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2 **Supplemental Table 1.** The animals used for this study were subject to a variety of  
3 treatments. Some were vaccinated, some were infected with versions of SIVmac239 that  
4 contained engineered mutations. These are listed in this table. Additionally, we have  
5 included references for the publications in which these animals are included and which  
6 epitopes were found in which animals.

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8 **Supplemental Table 2.** Mamu-A1\*007:01 binding capacity of a panel of 42 endogenous  
9 ligands eluted and sequenced from soluble Mamu-A1\*007:01.

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11 **Supplemental Table 3.** A complete list of all of the SIV<sub>mac239</sub>-derived peptides tested for  
12 Mamu-A1\*007:01-binding.

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14 **Supplemental Table 4.** Comparison of peptide binding to Mamu A1\*007:01 versus HLA  
15 B\*3801.

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17 **Supplemental Figure 1.** An amino acid alignment of the seven subtypes of the A1\*007:01  
18 family. Changes that do not affect the peptide-binding of the class I molecule are shown in  
19 yellow. Changes highlighted in red are residues that contact the peptide, and could  
20 therefore, affect the binding affinity.

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**Supplemental Table 1. Animal treatments, infecting virus and epitopes recognized.**

Animal ID	Vaccination	Infecting virus	Epitopes recognized	Reference
r97113	Gag,Tat,Rev, Nef by DNA/Ad5	SIVmac239	Pol YL8, Pol YF10, Vpr NL11, Gag DL9, Gag DL10	Wilson, et al 2006
r99006	-	SIVmac239 with 2 A1*001:01 and B*017:01 escape mutations	Vpr NL11, Pol YL8	Friedrich et al 2004b
rhas78	-	SIVmac239 with 3 B*017:01 escape mutations		Weinfurter et al, 2009
r98030		SIVmac239 with 8 B*008:01 escape mutations	Vpr NL11, Pol TL9, Pol YL8, Pol YF10; Pol IL9 and Env FL11(unconfirmed epitopes)	Valentine, et al., 2009
rh2122	Tat, Rev, Nef, A1*001:01 epitopes	SIVmac239	Vpr NL11	Vogel et al., 2003
r97073	DNA all SIV pns MVA Gag, Pol, Env, Nef, Tat, Rev	SIVmac239	Pol YL8, Pol SL10	Horton, et al., 2002
rh2161	DNA/NYVAC	SIVmac239		Unpublished
rh2001	Gag, Nef, Vif by DNA/Ad5	-		Wilson, pers. comm..
r99088	Gag, Nef, Vif by DNA/rYF/Ad5	-	Vif VL9	Wilson, pers. comm..
r96067		SIVmac239	Vpr NL11	
r98016		SIVmac239	Vif SL11 (unconfirmed epitope)	
r99019		SIVmac239	Pol SL10	
r01064		SIVmac239	Vpr NL11	
r99005		SIVmac239	Pol YL8	
rhav77		SIVmac239		
r92086		SIVmac239		
r96107		SIVmac239	Pol YL8, Pol SL10	

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**Supplemental Table 2. Mamu-A1\*007:01 binding capacity of ligands eluted from purified Mamu-A1\*007:01 molecules**

