

VI

Other SIV proteins

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Gag	570
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Table 1: Table of other SIV Amino Acid Alignments

Name	Accession	Region	Author	Reference
AGMGRI_677	M66437	Complete	Fomsgaard, A	Virology 182(1):397-402 (1991)
AGMGRI_2E	U03995	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMGRI_3E	U03994	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMGRI_2L	U04007	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMGRI_3L	U04006	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMGRI_TYOAA	M63386	Nef	Sakuragi, Ji	Virology 185:455-459 (1991)
AGMSAB_1C	U04005	Complete	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_266	M22974	Pol	Li, Y	J Virol 63:1800-1802 (1989)
AGMSAB_381	M73537	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_384	M73539	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_385	M21311	Pol	Daniel, MD	J Virol 62:4123-4128 (1988)
AGMSAB_385A	M81730	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_385B	M81731	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_385C	M81732	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_385D	M81733	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_386	M81734	Pol	Allan, JS	J Virol 65:2816-2828 (1991)
AGMSAB_D37P	U04018	Pol	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_D30	U20812	Tat	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_D42	U20814	Tat	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_D30	U20965	Vpx	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_D42	U20967	Vpx	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_D30	U20966	Rev	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_D42	U20968	Rev	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_2E	U03996	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_3E	U03997	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_4E	U03998	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_1L14	U04009	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_1L15	U04008	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_2L16	U04010	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_2L17	U04011	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_3L18	U04012	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_3L19	U04013	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_4L4	U04015	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_4L10	U04014	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMSAB_U20811	U20811	Nef	Jubier-Maurin, VJ	J Virol 69(11):7349-7353 (1995)
AGMSAB_U20813	U20813	Nef	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_U20893	U20893	Nef	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_U20897	U20897	Nef	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_U20898	U20898	Nef	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMSAB_U20899	U20899	Nef	Jubier-Maurin, V	J Virol 69(11):7349-7353 (1995)
AGMTAN_9	L19254	Gag, Pol	Hirsch, VM	Virology 197:426-430 (1993)
AGMTAN_17	L19250	Gag, Pol	Hirsch, VM	Virology 197:426-430 (1993)
AGMTAN_27	L19251	Gag, Pol	Hirsch, VM	Virology 197:426-430 (1993)
AGMTAN_40	L19252	Gag, Pol	Hirsch, VM	Virology 197:426-430 (1993)
AGMTAN_49	L19253	Gag, Pol	Hirsch, VM	Virology 197:426-430 (1993)
AGMTAN_692	M29974	Gag	Johnson, PR	J Virol 64(3):1086-1092 (1990)

Table 1: cont.

Name	Accession	Region	Author	Reference
AGMTAN_TAN1	U58991	Complete	Stivahtis, GL	Virology 228:394-399 (1997)
AGMTAN_1E	U03999	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMTAN_17E	U04000	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMTAN_40E	U04001	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMTAN_49E	U04002	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMTAN_B05	M81070	Env	Muller, M	J Virol 67, 1227-1235 (1993)
AGMTAN_B14	M80208	Env	Nerrienet, E	Unpublished(1992)
AGMTAN_U04016	U04016	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMVER_3	M30931	Complete	Baier, M	Virology 176(1):216-221 (1990)
AGMVER_155	M29975	Complete	Johnson, PR	J Virol 64(3):1086-1092 (1990)
AGMVER_963	L40990	Complete	Hirsch, VM	J Virol 69(2):955-967 (1995)
AGMVER_2010G	U10899	Gag	Jin, MJ	J Virol 68(12):8454-8460 (1994)
AGMVER_TYO	X07805	Complete	Fukasawa, M	Nature 333:457-461 (1988)
AGMVER_1E	U04003	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMVER_2E	U04004	Env	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMVER_266E	U10896	Env	Jin, MJ	J Virol 68(12):8454-8460 (1994)
AGMVER_385E	U10898	Env	Jin, MJ	J Virol 68(12):8454-8460 (1994)
AGMVER_2010E	U10897	Env	Jin, MJ	J Virol 68(12):8454-8460 (1994)
AGMVER_2L	U04017	Nef	Jin, MJ	EMBO J 13(12):2935-2947 (1994)
AGMVER_691	M33719	Nef	Johnson, PR	J Virol 64(3):1086-1092 (1990)
AGMVER_TYOAB	M63387	Nef	Sakuragi, Ji	Virology 185:455-459 (1991)
SIVLHOEST	AF075269	Complete	Hirsch, VM	J Virol 73(2):1036-1045 (1999)
LHOEST447	AF188114	Complete	Beer, BE	J Virol 74(8):3892-3898 (2000)
LHOEST485	AF188115	Complete	Beer, BE	J Virol 74(8):3892-3898 (2000)
LHOEST524	AF188116	Complete	Beer, BE	J Virol 74(8):3892-3898 (2000)
RCM_Ngm				
SIV_SUN	AF131870	Complete	Beer, BE	J Virol 73(9):7734-7744 (1999)
SIV_SYK	L06042	Complete	Hirsch, VM	J Virol 67(3):1517-1528 (1993)
SMN_DGB1	M27470	Vpr	Tsujimoto, H	Nature 341:539-541 (1989)
COL_CGU1	AF301156	Complete	Courgnaud, V	J. Virol 75(2):857-866 (2001)

AGMGR1_677	MGGGHS.A.LSGRSLDPTFEKIRLRPNKGKKYQIKHLIWAAGKEMERFGLHEKLLFTKEGCKQIIIEVLTPLPPTGSEGLKALFNLCVVICIHAEQKVKDTEEAUVTVKQHYHLVDKNEKA	117
AGMSAB_1C	MGASNSV.LSQRKLDFAFESVRLRPNKGKKYKLRHLVWASKELDRF.SILSALNFTKGVVKKILSVLPLVPTGSENLIALFNLCVVICIHAIEIKVKDTEEAQKAKVKEV.PAEMTESA	116
CONSENSUS_TAN		
AGMTAN_9	MGaGhSa.LsgRnldTfEkIRLrPngkKkYqIkHlIwAgKeMeRfGfLHeKlLlFtRgCkQIIEVlLaPlEpTgSeGlKsLfNlccVwCiHaEqVkvDteEAv?lvQ?cHlVeKeKta	115
AGMTAN_17	V-----A-----R-----K-----S-----P-----T-----K-----Q-----H-----G-----	117
AGMTAN_27	-----R-----A-----T-----S-----V-----H-----I-----H-----A-----T-----R-----H-----S-----	116
AGMTAN_40	-----R-----A-----T-----S-----V-----H-----I-----H-----A-----T-----R-----H-----S-----	117
AGMTAN_49	-----R-----A-----T-----S-----V-----H-----I-----H-----A-----T-----R-----H-----S-----	117
AGMTAN_692	-----R-----A-----T-----S-----V-----H-----I-----H-----A-----T-----R-----H-----S-----	117
AGMTAN_TAN1	-----R-----A-----T-----S-----V-----H-----I-----H-----A-----T-----R-----H-----S-----	117
CONSENSUS_VER		
AGMVER_3	MGAATSA.LmrRQLD?FE?IRLRPNgkKkYqIKHLIwAgKeMeRfGfLHeRlLlFtEgCkKIIIEVl?c?h?e?kvkDteEavAtVRQcChLlVeKeK?A.....???	109
AGMVER_155	K-H-----T-----S-----Y-----F-----V-----K-----D-----K-----E-----I-----R-----N-----E-----R-----N-----	120
AGMVER_963	E-H-----K-----D-----K-----M-----Y-----L-----V-----Q-----K-----L-----I-----D-----T-----	117
AGMVER_2010G	KG-----Q-----K-----D-----D-----D-----F-----Y-----I-----R-----Q-----R-----	117
AGMVER_TYO	Q-----K-----R-----Y-----L-----K-----Q-----H-----	117
CONS_LHOEST	MGSGNSV.LSRQIEP?FCs?RLRfPgSKtYQKRhVvWATfELDRFGlGahLlLlEtA?GCKkIlLgVwPlyS?TGSKNLkAlVgTvcV?CCChLlGi??adTqEA?gk?KlEptcqe?rqr???	104
LHOEST447	-----G-----E-----I-----I-----D-----L-----R-----D-----D-----D-----L-----L-----K-----I-----N-----A-----M-----I-----E-----	114
LHOEST485	-----G-----E-----I-----I-----D-----L-----R-----D-----D-----D-----L-----L-----K-----I-----N-----A-----M-----I-----E-----	114
SIVLHOEST	-----K-----D-----V-----E-----E-----S-----Q-----E-----I-----V-----R-----I-----S-----V-----A-----P-----A-----A-----G-----K-----Q-----	112
RCM_Ngm	MGARASI.LSGKKLDAMFQVRLRfPgGkKkYqIkHlVwAcReLrFgLSdTLlESaRGIQkIIGVlLPlVPTGSEGLKsLfNlccVlWcHkVkvDTEEAUVHVKQChLlVdKdENAGE	119
SIV_SUN	MGAAGNST.VDRVRSFRVAlKpGgKkYqIqArHlVwAgKeLDRfGfLkKELlRfTVEgCkQIlLsVcWpLySgSKNlKAlVgTvcVlAcHogIcVtQeAlKkVrLEPaKNEEAQASQ	118
SIV_SYK	MGAAGSAILTGRELDryEKIRLRPKgkRyLrHlVwAgKeLDRfGfLkKELlRfTVEgCkQIlLlVlLlFgANgSKLlFgIISVWAVhAKKEVDEtQAKOKKvEACNWKDDPAtSGGSESSQNM	130
COL_CGU1	MGNEQGL.LGKkTLlEdLQvRLkKkYqIkHVRWmCTeVSRcVlIeLLkSATgVAIlEKVtPlVDTGSEvLRSlyG.CSVCYCLHRkWNlEdTQEAkKvEAYkKQAMlEWASKEE	121
AGMGR1_677AK.....KkNETTAPPgESrNpYpVvNQ.NNAwHQP.LSPRTLNAwKvVEEKNGAEVVPmFOALSEGLSDYDVNQMLNVIgDHOGALQILlKEVINEEAAEWDRThPPAgPLPaGQLRDP	233
AGMSAB_1C	.TATSSGQTKELQAKKkNEPTVfPSSGSRNPYIVSVV.NNqWvHQP.LSPRTLNAwKvVEEKfSAEVPmFSALAEgALPYdINQMLNAVGEHGALQIVKDVINEEAAWDLRHPpPaGQVLrDP	244
CONSENSUS_TAN	.a?psggq.....?kqnyntaappgzhgnYpvyvQQ.NNGwHtP.LSPRTLNAwKtVbEeKfFGAEI.VPMFOALSEGLsYDiNqMLNVIgDHOGAMQIiKEVINEEAAQWDItHPPpPaGPLPaGQLRDP	236
AGMTAN_9	-----A-----Q-----L-----Q-----V-----N-----L-----A-----	239
AGMTAN_17	-----T-----N-----C-----Y-----V-----M-----C-----M-----Y-----I-----V-----S-----L-----	237
AGMTAN_27	-----Q-----L-----D-----Q-----Y-----V-----M-----C-----M-----Y-----I-----V-----S-----L-----	239
AGMTAN_40	-----TE-----S-----HSRDP-----SR-----Q-----	239
AGMTAN_49	-----T-----Q-----T-----S-----Q-----A-----Q-----V-----V-----VI-----K-----L-----L-----V-----	239
AGMTAN_692	-----A-----G-----I-----D-----K-----T-----P-----S-----Q-----A-----Q-----V-----V-----VI-----K-----L-----L-----V-----	233
AGMTAN_TAN1	-----A-----Q-----T-----S-----Q-----A-----Q-----V-----V-----VI-----K-----L-----L-----V-----	239
CONSENSUS_VER	?tetsGq.....kKnd?g?taPpGg.SQNFPAQQQ.GNAwVHVPLSPRTLNAwKvEeKfFGAEI.VPMFOALSEGCtPYdINQMLNVIgDHOGALQIVKEIINEEAAQWDytHPPpPaGQLRDP	229
AGMVER_3	-----K-----V-----V-----I-----	243
AGMVER_155	.VTPPG-----Q-----NT-----G-----T-----	239
AGMVER_963	-----P-----E-----SNRET-----	239
AGMVER_2010G	.A-----R-----Q-----R-----S-----T-----S-----Q-----T-----	139
AGMVER_TYO	-----K-----I-----A-----C-----	239
CONS_LHOESTpksgNYPliRENO.RwvHTPLSPRTIOTWkIVeDRGkWPtVAMfSALTEKAlPdLNLMLNAIGDHOGAMQIiKDHlVEEgEwDRghFOQOOPaQPGGLRTP	208
LHOEST447	-----K-----V-----V-----I-----	218
LHOEST485	-----E-----K-----F-----	218
LHOEST524	-----E-----K-----F-----	216
SIVLHOESTTG.....	221
RCM_NgmQEKGATVTSsGQRGNpYIVTINQ.QPEHQPI.SPRTLNAwKvVEEKfFGAEVVPmFSALSEGCIPdYDVNQMLNAIGEHOGALQIVKEIINEEAAWDLRHPpPaGQLRDP	232
SIV_SUNNFPVOREGQ.NYIHQP.LSPRTVQWVKIVeEKGKWPtVAMfSALMGTGAIPeDINVMlNAIGEHOGAMQILKHlVEEAWDRHHPpPaGQGLRTP	218
SIV_SYK	ASETSsGQKvVQEEKQK.....AATPEPRG.NYPLRNPONQIHITGVVPRTLKTPVEAVNSKKFDASIVPLFQALTEGfPYDLNGLMNAVGDHGQAMQIVLIDINEEAAWDLRHPpPaGQLRDP	256
COL_CGU1KAKKEAEKLDMP.IVTGPQ.GPVHQPLSPRTLGAwKVCV.EGGIATPslAPMfLAYSTGAIAyDMNMLNlLDTHQGFQVLKDEINKKAEEDYLLHFVQVP.QOQOAGLRQP	228

