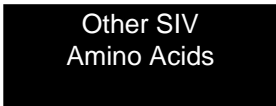


Other SIV  
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CONSENSUS_VER	Mk?t..lgi?gil?IGIgivls?kqQW?TVFYG?PVWK.NSSVQAFCMPTTrLWATTNcIPDDHDYT..EVPL.NIT.EPFEAWaDRNPLvQAgsNIHLLFEQTlKPCVKLSPLCIKM?CVELnssr??	115
VER_TYO	-RY-.IITL-IV-----I-I-----S-----G-I-A-----M-----N-----T-ER	122
VER_3	--L-.L.I-IV--V-NTR--V--V-----S-----S-----	123
VER_155	-TKF---FIV-G---GI-T--I--V-----I-----N---KG-ATS	124
VER_963	--PL---VL-AI---SSL--.ER--V---I-----S-----R-N	123
VER_1E	.....	0
VER_2E	.....	0
VER_266E	.....	0
VER_2010E	.....	0
VER_385E	.....	0
CONSENSUS_GRI	MGRL..LIKILIIAIGISIGIG..NLYVTVFYGIPVWK.NSTVQAFCMTPNTNMWATTNcIPDDHDNT..EVPL.NIT.EAFEAW.D.NPLVKQAESNIHLLFEQTMRPCVKLSPICIKMSCVELNGTATT	120
GRI_3E	.....	0
GRI_677	.....	120
GRI_2E	.....	0
CONSENSUS_TAN	MGPLRGKGVLLVILGSLIGLlyGTQYITVFYgIPVWK.NSS?QAFCMTPNTNLWATTNcIPDDH?YT..EVQL.NVS.EKFEAWKDRNPLVAQAESNIHLLFEStLKPCVKLTPMCI?MNCT?L?S??P?	118
TAN_B05	.....	0
TAN_TAN1	-----V-----D-----K---K-T-TA-T	126
TAN_B30	.....	0
TAN_B53	.....	0
TAN_B14	.....X-----N-----R---R-P-PT-S	85
TAN_1E	.....	0
TAN_17E	.....	0
TAN_40E	.....	0
TAN_49E	.....	0
CONSENSUS_SAB	MKLL..TVLLWLSGCWslVWL..VQYVTVFYGIPVWK.NSSVQAFCCKTPNTNLWASTNcIPDDEPEGTIAEVPIPNIT.EKFDAWKNRNPLVQAESNIHLLFEStLKPCVKLSpmCIKMNCYRLEGGAAAT	125
SAB_1C	.....	125
SAB_SD29	.....	0
SAB_SD30	.....	0
SAB_SD37	.....	0
SAB_SD45	.....	0
SAB_2E	.....	0
SAB_3E	.....	0
SAB_4E	.....	0
SYK_SYK	MAAF..RTYIVCLFSLISLGFMEKQYVTVFYGIPHWED.AYAPLFCTTSHKGGWATKNCVP.SADQI..EVRV.NITGEYFPAWSSHMIRQQILEDMSALFLQANRPCVKLAPMCIRMLCTLDNSPATS	124
LHOEST_LHOEST	MACP..GLGILLLLGIW..KQYVTVFYGVPNWDNVSVPLICASANTSLWVTTSClPDLQSYA..EVPIYNISENFTIPVKDNQVI.QQAWsAMNAMVDSIMKPCVKINPYCVRMQCGEVTKTPTT	122
SUN_SUN	MRCP..EILIGFSLLLSIA...IQYVTVFYGTPKWE.PAVVPLICASANNslWVTTSClPDLQTYA...EVPITGLEENFTEGISNNQIV.QQAWQAMTSMVDAIMKPCVKINPYCVMKCPKPTTPSS	121

CONSENSUS_VER	ttptstta?tt?????g1PCv??nkt??nLqsCNa?iIEkE??E?ASNCTFAMAGY?RDQKKn?YSVVWDAElyCkn?t??Ns??kE.....CYMIHCNDSVIKEACdKTYWDeLRLRYCAPAG	214
VER_TYO	A-TPT--PKS-.....G.PTSGE---S--R-MED-P-----V-----Y-----K-..TS-----Q-----	235
VER_3	---K---S--NITASTTT---Q---STV-E--ET---LNE-P-----V-----K-----M--.KG.-NSNR-----	241
VER_155	-PA---G-K.....R---DS---DT---MND-A-----I-----F--RS-SH-GT-----	236
