

**Table S3. Epitope and paratope residues within 6Å between the DH1017.Fab and E ectodomain fitted structures to the cryo-EM density map of the Fab-bound Zika virion. Related to Figure 6.**

Fab footprint conserved residues at i2f and q2f symmetry axes

Residue number(s)	Amino Acid	Domain/chain /axis
120-126	ACSKKMT	DII, A, C, i2f, q2f
205,207,208	T, N, N	DII, A, C, i2f, q2f
230-232	DTG	DII, A, C, i2f, q2f
278-280	DGA	DII, A, C, i2f, q2f

Fab footprint unique residues at i2f and q2f symmetry axes

Residue number(s)	Amino Acid	Domain/chain /axis
61-66	YEASIS	DII, A, i2f
206,228,229	M, G, A	DII, A, i2f
277	M	DI, A, i2f
127,128	G, K	DII, C, q2f
233-235	TPH	DII, C, q2f
281	K	DI, E, q2f

Paratope footprint residues at i2f axis

Residue number(s)	Amino Acid	Chain/region
26-35	GGSISSGDSY	VH, CDR1
54-59	YYSGST	VH, CDR2
75-77	TSK	VH, FR3
101-106	VGDLRV	VH, CDR3

Paratope footprint residues at q2f axis

Residue number(s)	Amino Acid	Chain/region
26-28	GGG	VH, CDR1
30-33	SSGD	VH, CDR1
75-78	TSKN	VH, FR3
101-106	VGDLRV	VH, CDR3
57, 58	G, I	VL, FR3