AGMRI_677	TGSDIAGTSSIQEQIEWTF..NANPRIDYGAQYRKWVILGLQKVVQVMNPQKVLDIRQPKPEPFQDYVDRFYKALRAEQAPQDVKNMWMTQLLIQANPDPCKLILKGLGMNPTLEEMLTACQGVGGPQH	361
AGMSAB_1C	QGSDIAGTSSIQEQIEWTT..RAQNAVNVGNIIYKGIWIIILGLQKCVKRMNPVNIILDKQPKPEPFQDYVDRFYKALRAEQADPAVKNMWMTQSLLIQANPDPCKTLVGLGMNPTLEEMLTACQGIIGGAGH	372
CONSENSUS_ITAN	RGSDIAGTSSIQEQIEWTf..nAnPrvDVGrIYRgWVIlIgLQKCVkMvNp?sVLDiRQgAkEpFkDYvDRFYgALRAEQpQDvKnWMTeTLlIqNANpdcKlVlKgLgLGmhPTLEEmLTACQgVgGpGh	363
AGWTAN_9	-----V-----	363
AGWTAN_17	-----I-----	363
AGWTAN_27	-----T-K-----S-R-----G-----R-----H-R-----I-----	363
AGWTAN_40	-----S-----	363
AGWTAN_49	-----SI-----	367
AGWTAN_62	-----K-----L-----	367
AGWTAN_TANI	-----I-----L-----Y-----T-----I-----A-----R-----A-----R-----S-----S-----K-----T-----O-----N-----	361
CONSENSUS_VER	rGSDIAGTSSIQEQLEWiy..TANPRvDvGAIYRRwIILGLQKCVkRMvNpVsVLDiRQgKPEpFkDYvDRFYkaIRAEQASgEVkQvMTeSLlIQANPDPCKVIlKGLGMhPTLEEMLTACQGVGGPSY	357
AGWVER_3	-----A-----	371
AGWVER_155	-----G-----	367
AGWVER_963	-----V-----	367
AGWVER_2010G	-----I-----K-----RT-----	224
AGWVER_TYO	-----S-----	367
CONS_LHOEST	NATDVAGVTSIVVEEQIawTtT...ADTPvDvGKIYkEWVIQAMEKVVRLIHQpVsvMdiKQgKPEpFkEYADRFfKALRAEQSGSHEVKEWMEKMLVQANPDPCKrVlKALGEGA?LlEEMkACQGVGGPAH	334
LHOEST447	-----I-----	345
LHOEST485	-----O-----	345
LHOEST524	-----I-----	343
SIVLHOEST	-----I-----Q-----T-----D-----D-----K-----K-----L-----S-----	348
RCM_Ngm	TGSDIAGTSSIAEQIAWtTR..ANNPfIaVgNIYRNwIILGLQKCVkRMvNpVNIILDKQPKPEpFkDYvDRFYKALRAEQADPAVKNMWMTQSLLIQANPDPCKTLVGLGMNPTLEEMLTACQAGGPPQH	360
SIV_SUN	NGTDIAGVTSIVVEEQIOWIYGLNGATRVAVQDIYKGIWVIEGMRVVRLLHQTTSVVEIRIQGPKPEPFDYDRFFKALRAESGSEEVKEMWKEMLVQANPDPCKLILKALGETPSLEEMWRAQCGVGGPSH	348
SIV_SVK	SASDIAGTSSIAEQIEW..ITRQNNPvQVGEIYRRwIILGLQKCVQvYvNpVsVLDiKQgKPEIIFkDYvDRFYgALRAEQADPAVKNMWMTQLLIQANPDPCKLILKAM.VKPTLEEMLQACQGVGGPLH	383
COL_CGU1	TASDITGNTSSVAEQVANGe.....PIANIYRGwIvQSLekVIQlARpSSVLDiRQgSKEDfKSYvDRFYsALRAEQAPAAgEIKAMwANNLLIqHANPDPCKRILKLGQ.KPFSLEDMLAAQCGVGGPDDH	349
AGMRI_677	KAKLVMEMM..SN..GO..NM..VOQG.....POKGRGPRGLKCFNGCKGFHMQRECKAPR..OIKCFKCKGIHMAKDKCN.....GOANFLGYG..HWG	440
AGMSAB_1C	KARLMAEAMTAFAQQOITVGNIFVQGGARPRG.....PLGGRGRFLNPNIKYCNCKGKPEHLARFCCKAPR...ROGCKWCCGSPDHQMKDCQK.....QVNFILGFG..FWG	465
CONSENSUS_TAN	KAKLMAEaM...qmQGV.nM.vqGg?.....prgGRGRgRg.....PPrCfkCGqIghIqKqCprgG...P?kCLkCKGKpGhMaKDCRS.....GqaNFIgrmptpw	445
AGMTAN_9	-----N-----I-----T-----AQG-----	449
AGMTAN_17	-----I-----H-----SK-----V-----I-----R-----L-----R-----T-----	446
AGMTAN_27	-----N-----I-----P-----	451
AGMTAN_40	-----N-----I-----T-----AQG-----	449
AGMTAN_49	-----V-----V-----P-----S-----V-----R-----K-----I-----	451
AGMTAN_692	-----V-----M-----N-----OA-----GI-----VK-----Y-----KP-----V-----N-----TOK-----V-----F-----R-----AV-----YG.RWM	442
AGWTAN_TANI	-----V-----A-----	450
CONSENSUS_VER	KakVMAEMM...QmmQ?q..NM..vQGG??.....G??P?RPP?kCYNCKGKGFHMQROCbEPR...K?kCLKCKG?GHlAKDCR.....GQVNFILGYG..Rhm	429
AGWVER_3	-----L-----S-----M-----	451
AGWVER_155	-----L-----S-----	447
AGWVER_963	-----R-----T-----N-----AA-----	449
AGWVER_TYO	-----T-----N-----	446
CONS_LHOEST	Kgk-IILAEAMtAmQsOmrcqmM.VQ.vTppRNaQGR.....FVRTGGGPRkPLtCFNCGKpGHTArMCRQPR...QBGWCWCGSkGhRfAQCpKPK.....GKVNfILGYGPW..r	432
LHOEST447	-----R-----	443
LHOEST485	-----R-----T-----	443
LHOEST524	-----R-----G-----KHL-----O-----R-----S-----K-----	441
SIVLHOEST	-----S-----I-----Q-----V-----L-----	446
RCM_Ngm	KARVLAEAMQ...MvQSNlMAQCGGRPRGPKL.....GGGPRILKYNGKtGCHTARyCKTSR..KKGWRCGEEGHLMKDCPKL	447
SIV_SUN	KGKILAEAMASAFQOVGRQAMVQNNLPPRNSQGR.....FVRIggGRPKPMtCFNCKGKPEHLAQCRBPkGpPpGSSCKGKGGHKQACpQK.....QVNFILGYGPW..N	450
SIV_SVK	KAKLMAEAMWMAQQSV.NM.VQ.....GPKSRSMIKCYNCGQIGHWQKCKKPL...KAKCFNCKGTGHLARACHQPKRNQDPPVAQANFLIGKGGVGS	472
COL_CGU1	KAKVLAEAMQFQOEBRTNMIeVKTAKCFNCGQIGHLARMCPRKPIGGAGRGRGRGRGPRFVRFCFTCNQEGHWQRDCPNK.....QANFLIGATRgVE	446

