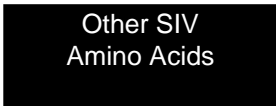


CONSENSUS_VER	MGAATSA.LnrRQLDqFE?IRLRPnGKKKYQIKHLIWAGKeMeRFLGHerLLEtEeGCKkIIEVLyPLEPTGSEGLKSLfNLVcVlyCvHke?kVKDTEEAAtVRQcCHLVEkEsA.....????t	116
AGMVER_TYO	-----K-----R-----L-----Q-----H-----	118
AGMVER_155	-----E-H-----K-D-----K-----S-----M-Y-----L-Q-----L-I-----D-T-----V	118
AGMVER_3	-----K-H-----T-----S-----F-----DKE-----I-----RN-----ERNT-	122
AGMVER_963	-----KG-----K-----D-----D-----F-----I-R-Q-----R-----	118
AGMVER_2010G	-----K-----	18
AGMGRI_677	MGGGHSa.LSGRSLDTFEKIRLRPNgKKKYQIKHLIWAGKEMERFGLHEKLEtKEGcQKIIEVLTPLPTGSEGLKALFNLCcVIWCIHAEQKVKDTEEAvtVVKQHYHLVdKNEKA.....	117
CONSENSUS_TAN	MGaGhSa.LsgRnLdtFEKIRLRPNgKKKYqLKHLIWAGKeMERFGLHekLLEtKEGcQKIIEVLaPLepTGSEGLKSLfNLccVIwCiHaEqKVKDTEEAvtvkvQhcHLveKekta.....a	118
AGMTAN_9	--V-----A-----R-----K-----R-----T-----S-----VY-----A-----QS-----	118
AGMTAN_17	-----R-----S-----	117
AGMTAN_27	--S---T-----R-----D-----I-----	118
AGMTAN_40	-----P-----D-----T-----V-----AT-R-----ST-----T	118
AGMTAN_49	-----T-----DR-----Y-----R-----A-----	118
AGMTAN_1	-----K-----S-----L-----R-----	118
AGMTAN_692	--S-S---K-Q-H-----E-K-----L-----T-----C-----Q-A-----IRI-Q-----D-GEN-----	117
AGMSAB_1C	MGASNSV.LSGRKLDAFESVRLRPNGKKKYKLRHLVWASKELDRFSLSANLEtKEGVVKILSVLLPLVPTGSENLIAlFNLCcVLACIHAEIKVKDTEEAkAKVKEEV.PAEMTESA.....T	117
SYK_SYK173	MGAAGSAILtGRELDryEKIRLRPKGKKRYLVRHLVWAKKELDRFGLSDQLMESKEGCEKILtVLLPLLeANGSENLSLFGIISVVWAVHAKKEVEDTEQAKQKVKKEACNWKDDPPATSGGQSENSSQNMA	132
LHOEST_LHOEST	MGSNSV.LSRQIEKDFCSVRLRPgSKKTYQRHrVewATKELDRFGLSGLLEtAEGcKILSVcWPLyATGSKNLKALVGTVCVICCHLGVRIStQEAISKVKIEPAPeAAGKQq.....	118
SUN_SUN	MGAGNST.VDREVVRSFERVALKPGGKTYQARHVWAGKELDRFGLNkELLRtVEGcQKILSVcWPLyASGSKNLKALVGTVCVLACCHQgIPVKDtQeAlKkVrLEfAKNEEAQASq.....	118
CONSENSUS_VER	etssGq.....kKnd?gttappGg.SQNfPAQQQ.GNaWvHvPLSPRTLNAWVKAVEEKFGAEIVPMFQALSEGCTPYDINQMLNVLGDHOGALQIVKEIINEEAAQWDvtHPPpAGPLPaGQLRDPrg	238
AGMVER_TYO	-----K-IA-----C-----L-----	241
AGMVER_155	TPPG-----Q-NT-G-T-----G-----	241
AGMVER_3	-----K-V-V-----I-----IA-----	245
AGMVER_963	-P---E-----SNRE-----P-----	241
AGMVER_2010G	-----R-----Q---RS-ATSS-Q-----T-----IQ-----	141
AGMGRI_677	.....AKKkNE..TTAPPGGESRNYpVVNQ..NNaWVhQPLSPRTLNAWVKVEEKRWGAeVvPMFQALSEGCLSYDvNqMLNVLGDHOGALQILKEVINeEAAEDWDRTHRPPpAGPLPaGQLRDPrg	235
CONSENSUS_TAN	apsggq....???qny.n.taappgGrhgNYPvvQQ.NNqWVhtP1SPRTLNAWVKtVEEKrFGAEiVPMFQALSEGclSYDINQmLNvIGDHOGAmQIiKEVINeEAAqWdItHPPpAGPLPaGQLRDPrg	240
AGMTAN_9	-----Q-----L-----Q-----V-----N-----LA-----V-----	241
AGMTAN_17	T-----K-----N-----S-----L-----	239
AGMTAN_27	-----Q-----L-----D-----Q-----YV-M-----C-----M-----YI-----V-----	241