Sequence	Source protein	Length	IC50 nM
DHSFSLEL	cAMP response element regulatory protein	8	2.0
NHIEPLKIQL	thymidylate synthase	10	10
SHSHVGYTL	Hematopoietic SH2 Domain Containing	9	10
NHQDVAGVFAL	lysophospholipase-like 1	11	12
NHDFQALAL	pumilio homolog 2	9	13
NHINVELSL	Ribosomal protein L9	9	13
THYDHLIEL	minichromosome maintenance complex 6	10	14
NHAPSVQI	PRO1670	8	17
NHQGATPLVL	ankyrin repeat domain 46	10	18
SHAQTVVL	Ribosomal Protein S27	8	18
QHTPTSITL	HDCMC04P	9	19
NHIKYAVTT	Coatomer subunit alpha	9	20
NHLREIWEL	Protein Regulator of Cytokinesis 1	9	20
HHGPMVAFA	Cathepsin C	9	21
NHALPLPGF	Solute carrier family 35 member B4	9	21
NHVFPLLL	Importin-8 (Imp8; RanBP8)	8	25
LHGWAFTL	eukaryotic translation elongation factor 2	8	32
NHQKDIQVL	Meiotic Nuclear Division 5 Homolog A	9	32
NHQKNLVEL	programmed cell death 11	9	33
NHTALTVVM	GARS Protein	9	34
HSPVVNEL	HSPC120	8	37
SHVSLVQLTL	proliferating cell nuclear antigen	10	43
DHAVSPRQL	Cyclin D3	9	63
NHMDGESLKL	MORC3 Protein	10	65
NHSAASAMAL	Muscleblind-like 3	10	70
VHAQIVSTL	MON1 homolog B	9	74
NQQPSNYGPM	hnRNP A2 protein	10	77
EHAHNMRVM	Eukaryotic Translation Elongation Factor 2	9	84
AHSPLAAQL	KIAA1631 protein	9	87
NHVITKTMEL	Nucleoporin	10	93
VHFIKPLLL	ICB-1	9	103
THFLQPIYL	RNA adenosine deaminase	9	129

SHSGREVV	Membrane-Associated Ring Finger	9	133
NHTIYINNM	small ribonucleoprotein B	9	137
VHAELADVL	chaperonin containing TCP1, subunit 6A	9	139
NHISELVQL	RAS guanyl releasing protein 1	9	143
NHTIYINNL	small ribonucleoprotein A	9	143
VHMPKHPEL	Ribosomal Protein S10	9	180
VHKPGPITL	protein kinase C-binding protein RACK8	9	181
THSSTFDAGAGIAL	glyceraldehyde-3-phosphate dehydrogenase	14	470
SHSSDLSTI	spectrin repeat containing, nuclear envelope 1	9	919
NHVFFLL	fatty acid desaturase 1	7	1515

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**Supplemental Table 3. Mamu A1\*007:01 binding of SIV-derived peptides**

Protein	Amino acid positions	Length	Sequence	IC50 (nM)
Vpr	45-55	11	NHIYNRHGDTL	0.20
Env	764-772	9	WQIEYIHFL	3.2
Pol	782-789	8	YHSNVKEL	5.8
Pol	782-791	10	YHSNVKELVF	6.2
Vif	22-29	8	WHSLIKYL	10
Pol	279-288	10	WRMLIDFREL	10
Vif	145-153	9	VPSLQYLAL	13
Pol	567-575	9	THTNGVRL	13
Env	795-802	8	YQILQPIL	24
Pol	332-340	9	FRQYTAFTL	39
Pol	817-825	9	IHGQANSDL	65
Env	230-240	11	FRYCAPPGYAL	101
Vpx	38-46	9	NHLPRELIF	144
Env	184-192	9	NETWYSADL	147
Pol	333-340	8	RQYTAFTL	151
Gag	42-50	9	DRFGLAESL	177
Env	35-42	8	WRNATIPL	200
Vif	65-75	11	SHLEVQGYWHL	209
Env	769-776	8	IHFLIRQL	223
Vpr	33-43	11	KHFDPRLLTAL	227