AGWGRI_677	GAKPRNFVQYRGDTVGLPPTAPPME.....TAYDPAAKLLQOYAEKGORLREEREO..TRKOKEKEVEDYSLSLFGGDQ	513
AGWSAB_1C	RGKPRNFPLT.....SIRPTAPPMDYSRPEENWYADRPPTRGPGDDPATALLKQYAVQGRKQKQWQHSPQSQSFYEAAYSLRSLFGEQD	554
CONSENSUS_TAN	GskKPrNFL.....EgggvaVptApp?paH.....gfptgpp?a?GAYDpAKrLLLeqYakkg?????dq.lrkQkekeLEdYSLsLFGeDQ	516
AGMTAN_9	-----D-----L-----IA-----R-----KRW-----M-----T-----RL-----T-----V-----SDMR-----NP-----E-----T-----K-----TQE-----AQORRKYE.....KSS-----AGR-----E-----K-----	522
AGMTAN_17	-----L-----D-----VA-----G-----R-----	523
AGMTAN_27	-----R-----KRW-----M-----T-----RL-----T-----V-----SDMR-----NP-----E-----T-----K-----TQE-----AQORRKYE.....KSS-----AGR-----E-----K-----	524
AGMTAN_40	-----L-----D-----VA-----G-----R-----	525
AGMTAN_49	-----R-----KRW-----M-----T-----RL-----T-----V-----SDMR-----NP-----E-----T-----K-----TQE-----AQORRKYE.....KSS-----AGR-----E-----K-----	526
AGMTAN_692	-----L-----D-----VA-----G-----R-----	527
AGMTAN_TAN1	-----R-----KRW-----M-----T-----RL-----T-----V-----SDMR-----NP-----E-----T-----K-----TQE-----AQORRKYE.....KSS-----AGR-----E-----K-----	528
CONSENSUS_VBR	G?KPRNFp...AATIG?PpsAPPpp?.....??LPYDPAAKLLQOYAEKGORLreO???pPa?NPDW?EGYSLNSLFGEDQ	492
AGMVER_3	-A-----V-----T-----S-----	521
AGMVER_155	-T-----L-----A-----H-----V-----A-----N-----NS-----D-----M-----N-----NRN-----N-----N-----	520
AGMVER_963	-A-----L-----L-----H-----V-----A-----N-----NS-----D-----M-----N-----NRN-----N-----N-----	519
AGMVER_TYO	-A-----L-----L-----H-----V-----A-----N-----NS-----D-----M-----N-----NRN-----N-----N-----	519
CONS_LHOEST	?gPpGNfPlm.GG?AGv?PSAPPMEr?p.....?TKAERALETYRnLGGQLr?OQQ?...vPQKCVDEPCL?ffffPDDQ\$	495
LHOEST447	S-----N-----V-----S-----Q-----R-----I-----	512
LHOEST485	N-----I-----N-----V-----NS-----K-----K-----	512
LHOEST524	N-----S-----I-----A-----I-----KV-----P-----R-----I-----T-----KR-----Q-----NSL-----	511
SIVLHOEST	SK-----Y-----L-----A-----RI-----SA-----	515
RCM_Ngm	GKPR.NLPL.....TSLRPTAPGRE.....EGWNPOYDPAEEMLRKYLALGRQHKOFORKEKKEKGRAYEDALSLSLNSLFGSDL\$	521
SIV_SUN	RGPGGNFPVM.....PSAPPLEDLTLGNRWT.....PPOSKAERALETYRnLGGQLRAGQORR...ERGECQEPCL.LANMLFEED\$	521
SIV_SVK	REPPANFVR.....SEPSAPPLEDLIEDGPWLTWSAQMSQQAQAQNSPSSKPPPTNREVLSPRESSGKERTKSLYP.....SLSLFGEDQ	554
COL_CGU1	LQTAIFPPKM.....SKDLPFR.....EKGESLYP.....SLKSLFGDDQ\$	482


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AGMGRI_677      PAVCREGTAPER...GERTDKETEGERSGGCFLEL.PLWRRRPMKRVIIEGTPVQALLDTGADDTIIQEKDLHFPHPKWRKRVVGGIIGGIIHVKEYQGVQVLEDKIIT.....GSILIGSTPINIIIGRNI 182
AGMSAB_IC      KAVCCSGETAETAFAK.PLATTEPLR.GGLQLPQVSLWRRPMKTVYIEGQKVTALLDTGADDSVIQGIELGDN...WKPRIIIGGIGGCINVKAYHNQEVKIEDKTKC.....ATILVGETFPVNIIGRNV 177
AGMSAB_166
AGMSAB_381
AGMSAB_384
AGMSAB_385
AGMSAB_385A
AGMSAB_385B
AGMSAB_385C
AGMSAB_386
AGMSAB_D37P
CONSENSUS_TAN
AGWTAN_9
AGWTAN_17
AGWTAN_27
AGWTAN_40
AGWTAN_49
AGWTAN_TAN1
CONSENSUS_VER
AGMVER_3
AGMVER_155
AGMVER_363
AGMVER_TYO
CONS_LHOEST
LHOEST447
LHOEST485
LHOEST524
SIVLHOEST
RCM_Ngm
SIV_SUN
SIV_SYK
COL_CGU1
S.....GESLRGCVLIPQF.SLWKRPTVWEIEGQKVEALLDTGADTVIQ...NLIDIGEN..WKPKIIGGIGGYINVKQFNHCKITTIAGKTHH.....AHVIVGPTPVNIIGRNV 163
KGRESSGDLQIVRTGPOSTAEIEGKGGMSAMLEYALSRRPLEKVFINGOPVALLDTGADDTIIVSEDSVSEGH..WKPRVGGIIGGQIRVKEYADVFEIRDKTAT.....GTVLVGETFPVNIIGRNV 158
ELSLLETPHQQGSALAEQEQ.WEGGDQESLSQLSLWRRPMLIEVDVEGDLVQMLVDTGADDTIIREEDIQLHQP..WSPKIVGSLGGNIITVRYRNIIRFTVVKPSGKRKQVEGTLIVGPTPVNIIGRNI 178
.....GGESISLLEVSLSRRRPIVIVEVEGQKCOALLDTGADDTVFKEDVQLTGA..WTAVQIQIGGAIIRVKQYRDKILKMGGKEYR.....GDILLIGHTPINIVGRNM 127
gtvckkkg.....ptkeaegegtGGLFLEF.plwirfp
-A-K-.....PAE-----#
-A-K-RR.....P--KR-----#
-I-K-.....SV-----I#
--EE.....P-EKT-R-I-----#
R--HEER.....T--T-----#
-A--Q--R.....MSKIYIQGQPVQVLLDTGADDTIIKEEDIHLEGR..WRPKVVGIGGGISVKQYDNLILVNIIDGKETR.....GNVLIGETPINIVGRNI 212
AA?CRE?etvEg..tke??tsneSrlargIFFEL.PLWRRRPIKTV?IeGvp?kaLLDTGADDTIIketDlQlsG..pWrpkiIGGIGGGLNVKEYS??EVk?EDKILR.....GT?L?GaTPINIIGRNI 160
-I--OG-A.....-KT-S-----#
-V--R-N-K...SEOKPP-EQ--E-----R-CI-G-TAV--D--R--L--S--V--V--DNV--QL.....-V-I--S-----I 184
--V--GK.....-R-EN-T-K--GGR.....-I--V-V-----I--T-----V-----NV--I-----V-L----- 179
--I--R-T...A--ES-G--G-----Y-----I-----N-----NDR--I-----I-L----- 176
SRESlr?iOepRTT?Ee?Atas?TEmCGRA?PEFllLSRRRPIEniLVNGOpVsALLDTGADDTIFSENSVrIEGP..YTPRVVGGIIGGOIIVKEY?DVFFIeIAGKTTV...GTVLLGPTPVDIVGRNI 151
--N--A.....DP-----M-----K-----K----- 159
---GN-D---T---T-S-V---L---KV---E-T---R---K---FR---Q--- 160
---IGDL-DF--A-KA-A-p-----L---T-----S-----R----- 156
S.....GESLRGCVLIPQF.SLWKRPTVWEIEGQKVEALLDTGADTVIQ...NLIDIGEN..WKPKIIGGIGGYINVKQFNHCKITTIAGKTHH.....AHVIVGPTPVNIIGRNV 163
KGRESSGDLQIVRTGPOSTAEIEGKGGMSAMLEYALSRRPLEKVFINGOPVALLDTGADDTIIVSEDSVSEGH..WKPRVGGIIGGQIRVKEYADVFEIRDKTAT.....GTVLVGETFPVNIIGRNV 158
ELSLLETPHQQGSALAEQEQ.WEGGDQESLSQLSLWRRPMLIEVDVEGDLVQMLVDTGADDTIIREEDIQLHQP..WSPKIVGSLGGNIITVRYRNIIRFTVVKPSGKRKQVEGTLIVGPTPVNIIGRNI 178
.....GGESISLLEVSLSRRRPIVIVEVEGQKCOALLDTGADDTVFKEDVQLTGA..WTAVQIQIGGAIIRVKQYRDKILKMGGKEYR.....GDILLIGHTPINIVGRNM 127

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AGMGR1_677 LAQAGMKLVMGVLSQIETTKVQLKEGKDGPKLKQWPLSREKIEALTEICKQMEEEKLSRIGGENPNYNTPVFAIKKKDKTQWRMLVDFRELNKATQDFEVQLGIPHPAGLQKQKQITVVIDIGDAYYSI 312

AGMSAB_1C LAQLGVTLNLAQ.REIEPI.KVHLKPGQDGPRIQWPLSKEKIEALKATCEIDLEKQGHLEIRIGPENPNYNTPVFAIRKKDKTQWRILLMDFRFLNKSTQDFEVQLGIPHPAGLQORREQITVVIDIGDAYFSC 305

AGMSAB_266 0

AGMSAB_381 0

AGMSAB_384 0

AGMSAB_385 0

AGMSAB_385A 0

AGMSAB_385B 0

AGMSAB_385C 0

AGMSAB_385D 0

AGMSAB_386 0

AGMSAB_D37P 187

AGMTAN_TAN1 342

CONSENSUS_VBR LAPAga?LVMGQLeqIPiTPVklKeGARGp?lKOWPLSKEKIKALqEiC?qlEKEGKlS??GGeNAYNTP?FCI?KKDKsQWRMLVDVDFRELNKATODFFEVQLGIPHPAGL?KMKqITVLD?GDAYYSI 281