AGMTAN_40	E-S-----K-HSR.PD-SR-Q-----L-----	241
AGMTAN_49	T-----K-----T-----Q-----I-----V-----	241
AGMTAN_1	-----Q-----T-S-----D-----	241
AGMTAN_692	.....AKGIDK..-TPT-S--SQ--AQ--.V--V-----VI--K-----TP--V-----L-----L--V-----	235
AGMSAB_1C	ATSSGQTKELQAKKkNE..PTVTPSGGSRNYPVSV.NNqWVhQPLSPRTLNAWVKVEEKrFGAEiVPMFQALSEGclSYDINQmLNvIGDHOGAmQIiKEVINeEAAEDWDRTHRPPpAGPLPaGQLRDPrg	246
SYK_SYK173	ETSSGQKVVQqEKQK...AATPPPRG...NYPLLRNPQNQWIHTGVPVrTLKtWVEAVNSKkFDASiVPLFQALTEGFIPYDLNGLNAVGDHOGAMQVIKDIINEEGAADLEHPQPPAPQAGLRDPsa	258
LHOEST_LHOEST	.....TGG..NYPLIRENQ.RWVHTPLSPRTIQTWVKIVEDRGWKpETVAMFSALTEKALPDDLNVMLNAIGDHOGAMQIKDHIVEEGAEDWRQHPQPPAPQPGGLRTPna	223
SUN_SUN	.....NFPVQREGQ.NYIHQPLSPRTVQTWVKIVEEKGWKpETVAMFAALMTGAIPEDINVMLNAIGEHOGAMQIKDHIVEESAEDWRMHPQPPAPQPGGLRTPna	220



Other SIV  
Amino Acids

CONSENSUS_VER	SDIAGTTStVQEQLewIY..TANPRVDVGAIYRRWIIILGLQKCVKMYNPVsvLDIrQGPKepFKDYVDRFYkaIRAEQASGEVKQWMTESLLIQNANPDCKvILKGLGMHPTLEEMLTACQGVGGPSYKakV	368
AGMVER_TYO	-----S-----	371
AGMVER_155	-----	371
AGMVER_3	-----A-----	375
AGMVER_963	-----R-----	371
AGMVER_2010G	--V-----I--K-----RT-----	224
AGMGRI_677	SDIAGTTSSIQEQIEWTF..NANPRIDVGAQYRKWVILGLQKVVMYNPQVLDIRQGPKepFKDYVDRFYKALRAEQAPQDVKNWMTQTLLIQNANPDCKLILKGLGMNPTLEEMLIACQGVGGPQHkAKL	365
CONSENSUS_TAN	SDIAGTTStVqEQIEWtf..nAnPrvDVGriYRgwVilgLQKCVKMYNP?sVLDIRQgakepFkDYVDRFYqALRaEQtpQDvKnmWteTLLIqNANPdcKlvLKgLGmhPTLEEmLTACQGVGGPghKAKL	369
AGMTAN_9	-----I--T-----	371
AGMTAN_17	-----S-----T-K-----\$--R-----I-----G-----R-----E-----H-----R-----I-----	367
AGMTAN_27	-----SI-----K-----S-----V-----A-----E-----E-----V-----I-----	371
AGMTAN_40	-----L-----I-----	371
AGMTAN_49	-----K-----V-----T--Q-----N-----	371
AGMTAN_1	-----S-A-----I-----	371
AGMTAN_692	-----I--L--IY..T--I--A--R--A--R--TG-----PR-S-S-----K-----AS-----D-----E-VI-----QY-----	365
AGMSAB_1C	SDIAGTTSTIQEQIEWTT..RAQNAVNVGNIYKGWIIILGLQKCVKMYNPVNIILDIKQGPKEPFkDYVDRFYKALRAEQTPAVKNWMTQSLLIQNANPDCKTVLkGLGMNPTLEEMLTACQGIgGAQHkARL	376
SYK_SYK173	SDIAGTTSSIAEQIEWIT..RQNNPVQVGEIYRRWIIILGLQKCVQVYNPVSILDIKQGPKEIFkDYVDRFYHCLRAEQADPSVKWGLTQTLLIQNANPECRQILKAM.VKPTLEEMLTACQGVGGPLHkAKL	387
LHOEST_LHOEST	TDVAGVTSTVEEQLAWTT..ADTPVDVGKIYKEWVIQAMEKVVRiHQPVSVMDIKQGPKEPFkEYADRFFKALRAEGGSHEVKEMWKEKMLVQANANPDCLRVIKALGEGASLEEMMKACQGVGGPAHkGKI	352
SUN_SUN	TDIAGVTSTVEEQIQWiyGLNGATRVAVQDIYKGVWIEGEMERVRLHQTTSSVVEIRQGPKepFRDYTDFFKALRAESGSEVKEWMEKMLVQANANPDCKLVIKALGETPSLEEMMRACQGVGGPSHkGKI	352
CONSENSUS_VER	MAEMM...QnmQsQ.NM.vQqG??.....GgrgR?RP...PlkCYNCGKFGHMQRQCpEPRK...ikCLKCGK?GHLAKDCR.....GQVNFLGYG.RWmG?KPRNFp...AATlG?EPsAPPPP	462
AGMVER_TYO	-----T--N-----PK--Q-----R-----T-----L-----A-----A-----	468
