

This is an electronic appendix to the Biology Letter by Zafiropoulos *et al.* 2004 Analysis of 'driver' and 'passenger' CD8⁺ T-cell responses against variable viruses. *Proc. R. Soc. Lond. B (Suppl.)* **271**, S53–S56. (DOI 10.1098/rsbl.2003.0088.)

Electronic appendices are refereed with the text. However, no attempt has been made to impose a uniform editorial style on the electronic appendices.

Electronic Appendix A

Table 1: “Selected” and “nonselected” epitopes from HIV RT studied in the paper of Moore *et al* (2002). For each the binding score represents the estimated half-life of dissociation. Selection += positively selected 0=not selected -= evidence of negative selection (i.e conservation).

Table 2: *Nonprotective passenger responses from the paper of Altfeld et al (2002).* Analysis as of predicted binding and variability.

Further tables: Estimated binding and variability for HIV derived peptides.

Table 3: Epitopes restricted by HLA-A alleles. All epitopes derived from the best defined epitope list from HIV molecular immunology database 2001. **Table 4:** Equivalent data for HLA B and a single C allele. Estimated “off-rate” is described as “Bimas affinity”. **Table 5:** Restricted epitopes with limited variability. Those marked in bold represent those with the slowest estimated binding off rates (>40 hrs)

In all cases estimated BIMAS affinity is the predicted half life of decay expressed in hours. % variability at a locus is the % of strains differing from the consensus sequence. This can be applied to the residue or the epitope across strains described in the Clade B database (see methods/Fig 2).

Table 1

HLA	Sequence	Length	Residues	Bimas affinity	Variability Anchor 1	Variability Anchor 2	Percentage Strains Different	Percentage residues different	Selected?
A0301	GIPHPAGLK	9	RT 93-101	2.7	0	0	7.7	0.8	+
B3501	TVLDVGDY	9	RT 107-115	4	7.7	0	7.7	0.9	0
A0201	VLDVGDYFSV	11	RT 108-118	?	0	0	7.7	0.7	0
A9	DAYFSVPL	8	RT113-120	?	0	0	0	0	+
B5101	DAYFSVPL	8	RT113-120	?	0	0	0	0	0
B3501	VPLDKDFRKY	10	RT 118-127	120	0	0	31	4	+
A0201	YTAFTIPSI	9	RT 127-135	1.53	0	31	31	3.4	0
B5101	TAFTIPSI	8	RT 128-135	?	0	31	31	3.8	+
B5101	QGWKGSPI	9	RT 151-159	194	0	0	0	0	0
B7	SPAIFQSSM	9	RT 156-164	20	0	0	15	1.7	+
B3501	SPAIFQSSM	9	RT 156-164	40	0	0	15	1.7	0
B7	SPAIFQSSMT	10	RT 156-165	2	0	0	15	1.5	+
A0301	AIFQSSMTK	9	RT 158-166	20	0	15	31	3	0
A11	AIFQSSMTK	9	RT 158-166	1.2	0	15	31	3	+
A7401	AIFQSSMTK	9	RT 158-166	1.2	0	15	31	3	0
A28	AIFQSSMTK	9	RT 158-166	1.2	0	15	31	3	0
A7401	KQNPDIYIY	9	RT 173-181	?	0	0	31	3.4	+
B3501	NPDIYIYQY	9	RT 175-183	12	0	0	23	2.6	+
A0201	VIYQYMDL	9	RT179-187	18	0	0	15	0.02	0
A0201	YQYMDL	9	RT 181-89	570	0	0	0	0	0
A3	DLEIGQHRTK	10	RT 192-201	0.6	0	0	54	6.2	0
A2	KIEELRQHL	9	RT 201-209	2.7	7.7	0	23	2.6	0
B40	IEELRQHLL	9	RT 202-210	10	0	0	23	2.6	+
B44	EELRQHLLRW	10	RT 203-210	36	0	0	31	3.1	+
A2	LLRWGLTTPDKK	12	RT 209-220	?	0	0	38	3.2	-

