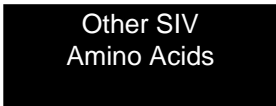


Other SIV  
Amino Acids

CONSENSUS_VER	.....LWKIWPYAKTMSGTK??M?mW?ar?psKRLQ.gTGeFFRVW.?VDGdkTeKf....SRr?SW?Gte.cApSte???.....tiRPsKEAPAA	69
AGMVER_TYO	.....-ENK-SKV-KIGT-----T--G-----Y-S-----S--RHH.....P-----	82
AGMVER_3	.....-KDE-LE-ET-AF-----R-K-----P--SE-Q--.....Y-G-AN-----S--C-----	66
AGMVER_155	.....-K-AL-----P-----K-----SH-G-K-----QLY.....L-----	61
AGMVER_963	.....E-T-G-----T-----L.....CH-S-----R---D.....	58
AGMGRI_677	.....VRQNPYGKRLQEWTKGFFRVW.PLGRSETKKF.CAIQRHSWSGTN.SPPNGN.....SLRSSKEAPPA	62
CONSENSUS_TAN	SNAKHARDHNGRSRTKRK?Q?R??PLLQMWtnw?ytkRLsksRT?q??qmW?Rt??KrLq?rtGgFFreNantmgfqaAQF.FRARRsRSDGSpda?AriphRsas?cgS.....?RpSQetpg?	103
AGMTAN_T9	-----R-GK-TY-----RPHSE--PQG--K-VS---KT--LS-G--D-A-K--K-D---IE-----I-C--DLR--H-.T---I---T-V-A	119
AGMTAN_T17	-----K-----R--LR-----R--W-----R-.....L-S-----A	58
AGMTAN_T27	-----PD-T-----NEVP-V-ET-AHG---KW---P---T---T---K-R-----L--A--T	90
AGMTAN_T40	.....R-NKMS--KA-HG---V-A-K---D---IE-----TH-N-----S-.T---I---II-T	77
AGMTAN_T49	.....I-N-WGS--VRLA--L--A--R-T	54
AGMTAN_TAN1	.....X-RQ-PT-----A-----K-MPK--EA--LS---PQW-----ANL-NK-----C-----F--I---A-A	101
CONSENSUS_SAB	.....FFRVW.PLGQRETQEF.PSDLHQTNSSPNGTGLQQAGGKLVCRQTSQDTRARRSSNSPVKAVCC	63
AGMSAB_1C	.....	63
AGMSAB_D37P	.....	0
AGMSAB_266	.....	0
AGMSAB_385	.....	0
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	.....FFRERMGLQEQAPSQLPSEERAICSPSGHRRWAMAH....MVSTDEP.....TSTSE.GTEL	53
SIVLHOEST	.....XWSLEQQTSQLSSTGRSCRENISSPNGECSN..KS	35
SIV-SUN	.....XWPLEQQAARELSSHAFCSASRGSDDIGEQNDTTPVKG	37
CONSENSUS_VER	?Cre?etvEg..tke??tsneSrLdrgI.FFELPLWRRPIkTv?IeGvp?kaLLDTGADDTIIKetDlQLsG..pWrPKiIGGIGGLNVKEYs?....?EVk?EDKILRGT?L?GaTPINIIGRNILApA	180
AGMVER_TYO	I--R--T-.A--ES-G--G-----Y--I-----N-----ND....R--I-----I-L-----	204
AGMVER_3	I--QG-A-----KT--S-----Y--IR-----A-----T-K-----D....R--RL-----I-I-S-----I---	188
AGMVER_155	V--R--N-K..SEQKPP-EQ--E---R-CI-G-TAV-----D---R..S-----V-----DN....V--QL-----V-I-----F--Q-	183