VER_963	P---ASTTKA...PKT-D--IKSTNNNV---P---SL--E-LEE-A-----I-----SSSS--ST-----E-----	241
VER_1E	.....	11
VER_2E	.....	11
VER_266E	.....	11
VER_2010E	.....	0
VER_385E	.....	11
CONSENSUS_GRI	KATTTATTTMT.....TPC.....QNCSTEQIEGEMAEEPASNCTFAIAGYQRDVKKN.YSMTWYDQELVCNKTGSEKGSKD.....CYMIHCNDSVIKEACDkTYWDTLrVRYCAPAG	224
GRI_3E	.....	11
GRI_677	.....	224
GRI_2E	.....L-----	11
CONSENSUS_TAN	SS??T?????.....?PCP??T???.??CN??LVTNSM??ENSS?C?FAMAGY?RD?KK?.YNSTWYD?EL?CE?E???.???.RG.....CYMIHCNDSVIKEACEKTYWDTLRLRYCAPAG	194
TAN_B05	.....	0
TAN_TAN1	--TP-SSSTT.....D--N-DES...S--AT---DY---I-S-----R--V--K-----Q--V--K-NNT.TGT--	233
TAN_B30	.....	0
TAN_B53	.....	0
TAN_B14	--ST-RTRN.....G-TN...DE--SH-----EF---M-T-----M-Q-T-----A-M-P-SKK.NS--	190
TAN_1E	.....	11
TAN_17E	.....	11
TAN_40E	.....	11
TAN_49E	.....	11
CONSENSUS_SAB	TTSPSTSTA.....RPEVVSVGF.....NDSVIEQEMEKEQAMNCSFAMAGYRRDVKKN.YSTVWDDQEVVCEEGRKSNATHTVG.....CYMIHCNTSVIKEACDkTYWDTFRLRYCAPAG	232
SAB_1C	.....	232
SAB_SD29	.....	0
SAB_SD30	.....	0
SAB_SD37	.....	0
SAB_SD45	.....	0
SAB_2E	.....	11
SAB_3E	.....	11
SAB_4E	.....	11
SYK_SYK	TPTTSPPTT.....PPNETWWDGNSTEPFNCSFNLTGGFKDKKQQ.YRAFFYKDDLMEEGNSSY.....YYLLHCNTSVISAACEKQTFQFPPIQYCAPPG	216
LHOEST_LHOEST	TPKTTTQ.....MPCFINEQVTVKNPNETRLEEDLNCTRGLNETTERNAECQYNVTGLCRDCRTEIKQSFYRDDVTCSEGERENRTCYMTHCNDSIITQDCNKGVMQNAYFRLCAPAG	235
SUN_SUN	NSTVKSS...CDYWTTTTAKTTTQTTSST.....SSTASTTTPMPLDWNCTDTENIA.ESNKVCKYNVTGLCRDCKTEVEQNFRDTEVTCNG...NDTCYMTHCNDSIITQDCHKGIMQNAYFRLCAPAG	239



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CONSENSUS_VER	* ?ALLKcNd?dYnGfkqnCsNVSvVHCTgLmNTTvtTGLLLNGSYsENrTqIWq...KHrvsNgsvlil?NKhyNLtvtCkRPGNKtVLPVTIMAG...lVFHSQkYNT...rLRQAWCHFqgnWrgAWkEvkq	335
VER_TYO	Y-----E---Y-----H-----...-N-NT--F---S--R-----...-----M..K-----E-----R---	359
VER_3	F-----Y-A--T-----N-I-----...-----V-F-----R-----...-----R-----N	365
VER_155	Y-----W-A--PE-----T-----...-----G-----L-----...-----K-----Q-E	360
VER_963	F-----H-H--Y-----S-----...-----N--IV-F--Y-----...-----K-----R--E-----E	365
VER_1E	Y-----RN-T--APR-R-----S-----T-----E-----...-K--N--I-RI-----IR-V-----...-----K-----K-D-----R-I--	135
VER_2E	Y-----H--Y-----R-----...-G-----I--I-AF-----R-----...-----L-----E-IR-	135
VER_266E	F-----A-D--T-----N-----...-T-----A--L-----...-----L-----PS--K-----E	135