Pol	368-376	9	FQYTMRHVL	234
Pol	760-769	10	SQGIRQVLFL	242
Env	562-569	8	VQQQQQLL	254
Env	735-743	9	THIQQDPAL	306
Env	792-802	11	SRVYQILQPIL	310
Pol	104-114	11	DRGFAAPQFSL	322
Gag	42-51	10	DRFGLAESLL	325
Pol	105-114	10	RGFAAPQFSL	359
Env	782-790	9	WLFSNCRTL	379
Gag	195-202	8	DHQAAMQI	380
Pol	289-298	10	NRVTQDFTEV	447
Gag	195-203	9	DHQAAMQII	473
Vpr	71-78	8	MHFRGGCI	498
Pol	321-328	8	DAYFSIPL	520
Pol	364-372	9	SPAIFQYTM	523
Env	768-776	9	YIHFLIRQL	538
Env	35-43	9	WRNATIPLF	599
Vpr	33-40	8	KHFDPRLL	627
Env	769-777	9	IHFLIRQLI	683
Nef open	165-174	10	IRYPKTFGWL	837
Gag	196-203	8	HQAAMQII	853
Env	769-779	11	IHFLIRQLIRL	879
Pol	192-202	11	NIFGRNLLTAL	880
Env	441-450	10	WHKVGKNVYL	882
Rev	73-81	9	IQQLQNLAI	886
Rev	45-53	9	RRWQQLLAL	900
Env	476-484	9	NQTNITMSA	932
Vif	109-117	9	LHSTYFPCF	949
Pol	567-574	8	THTNGVRL	962
Vif	140-148	9	AHKYQVPSL	966
Gag	275-284	10	VRMYNPTNIL	1000
Env	6-14	9	NQLLIAILL	1140
Env	870-878	9	IRQGLELTL	1154
Env	764-771	8	WQIEYIHF	1243
Rev	43-53	11	WRRRWQQLLAL	1265
Vpr	66-73	8	QRALFMHF	1313
Pol	389-396	8	VQYMDDIL	1477
Pol	366-376	11	AIFQYTMRHVL	1543
Pol	621-629	9	WDFISTPPL	1549
Pol	320-328	9	GDAYFSIPL	1551
Pol	192-201	10	NIFGRNLLTA	1666

Env	232-240	9	YCAPPGYAL	1750
Pol	759-769	11	VSQGIRQVLFL	1754
Env	209-216	8	NHCNTSVI	1777
Vpr	71-80	10	MHFRGGCIHS	1888
Gag	263-271	9	YRRWIQLGL	1984
Pol	844-851	8	VHVASGFI	1986
Env	476-486	11	NQTNITMSAEV	2046
Gag	145-154	10	VHLPLSPRTL	2272
Env	6-13	8	NQLLIAIL	2382
Gag	32-41	10	KHVVWAANEL	2471
Pol	844-852	9	VHVASGFIE	2498
Env	541-550	10	SAMGAASLTL	2509
Pol	862-871	10	RQTALFLLKL	2545
Env	792-801	10	SRVYQILQPI	2573
Env	691-699	9	IQYGVYIVV	2599
Vpr	71-81	11	MHFRGGCIHSR	2731
Env	554-562	9	SRTLLAGIV	2958
Pol	760-767	8	SQGIRQVL	3022
Pol	844-853	10	VHVASGFIEA	3053
Gag	429-437	9	DRQAGFLGL	3228
Env	838-845	8	WRSATETL	3351
Pol	433-442	10	PPFQWMGYEL	3523
Gag	57-64	8	CQKILSVL	3891
Env	522-530	9	RNKRGVFL	3911
Env	290-298	9	WHGRDNRTI	4204
Pol	977-987	11	IQFQQSKNSKF	4222
Vif	22-30	9	WHSLIKYLK	4487
Env	823-830	8	LQYGWSYF	4511
Gag	261-269	9	NIYRRWIQL	4680
Vpx	38-48	11	NHLPRELIFQV	4694
Nef open	138-146	9	RHRILDIYL	4763
Pol	677-686	10	EQTTNQQAEL	4880
Env	521-530	10	SRNKRGVFL	4904
Nef open	120-129	10	SHFIKEKGGL	4996
Env	773-780	8	IRQLIRLL	5140
Pol	104-112	9	DRGFAAPQF	5803
Env	48-58	11	NRDTWGTTQCL	5992
Gag	430-437	8	RQAGFLGL	6002
Env	782-791	10	WLFSNCRTLL	6561
Env	707-714	8	VIYIVQML	6688
Env	834-842	9	VQAVWRSAT	6827