AGMVER_3 ---K---K---QT---R---D---HL---CVR---K---V--- 314

AGMVER_155 ---Q---K---QT---R---D---HL---CVR---K---V--- 309

AGMVER_963 ---R---K---QT---R---D---HL---CVR---K---V--- 306

AGMVER_TYO ---VPR---K---V--- 330

CONS_LHOEST Lc?VGA?LVLaQLSgkIPiTKV?LKPGDGPRIQWPLSKEKIEALTEICEQLEKEGHLEIRIGPENPNYNTPVFAIRKKDKSQRWMLMDVDFRELNKATQDFEVQLGIPHPAGLQORREQITVVIDIADAYFSC 272

LHOEST447 ---N---R---S--- 289

LHOEST485 ---S---K---R--- 289

LHOEST524 ---NPL---R---E---H--- 290

SIVLHOEST ---AM---K---I---S--- 286

RCM_Ngm LSKLGASLNFFPISKA.ETI.KVELKPGDGPRIQWPLSKEKIEALTEICNAMEKEGKISRIGPENPNYNTPVFAIKKKDKSTKWRKLVDFRELNKRTODFFEVQLGIPHPAGLQKOCROITVVIDIGDAYFSC 291

SIV_SUN LSAALGRLVLAATLSEKIPiTKVklKeGAGPKYKQWPLSREKIEGLQKCDRLFAEGKISRADGPNPNYNTPVFAIKKKDKNEWRKLVDFRVLNGWTDFFELQGLGIPHPAGLKKCKQITVVDIGDAYFSC 288

SIV_SVK LTKLGVLMVVO.PALEPV.KVSLKPKDELPLKQWPLSVEKLEALKAVEMLKAGOLEKASPTNPNYNTPVFAIRKKDKKWRMLIDFRKLNATODFFEVQLGIPHPAGL.KOKLITLIDLKDAYSV 305

COL_CGU1 L.KEG.KLVVAQSLDRIPVTKVTLKEGMDGPKYKQWPLSKEKIEGLQKICERLEAEGKIEKAELELGNPNYNTPVFAIRKKDKKNEWRKLVDFRELNKRTODFFEVQLGIPHPAGLQKTHITVVIDIGDAYFSC 255

AGMGR1_677 PLCKEFRKYTAFTIPSVNNTPGFGIRYQFNCLIPQGWKGSPTIFQNTAANILEETIKRHTPGLIEIQVMDDLIWLASDHDETRHNQVDIVRKMMLLEKLETPDKKQVOREPPEWMMGYKLIHPNKNWTTINKIELEPP 442

AGMSAB_1C PLDDPDKYTAFTIPSVNNREPFGIRYQYKVLIPQGWKGSPTIFQTTANKILQEFRQKNPVDVIQYMDMMLIASDRPKAEHLVMVQQLRDYLETWGFKTPEKKTQKDPYLLMVGLEYELPKKQWQLEITLPE 435

AGMSAB_266 0

AGMSAB_381 0

AGMSAB_384 0

AGMSAB_385 0

AGMSAB_385A 0

AGMSAB_385B 0

AGMSAB_385C 0

AGMSAB_385D 0

AGMSAB_386 0

AGMSAB_D37P 217

AGMTAN_TAN1 PLDDPEFRPYTAFTIPQVNNVGGFIRYQFNCLIPQGWKGSPTIFQHTAQVRLKEIGKKVQDLEIQYMDDMWIGSGLPEKEHDEKVEVRKLLLRGFTFPDKVKYQKRPYDWMGKLYPSHWSLNKIEIPE 472

CONSENSUS_VBR PLDDPEFRKYTAFTIP?VNNGGFIRYQFNCLIPQGWKGSPTIFONTAa?ILIEeIKKeLkPliTVQYMDLLIWSQDeYtHDKLYeqlR?klqaWGLETP?KkYqk?PpYEWMMGYKLiWPhKwqlsIeLFe 406

AGMVER_155 ---S---T---E---V--- 444

AGMVER_963 ---T---E---S---K---V--- 439

AGMVER_TYO ---N---N---T--- 436

CONS_LHOEST PLDDPDKYTAFTIP?PS?NNQEPG?RYQVNVLPQGWKGSPTIFQaTvAGLLSsFRKLNpDpi.IIQYMDLLfIGSDR?kkChQaVkeLReLumTWNLepEKKQaepPYHWMMGYVlHPDRWEIEkvkLP? 397

LHOEST447 ---V---I---R--- 419

LHOEST485 ---I---L---K--- 419

LHOEST524 ---I---L---L---K--- 420

SIVLHOEST ---N---K---I---L---L---K--- 416

RCM_Ngm PLYEPRKYTAFTIIAIANNQGFIRYQVNVLPQGWKGSPTIFQNTANKILIEPRFRKPNPDVLIQYMDLLVGSDRTAHESHQMIKRLRHLLTWGFTFPDKKQKPPPEWMMGYVlHPDKWTTVQeIkLLE 421

SIV_SUN PLDDPDKYTAFTIPSVNNQAPGKRYVNVLPQGWKGSPTIFQGTVASSLLEKPRQYQWVLYQYMDLLIGSDYKKEKHEIVKQLRQLLMEWNLLETPEKPYQEPYKMMGYlLHPDRWEIEKIKLPP 418

SIV_SVK PLDKFRPYTAFTIPSVNNASPGERYQFTVLPQGWKGSPTIFOSTINILQEPKRYSDLIITQYMDLLIGTDRSEKAHGEIYQOIIVTALLKYGKVPKQWQDOYPMQWLYTlHPDKWOLQKLELN 435

COL_CGU1 PLDDPDKYTAFTIPSVNNLAPGTRYVYKVLIPQGWKGSPTIFQGTVARILIEPRKR.GQLQIAQYMDLLYLGSDLLPLEEHRRAYQELRDALLYGLETFPEKPYQADPPYKMMGYELHPKQWIKQVKIPE 384

Other SIV proteins


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AGMGRI_677
AGMSAB_IC 826
AGMSAB_381
AGMSAB_384
AGMSAB_385A
AGMSAB_385B
AGMSAB_385C
AGMSAB_385D
AGMSAB_386
AGMTAN_TAN1 855
CONSENSUS_VER
AGWVER_3 759
AGWVER_155 827
AGWVER_963 822
AGWVER_TYO 819
AGWVER_TYO 842
CONS_LHOEST 764
LHOEST447 806
LHOEST485 807
SIVLHOEST 803
RCM_Ngm 805
SIV_SUN 803
SIV_SYK 821
COL_CGU1 765
AGMGRI_677 956
CONSENSUS_SAB 91
AGMSAB_IC 949
AGMSAB_381 94
AGMSAB_384 94
AGMSAB_385A 93
AGMSAB_385B 94
AGMSAB_385C 94
AGMSAB_385D 94
AGMSAB_386 94
AGMTAN_TAN1 985
CONSENSUS_VER 888
AGWVER_3 957
AGWVER_155 952
AGWVER_963 949
AGWVER_TYO 972
CONS_LHOEST 891
LHOEST447 936
LHOEST485 936
LHOEST524 937
SIVLHOEST 933
RCM_Ngm 935
SIV_SUN 933
SIV_SYK 951
COL_CGU1 895
IIITACPOESNSPLVEQIIIQALMKKRQVYLOWVPAHKHGIQGNTEIDKLVSGKIR..QILFLDRIEEAQDDHAKYHNNWRSVMVQEFGLPNIVAKEIVAACPCKQIRGEPKHGQVDASLETWQMDCTHLEGGV
IIAGEPTESDNNIVQOIIIEELIKKEAVYIAWVPAHKGVGGNEEIDKLVSGQIR..QVLEFLDRIEEAQEBHDKYHANWRSMQOQEFGLPAIVAKEIVAACPCKQIKGESVHGQVDASPGVWQMDCTHLEGGKI
IIAQPTQSDSPLVBEQIIIALMvqk??IYLQWVPAHKHGIQGNTEIDKLVSGQIR..QVLFDRMEBAQESHDKYHTNWQFIRDAFGIPALVAKEIVAACPCKQIRGEPKHGQVDASVGVWQMDCTHLEGGKI
IIAQPTQSDSPLVBEQIIIALMvqk??IYEAQEBGH?RYH7NW7NLADT?GLPQIVAKEIVAMCPKcqiKGEF?HQQVDASPGVWQMDCTHLEGGK?
AGWVER_3 HQ--Q-M--KI--LEK--E--N--R--Y--V--
AGWVER_155 Q--EA--I--IGR--D--S--R--F--I--
AGWVER_963 K--RA--V--IGR--D--S--K--F--I--NAK--I--
AGWVER_TYO I--QQ--K--E--N--K--Y--V--LEK--K--E--N--K--Y--V--
VLSQRPTETHP?VKqIIeeckkKdqVYLGWVPAHKHGIQGNQEVdHlVskGIRkQV?FLekIEPA?EEhskFHNNAKDLBEKfh?PPMVAKQIVNSc?kCQtkGEAITGQVD?S?GIWQ?DCTH?EGQV
V--L--G--Q--Y--I--N--K--LQ--A--I--L--M--V--G--YGI--E--A--Q--K--
I--N--K--LQ--A--I--Q--I--T--M--V--G--YGI--E--A--Q--K--
I--D--Q--Q--M--V--V--NL--D--AN--K--
IIAGSPDTSESPVQOIIIEQMIGKEEYVLSWVPAHKHGIQGNQEVdKLVSGKIRQ..VLFLDGIGKAQEBEHEKYSNRAMAEFFQIPQIVAKEIVAACPCKQVKGAEVHGQVDASPGTQMDCTHLEGGKI
LLSKRPTETSELVKEIIVELIRQKDVYLGWVPAHKHGIQGNQEVdKLVSGKIRKQVMPTEKIEPAVEBHGKFNNAASLQEMFEDIPVAVAKQIVNECAQCOQGEAITGQVDASVGIWQMDCTHMEEKV
IIMTCTPTNTEHPVBOIIIOEAIKKEALVYTWVPAHKHGIQGNQEVdKLVSGKIR..KILFLERIPQAEDEHRYHNSMELYRQEFHLPVQAKALIOCPKQNRGEPKHGQVDVYIYNWQMDCTHBEKGV
IITGQYDQLPSSRGEIIIQAGMAKEAIIHVAWCVPAHKHGIQGNELIDQKV..GVRQ..VMWIDKIEAAEEDHQFHSNVQYLYKQFGLPTVVAKEIWERCSQCNKQGVAVHQLDYSYGLWQLDCTHBEKGV
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGISSAERLIVN
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDAERLETAQV?#
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDAERLETAQV?#
--Q--AK--P--F--E--L--
--Q--K--K--Y--SE--Y--L--
--I--K--K--Y--L--
--K--K--Y--L--
--K--K--Y--L--
--H--H--I--F--I--
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
VIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
I--R--IG--H--M--V--I--V--A--A--IL--Q--S--
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
--H--O--V--I--A--T--
--I--C--N--O--V--S--
-M--M--N--K--I--D--S--I--
--SH--K--I--S--T--
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
IIIVAVHVASGFTEAEVIAETGKETAFHLLKLLARWPVKHLHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
ICVAVNTASGYETKILKRETDGETALFLMQIASRWP IKQIHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN
IIIVAVHVVCTLFCWATILKRETDGETALFLMQIASRWP IKQIHTDNGENFTSQNVAAVWVWGNIEHTTGIYNPQSGSVESMNRQLKEIISQIRDDCERLETAQVOMATHHNFKRGKGGIGGIMTPAERLIN