VER_2010E	.....S-----K-----...-N-----L-----I-----...M-----N-----E--R	90
VER_385E	F-----Y-D-----...-----QI-----I-----...-----H-----I--	135
CONSENSUS_GRI	yALLkCnDKdYnGFAPkCKNVsVvHCTRLINTTitTGIGLNGSR?ENRTEIWQ...ekGNSNdTVIIKLNKFYNLTVRCRRPGNKtVLPVTIMAG...lVFHSQkYNT...rLRQAWCHFqGdW?GAWKEVre	346
GRI_3E	-----V-----...-----I-----...R-----K-----S--N--L-----	135
GRI_677	-----R-----...-S-----...KG--D-----...-----K-----	348
GRI_2E	F--R-L--N-----S--T-T-----VS-----A-----...-N-----...-----H-----KQ	135
CONSENSUS_TAN	fAiLkCkDNTNytGfG.iCrNVSVVSTGLMNTTvsSAFGLNGSQAENRTEiWQ...KHgvsNdSVIIKLNKhYkL?ivCrRPGnKTVLPVTiMaG...lVFHSQkyNT...kLRQAWCHFqGdWkGAWkEvre	316
TAN_B05	.....Q-T-----K-----M-----...-Q-----...-----R--K	71
TAN_TAN1	-----V-----I-----...-N-----K-----...-Q-----...-----S-----Q--Q	356
TAN_B30	.....T-----M-----...-----S-----Q--Q	34
TAN_B53	.....I-----...-N-T-L-----...M-----I-H-----S-K--E--E--K-	26
TAN_B14	V-----T-----...-----N-T-L-----...M-----...-----R--K	313
TAN_1E	-----V-----I-----...-N-----K-----...-Q-----...-----R--K	134
TAN_17E	-----V-----...-F-N-T-K-----...R-----K--E-----	134
TAN_40E	--L--R--A--N-----I-----...-N-----Q-K-K-I-----...-----K--E-----	134
TAN_49E	-----Y-----...-RIN-----Y--GVT-----...-----H-----	134
CONSENSUS_SAB	YALLRCaDtDYsGHK.aCkNVtVSACTRLINTTvsTGIGINGSYVANRTEIWQ...kNGNSNd?vIIRLNR?fNLTIRCRrPGNKtVLPVTImAG...LvfHSQkYNT...rLrQAWCWFgGnWrgAWqEvkE	353
SAB_1C	-----R-----...-S-----Y-----...-K-----K-----	355
SAB_SD29	.....I-----A-----...-I-----...-V-----K-A--	49
SAB_SD30	.....K-----K--S--K--R--	49
SAB_SD37	.....N-----KF-----N-----	30
SAB_SD45	.....T-----K--R--	47
SAB_2E	-----I-----...-A-HT-----H-----...K-----D-----	134
SAB_3E	-----K-----...-S-----H-----...K-----K-----	134
SAB_4E	-----R-S--R--N-Q-S-----...E--NTA--YY-----...-----K-----A--	134
SYK_SYK	YSLKcNDNTFEGDD.VCTNVTAVSCTQEFNTLASTWFQLNGTYKAKDKVRFI...KQKDKNESVILVPEALRLQIICERPGNESIKNIQLAAGYFLPVIQgkLkTGRDAKRAFRCrVTGNWTEFFKQVHE	343
LHOEST_LHOEST	YMLLRcNeQLNfSKK..CENITATPCTGYMLSSVSSFFGNGTNRHDELIPIN.KVGGQAGEGYVVKVAkWGLVIQcIRKGNRS.QVSTISSTGLLFYyGLEPGS..KLRLAQCKfVgQWGRAfATLKG	362
SUN_SUN	YMLLRcDeKLNATKk..CKNITATPCTNYMTSTVSSFFGNGTRHKEDELIPIN.KVGGQAGEGYVVKVAkWGLVIQcIRKGNRS.QVSTISSTGLLFYyGLEPGS..KLRLAQCKfVgQWGRAfATLKG	365

