAERPNDGGQDRGGESSSKLIR.....LQEESS	750
TANTALUS_UG.TANI	EANISRIILEQAHEQEQKNLDSYQKLSWSDQFWSWFDLTKWGMKTAIM...VIAGIIVARVLLVIGILRRFRKGYA...PLSSLPSH	723
LHOEST_CD.SIV1hoest447	eaNI?TLQEAAYTTELENrNaFKKLoF.NFWSwldilSfWfYiKYAVL...IiigIIVLR?SFI?Qn?VKMCRGVRV...LaPSAYvOdyKwEKgEnqEOPDkEgEiekDkEn.....	726
LHOEST_CD.SIV1hoest485	---S-----N-----V-V-I-----W-V-I-----C-R-----D-----	755
LHOEST_CD.SIV1hoest524	---K-----IV-V-I-----IV-V-I-----F-N-S-----T---R--	780
LHOEST_KE.SIV1hoest	DK--TS-----Q-K-----SH--T-V-----LV-G-VL-----I-V-----S-V-I-----R-E-KGA-T-I.....	778
MANDRIL-1.GA.MNDGB1	QONITEMLKOAYDREORNTVELOKLDLTSWASWFDFTWVQYLKWCVF...LVLGIIGLRLILLALWNTIISFRQYRVPFSODCOQNLVYKRPDNDGEEESNSLELGEHNSENLK.....EESLNR	809
COLOBUS_CM.COLCGUI	TDIIEADLVAYDLQEQENKELKLAELGDWLNWFS...GFLFLNLFKYLVAAYVGGILGLRIIMVVIACIRGAFRVGF.QOIGRTNVSSQIRGQDREW.EQDPNAAEIHROEQN.....SSSRFW	747
RCM_NG.RCMNG411	EGNISVALQDAQEQHERNVHDEKLSWGMNMDWMLKYRIGIF...IIGLIGLRIIFLLWSCVSKLRAGYF...PLSPPCYQIQQLPIRNRREQLKGEKGGSGGGHKYNNWQRYFYFIL	755
SUN_GA.SIVSUN	DDNITALLQEAAYTELENNQNFKQLQEF.NFWSWLDLSQWFLYKYAVL...IIGIITAAARLLSFIQQIYRMCQGYRV...LSPSAYVEDWLOETCPKPT...DKBEETEETER.....IYINLE	788
SYKES_KE.SYK173	TDHIDGLLREAEQEQQRNVHDLTKLQEWDSLWSWFDLSKWFYLYKIGFY...VIGALVLLRLVSVSFGVGIKKNLLGGYV...PILQNPYQGRKDPGKPADEEGSGDREGLNVST.....FSRESL	744