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AGMGRI_677	MLTTQLELNTLQNQIQKILNFKVYVYREGDRDPVWKGPARLIWKGEGAVIKEGED.IKVVPRRKAKIIKDYGERKTMDSGSMGVYREANKQMEGSDLQDQE	1057
AGMSAB_1C	IIHTELETKTLQKKISKIQNFRVYVYREGDRDPVWKGPAKLIWKGEGAVIQEQE.LKTIIPRRKAKIIKDYG..KALDSQAPLEGNRTRAGEVD	1039
AGWTAN_TAN1	MITTTQLEIQHIQTQQQKISNFKVYVYREGDRDPVWKGPAKLIWKGEGAVIKEGEE.LKVYPRRKAKIIKDYGERKTVGDKTNMEG\$	1068
CONSENSUS_VER	mITTTQLE?c?LQTKIQKILNFRVYVYREGDRDPVWKGPaLIWKGEGAVV?KeGee.LKvYPRRKAKIIKDYEP?k?mGdEgnlEGa?Gsdn	973
AGMVER_3	-----L-H-----I-G-V.-.-EY-----S-----G-A	1046
AGMVER_155	-----L-T-----L-----R-----I-----TL-----TH-----G-HOMAGDS	1047
AGMVER_963	-----L-T-----L-----I-----M-----LR-P--QMARNSQLDD\$	1049
AGMVER_TY0	-----I-H-----L-D-SD.-----KQ-V-N-DV--TR-----	1061
CONS_LHOEST	MINAGLETQYIQKLNLSKILKFKVYVYRQDRDPQWKGPAQIILWKGEGAVVYKEG?.?IFSVPRRKAKIIKDYGEGPKDSE?siIdnH\$#	972
LHOEST447	-----D.T-----GG-H--\$	1019
LHOEST485	-----D.T-----G-----\$	1019
LHOEST524	-----I-----R-----E.N-I-----OS-M-Q\$	1020
SIVLHOEST	-----E-----E.N-----S-----\$	1017
RCM_Ngm	ITASDLOTTKLNQIISKIQNFRVYVYREGDRDQWKGPAKLIWEGEGAVIODOE.DLKVVYPRRKCKIIKDYGKVDRETNMEGRQEE\$	1022
SIV_SUN	MINADLETQYIQKLNLSKILKFKVYVYREGDRDPQWKGPAKLIWKGEGAVIKEQE.NILVYPRRKAKIIKDYCGESSSVEVVG#	1014
SIV_SYK	MLYTELQIQ.QNTISPKFSNFRVYVYRQKNE.WKGPAPLWKGEGAVVYQTEGDIFAVPRRKAKIITDHDG.ERMDS.GSHVENDPKTD	1036
COL_CGU1	RAIIIELDTONLTKLQNKQKFKNFKAYWKEHTGEMQGGPGLVWKGEGAVVIRNSQGLLFFVPRRKVKIIRLQYGEDVGVSENLLSNGQKEAET	985

AGMGRI_677 MEREKQWIVRVRVRSERQISRMRGIIVTYKIR.NKQLP.WEYR.....HHWQVQWFMTYSQFIPLSKDDYIEVNIYHNLTPERGWLSSHGVLGSY.HQKG.YKTEVDPGTFADRMIHL
AGMSAB_1C M.EKHIVRPLMKVYGGQQRWTSLVKYHHMYSKQCVHWRYT.....PHTKIRWNYSYQEWIPLKDGALIKVWNYWHLLTPKGLWLEYATGIGY...SKGEWTELDPPWTADHI IHH
AGMTAN_TAN1 MEREKLWVTRLTWRVSGEHIDKMGIVKYHMR.NR.LQDWTYL.....MHYQCGAWYTCRSRFLIPLGEGEKIVVDCYVHLLTPQQGLWSTYAVAISF.ENWQNTYKTEVTPDADVADHMIHC
CONSENSUS_VER MhqKeWmRvTWKvp??LIITKOGIvYvMmr.kRnLk.WY?.....MHYQITWAWYTMsrYvIp?q?hGeIIVDIYWHLLPegQWLSlTYAVGIQY?sn??kyrTELDpPaTAdsmIH?
AGWVER_3 EE-T-K-D-K-R.....E-L-Q-S.....K.....E-L-RDPW-----L-L-T
AGWVER_155 -S-H-L-OEEV-N-E-K.....-LPGS-I-A-K-----V-LVND-----N-----C
AGWVER_963 ---GD---K-T---Q-M.....-N-C-I-I-L-E-QI-C-----R-----I-L.GAVGNF-----G-L
AGWVER_TY0 ---PN-----G-D-----Q-----N-Y.....I-K-C-----V-L-ES-----I-L-G
CONS_LHOEST MERDQIRVRAwITLrSL?EKFLDIrRahKet?ndWVSLHGtG.....VGEFFTYnK?vIpLletGTLVVR?YAHUaAGRWISQMAVSIeW...iYgnYQTEIDPILlAQMIHC
LHOEST447 ---Y-----V-----Q-----NI-----C.....C.....-N-----N
LHOEST485 ---N-I-----QV-----I-----I-----C.....-N-----N
LHOEST524 ---N-V-----K-N-S-SK-----L-L-D-----I-----V-----V-L-V
SIVLHOEST ---I-----V-LNT-AKEN-G-----H-L-S-----I-----V-RD-----Y
SIV_SUN MEENPPQWRWDE..REWEDRRQYKIVIRIVMLDRIAEKFLDLRRMhRETkdDwVSYGTGTGWEWYTYnKIIIPVtYGTWVvRI.YGHlLTPAKGLINOWGCSMEW...IYNSYOTEIDPILVADQMIHF
SIV_SYK M..EKEWIVPWRWTPrQIDRLQhIikTKhKSKLEKATYK.....HHYQIEWQWYTYCQWtIPVg.DGTIWIvFVHNLAPeRGWLHMQGIRIQY...QWNQWNTDLTPAVADRLIHN

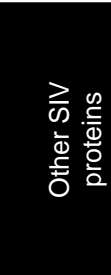
AGMGRI_677 YVFNCFTRAIQQAIRGEKYT.WCTFKEGHK.....GOVQSLQLLAIvAYT.....NGIRKRSKRTFFTRMAGNLGSRQGM...GRMATRHAQ.....GSKRRSOKALMNEHANPSMELLc
AGMSAB_1C SYFPCFTRAVQQAIRGEKYL.WCKHQVGHQPT...GOVPSLQYLAIRVYt.....NGLRRVAPT...SRRSSQGSQESQRDRTRWARRMNGFAORAVRRMARPHRVTPQFRGFPFLPKESFPPLVVEYC
AGMTAN_TAN1 HYFPCFTRAIQQAIRGESFL.WCTYKEGhVAENHNGVRSLSQLALTvYTDfLR.NGRKRfOGKTRMVRNLGSOQgAV...GRMIKRHGS.....RTQSGSTTFPFWERTPLPSMELLs
CONSENSUS_VER HYFtCtTeRAIq?AlrGpRFV.FCQFPpEGHK?T...GqVPSLQVLAAllAHQ.....NGLReRSqRgktrr?RnLgSkQgav...GrWAKr?vI.....RSQsgsq?afw?R?PvPsmELLs
AGWVER_3 ---RK-L-Q-T---K-----Q-S---GGT-M-FE-----HA-----Y-----D---A-A
AGWVER_155 ---D-O-N-I---G-L-----K-E-T---O-----O-YG-----N-OR---P-T-I---
AGWVER_963 ---S---K-I-E---T---K-----I---KQA-S-D---RTM-----GH-----IT-O-A-L-L
AGWVER_TY0 ---N-K---Q-H-----S.....Q-----Y-T-----P-GEA---E-T-----
CONS_LHOEST KYFncfstrDIr?AlwGEkIma?CamPtGhKG.....CVLSLQfLCURQLO...HVQ?KaakeSKtERGLW?kzrAMGMSaSRHhGCKgk.....GqTFPPrsnFGPSlGIIc
LHOEST447 ---K-----F-----N-----A-G-----R-----N-----R
LHOEST485 ---D-WVH---VR-IR---LHS-K-----Y-----T-T-AQP--AP--SS-----N---Q-R.....-H
SIVLHOEST ---IQ---R-L-R-TMC-Q.-L-----I-----A

AGMGRI_677 KYFCWTSRCIRRAMLGEKILHECRNOVAHKG.....LVLSLQFLCIRVLH.....GQQE
AGMSAB_1C FYFPCFTRAVNAQAVRGELLTShCWTP..HTD.....QVPSLQYLAIQVY...LKDGGGfLQSLPACARNTWVLHsKKCRVDPKRdQChCKGR.....TGSDRSIQAFYSSRNiWSLESL
AGMTAN_TAN1
CONSENSUS_VER
AGWVER_3 GGrr?tg?shdGkGl.\$
AGWVER_155 ---G-KESH--AR---
AGWVER_963 ---E-KT-S---I.
AGWVER_TY0 ---E-SPN-E-\$.
SIV_SUN QQYRVrgsLHEIHhYhSk
LHOEST447 ---E-----\$
LHOEST485 ---R-G-----HF-\$
SIV_SYK KRRGRD