CONSENSUS_VER	eIvkLpk.....drY?GTNdtekIylqRqfGDPEaaNLWFNCqGEFFYcKMDWfLNYlNNlt.....vdadH?NqC?n?t??k?kg?raPGPCvQRTYVacHIRSVindwytiskK	433
VER_TYO	K-E---K-N-H-W---S---K.....W-Y-..F-SS...-K-.H-----Y-----S-L---	459
VER_3	---Q---E---L-----R-----P---P---G---G---K-----A-----L-R-	466
VER_155	---E-Q---N-F-----R-----H-K-N...AG...-S-----L---	461
VER_963	---I-----R-----S-E...K-.N-----QS.....-N-----K-.N-----	466
VER_1E	K-E---E-Q---KQ-F---W---S---H-----M---I---...-N...-N...-S-QG...KR-----G-----KLAR-	234
VER_2E	---T---P---HK-R---F-----S---GSR.TSP...-----A-----	236
VER_266E	---N---E-R---PKR-FF---W---T---H-----E-K-TSGT-SGNK-----IWLE---	240
VER_2010E	---Q---AQ-----I-----N-NT-R...-K-G.-TS...A-----V---V-L	193
VER_385E	---R---Q---T-W-----S---K.....WN---D-S...-TG...	236
CONSENSUS_GRI	evKk?.....KNLTev?ienIhLRRqWGDPEaaANFWFnCqGEFFYcKMDWfINylNN?T.....vdAdG???C?...???kqp?.GPGPCvqrTYVACHIRQVVDWYtltKK	434
GRI_3E	KI-EE...K-----H-----Q.....KS...TSH--GQ...-AKK-----VS--	232
GRI_677	---V-----S-----I---S-----R-----E--E-TNRT-D...KG--	445
GRI_2E	---A-----TDD-K-----S-----I-E-----NK...NKP-G...	228
CONSENSUS_TAN	TivkLpk.....ekYqGTnntkqIWLrRQWGDPEaaNIwFNCqGEFFYCTPDWfvNwLNNeSasgrnvdVEG..N?C?n?t...tgglts?rkClKrtYvacHIRSVVDWYtLsKK	420
TAN_B05	---T---V-----N-T-L---K-PDR...S-----	178
TAN_TAN1	---E---R---R---S---L-----N-----N-TT...-KDKP-Y---P---I-----	457
TAN_B30	---A---P---D-E-AQK...-D-P-T...M-----Q-	141
TAN_B53	---A---HS-----KQ-----Y---ED-TLL...-K-A-T...-PP---T---S---I---FH-	134
TAN_B14	---H---D-K-----S---L-----L-Y---SE-SFT...-R-S-I...S---T---GL---LQ-	421
TAN_1E	---E---R---R---S---L-----N-----T-KD...KR-Y---P---I-----	235
TAN_17E	---R---D-K-----Y---D-RR-KE...-D...KD...P---F-S-P-----	233
TAN_40E	---K-TE-----M---D-KS-N...-T...-PEKD...-L-K-----	235
TAN_49E	---R---DR-S---N-----G-NYT...-P-S-S...K-M-----G-----S---	241
CONSENSUS_SAB	tivklpp.....?rYsGTndtskIFLQRQWGDPEaaEfffFnCQGEFFYcKMDWfLNyLNNqs....VdPdH..NpC.....???tknndkkCWgRtYvPCHIrQvVNDWYtLsKK	448
SAB_1C	---R---KK---N-----S---K-----N-----A---T-P-----	451
SAB_SD29	EL---EK-Q-----L-W-----LT.....-K-----NKG-----	144
SAB_SD30	---K---D-----S-----F-----N-----Q-----I-----	145
SAB_SD37	E---K---EK-Q---H-EQ-----S-I---K-----G-----S---R---N-----A---	126
SAB_SD45	---AAM-N...ST-T-RNI-Q-----S-NLL...-N---Q-----KT---A-N-----A---	143