AGMVER_963	V---GK---R-EN-T-K---GGR--I---V-V-----I--T--V-----V-----N....V--I-----V-L-----	180
AGMGRI_677	VCREGTAPER..GERTDKETEGERSGGC.FLELPLWRRPMKRVIEGTVPVQALLDTGADDTIIQEKDLHFPPHPKWRSKVVGIGGGIHVKEYQG....VQVQLEDKIIITGSILIGSTPINIIGRNILApA	186
CONSENSUS_TAN	vckkgg.....pt?eaegegtGGL.FLEFpLWRRP?????QGGPQVQLLDTGADDTIIKEEDIHLEGR..WRPKVVGIGGGISVKQYDN....ILVNIDGKETRGNVLIGPTPINIVGRNILLAPL	211
AGMTAN_T9	-----AE-----1	148
AGMTAN_T17	----RR.....-K--KR-----1	81
AGMTAN_T27	I-----SVK---KRA---I-----I1	120
AGMTAN_T40	--EE-----EKT-R--I-----1	106
AGMTAN_T49	-----HEER-----T-K-T-----1	83
AGMTAN_TAN1	--Q--R.....SIEK-----MSKIYI-----	216
CONSENSUS_SAB	SGETAETAVAKPLA.TTEPLR...GGLQLPQVSLWRRPMKTVYIEGQKVTALLDTGADDSVIQ?ELGDN...WKPRIIGGIGGINV?AYHN....QEV?IE?K?CKATILV?TPVNIIGRNVLApL	175
AGMSAB_1C	-----I-----K-----K--D-T-----E-----	181
AGMSAB_D37P	.....L-----R-----E--G--G-----D-----	63
AGMSAB_266	.....	0
AGMSAB_385	.....	0
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	SLEETPHQQGSALAEQEQ.WEGGDQESLSLSQLSLWRRPMIEVDVVEGDLVQMLVDTGADDTIIEEDIQLHQP..WSPKIVGGLGNITVRQYRNIRFTVVKPSGKRKQVEGTLVGPVNIIGRNILTKL	182
SIVLHOEST	RESTGLDQFRTTAEKAAAASPTMCGRALPEFTLSRRPIESILVNGQPVSALLDTGADDTIFSNSVRIEGP..YTPRVVVGIGGQIRVKEYRDFVIEIAGKTTV....GTVLLGPTPVDIVGRNILTAM	160
SIV-SUN	RESSGDLQTVRTGPPQSTAAEEGKGGMSGAMLEYALSRRPLEKVFINGQPVTALLDTGADDTIVSEDSVSIIEGH..WKPRVVGIGGQIRVKEYADVFVEIRDKTAT....GTVLLGPTPVDIIGRNILSAL	162

CONSENSUS_VER	ga?LVMGQLSeqIPiTFVklKeGARGP?lkQWPLSKEKIkALqEIC?qLEkEGkIS??GGeNAYNTP?FCI?KKDKsQWRMLVDFRELNKaTQDFFEVQLGIPHPaGl?KMkqITvLD?GDAYYSIPLDPeF	303
AGMVER_TYO	VPR-----K-V-----CVR-----E-----S--Q---RV-----I--K-----R--R-----V-----N-	336
AGMVER_3	--K-----F-----D-----KI-----V--K-----S-FE--TE--I-----N-	320
AGMVER_155	--K-----QT-----R-----R-----I-----KT--E--L-RV--D-----V--R-----K-----II-V-----	315
AGMVER_963	--R-----D-----HI-----T--E-----KI-----I--R--T-----V-----Q-----I-----	312
AGMGR_I_677	GMKLVMGVLLSSQIEETKVQLKEGKDGPKLKQWPLSREKIEALTEICKQMEEEGKLSRIGGENPYNTPVFAIKKKDKTQWRMLVDFRELNKATQDFFEVQLGIPHPAGLQKKKQITVIDIGDAYYSIPLCKEF	318