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AGMGRI_677      MDKEE.EPHELQDL...HRPLQPCTNKCYCKKCCYHCELCFLQKGLGVRYHYSRKRRTKSTQDNQDP.IRQOSI.STV.QRNGQTTEGKTEVE      88
CONSENSUS_SAB  MdQe?earpQVWEELQEEI?RPLQACDNECYCK?CCfHC?LCF??KALGIcYVYPR?RR?skKIqmkNkVpvhN$      65
AGMSAB_1C      -O-----H-----F-V-----I-HK-----R-----P-A-----SH-O-SL--      73
AGMSAB_D30     -A-E-.-.-.-.-O-----P-----K-Y-S-----TR-----K-RA-----S      71
AGMSAB_D42     --VR-G-----R-----R-----N-----V-----NQ-----T-----H-----T-----H-----N-----Q-----$      73
AGWTAN_TAN1    MSEGDMAESLLODLH...RPLTPCTNKCFKRCYHCQVCFLOKGLGITYHYVSRIRPRPKKNHSHQNLVSOQSISAWGNSQTTQEEKTKIPAAAETSRRPQ$      101
CONSENSUS_VER  MDKGEeeq?vsHQDLi.ecykkpL?tCtNKcFkKCCYHCQICFLqKGLGVTYHApRrRkKiasl?r?P?c?QsIstr?GRD?QtTqesQ?KVet?a?c??lgrknl????r?avga??      99
AGMVER_3      ---D-GAY---L-A-KR---Y-C-----I-----P-D-F-E-K-----S---KG-E---S-R-APS-----AQQSGR-T---S      118
AGMVER_155     ---D-D---K-R-E---T-R-----F--R--I---F-----AD-I-VFQ---I-.---S---K---EQ-KANLRIS---GDET-GP---G      118
AGMVER_363     ---RT-L---R-----T-R-----R-----SVQPN-LSQ-D-----G-A---K---RETT-AQI-----D-ERDK-E---NA$      119
AGMVER_TYO     ---A-I---S-D-Q---Q-K-----T-----LH-----K-----#RTTSGRKKRtKNSQTE--RKEQIQRLSTST$#      100
CONS_LHOEST    MOQ?EQEQlt?OKQHqdpIke?YkEAvTkpL?acQnkCccKkCfHCILCFQOKGLGirYyVHR*RRrVtgvfedkqdpRtknsqtKker??????T#      88
LHOEST447      ---O---R---N-----T-----S-N-----K-A-----S-----$      90
LHOEST485      ---O---R---N-----I-----SV-D---R-----H-V-----A-----T-----YIL-TE---A---ORkTEKtStS-$      90
LHOEST524      ---P---H-O---L-O-E-I---I-D-OS---H-----A-----LH-----K-----#RTTSGRKKRtKNSQTE--RKEQIQRLSTST$#      101
SIVLHOEST      ---P---PIQ-----LM--T-N-----A-Q-----T-----LH-----K-----#RTTSGRKKRtKNSQTE--RKEQIQRLSTST$#      101
SIV_SUN        MSTQGHQDDQDGKGTLEEAyKtNLEACDNKcWCRRCfHCQLCFLOKGLGIHYVY. YRGRQHRIgSRKpAPNPQTKKKKQRKKESTST$#      93
SIV_SYK        MSSTDQICQrVPPSPfLEGTFLE:KGPPTPC.NKCFCKNCCYHCQVCFLOKGLGITYARPRKRAARSISEDSDAPTGLPRAGRTOANPQTKKKKAVETEKDKDSTSLPSAENL      110

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CONSENSUS_VER	MP.LGpEE..RrllrLiAfL?rTNPYPp?VE....GTARQRRRRRRRw?qrQlraLaERiW?r?r?BESQLVqaiDgtvlq?QHLaI...QqL.....PDPpP?s??	90
AGWVER_IYO	...FV--WL--YS--SG--O-D-I-V-V--L...-Y-V-R-ADEA...H-A	84
AGWVER_I55	...S...-KN-K-IY--GT--D--T--VT...-SQA	89
AGWVER_3	...S...-NKN--HS-V--O--S-S	89
AGWVER_963	...-KVFS--Y-N--E-R--F--NETK-R--E-TL--A--V--H--N-S-\$	89
AGMGI_677	MS.LGKEE..KQALKIKIILYGSNPYPQ.PS....GTARQRRRARQWRKQOQIDKIAGRVLNTFEDQQLVAQLQELQLENKDLVL...QHL.....PDPpPHIH	89
CONSENSUS_SAB	MS.LGqBe?LRRF.RIKYLYTNPYP.PG....GTARQRRRARQWAKORQOiiHLAERll...QTPVSOIDnLAQEFDQVLVDNLQOP.....Pp1pppghpses??SS??\$	99
AGMSAB_I1C	...EL--F--V--H--S--I-NQTAN--S-\$	99
AGMSAB_D30	...K-EE--L--L--A--KNLE--A-\$	99
AGMSAB_D42	...P-DI--H--C--S--EDQAVQ-S-\$	92
AGMTAN_TAN1	MS.LGSEDL.RRIIQIIRILYHSNQYPP.GE....GTARQRRRRRQFOOQOQFQAALSERIFI AQORRDPSGGE.SLA AA F D Q L V L D N . Q O L V I E T L P D P P O E P H D S S T A \$	103
SIV_SYK	MPDQGEQL.AVFLRMI AHL..QEPYFG.PE....GPRQTRRRRRRQWRQRTORLYLQORIFEAFGSRATALEDSL.....QQLQIISD	77
CONS_LHOEST	MS.TGGe?ElPrYlk?S?IL?????????EPRTARQRRRDRGRKHLHLR?VOERIF.....??TVERGLERAFt?ltVcDSEV?G?N?sPgcVAVPf?ArPfdDPFLPWTAts1?sq	96
LHOEST447	...K-S--I-K--T--HS--D--LW-S--V--SE-L	109
LHOEST485	...E--I-K--R--HS--G--D--TW-S--V--E-L	109
LHOEST524	...P-G--T--L-R--A--QA--AE-VG-TA-H-R--I-HL-GTY--P--ANP	109
SIVLHOEST	...-NGD--KL-R--WIGHIGLVGERR--E-S-Y-DY--A--R-A-S--A--RG-TP-ITS--E-QL-VA-V--K--P-AD-	122
SIV_SUN	MS.TGDDSI.NQYLRI SKRLYEGTGLAP.GN...LPQTHRQRRRRDRERKNIHLRAVQERIF.....ATTLD SRLGRAPERLSVSDSSQVAESLGNSFSTKHLPPAKFLVAVTYDFLPSWATFLADP	118
CONS_LHOEST	QrwdGgkrSedcclle?eqdQKE0?rhIssSc???GTGKE?MELIQR?KkVWSQ\$	143
LHOEST447	--TG-----L-----K-----KKP-----E-----K-----\$	163
LHOEST485	--R-----A-----L-----K-----ERH-----K-----E-----\$	163
LHOEST524	--IP--EC--N--DO--E--R-A-KN\$	138
SIVLHOEST	-----S--AQGEM-----RTV-EH\$	151
SIV_SUN	QRLAGFAPYSGYEQDQERVQNQGESIIVSEGKk\$	152


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AGMGRI_677      MASG.....RDPREPLPGWLEIWDLDREPDEWLDQMLRDLNLEAEARRHFGMNMLIRVWNYCVEE.GRRHNTPWNEIGYKYRIVQKSMFVHFRCGRRRGGPFSPY.....EERRNG.QG      107
CONS_AGMSAB    MASGGWLP?GGPPKDPKPNREEI?PGWLETWDL?REPFDEWLRDMLQDLNgEAQCHFRNLLFRLWNNIVEEPAIDiGQ?RIEGWKYRILQKALFVHMKGRCCKPKTHPAYGPGGgGgPPPLG.Ga      129
AGMSAB_1C     -V-----P-----H-T-L-----C-----G-----G-----T-----      129
AGMSAB_D30    -T-----R-O-----V-----D-----S-----Y-----S-L-----V-----G-----G-----T-----      127
AGMSAB_D42    -M-----A-----A-----Y-----Y-----P-I-----Y-----G-----G-----T-----      129
AGMTAN_TAN1   MAEG.....RDSRERPGWLEIWDLSREPWDE$LRDMVAELNQEQRHFGRELLFQVWNFCQEE.GERNGAPMIERAYRYRLVQKALFVHFRCGRRRTPEFPY.....EERRNGVGG      107
CONS_AGMVER   MASG.....RdPRE?RPGe?EiWDLsREPWDEWLRDMLed?NgEak.lHfGREllfQVWNYCQEE.GER?S?Pn?ERAYKYRILVQKALFVHFRCGRRRQPFEPY.....EERRdG.QG      107
AGMVER_3     -A-----L-----I-----KM-----NRT-L-----K-----K-----K-----N-----      107
AGMVER_155    -E-----GL-----V-EI-N-K-----Y-----Q-R-IA-----R-----N-----N-----      107
AGMVER_963    -G-----N-----V-----N-----L-----K-----R-----A-----T-----R-----R-----A-----T-----      107
AGMVER_TYO   -A-----V-----A-----K-----Q-L-----R-----R-----H-T-M-----M-----      107

AGMGRI_677      GG.APPPPPGGL      117
CONS_AGMSAB   PGGAaaAaPGL      141
AGMSAB_1C     S-----S-----      140
AGMSAB_D30    -----P-----$      138
AGMSAB_D42    -----S-----$      140
AGMTAN_TAN1   GRDGREPPPGGLA$      119
CONS_AGMVER   GGRa?RVvPPGLd      120
AGMVER_3     -G-----      119
AGMVER_155    -PG-----      119
AGMVER_963    -N-A-----      119
AGMVER_TYO   -N-----E      119
    