Table 2

Atfeld et al: Strong responses which do not protect

HLA allele	Peptide Sequence	Mer	Protein Region	BIMAS Estimated Binding Affinity	Variability Anchor 1	Variability Anchor 2	Percentage B Clade Strains Different	Percentage Residues Mutated Amongst B Clade strains
A0301	GIPHPAGLK	9	RT 93-101	2.7	0	0	7.7	0.8
A3	KLVDFRELNK	10	RT 73-82	180	0	8	8	0.8
B7	SPRTLNAWV	9	p24 16-24	40	0	0	4.2	0.5
B7	TPQDLNTML	9	p24 48-56	80	3.8	0	4.2	0.5
B7	GPGHKARVL	9	p24 223-231	80	0	0	33	5.5
B7	SPAIFQSSM	9	RT 156-164	20	0	0	15	1.7
A0301	KIRLRPGGK	9	p17 18-26	1.8	4.2	0	12.5	1.9

Table 3

HLA allele	Peptide Sequence	Mer	Protein Region	BIMAS Estimated Binding Affinity	Variability Anchor 1	Variability Anchor 2	Percentage B Clade Strains Different	Percentage Residues Mutated Amongst B Clade strains
A0201	KLTPLCVTL	9	gp160 121-129	74.77	4.5	0	14	1.5
A0201	RGPGRAFVTI	10	gp160 311-320	0.13	9.1	12.5	75	14
A0201	SLLNATDIAV	10	gp160 813-822	257.34	27	0	59	10
A0201	PLTFGWCYKL	10	Nef 136-145	0.47	3.8	0	12	1.5
A0201	LTFGWCFKLV	10	Nef 137-146	11.54	7.7	3.8	15	1.9
A0201	VLEWRFD SRL	10	Nef 180-189	8.83	27	0	65	12.6
A0201	FLGKIWPSYK	10	p1 1-10	0.38	0	4.2	29	2.9
A0201	SLYNTVATL	9	p17 77-85	157	4.2	0	58	9.7
A0201	VLAEMSQV	9	p24/p2 230-237	1115	0	17	21	4
A0201	LVGPTPVNI	9	Protease 76-84	1.55	8	0	8	0.9
A0201	YTAFTIPSI	9	RT 127-135	1.53	0	31	31	3.4
A0201	ILKEPVHGV	9	RT 309-317	39.03	0	0	31	4.3
A0201	ALVEICTEM	9	RT 33-41	20.4	0	0	23	4.2
A0201	VIYQYMDDL	9	RT179-187	18	0	0	15	0.02
A0201	AIIRILQQL	9	Vpr 59-67	6.76	24	0	29	5.2
A0201	RILQQLFI	9	Vpr 62-70	67.14	24	0	24	2.6
A0205	SLYNTVATL	9	p17 77-85	42	4.2	0	58	9.7
A0301	TVYYGVPVWK	10	gp160 37-46	15	0	4.5	4.5	0.5
A0301	QVPLRPMTYK	10	Nef 73-82	4.5	0	11.5	19	3.4
A0301	KIRLRPGGK	9	p17 18-26	1.8	4.2	0	12.5	1.9
A0301	RLRPGGKKK	9	p17 20-29	15	0	21	21	2.8
A0301	AIFQSSMTK	9	RT 158-166	20	0	15	31	3
A0301	QIYPGIKVR	9	RT 269-277	2.25	0	31	31	4.3
A0301	GIPHPAGLK	9	RT 93-101	2.7	0	0	7.7	0.8
A0301	RIRTWKSLVK	10	Vif 17-26	4	14	4.8	48	5.2
A1101	SVITQACPK	9	gp160 199-207	3	9.1	0	18	2.5
A1101	AVFIHNFKRK	10	Integrase 179-188	2	0	0	0	0
A1101	QVPLRPMTYK	10	Nef 73-82	2	0	12	19	3.4
A1101	AVDLSHFLK	9	Nef 84-92	6	50	19.2	69	9.4
A1101	TLYCVHQRI	9	p17 84-92	0.008	0	0	75	9.7
A1101	QIIEQLIKK	9	RNase 80-88	1.2	0	0	23	2.6
A1101	AIFQSSMTK	9	RT 158-166	1.2	0	15	31	3
A1101	IYQEPFKLNK	10	RT 341-350	0.4	0	0	38	4.6
A24	LFCASDAKAY	10	gp160 52-61	0.5	0	9	23	3
A24	RYLKDQQLL	9	gp160 585-593	720	0	9	64	8
A24	KYKCLKHIVW	9	p17 28-36	10	0	0	66.7	11
A3	AVFIHNFKRK	10	Integrase 179-188	15	0	0	0	0
A3	AVDLSHFLK	9	Nef 84-92	6	50	19.2	69	9.4
A3	ERILSTYLGR	10	Rev 57-66	0.004	0	5.3	84	17
A3	KLVDFRELNK	10	RT 73-82	180	0	8	8	0.8
A3	HMYISKKAK	9	Vif 28-36	50	5	10	76	13
A3302	EYRKILRQR	9	Vpu 29-37	45	5	20	40	9
A68	IVTRIVELL	9	gp160 777-785	4	23	0	73	14
A68	ITLWQRPLV	9	Protease 3-11	2	0	0	23	2.6
A68	DTVLEEWNL	9	Protease 30-38	9	0	0	54	9