CONSENSUS_TAN	GARLIMGQLNEKIPITKVQLKPGMSGPKLKQWPLSSEKIKALTEITQALEKEGKISKVGGENPYNTPVFCIRKKDKTQWRMLIDFRALNKATQDFFEVQLGIPHPAGLKRKKQITVLDIGDAYYSIPLDPEF	343
AGMTAN_TAN1	-----	348
CONSENSUS_SAB	GVTLNL??..??I?PIKV?LKPQ?DGPR?RQWPLSKEKIEAL??ICE?LEK?GHLERIGPENPYNTPVFAIRKKDK?QWR?LMDFR?LNK?TQDFQEVQLGIPHPAGLQOREQITVLDI?DAYFSCPLD?DF	287
AGMSAB_1C	-----TQ..RE-E--H---Q---I-----KA--D--Q-----T--I---Q--S-----G-----P--	311
AGMSAB_D37P	-----VA..KT-L---Q---K---L-----RT--Q---E-----S--M---E--A-----A-----E--	193
AGMSAB_266	.....	0
AGMSAB_385	.....	0
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	GVKLVVMVQ..TALEPVKVS LKPKDELPR LKQWPLSVEKLEALKAIVEDMLKAGQLEKASPTNPYNTPV FVIRKKDKKWRMLIDFRKLNELTQDFFEVQLGIPHPGGLK.RQKLTIIDLKDAYYSVPLDKEF	311
SIVLHOEST	GAKLILAQLSDKIPITKVSLKPGCDGPRVKQWPLSKEKIEGLQAICDRLEKEGKISPVDPGNPYNTPIFAIAKKKDKNEWRKLDIFRKLNELTQDFHELQLGIPHPAGIKKCKQITVVDIGDAYYSIPLDPNY	292
SIV-SUN	GGRVLVATLSEKIPITKVKLKEGAAGPKVKQWPLSREKIEGLQKICDRLEAEGKISRADPGNPYNTPIFAIAKKKDKNEWRKLDIFRVLNGMTQDFHELQLGIPHPAGLKKCKQITVVDVGDAYYSIPLDPDY	294
CONSENSUS_VER	RKYTAFTIP?VNNqGPGiRYQFNCLPQGKGSPTIFQNTAA?ILEeIKkeLkpLTIIVQYMDLLWVGSQEdEytHDkLveqLR?kLqaWGLETP?KKvQk?PPyEWMGYKLWPhKWqlssIeLEe.Ke?.WTW	427
AGMVER_TYO	-----T-----S-----RN-PA-----N-H-----T-----E-M-E-----E-R-Q---.DE.---	466
AGMVER_3	-----S-----T-----S-----R-----M--S-----D-----K-----I-----D---E.---	450
AGMVER_155	-----T--E-----SK-----Q-----EGPK--Q--QT--NR--E-----E--RE--F-----K-Q---K---Q.---	445
AGMVER_963	-----S-----V-----K--K--E-----V--KT-----D---K-----Q---N--N---.Q.---	442
AGMGR_I_677	RKYTAFTIPSVNNTGPGIRYQFNCLPQGKGSPTIFQNTAANILEEIKRHTPGLEIVQYMDLLWLASDHDTRHNQVDIVIRKMLLEKGLTPDKKQVREPPWEWMGYKLHPNKWTINKIELPPEGE.WTW	449
CONSENSUS_TAN	RPYTAFTIPQVNNVGPGRYQFNCLPQGKGSPTIFQHTAQRVLKEIGKKVQDLEIIQYMDDMWIGSDLPEKEHDEKVEVRKLLLLRGFETPDKKVQKRPPYDWMGYKLYPSHWSLNKIEIPE.QEH.WTW	473
AGMTAN_TAN1	-----	478
CONSENSUS_SAB	QKYTAFTIPSVNNTGPGIRYQFNCLPQGKGSPTIFQNTANKILQEFRQKNPDVDIYQYMDMLIASDRPKAEHLVMVQQLRDYLETWGFKTPEKKFQKDPPLWWMGYELYPKKWQLQEITLPE.REE.WTW	413
AGMSAB_1C	-----R--I-Y--L-----	441