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CONSENSUS_VER      AWKEVKeIvKkLpK.....drY?GTNdtE?Iy1qRqfGDPPEaaNLWfNCqGGEFFYcKMDWfLNYLNNIt.....vdadh?N?Cn????k??g??aPpCvQRTYYvachIRSVI
AGWVER_1E          -R-I-QK-E-E-----E-Q-----KQ-F-W-S-----H-----N-----N-----STQG.....KR-----G-----
AGWVER_2E          -E-IRQ-T-P-----HK-R-----K-F-----L-----S-----GSR.TSP.R-----A-----
AGWVER_3           -N-----O-----E-----L-----R-----P-----GT-----GK-K-A-----
AGWVER_155        -OE-----N-----NK-F-----W-----T-----H-----K-N-----AGK-RS-----
AGWVER_266E       -I-Q-----R-----R-----PKR-FF-W-----S-----WN-----O-D-ST-----TG-R-----
AGWVER_385E       -R-----I-----R-----Q-----K-----QS-----N-----O-S-EI-----KK-N-----
AGWVER_2010E      -E-----R-----Q-----K-----I-----QS-----N-----NT-R-NKtG-----TS-----A-----
AGWVER_TYO       -R-----QK-E-----K-----N-----H-----W-----S-----K-----W-----Y-----F-SS-----KK-H-----Y-----
CONSENSUS_GRI     AWKEV?ee?kk???.....?Knltev??enHlRqWGDPPE?anFwFncGGEFFYcKMDWfLNYLNNIt.....vdDads?n?C?.....??kKp??gPpCvqrTYVaCHIRQVY
AGMGR1_2E         -KQ-V-A-----TDD-K-----A-----S-----I-----E-----K-----NKP-G-----
AGMGR1_3E         -R-KI-EE-----KI-----A-----H-----A-----H-----KS-----TSH-GQ-----AKK-----
AGMGR1_677       -R-V-V-----SI-----I-----S-----R-----R-----E-E-TNRT-D-----KG-----
CONSENSUS_SAB     AWqEvKELIValpP.....drYsGT?dtnkIFLQRQMGdPEaEFFFNCqGGEFFYcKMDWfLNYLNNqS.....VDPdH_NpC.....????kn?dkkCwQRTYvPCHIRQVY
AGMSAB_1C        -K-----R-----K-----N-----N-----S-----S-----K-----N-----A-----NT-P-----
AGMSAB_2E        -A-----E-----K-----S-----E-----E-----E-----E-----G-----GND-N-R-----N-TS-----N-A-----
AGMSAB_3E        -E-----K-----S-----KN-SQ-----G-----G-----N-----T-----TPKS-R-----
CONSENSUS_TAN     AWKEVREtIvKkLpK.....ekY?GTnnt?qIWLzRQMGDPPEAAhIWfNCqGGEFFYcKMDWfVNWLNNEs??g??dVEG..NpC????..??g??g??rkC?KRtYV?cHIRSVY
AGMTAN_1E        -R-K-E-----R-----R-----S-----L-----L-----NS-RNV-----N-----TT-KD-----KR-Y-----P-----L-----
AGMTAN_17E       -R-----D-----K-----K-----TE-----M-----Y-----D-ARRKE-----D-----KD.-P-F-S-P-----A-----
AGMTAN_40E       -R-----Q-----K-----TE-----N-----M-----M-----DS-KSVN-----T-----TPEKD-----L-K-----A-----
AGMTAN_49E       -T-----R-----DR-S-----N-----N-----Y-----AG-NYT-----P-SNST.-KG-MT-S-----L-----G-----
AGMTAN_B05       -T-----V-----O-----K-----K-----L-----Y-----AN-TNL-----K-PDRT.-SG-LT-S-----L-----A-----
AGMTAN_B14       -R-----K-----E-----R-----R-----S-----L-----L-----H-O-D-KK-----R-SNIT.-SG-LT-ST-----L-----GL-----
AGMTAN_TAN1      -R-----K-----E-----R-----R-----S-----L-----L-----NS-RNV-----N-TT-----KDKP-Y-----P-----L-----
CONS_LHOEST       MFnNLGkMLkLNa tAMNYteGh...?C??kKpCGRqLkGLPIAMWTRrG7dLATEMLMHTCGEEMFFCNVTRIFQEWNNKN..SDKWYP.....WANCHIKSTI
LHOEST447        -H-----N-----R-----H-----IDNT-----GND-----GN-----
LHOEST485        -Q-----N-----Q-----PEG-Q-----H-----E-----V-----I-----L-----L-----V-----
LHOEST524        -R-----E-----K-----T-----STPG-----EG-----
SIVLHOEST        -E-----E-----T-----T-----GT-DSK-TT-----K-----H-----A-----
RCM_Ngm          AWKEVKEAIKTKYKGTROP.....ENITIRSVYGGDEAKCFWLNCDGEFLYCKMWfLNYLNNKtI..EGNKNEARQAM.....FVPCITKMWV
SIV_SUN          AFATILKLLROVEPLANMSNGCTFDNITKTCRFTNGTDFKMLKFKPMEKHGADAATEMLMWTTCGEEMFFCNLTRIFKVMNDIT..SNKWYP.....WANCHIKSVI
SIV_SVK          FPKOVHEOATKW.....KNVNTTWRSQPGDLEVRTHWFQCGEYFCNVSKLFANITNGN.ASKNNYASNLR.....LSCAIROFI
COL_CGU1        NCKNKTKQFAIBKIKKNTAWLERISR.....KNITITPENGRTSDPEATFTFVICHLEFFYCN.....ASSLWKHDSIP.....VMNCTIRKLV

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CONSENSUS_VER          *      ^^^      ^^^
AGWVER_1E              .LqCtStVtGmTVELN_Yn?nRT.....NVTLSPQIE?IWAaELgRYKlVEITPIGFAPTeVRRYTG...herqKR.vPFVlGfLgFLGAAAGTAMGAAaAtALTVOs
AGWVER_2E              .---KLAR---A---IHK---A---S---P---P---S---E---
AGWVER_3E              .---L-R---S---SR---S---D---D---Q---T---
AGWVER_155             .IwLE---E---NO---T---IPK---Q---
AGWVER_266E           .---V---L---IND---T---SP---I---
AGWVER_365E           .---S---L---R---SK---S---NQS---Q---OD---S---A---
AGWVER_2010E          .---S---L---R---SK---S---NQS---Q---OD---S---A---
AGWVER_TYO            .---S---L---R---SK---S---NQS---Q---OD---S---A---

CONSENSUS_GRI
AGMGR1_2E             .NDWYtlSkktYAPPRGH...LECNStAtALyVELn_YNSKNRT.....NVTLSPqIeSIWANELGDYKlVEIKPIGFAPTeVRRYTGp...ERQKR.VPFVlGfLgFLGAAAGTAMGAAaAtALTVOs
AGMGR1_3E             .---T---R---Q---S---E---I---KQ---
AGMGR1_49E            .---T---S---V---S---E---
AGMGR1_677            .---VS---V---S---A---D---V---E---

CONSENSUS_SAB
AGMSAB_1C             .NDWYtlSkktYAPPRGH...LECNStAtALyVELn_YNSKNRT.....NVTLSPqIeSIWANELGDYKlVEIKPIGFAPTeVRRYTGp...ERQKR.VPFVlGfLgFLGAAAGTAMGAAaAtALTVOs
AGMSAB_2E             .---L---L---H---K---
AGMSAB_3E             .---L---L---H---K---
AGMSAB_4E             .---L---L---H---K---

CONSENSUS_TAN
AGMTAN_1E             .NDWYtlSkktYAPPRGH...LECNStAtALyVELn_YNSKNRT.....NVTLSPqIeSIWANELGDYKlVEIKPIGFAPTeVRRYTGp...ERQKR.VPFVlGfLgFLGAAAGTAMGAAaAtALTVOs
AGMTAN_17E            .---I---ER---
AGMTAN_40E            .---I---IA---N---I---LY---
AGMTAN_49E            .---S---N---K---
AGMTAN_B05            .---LQ-R---R---L---D---ER---I---#---
AGMTAN_B14            .---LQ-R---R---L---D---ER---I---#---
AGMTAN_TAN1           .---LQ-R---R---L---D---ER---I---#---

CONS_LHOEST
LHOEST447             .DDWAlVgKkIYlPPTSGFNnRIRCTHRVTEWwFemEKwEP?E?lGgNLS.??FLPPSWETnQFVAtGahYKlLlRlPPIGFAPTeHrY.AP...??Q?RAAPLALGALGLLSAAGTAMGLVSTlLTVOA
LHOEST485             .---I---Q---F---E---N---VR---
LHOEST524             .---L---L---E---N---VR---A---Q---SSK-K---
SIVLHOEST             .---I---H---D---IK---H---D---IK---F---SK---K---N---RGR-T---

RCM_Ngm
SIV_SUN               .NDWYtSRKvYTPRPDA...lRCNAtVtYllADID...YTDNMt.....NVTLsAEYDIWAaELGRYKlVEIMPIGyAPtNVRrYET...KQKR.VPlVlGfLgFLSAAAGTAMGAAaAtALTVOs
SIV_SVK               .DDWAlVgKkIYlPPTSGFNnRIRCANRvTEAWFTLrEVEDWkVNGSNIsvAFOPPTnTlNOFvStGAHkYKlVlRlRPIGFAPTeHrY.AP...RKEKRAAPVAlGALAlLSAAAGTAMGLVSTlLTVOA
COL_CGU1              .NSWVTHARlLYGPPGgH...lQCnWEKQPIAFPMGTIEGDNDGNC...AYPAAEFKHALStLElGRYKlVWRITTYVPTDIKRsvNVNWHHGQRK.GlFAFSlLAlLSGAGAAAGSASVALTIQA

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CONSENSUS_VER      qHLLAGIILQOQK... 643
AGMVER_1E          ----- 372
AGMVER_2E          ----- 375
AGMVER_3           ----- 693
AGMVER_155        ----- 687
AGMVER_266E      ----- 379
AGMVER_385E      ----- 275
AGMVER_363       ----- 993
AGMVER_2010E     ----- 302
AGMVER_TYO       ----- 686

CONSENSUS_GRI      rHLLAGIILQOQK... 347
AGMGR1_2E         ----- 367
AGMGR1_3E         ----- 371
AGMGR1_677       ----- 671

CONSENSUS_SAB      QOLLAGIILQOQK... 362
AGMSAB_1C         ----- 676
AGMSAB_2E         ----- 369
AGMSAB_3E         ----- 368
AGMSAB_4E         ----- 368

CONSENSUS_TAN      qqllegiilqgqk... 354
AGMTAN_1E         ----- 373
AGMTAN_17E        ----- 371
AGMTAN_40E        ----- 373
AGMTAN_49E        ----- 379
AGMTAN_TAN1       ----- 682

CONS_LHOEST        QvviLQOQKOLL... 670
LHOEST447         ----- 700
LHOEST485         ----- 699
SIVLHOEST         ----- 702
                   -A-L----- 697

RCM_Ngm           RHLLAGIILQOQK... 659
SIV_SUN           QAVLQOQKOLL... 703
SIV_SYK           OTLLAGIVQOQK... 658
COL_CGU1          QSLNGRASASSNR... 660