AGMVER_155	-----L-----P-----P-----T-----A-----	469
AGMVER_3	-----M-----Q--P-----V-----MR-----P-----A-----V--T-----	473
AGMVER_963	-----T-----AA.....VR-Q-----T-----L-----T-----L-----H-V-----	471
AGMGRI_677	MVEMM...SNGQ...NM.VQVG.....PQKKGPRG...PLKCFNCGKFGHMQRCKAPRQ...IKCFKCGKIGHMAKDCKN.....GQANFLGYG.HWGGAKPRNFVQYRGDTVGLLEPTAPPME	465
CONSENSUS_TAN	MaEaM...qqMQGv.nM.vqg?.....prgGRGRgRg.PprCfkCGqIGHiQKdCprgGP...ikCLKCGKPGHmAkDCRs.....GqaNFLgrmptpwGsKPrNFL...EggaVptAppmp	469
AGMTAN_9	-----N--I.T--AQG.....T-----L--R--T.....TPW.....D-----L-----	470
AGMTAN_17	-----I--H.....SK-----V-----R-----G.....R--A--\$-----R--KK--	467
AGMTAN_27	-----N-----I--P-----Q--A-----T-----R-----	472
AGMTAN_40	-----N--I.T--AQG.....S-----S--V--R-----R-----	470
AGMTAN_49	-V-V-----P-----S-----V-----L-----R-----	472
AGMTAN_1	-V-----A-----N-----L-----W--T-----	471
AGMTAN_692	-V-M...N-----QA.....GI-----VK-Y--KF--V--N-TQK--...VV-----F--R-----AV---YG.RWM-A--K---...HRA--S---P-	463
AGMSAB_1C	MAEAMTAAFQQTvGNIFVQqGARPRG...PLGGRGRPLNPNiKCYNCGKFGHLARFCKAPRR...QGCWKCSPDHQMKDCQK.....QVNFLGFG.PWGRGKPRNFPLT....SIRPTAPPME	485
SYK_SYK173	MAEAM...VMAQSV.NM.VQGP.....SKGRSM.....IKCYNCGQIGHMqKdCKKPLK...AKFCNCGKTGHLARACRQPKRNQGPVPAQANFLGKGWVSRRPANFPVR.....SEPSAPPLE	491
LHOEST_LHOEST	LAEAMASAIQQVVRQNM.VQ.VTPLRNAQGRFVRTGGGPRKPLTCFNCGKPGHTARMCRQPRQ...EGCWNCGSKEHRFAQCPKPK.....GKVNFLGYG.PWSSKPPGNYPLL.GGAAGRIPSAPPME	470
SUN_SUN	LAEAMASAFRQVGRQAMVQQLPPRNSQGRFVRIgGGGPRKPMTCFNCGKPGHLANQCREPKKPPGSCWKCgKMGHQAQCPQgK.....QVNFLGYG.PWNRGPPGNFPVM.....PSAPPLE	467

CONSENSUS_VER	?.....??tPYDPAKLLQQYAeKGKQlReQ??n.pPa?NPDWtEGY.SLNSLFGEDQ\$	507
AGMVER_TYO	S.....GT-----KR-.-M-----	519
AGMVER_155	N.....NS-----M-N-NR-.-N---N-----	520
AGMVER_3	.....S-----D-----RKK.-V-----	521
AGMVER_963	.....GKR.T-PT---A-----	519
AGMGRI_677	.....TAYDPAKLLQQYAeKQRLREEREQ.TRKQKEKEVEDV.SLSSLFGGDQ	513
CONSENSUS_TAN	aH.....gfptgpp?aaGAYDpAkrLLeqYakkg?????dq.lrkQkekELEDY.SLsSLFGeDQ\$	521
AGMTAN_9	-----ETSV--T.-R-----	522
AGMTAN_17	-----V-----G-----R-----	513
AGMTAN_27	-----V---L-.-R-----E.....-K-----	524
AGMTAN_40	T-----Q-----R-----	522
AGMTAN_49	T-----V---SDWR-----T-----E-----	525
AGMTAN_1	-----S-----RK-----G---	523
AGMTAN_692	-----NP---E-T---K-TQE-AQQRKVE..KSS-AGR-E---.-K-----	513
AGMSAB_1C	RDYSRPEENWYADRPPTRGPGPDDPATALLKQYAVQGKRQKQWQNHSPQQSP.YEEAYSSLRSLFGEDQ	554
SYK_SYK173	DI.....EDGPWLTWSAQMSQQAQAKAQNPSK.K.PPTNREVLSPKESGKEETKSLYPSLSSLFGEDQ	554
LHOEST_LHOEST	SA.....PTKAERALETYRTLGGQLKRQQ.....QVPQKVD...EPCLNSLFPDDQ\$	515
SUN_SUN	DLTLGNRMT.....PPQSKAERALETYRLLGQGLRAQQK.....RK.ERGECQ.EPCLNMLFPEDP\$	521