Supplementary material:

Figure S1:

Figure S2:

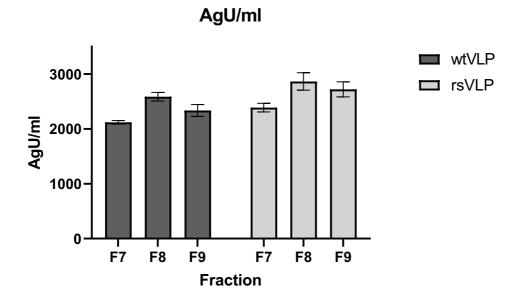


Figure S1: Antigen concentration (AgU/ml) of peak VLP fractions determined by the CT11F9 antibody relative to the 18/116 antigen standard.

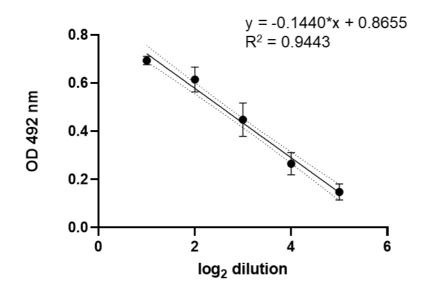


Figure S2: Relationship between OD and log_2 dilution of antigen, used to calculate the proportion of HAg in samples.



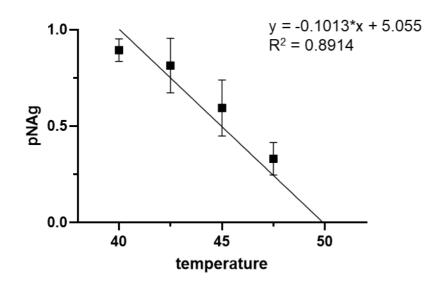


Figure S3: Linear regression to estimate antigenic conversion temperature of rsVLPs between 40°C and 50°C.

Figure S4:

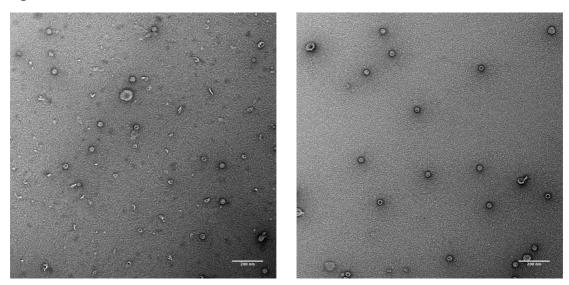


Figure S4: Negative stain TEM (using 2% UA) of samples of wtVLPs (left) and rsVLPs (right), scale bar = 200 nm.

Figure S5:

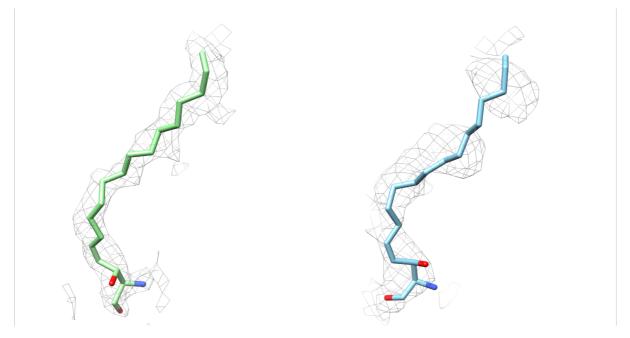


Figure S5: Density indicating occupancy of the pocket, present in the major population (left) and the minor population (right) shown at 2.5 rmsd.



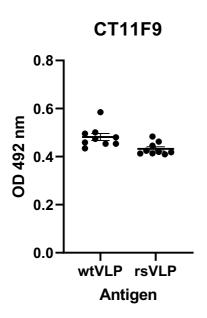


Figure S6: Reactivity of VLP (captured on ELISA plates) with CT11F9 antibody.

Antibody	Source	Specificity	Uses
CT11F9	mouse	NAg and HAg	ELISA
mAb 979	mouse	HAg	ELISA/western blot
16-2-2D scFv	human	NAg	ELISA

Table S1: specificity of the antibodies used to detect EVA71 antigenic states.

Table S2: Antigen composition of samples at a range of temperatures

proportion $HAg = 2^{(OD \ 4^{\circ}C \ -OD \ 55^{\circ}C)/incline}$

Temperature (°C)	pHAg rsVLP	pNAg rsVLP	pHAg wtVLP	pNAg wtVLP
4	0.13	0.87	1.11	-0.11
30	0.11	0.89	0.80	0.20
35	0.10	0.90	0.69	0.31
37.5	0.11	0.89	0.84	0.16
40	0.14	0.86	0.97	0.03
42.5	0.31	0.69	1.16	-0.16
45	0.46	0.54	1.18	-0.18
47.5	0.86	0.14	1.32	-0.32
50	1.10	-0.10	1.54	-0.54
52.5	1.07	-0.07	1.17	-0.17
55	1.00	0.00	1.00	0.00
60	0.80	0.20	0.73	0.27

Table S3:

rsVLP

Microscope	FEI Titan Krios
Detector mode	Counting
Camera	Falcon IV
Voltage (kV)	300
Pixel size (Å)	0.91
Nominal magnification	130,000×
Exposure time (s)	5
Total dose (e ⁻ /Ų)	31
Number of fractions	42
Defocus range (μm)	–0.8 to –2.9
Number of micrographs	20,419
Acquisition software	Thermo Scientific EPU

Table S4:

Model	rsVLP
EMDB ID	EMD-16450
PDB ID	PDB-8C6D
CryoEM map processing	
Symmetry imposed	11
Number of particles contributing to map	11,789
Map resolution (FSC = 0.143) (Å)	2.4
Map resolution range at atomic coordinates (Å)	2.4-2.8
Map sharpening B factor (Ų)	-133.6
Residues modelled	A 58-297
	B 13-45, 83-323
	C 1-242
RMSD	
Bond lengths (Å)	0.0096
Bond angles ()	1.33
Validation	
All-atom clashscore	8.17
MolProbity score	2.21
Rotamer outliers (%)	3.89
Ramachandran plot	
Favoured (%)	95.45
Allowed (%)	4.55
Outliers (%)	0.00