AGMSAB_D37P	-----K--M-F---I	217
AGMSAB_266	.....	0
AGMSAB_385	.....	0
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	RPYTAFTVPSINNAPGERYQFTVLPQGKGSPTIFQSTINQILQFRRKYSDLTLIYQYMDLLIGTDRSEKAHQEIVQQIVTALLKVGFKVPEKQWQDQYPMQWLGYTLHPDKWQLQKIELPNIDDEI.TV	442
SIVLHOEST	RKYTAFTIPSLNNQEPGKRYQYNVLPQGKGSPCIFQGTVAGLSEFRKLNPDMIYQYMDLLIGSDREKRGHDQAVKELRELLMTWNLETPEKKFQAEPYHWMGYVLHPDRWEIEKIKLPMDLTKTTV	424
SIV-SUN	RKYTAFTIPSVNNTGPGIRYQFNCLPQGKGSPTIFQHTVAVLLEKFRFRQYQEVQYQYMDLLIGSDYKHEEIVKQLRQLLEWNLLETPEKKYQGEPPYKWMGYILHPDRWEIEKIKLPPEEEP.TV	425



Other SV  
Amino Acids

CONSENSUS_VER	NDiQkLVGKLNWAAQLYPGLrTknIcKlIr?GKKNLLe?V?WT?EAEAEYaENkEILKTEQEGTY?PgkP?RAAVQKLe?GQWSYQFKQE..G??LKVgKy?K...QKnTHTNElR?LAGlVQKicKeaLV	543
AGMVER_TYO	-----K-R-----TG-----L-A-P-----A-----K-I-I-----G-----..QV-----T-----T-----	592
AGMVER_3	---R-----L-----L-----T-T-E-----K-R-I-----G-----..QV-----T-----K-F-V-----L-----S---	576
AGMVER_155	--L-----L-----L-----DV-E-P-----E-----A-E-L-----GD-----..KI-----FA-----A-----V-----V-----G-----	571
AGMVER_963	-----Q-R-----E-Q-E-----A-----L-----D-----..KI-----A-----T-----	568
AGMGRI_677	NKIQKVVGVNLNWSAQIYPGIKTKHTCAMLr.GKKNLLEIEVWTEEAEEYKNNQGIvQETQEGTYDPLKELIATVQKQEGQWTYQFTQE..GAVLKVGRYAK...QRETHNTDLRLTLAHLVQKICKEALT	575
CONSENSUS_TAN	NDiQkLVGVLNWSAQLYPGIKTKALCKLLr.GAQLDTAVVQWTEQAEEVFRQNQEILKEEQGAYYDPSKSLRATITKLLDDGQWGYQFKQEG..KVLKTGKYTK...SKNTHTNEFRVLGAMVQRVCKEAIT	599
AGMTAN_TAN1	-----	604
CONSENSUS_SAB	NDiQkLVGKLNWASQIYTGIKTKHLCLRLr.GARPLTEIVQWTEEAEELEENRQILRQKQGGYYDPALPLRAKVLKLDGGQWGYQIYQPE.NKILKVgKYAK...IKTAHTNELRMLAGLVLQKIGKE??V	538
AGMSAB_1C	-----SI-----	568
AGMSAB_266	.....	0
AGMSAB_385	.....-AL-	5
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	NQLKQLIGVLNWSAQIYSGIKTKELCKCIR.GTKQLTEVLTLEAAEELEENRQILKEEQAGSYDPPKPLEAHITKLSQQWGYMIKQEKGPPPLITGKTAK...TFAAHSNDYQSLAQLLNKIGIQSLW	570
SIVLHOEST	NQIQKLVGVLNWAAQLYDGIKTKELCKLr.GVKPLEEIIINWTEEAEEYQGNKEVLKEKMQGAYYDPEKELIVRVQNNKGIITFPQRQ..GNNILRAGRYQ...RQKAAHTNPLQKLVEAIQKIGKESIV	550