CONSENSUS_VBR	tr?????wckrLthwls.??stwLXnscLTLlhlR?AfOY4OYGLgELKtaOEAa??aLa?AQNAGhO.....IWL.ACRSAVR?Iins.PRRVROGLBeILN	825
VERVET_DE.AGM3	---AEWKN---C-IS-I-----N-----V-S-----A-VV-L-Y-----A-----G-----	877
VERVET_KE.AGM_VER-9063	S-----MO-A-T-RLN-----O-K-L-A-G-LLQT-GV-C-----N-V-----T-H-S-----	863
GRIVET_FT.AGM_GRI-677	---QRRGS-S-----TF-----G-W-----RL-V-F-----	877
TANTALUS_UG.TANI	TPSRINWNLNFK.SCSLRIRTWCYNICLTLTLFIRTVAVGYLQYGLQEQEAATGLAQAALARAAREAWGR.....LGA.IVRSAYRAVINS.PRRVROGLEKVLG	847
LHOEST_CD.SIV1hoest447	.VKESLIPNRGGIQAEEERAWRQHLLTNWCLTISWLLRLYQILRRSLITLLQLLREQCYIQYGMWQKFEKGAARFEEALASAAQASRTLWN.ACRSAVRAILEH.PRRMRQELERWFN	841
LHOEST_CD.SIV1hoest485	.IYINLEQcKkESrPpWNVdW?EPLODSLfVTLKkW?KafGILLLsLVWQELsWlghIvIlfghQhLw??sRw.mVEnAQkiasW?nkiRRNR?d?Sa?harnirLgqkkrWRFRFRGRSG...	872
LHOEST_CD.SIV1hoest524	---Y-----T-----I-----I-----R-KC-R-V-----W-----R-I-A-L-----	905
LHOEST_KE.SIV1hoest	---I-----S-----L-----KA-G-----R-W-----R-I-A-D-----	904
MANDRIL-1.GA.MNDGB1	---F-----N-----L-W-T-----I-----SYH-----L-S-----T-IR-S-----GEL-KTNGT---NR-----	906
COLOBUS_CM.COLCGUI	---L-----N-----L-EG-----S-----W-L-----N-R-QT-----Q-LRE-C-----GQL-STDRK-Q-K-K-L-G-----	902
RCM_NG.RCMNG411	SLIEDLTSFAFE	821
SUN_GA.SIVSUN	RIMBEWSSLIR.HCSNGILLVLP.OHPPTTSDKRSAMQTLRYLLVPRGSLILLETLOMLRSAAAR.....GWRRAPE.YLRGWI.....YDRP.OGPA	834
SYKES_KE.SYK173	ILRPFIEILCRLYQICS.NSLSVIYQSLQIPSRILLHLR.WIGAKLQDWQEFKGFSGSWLAEMRTINAY.....YTWKGLCA.VCRDDPAGWPAIL.CRRIRQGFERFLN	856
	QSKLESFPPTVTDWDEPLRDSLLVTLKWKAWGIVLQNIYHLLSFLWHLITTSFHGQLWGLRWG.....LGSHLIQATSRIRN.ACRSRRFRVSS.OKARSTFFSLGRKWRPKWNRTRGS	908
	RQSLFAGQQLWRV.CSSFR.....SLIRQLTITWGFISYG.FNELKIAAASLIGRETRDVAAIWQAIYAA.....TRRVVEAVAL.PRRIROGLEIYLN	832

CONSENSUS_LHO	.fpSetTETal	882
LHOEST_CD.SIV1hoest447	-----T-----	915
LHOEST_CD.SIV1hoest485	-----T-----	914
LHOEST_CD.SIV1hoest524	.LS-A-----	916
LHOEST_KE.SIV1hoest		912
SUN_GA.SIVSUN	RIPSETTETTL	919

