

Other SIV
Amino Acids

CONSENSUS_VER	MnqeKeWVMRvTWKvP?lITKWQGIVrYWMr.kRnLk.W?Y?.....MHYQItWAWYTMsrYvIP?g?hGeIhvDLYWHLtPeqGWLSTYAvGIQY?sn??kyrTELDPaTADsmIH?HY	104
AGMVER_TYO	--PN-----GD-----Q-----N-Y.....I-K---C-----V--LES-----I--G--	115
AGMVER_155	-S---H---L---QEEV-----N-----E-K.....LPGS-----I---A-K-----V-LVND-----N-----C--	115
AGMVER_3	-----EE-----T-K-D.-K-R.....E--L-Q-S-----E---L--RDPW-----L--T--	115
AGMVER_963	-----SGD-----K--T-----Q-M.....N-----C--I--I-LE---QI-C-----R-----I---L.GAVGNF-----G--L--	114
AGMRI_677	MEREKQWIVRVVWRVSRQISRWRGIVTYKIR.NKQLP.WEYR.....HHWQVQWQFWTYSQFIIPLSKDDYIEVNIYHNLTPERGWLSSHVGLSYY.HQKG.YKTEVDPGTADRMHLYY	113
AGMSAB_1C	M..EKHWIVRPLWKVVTGGQERWTSLVKYHMHVSKQCVHWRYT.....PHTKIRWNWYSYQEWVIPLKDGALIKVTNYWHLTPEKGWLETYATGIGY...SKGEWFTELDPWTADHIIHWSY	112
AGMTAN_TAN1	MEREKLVWTRLTRVSGEHIDKWKGIKHYHMR.NR.LQDWTYL.....MHYQCGAWYTCRFLIPLGGEGKIVVDCYWHLTPEQGWLSTYAVAI SF.ENWQNTYKTEVTPDVADHMIHCHY	114
SYK_SYK	M..EKEWIVVPTWRMTPRQIDRLQHIKTHKYKSKELEKATYK.....HHYQIEWQWYTYCQWTIPVG.DGTIWIWTFYHNLAPERGWLHMQGIRIQY...QWNQNTDLTPAVADRLIHNFY	111
SIVLHOEST	MERDQRIVRVAVITTRSLIEKFLDIVRLNTEAKENWVGLHGTG.....VGWEFYTYHKLVIPLS.SGTLVVRIYAHLAAGRGWISQWAVSIEW...VYRDYQTEIDPLADQMIHYKY	109
SIV-SUN	MEENPPQWRWDE..REWEDRRQYKIVRIVWLIDRIAEVKFLDLRRMHRET KDDWVSMYGTGTGWWEWYTYNKIIPVT.YGTVVVRVRYGHLTPAKGLINQWGCSEW...IYNSYQTEIDPLVADQMIHFKY	126
CONSENSUS_VER	FtCFteRAIq?AlrG?RFv.FCQFPeGHK?T...GqVPSLQYLALLAHQ...NG.lReRSqRgktrr?RnlGskQgav...GrMAkr?vr.....RsQsgsq?aFW?R?PvPsmELLSGGrr	202
AGMVER_TYO	-N--K-----Q---H---S.....K-----S-----Q---Y-T.....P-GEA---E-T-----G	221
AGMVER_155	-----D---Q---N--I---G---L.....K---E---T---Q-----Q-YG.....N-QR--T--P-T-I-----G	221
AGMVER_3	-----RK--L-Q--T-----K.....Q---S--GGT--M-FE-----HA.....Y---D---A-A-----G	221
AGMVER_963	-S-----K-I--E---T---K.....I-----KQA--S-D---RTM.....GH-----IT--Q-A-L--L-----	220
AGMRI_677	FNCFTDRAIQQAIRGEKYT.WCTFKEGHK...GQVQSLQLLALVAYT...NG.IRKRKRTFTRMAGNLGSRQGM...GRMATRHAQ.....GSKRRSQKALWNEHANPsmELLCRGK	217
AGMSAB_1C	FPCFTDRAVQQAIRGEKYL.WCKHQVGHQPT...GQVPSLQYLALRVYT...NG.LRRVAPT...SRRGSSQGSQESQRDRDTRMARNMGFAQRAVRRMAPRHVTGPQFRGPVPLPKESPPSLVEYCGRTS	233
AGMTAN_TAN1	FPCFTDRAIQQAIRGESFL.WCTYKEGHVAENHWQVRSLQFLALTYVDFLRNG.RRKRFGQKTRMVRNLGSSQGVAV...GRMIKRHGS.....RTQSGSTTPFWERTPLPSMELLSGRRG	227
SYK_SYK	FPCFTARAVNQAVRGELLTSHCWTP...HT...DQVPSLQYLALQVY...LKDGGGFLQSLPACARNTMVLHSSKCRVDPKRDQCHCKGR.....TGSDRSIQAFYSSRNISLESILKRRG	219
SIVLHOEST	FNCFIQRDIRRALLGERITMCCQ.PLGHK...GCVLSLQFICLRQLQ...HVQA	156
SIV-SUN	FDCWTSRCIRRAMLGEKILHECRNQVAHK...GLVLSLQFLCLRVLH...GQQE	174
CONSENSUS_VER	?tg?shdgkGl	211
AGMVER_TYO	K-WY-----	232
AGMVER_155	E--KT-S---I	232
AGMVER_3	KESH\AR---	232
AGMVER_963	E--SPN--E--.	231
AGMRI_677	ET	219
AGMSAB_1C	H.	234
AGMTAN_TAN1	KEWGTNDRKGL.	238
SYK_SYK	RD	221