SAB_2E	K-A---D-----N-----GGND---R-----I-----	232
SAB_3E	---A---D-Q-K-N-----N-TS...N-A-----	230
SAB_4E	E---S---E---KN-Q-----G-----N---T-----PKS--R-----	230
SYK_SYK	QATKTWK.....NVINTTWRsQPggDLEVRTHWFQCGEFFYcNvSKLfanITngnasknnyasnlr.....LsCAIRQIINDWRYVRKL	423
LHOEST_LHOEST	MLKELNAEAMNYTEGT...GTCDsKkTTCGRKLGPIANMTRHGADLATEMLMHTCGEEMFFCNVTRIFQEWNNKNSDKWYP.....WANCHIKSIIDDWATIGKK	461
SUN_SUN	LLRQVEPLANMSGCTFDNITKTCRFTNGTDFKMKIKFKPMEKHGADAATEMLMTCGEEMFFCNLTRIFKvWnDttSNkWyP.....WANCHIKSVIDDWASVGKK	467

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CONSENSUS_VER	tYAPPREGH...LqCtSTVTGMtVELN.YnnknRT.....NVTLSPQIEsIWAAELgRYKlVEITPIGFAPTeVRRYTGghergkRv.PFVlGfLgFLGAAGTAMGAAaAtaLTVQsghLLAGILQQQKNL	553
VER_TYO	-----R-----S-----NVTLSPQIEsIWAAELgRYKlVEITPIGFAPTeVRRYTGghergkRv.PFVlGfLgFLGAAGTAMGAAaAtaLTVQsghLLAGILQQQKNL	579
VER_3	-----S-----S-----T-----D-T-----	586
VER_155	-----Q-----T-----Q-----	581
VER_963	V-----E-----NY-----G-----N-----QD-S-----M-----	586
VER_1E	-----E-----A-----IH-----A-----S-----P-----P.S-E-----	353
VER_2E	-----SR-----D-----D-----Q-----T-----	356
VER_266E	-----E-----IP-----D-----	360
VER_2010E	-----E-R-----QS-----Q-----A-----D-----	302
VER_385E	-----I-D-----T-----SP-I-----	356
CONSENSUS_GRI	tYaPPREGH...LECNSsVTALYVeIn.YNNkSGPI.....NVTLSpQvRSIWAYELGDYKlVEITPIGFAPTDVRRYTGp.treKRV.PFVlGfLgFLGAAGTAMGAAaAtaLTVQSRHLLAGILQQQKNL	554
GRI_3E	-----T-----S-----	352
GRI_677	V-----A-D-----T-----	565
GRI_2E	--R---Q---E-----I-----KQ---	348
CONSENSUS_TAN	tYAPPREGH...LEcTSTVTSmmvSLD.YnsKnMnT.....NVTLSANLEniWAYELGrYkIeIkPIGFAPTeVRRYvGP.TREKRV.PFVlGfLgFLGrAGAAMGATaTaLTVQSQQLLAGILQQQKNL	539
TAN_B05	-----K-----	234
TAN_TAN1	-----ER-----E-----I-----A-----	576
TAN_B30	-----E-----	219
TAN_B53	-----I-----T-H-----N-N-----	185
TAN_B14	R-----R-----L-----D-----	487
TAN_1E	-----ER-----E-----I-----S-----A-----M-----	354
TAN_17E	-----VN-----I-----D-----S-----E-----	352
TAN_40E	-----IIA-----N-----I-LY-----	354
TAN_49E	-----E-E-----	360
CONSENSUS_SAB	TYAPPREGH...LEcNstATALYVELn.YNskNrT.....NVTLSpQIrSIWanELGdyKlVEIKPIGFAPTeVRRYtGP.ERQKRV.PFVlGfLgFLGAAGAAMGAAATaLTVQSQQLLAGILQQQKNL	567
SAB_1C	-----E-----K-----	570
SAB_SD29	-----T-----H-----	192
SAB_SD30	-----M-----L-----L-----F-----K-----	223
SAB_SD37	-----Q-----H-----G-----	162