Table 4

HLA allele	Peptide Sequence	Mer	Protein Region	BIMAS Estimated Binding Affinity	Variability Anchor 1	Variability Anchor 2	Percentage B Clade Strains Different	Percentage Residues Mutated Amongst B Clade strains
B14	ERYLKDQQL	9	gp160 584-592	300	0	9	64	8
B14	DRFYKTLRA	9	p24 166-174	15	0	4.2	8.3	0.9
B27	GRRGWEALKY	10	gp160 786-795	1000	9.1	0	64	7.7
B27	RRQDILDLWI	10	Nef 105-114	1800	3.8	27	62	9.2
B27	IRLRPGGKK	9	p17 19-27	2000	0	0	8	1
B27	KRWIILGLNK	10	p24 131-140	30000	0	0	4	4
B3501	TAVPWNASW	9	gp160 606-614	1.5	41	0	59	9.1
B3501	DPNPQEVVL	9	gp160 78-86	20	0	5	23	3
B3501	NSSKVSQNY	9	p17 124-132	10	29	0	46	10.2
B3501	WASRELERF	9	p17 36-44	4.5	0	0	0	0
B3501	PPIPVGDIY	9	p24 122-130	4	4.2	0	8.3	0.9
B3501	TVLDVGDAY	9	RT 107-115	4	7.7	0	7.7	0.9
B3501	VPLDEDFRKY	10	RT 118-127	120	0	0	31	4
B3501	NPDIVIQY	9	RT 175-183	12	0	0	23	2.6
B3701	YFPDWQNYT	9	Nef 120-128	0.1	3.8	0	19	3
B3901	GHQAAMQML	9	p24 61-69	135	0	0	58	10
B5101	LPCRIKQII	9	gp160 416-424	692.12	9	23	64	8
B5101	RAIEAQQHL	9	gp160 557-565	36.6	0	27	36	4.5
B5101	EKEGKISKI	9	RT 42-50	1.9	0	7.7	7.7	0.8
B5801	TSTLQEIQGW	10	p24 108-117	80	0	0	4.2	0.4
B5801	KAVRLIKFLY	10	Rev 14-23	13.5	11	0	47	6.8
B60	QELKNSAVSL	10	gp160 805-814	640	0	5	41	4.5
B60	KEKGGLEGL	9	Nef 92-100	160	7.7	0	27	4.3
B60	IEIKDTKEAL	10	p17 92-101	320	29	0	63	7.8
B60	SEGATPQDL	9	p24 44-52	160	0	0	12.5	1.4
B60	KELYPLTSL	9	p6 33-41	320	21	0	42	6
B60	IEELRQHLL	9	RT 202-210	160	0	0	23	2.6
B62	GLNKIVRMY	9	p24 137-145	80	0	0	0	0
B62	ILKEPVHGVY	10	RT 309-318	377.5	0	0	31	4
B7	RPNNNTRKSI	10	gp160 298-307	12	14	4.5	77	15
B7	IPRRIRQGL	9	gp160 843-851	1200	0	14	64	9
B7	TPGPGVRYPL	10	Nef 128-137	120	3.8	3.8	46	8
B7	FPVTPQVPLR	10	Nef 68-77	0.2	0	0	19	1.9
B7	TPQVPLRPM	9	Nef 71-79	30	0	3.8	19	2.6
B7	RPMTYKAAL	9	Nef 77-85	240	0	50	88	15
B7	SPRTLNAWV	9	p24 16-24	40	0	0	4.2	0.5
B7	GPGHKARVL	9	p24 223-231	80	0	0	33	5.5
B7	TPQDLNTML	9	p24 48-56	80	3.8	0	4.2	0.5
B7	HPVHAGPIA	9	p24 84-92	2	0	8.3	33	6
B7	HPRVSSEVHI	10	Vif 48-57	80	0	0	48	7.1
B7	FPRIWLHGL	9	Vpr 34-42	800	0	0	71	9.2
B8	GGKKKYKLG	9	p17 24-32	0.04	0	0	63	8.3
B8	ELRSLYNTV	9	p17 74-82	2.4	42	0	71	15.7
B8	DCKTTILKAL	9	p24 197-205	32	4.2	0	4.2	0.5
B8	GPKVKQWPL	9	RT 18-26	320	0	0	0	0
B8	RVKEKYQHL	9	gp160 2-10	60	36	9.1	77	24
Cw_0401	SFNCGGEFF	9	gp160 375-383	100	0	0	18	2