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CONSENSUS_VER	SCFWWFDFSKWLNILKIGFLVYVYGIIGLRLLTYVYSCIAVRQGYs...PLSPQIHIHPw?kG??PdnAgeP?EGGd?k??sewqk?s????ks??ckrltnwls.??stwlwnscitliihlr?afq	752
AGWVER_3	-----D-L-----Q-EG-G--KR-NS-P--E-GTAEW--NW-----C-.IS-I-----V--S--	819
AGWVER_155	-S-----A-I-V-----L-T-----O-E--RTG-SK-TH.....G-W-----G-W-----	768
AGWVER_963	-N-----I--G-----R-G--E--ERNDS-D--G-GTRQKRGWS.....TF-----TF-----	819
AGWVER_TYO	-M-----I-----G-V--V-----QVG-R--D-G--NSRIKL--\$-D-----R-MQ--A--T.RLN-----Q-K-----	806
AGWRI_677	SGFWWFSLWLVGVYKIGFLVIVIIIGLRFANVWLCIRNIQGYN..PL.PQIHHS.SAERPDNGGQDRGGESSKLLIRLQEBSSTPSRINNWLNFK.SCSLRIRFTWCYNICLTLILFIRTAVG	796
AGMSAB_1C	SDFWFWFDLTKWGMKTAIMVIAGIIVARVLLVIGILRRKFRKGYAPLSSPSSH\$	732
AGWTAN_TAN1	TSWMNIFDVSSFWFKWGFYIVIGLILFRMAMLIWCIARVQRGYF..PLSPQINIRL.GREQPDNA.....GGEDK.DSSSRDKSPSPKESLPLNRRGGIQAERAWRQHLTNWCCLTISWLLRLLYQ	803
CONSENSUS_HOEST	NFWsWldilswFqYikYAVLIIiGIIvLR??SFT?On?VKMCRGYRv...LapSaYveOdykWEkEngEQPDKEGEiekDkEnIYINLEQCKKESrPpWNVDMW?EPLODSlfVTLKKW?kafGILLIs	791
LHOEST447	-----N-----VV--V--I-----C-R-----Y--T-----S-----I-----	827
LHOEST485	-----M-LTT-----I--IL--I--SV-----F--N--S-----T--R--F--N-----L--W-----T	826
LHOEST524	-----SH--T--V-----LV--G--VL--I--V-----S--V--I-----E-----R--E--KGA--T--T-----L-----N-----L--EG-----	829
SIVLHOEST	-----DMLSWLNMDWMLKYIRIGIFLILGILIRLFLIWSGVSKIRAGYTELISPPPCVHQOIPINBEOPTEKGEKGGCGGKHYVNWQRYFYVILIRPEILCBRLYQCSNLSLVYQSLOSIPSR	824
RCM_Ngm	NFWsWLDLSOMFLYIKYAVLIIiGIIvLR??SFT?On?VKMCRGYRv...LapSaYveOdykWEkEngEQPDKEGEiekDkEnIYINLEQCKKESrPpWNVDMW?EPLODSlfVTLKKW?kafGILLIs	789
SIV_SUN	DLSWFDLSOMFLYIKYAVLIIiGIIvLR??SFT?On?VKMCRGYRv...LapSaYveOdykWEkEngEQPDKEGEiekDkEnIYINLEQCKKESrPpWNVDMW?EPLODSlfVTLKKW?kafGILLIs	828
SYK_SYK	NFWsFGFLNFIFKYVLYAAYVVGGLIGLRIIMVVIACIRGAFRVKGF..QOIGRTNVSSQIRGQDREWQPDNAEIIHREQENSSSRFWRLEEWWS.....	778
COL.CGUI	755
CONSENSUS_VER	YiQYGLgELktaQPa??aLAr?AQNAghQ.....IWLACRSaYR?Iins.....PRRVROGLEeILn	805
AGWVER_3	-----A-----VV--L--Y-----A-----A-----G--N-----	877
AGWVER_963	-----L--V--F-----RL--V--F-----T--H--S-----N--N-----	877
AGWVER_TYO	-L--A--G--ILQT--GV--C--.....N--V--.....	863
AGWRI_677	YLOYGLUQLOEAAATGLAQAARAREAWGR.....LGAIVRSAYRAVINS.....PRRVROGLEKVLG	854
AGWTAN_TAN1	ILRRSLTLLQLLREQEQYIQYQWQFKEGAARSFELASAAQSRTLWNACRSAYRAILEH..PRMRQELERWFN\$	879
CONS_LHOEST	LVMQELsWlghlVlLffqhQhLw??sSrW...mVEnAQKiasW?s?KIRRNr?d?Sa?...harniRlgqkkr?WRFRFrgrG...fpSEtTfTAl\$	873
LHOEST447	-----RKAC--R...V-----W-----R--I--A.....L-----L-----	915
LHOEST485	-----KA--G.....R--W-----R--I--A.....D-----D-----	914
LHOEST524	-----T--I--SYH-----QTL--F...L--S--T--IR--S-----GEL--KT...NGT-----NR--R-----L-----L-----T--\$	916
SIVLHOEST	-----S--W--L-----N--R--QT-----Q--LRE--C-----GQL--ST...DRK--Q--K--KR--L--G-----IS--A-----	912
RCM_Ngm	LLHLRWIGAKLQDQWQ.....EFKGFSSWLAEMARTWAYTYWRGLCAVCVCRDP.AGWPAATLCCR..IROGFERFLN\$	856
SIV_SUN	NIYHLLSFLWHLTTSPHHGRLWQTLRGW...LGSHLIQATSIRINACFTSRVSSS..OKARSRTFSLGRKWRKWNRTGRSRIPSETTITL\$	919
SIV_SYK	GFNELKIAAASLIGREIRDMVAIWOALYAA...TPRVVEAV...AALPRLRQGLELYLN	832
COL.CGUIPTTSDKRRSAWQTLIRVLLVPRGFSLIQILETLQEWLRSAAARG.WRRAPEYLRG..WIYDRPQGPAS\$	834

CONSENSUS_GRI	rREkILINLYALNwGIIIDDwQ?YtPpGFIIRYP?LFGFCFKLVFPVdl?EEARnCerH.CllHPAQAg?dpD???H.GEVLVWKFPpKLaVe??PwM...?kDMH??akr	92
AGMGR1_2L	L---G-R---L---#-S-A-Y---GSE-PSG---T--FK---T--FK---HR--EH-\$\$	102
AGMGR1_3L	M---K---T-S-Q-D---G-G-PSG---T--FK---FK---GME-K\$	104
AGMGR1_677	---M---A-S---H---M---M-E-GID---R---YR-D---F---EH---	223
AGMGR1_TYOAA	#-I---I---\$---A---H---H---I---L-E-GID---R---QYR-E...FT---GM---\$	102
AGMTAN_TANI	KREOILNLYALNwGIIIDDwQAYSPGpTRKPRCFGFCFLVVDVYSQEAQ_DERH.CllHPAQLEWESDPW...KETLVWKFNPllLAVOYNPDS...FKDMHGILVrKk\$	222
AGMTAN_U04016	KREOILNLYALNwSGIIDDwQAY#PGFTRKPRCFGFCFLVVDVYSQEAQ_DERH.CllHPAQLEWESDPW...KETLVWKFNPllLAVQYNPDS...FKDMHGILVrKk\$	107
CONSENSUS_VER	rRnkILINLYALNwGIIIDDwNAws?GFGiRyPrcFGFCFKLVFPVdlhERActCerH.cLvHPAQ?EDDDgi?H.gEFlvWkFPMLAVgydPr?yftDmh??vKpk?	186
AGMVER_2L	#---K---K---VR---N---V---N---V---N---V---N---V---N---V---T-E-E---ST-GTGN\$	107
AGMVER_3	---E---K---K---A---A---LH---N---I---A---N---K-L---DLG-R-	229
AGMVER_155	---Q---YTP---E---S---QG---EM---Y-A---IK---S---I---N---Q---E---AT-GK\$	230
AGMVER_691	---R---T---V---EM---Y-A---IK---S---I---N---Q---E---AT-GK\$	111
AGMVER_963	---A---K---K---V---MR---DPE-N-V---CKAS-GV...N-K-\$	229
AGMVER_TYO	---A---Q---YTP---V---MR---DPE-N-V---CKAS-GV...N-K-\$	229
AGMVER_TYOAB	---A---Q---YTP---V---MR---DPE-N-V---CKAS-GV...N-K-\$	110
CONSENSUS_SAB	#RkKILDLyALNwGIVDwQNYTDGFGtRyPk?FGwcfKLVFPVd?seea?n???H.CllHPAQ?ayEDDpW...KETLVWkFDP?LAVDyVwMRL.hPEQVpSvs?	91
AGMSAB_1C	R-----L---K-SEN-----V---A---L-----L-----AOQ\$	226
AGMSAB_1L14	-----L---K-SEN-----V---A---L-----L-----AOQ\$	102
AGMSAB_1L15	-----L---K-SEN-----V---A---L-----L-----AOQ\$	102
AGMSAB_2L16	-----M---HNDR-----I---W-----V-----A\$	102
AGMSAB_2L17	-----M---HNDR-----I---W-----V-----A\$	102
AGMSAB_3L18	-----C---K-RED-----L---K-RED-----V-----A\$	102
AGMSAB_3L19	-----C---K-RED-----L---K-RED-----V-----A\$	102
AGMSAB_4L14	-----O---F-----AL---A---Q-DEH-----I-----A\$	102
AGMSAB_4L10	-----O---F-----AL---A---Q-DEH-----I-----A\$	102
AGMSAB_U20811	R-----F---M---L---M-D-HSDT-----I-----Y-----F-----GL-A\$	226
AGMSAB_U20813	R-----M---L---M-D-HSDT-----I-----Y-----F-----GL-A\$	226
AGMSAB_U21093	R-----M---L---M-D-HSDT-----I-----Y-----F-----GL-A\$	110
CONS_LHOEST	RRqDILcLYCENEwGLIGDFM?YTDGFGtRyPl?FGWlwQLEPvACDEy?DPsDerQcLLHSSQlGV?BDPW...GERLIWHFpPMLAVD?vAlrK?qpskiqasa??lnckrK	195
LHOEST447	-----T---F---A-----T---Y-----Q-----Y-----IG-OR-\$	205
LHOEST485	-----N---T-----T---AS-----Q-----Y-----SLS-----\$	207
LHOEST524	-----N---A-----A-----FK-----L-----Y-----A-V-T-MRF-E-\$	206
SIVLHOEST	-----I---N-----T---K-----T-----L-----F---K-QFA-IQNTAFADCKRk\$	207
SIV_SUN	IFQEVEFPVRPQRPLCKPTYKQLIDLShFIKKGGLEGLwSRTRREEILDLyAENEwGFIITGWODyTKGpGVrPKAFGwLwKlAPVTTIDEDRDPNHPCQALIHSSQOwNEDPwGERLIWTFDFTLAY	186
SIV_SYK	KRDEILHLyQNEHGIIIDRI.NYtSGFTRyPLIFGwLwELVNEIeGCLyEBEHTLLHPASGSSMSGpHVELQPPFGYTPGwEMARLQLERQTGKPBQLSALSKNI\$	240
SIV_SUN	DFRAIQKHPEEFKHVTSLQ#	206