Pol	464-472	9	DIQKLVGVL	6888
Env	769-778	10	IHFLIRQLIR	7047
Vif	123-131	9	RRAIRGEQL	7053
Tat	61-68	8	YHCQFCFL	7461
Nef open	139-146	8	HRILDIYL	7550
Pol	613-623	11	WQVTWIPEWDF	7704
Pol	922-932	11	NHHLKNQIDRI	7714
Pol	862-869	8	RQTALFLL	7907
Pol	984-992	9	NSKFKNFRV	7913
Vpx	38-45	8	NHLPRELI	8058
Env	322-330	9	VTIMSGLVF	8215
Vif	43-51	9	PHFKVGWAW	8295
Pol	884-893	10	NGANFASQEV	8618
Env	700-708	9	GVILLRIVI	9330
Env	290-299	10	WHGRDNRTII	9744
Vif	87-96	10	VRITWYSKNF	9917
Pol	122-132	11	AHIEGQPVEVL	10494
Vif	141-151	11	HKYQVPSLQYL	11201
Env	708-717	10	IYIVQMLAKL	11254
Env	773-783	11	IRQLIRLLTWL	11977
Env	870-879	10	IRQGLELTLL	12516
Nef open	108-115	8	LRTMSYKL	13247
Pol	623-632	10	FISTPPLVRL	13793
Env	547-557	11	SLTLTAQSRTL	14009
Env	705-714	10	RIVYIVQML	14188
Env	795-805	11	YQILQPILQRL	14750
Gag	314-322	9	VKNWMTQTL	15268
Env	540-550	11	GSAMGAASLTL	15924
Pol	759-767	9	VSQGIRQVL	15943
Vif	202-210	9	NFPGLAKVL	16900
Rev	12-20	9	KRLRLIHLL	17284
Nef open	8-16	9	RRSRPSGDL	18041
Env	432-441	10	CHIRQIINTW	18059
Gag	371-379	9	ALAPVPIPF	19340
Env	6-15	10	NQLLIAILLL	19759
Pol	192-200	9	NIFGRNLLT	21621
Pol	192-199	8	NIFGRNLL	22948
Rev	43-51	9	WRRRWQQLL	23095
Pol	389-397	9	VQYMDDILI	25224
Env	479-487	9	NITMSAEVA	25358
Env	292-301	10	GRDNRTIISL	25541

Env	704-714	11	LRIVYIVQML	25774
Pol	292-300	9	TQDFTEVQL	25861
Env	311-320	10	CRRPGNKTVL	26175
Env	232-241	10	YCAPPGYALL	27487
Vif	135-145	11	CRFPRAHKYQV	27716
Vpx	33-40	8	NREAVNHL	29524
Env	868-876	9	RRIRQGLEL	30416
Env	787-797	11	CRTLLSRVYQI	30502
Env	717-725	9	LRQGYRPVF	31731
Pol	922-930	9	NHHLKNQID	32796
Vif	138-148	11	PRAHKYQVPSL	32852
Env	733-743	11	QQTHIQQDPAL	34417
Env	704-713	10	LRIVYIVQM	37943
Env	16-24	9	SVYGIYCTL	38700
Env	834-843	10	VQAVWRSATE	40365
Env	675-684	10	WDVFGNWFDL	41269
Gag	57-67	11	CQKILSVLAPL	43294
Env	691-701	11	IQYGVYIVVGV	44298
Env	823-831	9	LQYGWSYFH	46107
Vif	200-210	11	GANFPGLAKVL	46361
Vif	43-53	11	PHFKVGWAWWT	47973
Gag	261-271	11	NIYRRWIQLGL	48855
Pol	863-871	9	QTALFLLKL	50331
Env	725-732	8	FSSPPSYF	50331
Env	787-795	9	CRTLLSRVY	50999
Vpr	92-101	10	SAIPPSRSM	51261
Pol	922-929	8	NHHLKNQI	52705
Env	119-127	9	DRWGLTKSI	53723
Rev	43-50	8	WRRRWQQL	53931
Pol	298-308	11	VQLGIPHPAGL	55559
Pol	262-269	8	NPYNTPTF	59045
Gag	138-145	8	QQIGGNYV	63987
Env	486-494	9	VAELYRLEL	65932
Vpr	71-79	9	MHFRGGCIH	68519
Gag	277-284	8	MYNPTNIL	-
Gag	316-323	8	NWMTQTLL	-
Gag	297-305	9	YVDRFYKSL	-
Gag	299-307	9	DRFYKSLRA	-
Gag	487-495	9	SREKPYKEV	-
Gag	138-147	10	QQIGGNYVHL	-
Gag	151-160	10	PRTLNAWVKL	-



