Table S1. Hydrogen bonding contacts (≤ 3.2 Å) between the E2s epitope and the 8G12 Fab

8G12's epitope on E2s[1]		8G12 Fab residues		Distance (Å)[2]
$Glu479^{E2s(A)}$	(OE1)	Lys^{H63}	(NZ)	2.6
	(OE1)	Gln^{H60}	(OE1)	3.2
$Arg542^{E2s(B)}$	(NH1)	Gly^{H102}	(O)	3.0
$Glu549^{E2s(A)}$	(OE1)	Glu^{L93}	(OE1)	2.6
	(OE1)	Thr^{L94}	(N)	3.1
	(OE2)	Thr^{L94}	(OG1)	2.9
	(OE2)	Tyr^{H105}	(OH)	2.8
$Gly551^{E2s(A)}$	(O)	Gly^{H102}	(O)	3.0
	(O)	Asn^{H104}	(N)	2.9
$Thr553^{E2s(A)}$	(N)	Asn^{H104}	(OD1)	2.7
	(OG1)		(OD1)	3.2
	(OG1)		(ND2)	3.0
$Lys554^{E2s(A)}$	(NZ)	Glu^{L93}	(OE1)	2.6
$Thr564^{E2s(B)}$	(OG1)	Trp^{L92}	(NE1)	2.8
$Ser590^{E2s(A)}$	(N)[3]	Asp^{L1}	(OD1)	2.9
$Gly591^{E2s(A)}$	(O)	Gln^{H60}	(OE1)	2.7
$Pro592^{E2s(A)}$	(O)	Gln^{H58}	(N)	2.9

[1] The residues are labeled to indicate their location on E2s dimer molecule (A or B)

[2] The calculation is based on the $E2s^{HEV\text{-}4}$:8G12 Fab complex structure (2.3 Å resolution)

[3] For residue 590, a serine residue in genotype 4 but an alanine residue in the other genotypes