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GRIVET_ET.AGM_GRI-677  MG.....SSNSKRQOQGL.....LKLWRGLRGKPGADWVLLSDPLIGOSSTVQEECGKALKKSW...GKGKMTPDG.RRLQEGDITFDEWDD..DEEE.VGFFVQPRVPLRQMTYKLAVDVDFSHFLKSKGG 112
CONSENSUS_SAB
SABAEUS_.AGMSD42  MG.....gKSSKQgQgrS.....LWLWSKLRGaPaPeIrYDMLADPL?GOSSHIQEECAKSLsDGLIrQGDSsrTeEgIk?k?pGrQP.SWYD.??EEEVGFVVRPrVPLRmTYKLAIDFGHFLEKKG 111
SABAEUS_SN.AGMSp055  A.....R.....L.....E-O.....D-TMRH.....I-O-F.....DD.....E-K.....W-G-S.....DE.....S-K.....EE.....E.....DE.....CL..... 116
SABAEUS_SN.P056  N.....V.....I.....V.....I.....W-G-N.....DE.....E.....DE.....E..... 107
SABAEUS_SN.SABLC  RH.....V-Q.....L.....R.....V-M-HQ.....ED..... 116
TANTALUS_UG.TANI  MG.....GSNSKREOQGL.....LRLWRALRKAPVVRVYGMLADPLIGOSSNIQEECCKNWNNGS...TRRKSTPE.GRKLAAADD..TWDDWPEPEEEVGFVVRPrVPLRQMTYKLAVDVDFSHFLKSKGG 113
CONSENSUS_VER
VERVET_DE.AGM3  MG.....lgnSKPqHKKg.....lslWhALHkTyTrYGLLADPLIG?SST?QEecDK?LrKsLIRKrNGmTpeg.RrLQeGD?WdEWSd...?EdEVGFFVPrPRVPLRQMTYKLAVDVDFSHFLKSKGG 110
VERVET_KE.AGML55  S.....S.....TI-R-A-H.....Q-L.....A-KE.....K.....E.....D-Q.....D-Q.....E.....I..... 115
VERVET_KE.AGMTYO  SQ-A-Y...SK-Q-H.....T-V.....A-Q.....E-E.....D-E.....T-E.....D-E.....I..... 115
VERVET_KE.AGM_VER-9063  H.....V.....Q-K.....T-AV.....Y-G.....E.....D.....E.....K..... 115
CONSENSUS_LHO
LHOEST_CD.SIVLhoest447  MG.....NlFGkPaAdGw.....WktLRLrLRAG?Ghr?EGTee?YgqLmeeTsd.WgKrrr.....dgDsd...SeeEVGFFVPrPORPLCSpTYKTLIDLShfIkeKGG 86
LHOEST_CD.SIVLhoest485  A.....S.....T.....O.....R.....K..... 89
LHOEST_CD.SIVLhoest524  S-S.....-RV-K--S-A-S-K-Q-IG.-T.....EE-G...-DS.....S..... 88
LHOEST_KE.SIVLhoest  A-R.....-F--S-RNA--DS-RA-I-K-N.-A..... 89
PATAS_SN.PAMG3INEF
MANDRIL_I.GA.MNDGB1  MG.....GKSKQOQOHS.....LWLMSKLRQAPQIRYDMLADPLIGOSSNIQEecAKSLRDGSIKQDSsrTEEGIKYKQGRQP.SWYD..EDEEEVGFVVRPrVPLRmTYKLAVDVDF 107
COLOBUS_CM.COLCGUI  MG.....SSQKKRSEAW...VRYSSALRQLVGGVPTPDGYKQIESsQAEKQSLLRGRAYGTySEGLDKVQNDPLTKDEKLDLTQODPE...EEEVGFVCRQVSLRVPsYKDLIDFDShfIkeKGG 117
RCM_NG.RCMNG411  MG.....LMSLCLNIRQOPTRGGVLRGLFGlyWpYQAFRLRHFRGGYDLRRVAVGERLNIcEDYMTVKVLPNGPCPLCYRHPDVIYHNPEPEDEVEDVEAGCYVMSRLVFRQATIKLlVDIscFLKEKGG 130
SUN_GA.SIVSUN  MG.....GKSKKASAAGL...RRWFGMLTTPGEDYARFAFTLQDGGPRCAEGSGRASRDFLRGGFTTlEQOSVDAl.....DwyEDT.DDTLVGFFVPRQVPrIRPMSYKLAIDLShfIkeKGG 111
SYKES_KE.SYK173  MG.....NAFGRPSEVgw...VRTLFRLAGSGTTRAPAPAGREYHRLRQEVPLVSAENG.....GPNGI...EQEEVGFVPRPORPLCKPtyKQLIDLShfIkeKGG 92
MG.....STSKSQQLRSEgkYAlGWRLFGkYtTlPDELsrPLQPCRGGFDKAWRSTLTepIDPHGPRDRDWGSHGGQKfSPGDIVQDEg...DTGLVGFVFCPTPLRtlTYKLAIDLShfIknKGG 120