Table 5

Epitopes that have less than 10% variability									
HLA allele	Peptide Sequence	Mer	Protein Region	BIMAS Affinity	Variability Anchor 1	Variability Anchor 2	Percentage Strains Different	Percentage Residues Mutated	
A1101	AVFIHFKRKK	10	Integrase 179-188	2	0	0	0	0	
A3	AVFIHFKRKK	10	Integrase 179-188	15	0	0	0	0	
B3501	WASRELERF	9	p17 36-44	4.5	0	0	0	0	
B62	GLNKIVRMY	9	p24 137-145	80	0	0	0	0	
B8	GPKVKQWPL	9	RT 18-26	320	0	0	0	0	
B27	KRWILGLNK	10	p24 131-140	30000	0	0	4	4	
B5801	TSTLQEQIGW	10	p24 108-117	80	0	0	4.2	0.4	
B7	SPRTLNAWV	9	p24 16-24	40	0	0	4.2	0.5	
B7	TPQDLNTML	9	p24 48-56	80	3.8	0	4.2	0.5	
B8	DKKTILKAL	9	p24 197-205	32	4.2	0	4.2	0.5	
A0301	TVYYGVPVWK	10	gp160 37-46	15	0	4.5	4.5	0.5	
A0301	GIPHPAGLK	9	RT 93-101	2.7	0	0	7.7	0.8	
B3501	TVLDVGDAY	9	RT 107-115	4	7.7	0	7.7	0.9	
B5101	EKEGKISKI	9	RT 42-50	1.9	0	7.7	7.7	0.8	
A0201	LVGPTPVNI	9	Protease 76-84	1.55	8	0	8	0.9	
A3	KLVDFFRELNK	10	RT 73-82	180	0	8	8	0.8	
B27	IRLRPGGKK	9	p17 19-27	2000	0	0	8	1	
B14	DRFYKTLRA	9	p24 166-174	15	0	4.2	8.3	0.9	
B3501	PPIPVGDIY	9	p24 122-130	4	4.2	0	8.3	0.9	