SAB_SD45	-----Q-----T-----H-----SY---S-----	198
SAB_2E	-----L-----H-E-----	351
SAB_3E	-----E-----	349
SAB_4E	-----N-----	349
SYK_SYK	IYLPPTAGH...IKCTSNVTAVLTDIE.YYPGSTL.....NFTPTANVEDVWRADLFNYKLIQIKPIGFAPTDQRRYELPNTRKRAAPLALGFLGLLSAAGTAMGGAATALTlQSQTLLAGIVQQQKL	544
LHOEST_LHOEST	IYLPPTSGFNNRIRCTHRVTEMFFEMEKWEPHEDLGGNLS.IKFLPPSWETNQFVAEGSKYKLIKLNPIGFAPTDEHRY.APRGRQTRAAPLALGALGLLSAAGTAMGLVSTILTlVQAQAVLQGILQQQKL	591
SUN_SUN	IYLPPTSGFNNRIRCANRVTEAWFTLERVEDWKVNGSNISVVAFQPPTNTLNQVSTGAHYKLVIRIPIGFAPTDEHRY.AP.RKEKRAAPVALGALALLSAAGTAMGLVSTILTlVQAQAVLQGILQQQKL	597

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CONSENSUS_VER  LAAVeAQQQMLKLTIWGVKNLNARVTALEKYLEdQARLNaWGCawKQVCHTIVpW . . . . . qW?NrTPdW?NMTWLEWErQI??LEgNIT?QL?kAReQEEKNLDAyQkL?sWsdFWSWFDfSKWLNILKi 671
VER_TYO        -----S-----E- . . . . . P-T---Q-----AD-S--G-V-----T-----M 704
VER_3          ----- . . . . . -N---N-----SY---T--EE--A-----S----- 711
VER_155        ---G-----A----- . . . . . T--N--E-N-----K--EG---K--EQ-----SD--S----- 705
VER_963        -----V----- . . . . . -Q-M--N-Q-----GE---E--V-----R-T--N----- 711
VER_1E        ----- 372
VER_2E        ----- 375
VER_266E      ----- 379
VER_385E      ----- 375

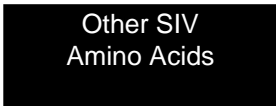
CONSENSUS_GRI  LaAVEQQQLLKLTIWGVKNLNARVTALEKYLEdQARLNSWGCawKQVCHTIVpW . . . . . KY.NNTPKWDNMTWLEWErQINALEGNITQLLEEAQNQESKNLDLYQKLDDWSGFWSWfSLSTWLGyVKI 678
GRI_3E        -V----- 371
GRI_677       ----- 689
GRI_2E        ----- 367

CONSENSUS_TAN  LAAVEQQQMLKLTIWGVKNLNARVTALEKYLEdQTRLNLWGCAfKQVCHTIVpW . . . . . TF.NNTPDWDNMTWQEWESQITALEGNISTTLVKAYEQEQKNMDTYQKLGWTSWwNIFDVSSWfWwIKW 663
TAN_TAN1     ----- 700
TAN_1E       ----- 373
TAN_17E      ----- 371
TAN_40E      ----- 373
TAN_49E      ----- 379

CONSENSUS_SAB  LAAVEQQqMLKLTIWGVKNLNARVTALEKYLEdQARLNIWGCafRQVCHTIVLW . . . . . KY.NNTPDwENMTWQEWERQIEKYeANISRILeQAHEQEQKNLDSYQKLVSdFWSWfDLTKWfGwMKI 691
SAB_1C       ----- 694
SAB_2E       ----- 369
SAB_3E       ----- 368
SAB_4E       ----- 368

SYK_SYK       LEAVEAQHLLGLTVGVKNLNARLTALETyLRDQAiLSNWGCafKQICHTAVTWekACGNNSNfCPKpQwKNMTWHRWEQeVDNLTDHIDGLLREaQEQeRNVHDLTkLQeWdSLWSWfDLSKwFFyLKI 676
LHOEST_LHOEST LVLVEKQQeLLRLTIWGVKNLQARLTALEeYVKHQALLASWGCQwKQVCHTnVew . . . . . TY.NITPNWTKDTWREWESKVAIYDKNITSLlQeAYTTeLENQNKfKkLQeF.NFWSWLDIshWfTYVKY 714