SIV-SUN	NDiQkIVGVINWASQLYEGLRTEKELCKLr.GNKP LAEKVKMTEEAAREEYQSNQEVLEQSVSGSYEYDPKELICRVQKVKQGITLFPQWLQ..GKQVLRVGRYQ...KRGAAHENPCQQLAALQKIGRESIV	551
CONSENSUS_VER	IWGELPv?ELP?ERevWEQWwADYwQVSWIPeW?FVS?PPLvKlWYtLTKEPI?EDVYYVdGACNRnSkEGKAGYITq?GkQrVekLEntTTNQQaELtAIKMALEDsgp?VNIvTDSQYAMGILTAQPTQS	669
AGMVER_TYO	---I---L---I-----D---T---L-----K-----S-----T-----K-----N-----	723
AGMVER_3	---L---L---I-----D---E---T-----K-----R-----M-----N-----	708
AGMVER_155	---Q---TF---V---DT-----D---V---T-----G-----Q-----Q-----K-----	703
AGMVER_963	---IF---V-----E---V-----G-----Q-----V-----EK-----	700
AGMGRI_677	IWGRlPRVQLPVDKKTWDMWQDYwQVSWIPeWfVSTPLLVKlWYSLVKEPIKGEDVYYVDGAASKVTKLGKAGYLSERgKSRIRELENTTNQQaELTAVKMALEDsgENvNIvTDSQYVMNILTACPQES	707
CONSENSUS_TAN	FWGKLPIMEVpVEREVWEQWwSDYwQVTLPEIEFISTPPLIKLWYNLVKDPiPKAKVYYCDGACNRNSKLGKAGFLTNTGESQVIELEDTTNQQaELQAVLLALKHskSKVNIvTDSQYVMGILTAQPTQS	731
AGMTAN_TAN1	-----	736
CONSENSUS_SAB	IWG??P?ELPVERE?WEQww?DYwQvsWIPeW?fVStPpl??LWYtLtKePIgEdVYYVdGACNRNSrEGKAGYITq?GkQrVekLEntTTNQQaEL?AI??AL?DSG??VNI?TDSQYA?GI IAGEPTES	652
AGMSAB_1C	---QI-IM-----L-----S-----T-----EM-----Q-IR---K-V-D---A-----A---K-----L-DR-D-K-VA-----K---E---LL---R---SK---I-----M-----	700
AGMSAB_266	.....X.Q---X---D-T---V---VT-----K-----Q-----T---KM---E---PR---V-----1	101
AGMSAB_385	---EL-TL-----V---A-----D-----WLK-----LAK-----Y-----1	100
AGMSAB_381	.....	0
AGMSAB_384	.....	0
AGMSAB_386	.....	0
AGMSAB_385A	.....	0
AGMSAB_385B	.....	0
AGMSAB_385C	.....	0
AGMSAB_385D	.....	0
SYK_SYK	YWGKVPtFHLpVKREWEKwWTDYwQATWVPEVKFISTPPLVrWYyNLVPEPIPEAVTFYVDGAANRSDSKTGNAGYVAsDGTQRVQYLEQTTNQQaELEGLLMALQDSKDKVNIvVDSQYSYGILMTCPTNT	702
SIVLHOEST	IWGFVPKIQVPVTREVWEHwSDHWQVtWIPDLFIStPQLEQEWYIWEAEPiIGVDTYyVDGAAEKVGKTKGAGYITQSGKEKVKELTDTTNQQaELEAVLLMALQDSNSKvNIvTDSQYVMKILSRPTET	682
SIV-SUN	IWGFVPKIQVPIQREIWSQWwADYwQCTWIPELEFVSTPKLEQEWYTLATEFPVPG.DTYyVDGAAEKLEKRGKAGYITQGGRSRVKLENTTNQQaELEAIKMALEDsRSsvNIvTDSQYALRLLSKRPTET	682

CONSENSUS_VER	DSPLvEQIIAlMvqK??IYLQWVPahKGIgGNEEIDKLVS?GiR..r?LF??IEEAQeEh?RYH?NW?NLADT?GLPQIVAKEIVAMCPKcqiKGEP?HGQVDASPGvWQMDCTHlEgK?vIVAVHVASGF	786