Gag	196-206	11	HQAAMQIIRDI	-
Pol	105-112	8	RGFAAPQF	-
Pol	828-835	8	WQMDCTHL	-
Pol	873-880	8	GRWPITHL	-
Pol	918-925	8	VEAMNHHL	-
Pol	195-203	9	GRNLLTALG	-
Pol	277-285	9	NKWRMLIDF	-
Pol	279-287	9	WRMLIDFRE	-
Pol	570-578	9	NGVRLLAHV	-
Pol	760-768	9	SQGIRQVLF	-
Pol	764-772	9	RQVLFLEKI	-
Pol	871-880	10	LAGRWPITHL	-
Pol	322-332	11	AYFSIPLDEEF	-
Pol	840-850	11	IIVAVHVASGF	-
Pol	844-854	11	VHVASGFIEAE	-
Vif	135-142	8	CRFPRAHK	-
Vif	171-179	9	WRRDNRRGL	-
Vif	175-183	9	NRRGLRMAK	-
Vif	43-52	10	PHFKVGWAWW	-
Vif	98-108	11	TDVTPNYADIL	-
Vpx	65-74	10	SYVKYRYLCL	-
Vpr	49-57	9	NRHGDTLEG	-
Vpr	62-70	9	IRILQRALF	-
Tat	103-111	9	NRTRHCQPE	-
Tat	63-72	10	CQFCFLKKGL	-
Tat	118-128	11	VEKAVATAPGL	-
Rev	70-79	10	DLAIQQLQNL	-
Rev	47-57	11	WQQLLALADRI	-
Env	244-251	8	NDTNYSGF	-
Env	295-302	8	NRTIISLN	-
Env	432-439	8	CHIRQIIN	-
Env	675-682	8	WDVFGNWF	-
Env	857-864	8	RRGGRWIL	-
Env	61-69	9	NGDYSEVAL	-
Env	222-230	9	KHYWDAIRF	-
Env	226-234	9	DAIRFRYCA	-
Env	284-292	9	NRTYIYWHG	-
Env	540-548	9	GSAMGAASL	-
Env	575-583	9	QQELLRLTV	-
Env	665-673	9	NMYELQKLN	-
Env	696-704	9	YIVVGVILL	-

Env	857-865	9	RRGGRWILA	-
Env	151-160	10	CIAQDNCTGL	-
Env	209-218	10	NHCNTSVIQE	-
Env	619-628	10	TTVPWPNASL	-
Env	823-832	10	LQYGWSYFHE	-
Env	456-466	11	DLTCNSTVTSL	-
Env	460-470	11	NSTVTSLIANI	-
Env	479-489	11	NITMSAEVAEL	-
Env	707-717	11	VIIYIVQMLAKL	-
Env	823-833	11	LQYGWSYFHEA	-
Env	834-844	11	VQAVWRSATET	-
Nef open	134-142	9	YSARRHRIL	-
Nef open	203-211	9	WDDPWGEVL	-
Nef open	245-253	9	RRRLTARGL	-
Nef open	21-31	11	LRARGETYGRL	-
Nef open	40-50	11	SQSPGGLDKGL	-

A dash indicates IC50 >70000 nM.

