

Additional file 3

Sl. No.	Amino acid substitutions positions in E protein	HLA-B alleles						
		HLA-B*07	HLA-B*27	HLA-B*40	HLA-B*44	HLA-B*51	HLA-B*53	HLA-B*3501
1	N2H	-	-	-	-	-	-	-
2	N8H	-	-	-	-	-	-	-
3	S64T	-	VRSYCYHAT (1.394)	-	-	-	-	-
4	N103K	-	-	-	-	-	-	-
5	F107L	-	-	-	-	CGLFGKGS (76.03)	-	-
6	S123R	-	TRKAIGRTI (1.277)	-	-	-	-	-
7	K138E	-	-	-	-	-	-	-
8	Q158P	-	-	-	-	-	-	-
9	V176I	TPNAPSITL (3.11)	-	-	-	TPNAPSITL (62.95)	-	-
10	A177T	TPNAPSITL (3.11)	-	-	-	TPNAPSITL (62.95)	-	-
11	A222S	-	-	REWFHDLSL (1.376)	REWFHDLSL (1.376)	-	-	-
12	G244E	-	-	-	-	-	-	-
13	G261S	-	-	-	-	-	-	-
14	H264Q	-	-	-	-	QALAGAIVV (82.79)	-	-
15	M279K	SVKLTSGHL (75.86)	-	VEYSSSVKL (1.505)	VEYSSSVKL (1.505)	-	-	-
16	E306G	-	-	-	-	-	-	-
17	A311R	-	FRKNPADTG (1.471)	-	-	-	-	-
18	V315A	-	-	-	-	-	-	-
	S327Q	-	-	-	-	-	-	-
19	S327T	-	-	-	-	-	-	-
20	S329T	-	-	-	-	TGSDGPCKI (3.24)	-	-
21	S331K	-	-	-	-	TGKDGPKCI (19.41)	-	-
22	A366S	-	-	TSSNSKVL (0.622)	TSSNSKVL (0.622)	-	-	-
23	V372L	-	-	-	-	-	-	-
24	M374I	-	-	-	-	-	-	-
	G388E	-	GREDKQINH (1.656)	-	-	-	-	-
25	G388K	VVGRKDKQI (45.19)	GRKDKQINH (1.672)	-	-	-	-	-
26	D389E	-	GRGEKQINH (1.660)	GEKQINHHW (1.094)	GEKQINHHW (1.094)	-	-	-
27	W396R	-	-	-	-	-	-	-
28	R416K	-	-	-	-	-	-	-
29	G432R	-	-	-	-	-	-	-
30	R439K	-	-	-	-	-	-	-
31	L463R	-	-	-	-	-	-	-
32	L467E	-	-	-	-	-	-	-
33	A481D	-	-	-	-	-	-	-

The values given within the bracket indicates the 50% inhibitory concentration (IC50) of the peptide, a measure of the binding affinity. An IC50 value < 50 is considered as a good affinity. Amino acid substitutions in the predicted epitopes of E protein are marked as bold.