AGMVER_TYO	-----I--QQ-----K-----V--LEK-----K-E--N-K--Y-----V-----T-----K-V-----	853
AGMVER_3	-----I-----HQ-----D-----Q-M..KI--LEK-----E--N-R--Y-----V-----VI-----	838
AGMVER_155	-----Q-----EA-----K-V..-I--IGR-----D--S-R--F-----V--I-----I--I-----	833
AGMVER_963	-----K-RA-----Q-----V--IGR-----D--S-K--F-----NAK-----I-----V--I-----	830
AGMGRI_677	NSPLVEQIIQALMKKRQVYLQWVPAHKGIGGNTeIDKLVSkgIR..QILFLDRIEEAQDDHAKYHNNWRSVMVEFGLPNIVAKEIVAACPkcQIRGEPKHGQVDASIEtWQMDCTHLEgKVIIVAVHVASGF	837
CONSENSUS_TAN	DSVLVNQIIIEEMINKDAIYLtWVPAHKGIGGNQeIDKLVSQgIR..QVLFldRMEEAQESHdKYHTNWqfIRDAFGIPALVAKEIVAACPkcQIRGEPiHGQVDASVgVWQMDCTHLEgKIIIVAVHVASGF	861
AGMTAN_TAN1	-----	866
CONSENSUS_SAB	DNNIVQQIIIEELIKKEAVYIAWVPAHKGVGNEEIDKLVSQgIR..QVLFldRIEEAQEEHdKYHANWRSMQQEFGLPAIVAKEIVAACPkcQIKGESVHGQVDASPGVWQMDCTHLEgKIIIVAVHVASx?	781
AGMSAB_1C	-----GF	830
AGMSAB_381	.....	1
AGMSAB_384	.....	1
AGMSAB_386	.....	1
AGMSAB_385A	.....	1
AGMSAB_385B	.....	1
AGMSAB_385C	.....	1
AGMSAB_385D	.....	1
SYK_SYK	EHPIVEQIIQeAIKKEAIYtWVPAHKGIGGNEAVDKLVSkgIR..KILFLERIPQAQEDHERYHSNMEYLRQEFHLPRQVAKAIIQcPKcQNRGEPKHGQVDVDIYNWQMDCTHEEGKVICVAVNTASGY	832
SIVLHOEST	EHPIVKDIIEQCKQKQDQVYLGWVPAHKGIGGNQeVDHLVSKGIRQKQVMFLKIEPAVEEHSKFHNNAKDLKEKFNLPMPVAKQIVNDcANCQKKGEAITGQVDVSVGIWQLDCTHLEgQVIIVAVHVASGF	814
SIV-SUN	DSELVKEIIVELIRQKQDQVYLGWVPAHKGIGGNQeIDQLVVSQgIRKQVMFIEKIEPAVEEHGKFHNNAASLQEMFDIPLVVAKEIVNECAQCQKGEAITGQVDASVGIWQIDCTHMEEKVIIVAVHVASGY	814
CONSENSUS_VER	IEAEVIPRETgkETAKFLlKILSRWPItqLHTDNGPNFTSQEVAA?CWWGkiEHTGvPYNPQSQGSiESMNKQLKEIIGKIRDDCQYtEtAVLMachiHNFKRKGGIGGLTpAERLINmITtQLE?q?LQT	915
AGMVER_TYO	-----I-----I-----A-----IL-----Q-S-----I-H-----	985
AGMVER_3	-----M-----M-----V-----A-----L-H-----	970
AGMVER_155	-----IG-----H-----M-----V-----A-----INT-----	965
AGMVER_963	-----R-----V-----I-----V-----L-T-----	962
AGMGRI_677	IEAEVIPRETgKETAhFLlKLLARWpVKHLHTDNGPNFTSQNVAAVCWwGNIeHTTGIPYNPQSQGSVESMNRQLKEIISQIRDDCERLETAVQMATHIHNFKRKGGIGGISSAERLVNMLTtQLELNTLQN	969