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**Supplemental Table 4.** Comparison of peptide binding to Mamu A1\*007:01 versus HLA B\*3801.

Protein	Amino acid positions	Length	Sequence	IC50 nM	HLA B*3801	Recognized	Optimal epitope	Final optimal
Vpr	45-55	11	NHIYNRHGDTL	0.20	<b>19</b>	Yes	Yes	1
Env	764-772	9	WQIEYIHFL	3.2	<b>2.4</b>	-	-	0
Pol	782-789	8	YHSNVKEL	5.8	<b>364</b>	Yes	Yes	1
Pol	782-791	10	YHSNVKELVF	6.2	<b>5.2</b>	Yes	-	0
Vif	22-29	8	WHSLIKYL	10	1630	-	-	0
Pol	279-288	10	WRMLIDFREL	10	<b>3.2</b>	-	-	0
Vif	145-153	9	VPSLQYLAL	13	1526	Yes	Yes	1
Pol	567-575	9	THTNGVRL	13	617	Yes	Yes	1
Env	795-802	8	YQILQPIL	24	39143	-	-	0
Pol	332-340	9	FRQYTAFTL	39	<b>17</b>	-	-	0
Pol	817-825	9	IHGQANSDL	65	2361	Yes	-	0

Env	230-240	11	FRYCAPPGYAL	101	<b>8.4</b>	Yes	-	0
Vpx	38-46	9	NHLPRELIF	144	1123	-	-	0
Env	184-192	9	NETWYSADL	147	3924	-	-	0
Pol	333-340	8	RQYTAFTL	151	1321	-	-	0
Gag	42-50	9	DRFGLAESL	177	<b>30</b>	Yes	Yes	1
Env	35-42	8	WRNATIPL	200	2259	-	-	0
Vif	65-75	11	SHLEVQGYWH L	209	<b>13</b>	Yes	-	0
Env	769-776	8	IHFLIRQL	223	11698	-	-	0
Vpr	33-43	11	KHFDPRLLTAL	227	1107	-	-	0
Pol	368-376	9	FQYTMRHVL	234	503	-	-	0
Pol	760-769	10	SQGIRQVLFL	242	<b>303</b>	Yes	Yes	1
Env	562-569	8	VQQQQQLL	254	-	-	-	0
Env	735-743	9	THIQQDPAL	306	<b>148</b>	-	-	0
Env	792-802	11	SRVYQILQPIL	310	<b>156</b>	-	-	0
Pol	104-114	11	DRGFAAPQFSL	322	581	-	-	0
Gag	42-51	10	DRFGLAESLL	325	<b>6.9</b>	Yes	-	0
Pol	105-114	10	RGFAAPQFSL	359	10522	-	-	0
Env	782-790	9	WLFSNCRTL	379	993	-	-	0
Gag	195-202	8	DHQAAMQI	380	827	-	-	0
Pol	289-298	10	NRVTQDFTEV	447	2380	-	-	0
Gag	195-203	9	DHQAAMQII	473	<b>125</b>	-	-	0
Vpr	71-78	8	MHFRGGCI	498	<b>445</b>	-	-	0