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CONSENSUS_GRI
GRIVET_1.GRI2L
GRIVET_1.GRI3L
GRIVET_FT.AGM_GRI-677

LDGIYSNRREKILNLYALNEWGI.....IDDWQGYLPGFGIRYPLtFGFCFKLVPV?..LseEA?NC?RHCLLHPAQAGd?DpsgHGEVlVWKFDPKLaVEfKpWm..hkDMHehah?
---A---X---A---Y---SE---T---R---
---M---K---Q---D---G---T---GMB-K
---E---A---S---RV---D---H---R---E---M---M---E---P---GID---YR-D---.F---R

LEGIVfSE?RKkIILDLyALNEWGI.....VDGMQNYTDGPGtRYPKGFgwcFKLlVPVd.?seeAhm??rHCLLHPAQlAyEDDpW..KetiLVWkFDPp?LAVDYvAWRL.hpEQVpvsva
---R---M---MTD---ND---S---Q---R---M---Y---GL-
X---DND---M---V---V---Y---
X---L---K-RED---V---SI---A---T---D
R---F---A.L-A-Q-DEH---I---M---GL-G
X---R---M---M---D---DSDT---V---M---F---GL-G
---Y-R---L---K-SEN---V---A---L---AQQ

LEGIYWSFKREIILNLYALNEWGI.....IDDWQAYSFGPGTRKPRCFGFCfELVPVD.VSQEAQ.DERHCLLHPAQlEWEsDpW..KETlLVWkFNPLlLAVQYNPDS..FKDMHGLVkrK

LDGIYSdrRukIILNLYALNEWGI.....IDDWnAwwskPGiRyPrCFgFCFKLlVPVd.lheEAetCERHclVHPAQ?gEDDPDGInHGE?LwKfDpMLAVgYqPnrEYftDmh?tv?rKkN
X---K---KH---V---T---E---S---GTG-
---O---E---E---Q---YTP---S---QG---VR---K---L---DLGK-
X---E---E---A---LH---I---A---S---CKAM-GV..N---A---GK-
---E---R---Q---F---K---I---A---L---L---S---L---L---L---S---GTG-
---E---R---T---V---V---Y---A---I---K---S---I---I---Q---E---AI-K-

LEGIYWSQRQdILcLYCENEWGL.....IGDFW?YTDGPGTRYPt?FGWLMQLEPVACDEY?DPSDer?CLLHSSQLGV?EDPW..GERLIWHFnpMLAVD?VALrKQgpksgasa??lnckrK
T---F---A---T---Y---Q---Y---IG-OR-
LHOEST_CD.SIVlhoest447
LHOEST_CD.SIVlhoest485
LHOEST_CD.SIVlhoest524
LHOEST_XE.SIVlhoest

LGGIYSRRREIILDLyAENEWGF.....EPGWOQYTTGPGTRYPKtFGfFKlEPVS.RAIGDEYAANNHLLHSSQLCPQEDPE..GETlMWSGTlLlPMTLOH
LEGIRPERDDLlEOYAlEWGLKGLWLEyDELGDGALKEDRkPLVAGWLMKlVLE.OL.GEYAYSVDLSlSVTSRkKkKkKPOQVALEWVD
LEGIVfSERREIILDLyMENEHGI.....IDPMQNYTGPgIRYPTMFGHlMQLVPVD.VSDEATENEHGHLLHEAETSgMDpW..GEVlAWKFKPLlAVDYAGYRLHPEfEGRKkNTK
LEGlMYSRTREIILDLyAENEWGF.....lIGWOYTKGPGVRYPkKfAGWLMKlAVPtlDEDRPNHCQALLHSSQGSVNEEDPW..GERLIWfDPTLADFRAlQKHPEEFKHVTSLQX
LQGMNCKRDEIILHLyLQNEHGI.....I.DRINYSgPGTRYPkKfLlFGWLMELVPElEGCLEYEEHT..LLLHPASGGSSSMG..EPHVELQPPPGYTPGWEWARKLQERQTKRPOELQSALSKNIS
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