SUN_SUN       LVLVEKQQeLLRLTIWGVKNLQARLTALEeYVQDQSLLASWGCQwKQVCHTnVpW . . . . . NY.NITPNWTKDTWMEWDRQVKMYDDNITALLQeAYVTeLENQNKfKkLQeF.NFWSWLDLSQwFLYIKY 720

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Other SIV  
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CONSENSUS_VER	GFLvVvGiI.GLRLLYTvYsCIaRVRQGYsPLSPQIHHPw?KG?PdNAgeP?EGGd??k??sesWQK?Sgt??ks?wckrLThWls.??stWLYNscLTLL.....ihLR?AfQYiQYGLgELKtaA	778
VER_TYO	---I-----G-V-----V-----QVG--R---D-G---NSRIKL---D-.....R.-MQ--A--T.RLN-----Q--K---L---A---G-	819
VER_3	---D-L-----Q-----EG-G---KR-NS--P---E---AEW--N-----C-.IS-I-----V--S-----A--	832
VER_155	---A-I-V-.-----L-T-----Q-----E---RTG-SK-TH	768
VER_963	-----I---G-----R-G---E---ERDNDSD---G---RQKRGS-S-----TF-----TF-----G-W-----	832
CONSENSUS_GRI	GF.LVIVIIILGLRFAWVLWGCIRNIRQGYNPL.PQIHHS.SAERPNDGGGQDRGESSSSKLIRLQESSTPSRINNWLNFK.SCSLRIRTWCYNICLTLL.....IFIRTAVGYLQYGLQQEQEAA	798
GRI_677	-----	809
CONSENSUS_TAN	GFYIVIGLIL.FRMAWLIWGCiARVRQGYFPLSPQINIRL.GREQPDNAGGEDK..DSSSSRDKSPPSVKESLLPNRGGIQAEERAWRQHLTNWCLTISSWLL.....RLYQILRRSLTLLQLLRQEC	783
TAN_TAN1	-----	820
CONSENSUS_SAB	AIMVIAGII.VARVLLVIGILRKRFRKGYAPLSSLPSSH	729
SAB_1C	-----	732
SYK_SYK	GFYVIGALV.LLRLVSFSVGIiKNLLGGYVPIQNPQTQ...GRKDPGKPA...DEEEGSGDREGLNVSTFSRESRLQSLAQGLWRTVCSSFRSLIRQLTIT.....WGFISYGFNELKIAAASLGREIR	795
LHOEST_LHOEST	AVLIILVII.GLRVLSFIIQNVVKMCRGYRVLSPSVYIEQDYKWEKEENQEQPDREEEKGADTETI...YINLEQCKKESRPLWN.VDWNPELQDSLIVTLLKWLKEGILLLSLVWQSLSWLWHLILLFF	841
SUN_SUN	AVLIIGIII.AARILSFIIQQIYRMCQGYRVLSPSAYVEQDWLQETCPKPT..DKEEEETEKERI...YINLEQSKKESLPPPWT.VDWEPLRDSLLVTLKWLKAWGIVLAQNIYHLLSFLWHLTTTSF	845
CONSENSUS_VER	QEa??alAr?AQNaghQ.....IWLACRSaYR?IinSPRRVRQGLEeILN.	819
VER_TYO	--ILQT--GV---C-----N-V-----	863
VER_3	---VV---L---Y-----A-----G---	877
VER_963	---RL-V--F-----T--H--S-----.	877
CONSENSUS_GRI	TGLAQALARAAREAWGR.....LGAIVRSAYRAVINSPRRVRQGLEKVLG	843
GRI_677	-----	854
CONSENSUS_TAN	QYIQYGWQPFKEGAARSFEALASAAQSASRTLWNACRSAYRAILEHPRMRQELERWFN	842
TAN_TAN1	-----	879
SYK_SYK	DWVAAIWQAIYAATRRVVEAVAL.....PRRLRQGLEIYLN	832
LHOEST_LHOEST	QNGQRLWQTSSRWMVENAQIQSWLREK.....CRRNRGQLSSTDRKNIQ...LGKKRWRLRFGRSGISSEATETAL	912
SUN_SUN	HHGQRLWQTLRGWLGSHLIQATSRI RNA.....CRTSRERVSSSQKARSRTFSLGRKWRPKWNRTRGSRIPSETTETTL	919