

Table 2. Amino acid differences between FVO, CAMP, 7G8, 3D7, HB3, DD2, M24, and D10 strains

	FVO	CAMP	7G8	HB3	DD2	M24	3D7	D10			3D7	D10	HB3	CAMP	M24	FVO	7G8	DD2
34	K	N	K	N	N	N	N	K		34	N	K	N	N	N	K	K	N
36	D	N	D	D	D	N	D	D		36	D	D	D	N	N	D	D	D
39	H	H	H	R	R	H	R	H		39	R	H	R	H	H	H	H	R
48	P	P	S	P	P	P	P	P		48	P	P	P	P	P	P	S	P
52	E	Q	S	E	E	Q	E	Q		52	E	Q	E	Q	Q	E	E	E
95	P	S	S	S	S	S	S	S		95	S	S	S	S	S	P	S	S
120	E	E	K	E	E	E	E	E		120	E	E	E	E	E	E	K	E
121	E	E	N	K	E	E	E	E		121	E	E	K	E	E	E	E	E
162	N	N	N	K	N	N	N	N		162	N	N	N	N	N	N	N	N
167	K	K	K	T	T	T	T	T		167	T	T	T	K	T	K	K	T
172	G	G	G	E	G	E	G	G		172	G	G	E	G	E	G	G	G
175	D	D	D	D	Y	D	Y	Y		175	Y	Y	D	D	D	D	D	Y
187	N	E	N	E	K	K	E	E		187	E	E	E	E	K	N	N	K
190	I	I	I	I	M	M	M	M		190	M	M	I	I	M	I	I	M
196	N	N	D	D	D	D	D	D		196	D	D	D	N	D	N	D	D
197	G	G	H	Q	D	Q	E	E		197	E	E	Q	G	Q	G	H	D
200	D	D	D	H	L	L	H	H		200	H	H	H	D	D	D	D	L
201	F	F	F	L	L	F	F	F		201	F	F	L	F	F	F	F	L
204	N	N	N	D	D	N	D	D		204	D	D	N	N	N	N	N	D
206	E	E	E	E	E	E	K	K		206	K	K	E	E	E	E	E	E
207	Y	Y	Y	Y	D	Y	Y	Y		207	Y	Y	Y	Y	Y	Y	Y	D
225	N	N	N	N	N	N	I	I		225	I	I	N	N	N	N	N	N
228	N	K	N	N	N	N	N	N		228	N	N	N	K	N	N	N	N
230	K	E	K	K	K	E	K	K		230	K	K	K	E	Y	K	K	K
242	Y	D	Y	Y	Y	D	D	D		242	D	D	Y	D	Y	Y	Y	Y
243	N	K	N	E	N	K	K	K		243	K	K	E	K	K	N	N	E
267	Q	E	E	E	E	Q	E	E		267	E	E	E	Q	Q	E	E	E
282	K	K	K	K	K	K	I	I		282	I	I	K	K	K	K	K	K
283	L	S	S	L	S	L	S	S		283	S	S	L	S	L	L	S	S
285	E	Q	Q	E	Q	E	Q	Q		285	Q	Q	E	Q	E	E	Q	Q
296	D	D	D	D	D	H	D	D		296	D	D	D	D	H	D	D	D
300	E	K	K	E	E	K	K	K		300	K	K	E	E	K	E	K	E
308	E	E	E	E	S	Q	Q	Q		308	Q	Q	E	E	E	E	E	E
330	S	S	S	S	S	S	P	S		330	P	S	S	S	S	S	S	S
332	N	N	N	N	N	N	I	I		332	I	I	N	N	N	N	N	N
393	H	H	R	R	H	R	H	H		393	H	H	R	R	H	R	H	H
404	R	R	R	T	R	T	T	T		404	T	T	T	R	T	R	R	R
405	E	K	K	E	K	K	E	E		405	E	E	E	K	K	E	K	K
407	Q	H	Q	Q	Q	Q	Q	Q		407	Q	Q	Q	H	Q	Q	Q	Q
435	I	I	N	N	I	I	I	I		435	I	I	I	N	I	I	N	I
439	H	N	H	N	H	H	N	H		439	N	H	N	N	H	H	N	H
448	D	N	D	D	D	D	D	D		448	D	N	D	N	D	D	D	D
451	K	M	K	K	K	K	M	M		451	M	M	K	K	K	K	K	K
485	K	K	I	K	I	I	K	K		485	K	K	K	K	I	K	I	K
496	M	M	I	I	I	M	M	I		496	M	I	I	M	M	M	I	I
503	R	R	N	N	N	R	R	N		503	R	N	N	R	R	R	N	N
505	F	F	F	F	F	Y	F	F		505	F	F	F	F	Y	F	F	F
512	R	R	K	K	K	R	R	R		512	R	R	K	R	R	R	K	K
544	N	N	K	N	K	N	K	K		544	K	N	N	N	N	N	K	K
581	Q	Q	E	Q	E	Q	E	E		581	E	E	Q	Q	Q	Q	E	E
584	H	D	D	H	D	D	D	H		584	D	H	H	D	D	H	D	D
589	T	T	N	N	N	T	N	N		589	N	N	N	T	T	T	N	N

High-impact AER residues of the C1-L and domain-2 clusters are boxed. Table on the left shows residues that are similar to FVO in green. The amino acid number is shown on the left. The shaded cells correspond to the sequence boundaries included in the AMA-1 constructs designed here. Yellow cells are domain 1, light blue are domain 2, and dark blue are domain 3. Table on the right shows residues that are similar to 3D7 in red. Strains FVO, 7G8, and CAMP belong to the “FVO inhibition group” (Fig. 7 and SI Fig. 15). Strains 3D7 and D10 belong to the “3D7 inhibition group” (1, 2). The AMA-1 sequences within members of the same inhibition group share similar residues in the C1-L and domain 2 AER cluster; therefore, the AER mapped here can predict antigenic escape.

1. Hodder AN, Crewther PE, Anders RF (2001) *Infect Immun* 69:3286-3294.

2. Kennedy MC, Wang J, Zhang Y, Miles AP, Chitsaz F, Saul A, Long CA, Miller LH, Stowers AW (2002) *Infect Immun* 70:6948-6960.