CONSENSUS_TAN	LEAEVIAREtGkETAKFLlKIIISRWPITKLHTDNGPNFVSQEVQTIcWwGQVEHTTGIPYNPQSQGSVESMNRQLKETIEKIREDCAFLETAVLMACHIHNFKRKGGIGGMPAERLINMITtQLEIqHIQT	993
AGMTAN_TAN1	-----	998
CONSENSUS_SAB	??AEVIPQETGKATAhFLlKLasRWPItkLHTDNGtNFTSQVAAIcWwGkiEHT?GVPYNPQSQGVVESMNKQLKEIIGQIRdDAERLETAVI?AVHIHNFKRKGGIGGYSAAERLINIiHTELETktLQQ	909
AGMSAB_1C	IE-----Q-----A-----P-----F-----IM-----	962
AGMSAB_381	..-----Q-----A-----P-----F-----E-----	93
AGMSAB_384	..-----Q-----A-----P-----F-----I-----	93
AGMSAB_386	..-----H-----F-----I-----	93
AGMSAB_385A	..-----Y-.E--Y-----	92
AGMSAB_385B	..-----Y-----	93
AGMSAB_385C	..-----Y-----	93
AGMSAB_385D	..-----Y-----	93
SYK_SYK	IETKILKREtGDEtALFLMQIASRWPIKQIHTDNGPNFVSDKfKAAcWwGIEHTTGIPYNPQSQGIVESKNRYLKEAISQIRDDVtHLQTAVAMATFIlnfKRKGGIGGISPGERYINMLYtELQlQ.QNT	963
SIVLHOEST	MVAEVIpDEtGKTtSHFLlKLCsRWpVKQIHTDNGPNFVSKEVQAVtWwIGIEHTTGIPYNPQSQGVVEAKNVLKQIISrIREDAQELKtAVLMaVHIHNFKQRGGLGGLtPAERfINMINAELETQYLQK	946
SIV-SUN	MVAEVLpNEQKtTATWLLKLCAMWpVKQIHTDNGPNFISKdVEAVcWwLGIQHTTGIPYNPQSQGVVEAKNVLKQIISrIREDAQELKtAVLMALHIHNFKQRGGLGGMtAAERfINMINADLETQYLQK	946
CONSENSUS_VER	KIQKILNFRVYYREGRDPVWKGPaqLIWKGEGA.VV?KeGee.LKvvPRRKAKIIKDYEPkrGdEgnlEGa?GsDn?MA??S?ILDD.	996
AGMVER_TYO	-----L-D-SD-----KQ-V-N--DV--TR----	1061
AGMVER_3	-----G-----I-G-V--EY-----S--G-A--	1046
AGMVER_155	-----R-----L-----TL---TH---G--HQ--GD-	1047
AGMVER_963	-----I-----I-----M--LR-P--Q--RN-Q----	1049
AGMGRI_677	QIQKILNFKVYYREGRDPVWKGPARLIWKGEGA.VVIKEGED.IKVvPRRKAKIIKDYGERKtMDSEGSMEGVREANKQMEGDSLDLQDQE	1057
CONSENSUS_TAN	QQQKISNFKVYYREGREPvWKGpATLLWKGEGA.VVIKEGEE.LKVvPRRKAKIIKEYGERKtVGDkTNMEG	1063
AGMTAN_TAN1	-----	1068
CONSENSUS_SAB	KISKIQNFRVYYREGRDPVWKGPAKLIWKGEGA.VVIQEQGE.LKtIPRRKAKIIKDYG..KALDSQAPLEGNGRTAGEVD	986
AGMSAB_1C	-----	1039
SYK_SYK	TSPKfSNFRVYYRQgKNE.WKGPARLLWKGEGA.VVvQTEEGDIFAVPRRKAKIITDHG..ERMDSGSHVENDPKTD	1036
SIVLHOEST	LNSKILKfKVYYRQGRDPQWKGPAQLLWKGEGA.VVvKEGE.NIFSVPRRKAKLVKDYEGEPKdSESSLDNN.	1016
SIV-SUN	INSKILKfKVYYREGRDPQWKGPAKLLWKGEGA.VVIKQGE.NILVvPRRKAKLVKDYGGESSVEMVG	1013