4/6 optimal

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Supplementary Figure 1

	Leader		1		30
A*07	MAVMAPRTLLLVL	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0702	~~~~~LS	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0702-like	~~~~~LS	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0703	MAVMAPRTLLLVL	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0704	~~~~~VLS	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0705	~~~~~VLS	GVLALTETWA	GSHSMRYFYT	SMSRPGRGQP	RFISVGYVDD
A*0706	~~~~~VLS	GVLALTETWA	GSHSMRYFYT	SMSR <b>H</b> GRGQP	RFISVGYVDD
			31		80
A*07	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKAN	TQTYRESLRN
A*0702	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKA <b>D</b>	TQTYRESLRN
A*0702-like	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKA <b>D</b>	TQTYRESLRN
A*0703	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKAN	TQTYRESLRN
A*0704	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKA <b>D</b>	TQTYRESLRN
A*0705	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKAN	TQTYRESLRN
A*0706	TQFVRFSDA	ESPREEPRAP	WVEQEGPEYW	DRNTRICKAN	TQTYRESLRN
			81		130
A*07	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGYEQFAYDG	RDYIALNEDL
A*0702	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGYEQFAYDG	RDYIALNEDL
A*0702-like	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGY <b>DQ</b> SAYDG	RDYIALNEDL
A*0703	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGY <b>DQ</b> SAYDG	RDYIALNEDL
A*0704	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGYEQFAYDG	RDYIALNEDL
A*0705	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGYEQFAYDG	RDYIALNEDL
A*0706	LLRYYNQSEA	GSHTIQRMYG	CDLGPDGRL	RGYEQFAYDG	RDYIALNEDL

	131				180
A*07	RSWTAADMAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ
A*0702	RSWTAADMAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ
A*0702-like	RSWTAADMAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ
A*0703	RSWTAADMAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ
A*0704	RSWTAADLAA	QNTQRKWEAA	GVAEQDRVYL	EGKCLEWLRR	HLENGKETLQ
A*0705	RSWTAADTAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ
A*0706	RSWTAADTAA	QNTQRKWEAA	GAAEQMRAYL	EGECLEWLRR	HLENGKETLQ

	181				230
A*07	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL
A*0702	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL
A*0702-like	RADPPKTHVT	HHPVSDHEAT	LRC~~~~~	~~~~~	~~~~~
A*0703	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL
A*0704	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL
A*0705	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL
A*0706	RADPPKTHVT	HHPVSDHEAT	LRCWALGFYP	AEITLTWORD	GEDQTQDTEL

	231				280
A*07	VETRPAGDGT	FQKWAAVVVP	SGKEQRYTCH	VQHEGLPKPL	TLRWEPSSES
A*0702	VETRPAGDGT	FQKWAAVVVP	SGKEQRYTCH	VQHEGLPKPL	TLRWEPSSES
A*0702-like	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
A*0703	VETRPAGDGT	FQKWAAVVVP	SGKEQRYTCH	VQHEGLPKPL	TLRWEPSSES
A*0704	VETRPAGDGT	FQKWAAVVVP	SGEQRYTCH	VQHEGLPEPL	TLRWEPSSES
A*0705	VETRPAGDGT	FQKWAAVVVP	SGKEQRYTCH	VQHEGLPKPL	TLRWEPSSES
A*0706	VETRPAGDGT	FQKWAAVVVP	SGKEQRYTCH	VQHEGLPKPL	TLRWEPSSES

	281				330
A*07	TIPIVGIIAG	LVLLGAVVTG	AVVAAVMWWR	KSSDRKGGSY	SQAASSDSAQ
A*0702	TIPIVGIIAG	LVLLGAVVTG	AVVAAVMWWR	KSSDRKGGSY	SQAASSDSAQ
A*0702-like	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
A*0703	TIPIVGIIAG	LVLLGAVVTG	AVVAAVMWWR	KSSDRKGGSY	SQAASSDSAQ
A*0704	TIPIVGIIAG	LVLLGAVVTG	AVVAVVMWRR	KSSDRKGGSY	SQAASSDSAQ
A*0705	TIPIVGIIAG	LVLLGAVVTG	AVVAAVMWWR	KSSDRKGGSY	SQAASSDSAQ
A*0706	TIPIVGIIAG	LVLLGAVVTG	AVVAAVMWWR	KSSDRKGGSY	SQAASSDSAQ

	331
A*07	GSDVSLTACKV
A*0702	GSDVSLTACKV
A*0702-like	~~~~~
A*0703	GSDVSLTACKV
A*0704	GSDVSLTACKV
A*0705	GSDVSLTACKV
A*0706	GSDVSLTACKV