SUPPLEMENTAL INFORMATION

Resurfaced ZIKV EDIII nanoparticle immunogens elicit immune-focused protective responses *in vivo*

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Figure S1, related to Figure 1. rsZDIII phage clone reactivity toward ZV-mAbs (ZV-2, ZV-64, and ZV-67) determined by ELISA. Data from a single experiment completed in duplicate are plotted as (mean OD_{450}) <u>+</u> SD.



Figure S2, **related to Figure 2**. Coomassie blue-stained gels for recombinant expressed rsZDIII variants following TEV cleavage of MBP-rsZDIII fusion proteins and purification by anion exchange chromatography.



Figure S3, related to Figure 2 and STAR methods. Biochemical characterization of rsZDIII variants. (A) Binding reactivity of ZV-mAbs (ZV-2, ZV-64, and ZV-67) to soluble rsZDIII variants determined by ELISA. Representative data from two independent experiments completed in triplicate are plotted as the (mean OD_{450}) + SD. (B) Binding interactions between MBP and ZV-mAbs (ZV-2, ZV-64, and ZV-67) by BLI. Representative data from two independent experiments is shown.



Figure S4, related to Figure 3. HSQC spectrum of rsZDIII-2.39 (shown in black contours) and the ZDIII-WT (BMRB 34167, shown as red crosses). Spectra shown was acquired from a single labelled protein preparation.



Figure S5, related to Figure 4. FRNT50 neutralization titers of D35 and D56 serum collected from immunized mice. Data from two independent experiments, completed in triplicate, are plotted as (mean FRNT₅₀) \pm SD.



Figure S6, related to Figure 6. Flow cytometry analysis of the frequency of ZDIII-WT antigen-reactive CD19+/ IgG+ splenic B cells in vaccinated animals.

(A) Gating strategy used for analysis. (B) ZDIII-WT reactive B cells in AaLS-ZDIII-WT immunized animals collected at D56, each plot represents an independent biological sample and experiment. (C) Frequencies of ZDIII-WT reactive B cells in AaLS-rsZDIII-2.39 immunized animals collected at D56, each dot plot represents an independent biological sample and experiment.

Table S1, related to Figure 1 and Star Methods.Amino acid sequences of proteinsand peptides described in this study.

Protein/ peptide	Amino acid sequence
SpyTag (SpT)	MAHIVMVDAYKPTK
SpyCatcher (SpC)	GAMVDTLSGLSSEQGQSGDMTIEEDSATHIKFSKRDEDGKELAGATMELRDSSGKTISTWIS DGQVKDFYLYPGKYTFVETAAPDGYEVATAITFTVNEQGQVTVNGKATKGDAHI
ZDIII-WT-SpT	GVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCKVPAQMAVDMQTLTPVGRLITANPVI TESTENSKMMLELDPPFGDSYIVIGVGEKKITHHWHRSGSTIGKGSGSMAHIVMVDAYKPTK
AaLS-SpC	MQIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAG ELARKEDIDAVIAIGVLIRGATPHFDYIASEVSKGLANLSLELRKPITFGVITADTLEQAIERAGTK HGNKGWEAALSAIEMANLFKSLRSGGGSGGGGAMVDTLSGLSSEQGQSGDMTIEEDSATHI KFSKRDEDGKELAGATMELRDSSGKTISTWISDGQVKDFYLYPGKYTFVETAAPDGYEVATAI TFTVNEQGQVTVNGKATKGDAHI

Position	Residue	н	NH	ΔH	∆NH	CSP
303	Val	7.82	119.2	-0.04	-0.35	0.081
304	Ser	8.18	119.66	-0.03	-0.26	0.060
305	Tyr	7.96	121.94	0.02	-0.03	0.021
307	Leu	8.5	122.25	-0.02	0.02	0.020
308	Cys	9.24	123.54	-0.01	0	0.010
309	Thr	8.63	114.3	-0.06	0.02	0.060
310	Ala	8.99	127.84	-0.03	0.05	0.032
311	Ala	7.73	119.05	-0.03	-0.06	0.032
312	Phe	9.03	119.32	-0.02	-0.26	0.056
313	Thr	8.58	109.77	-0.04	0.22	0.059
314	Phe	8.74	121.51	0.08	0.05	0.081
315	Thr	8.87	115.58	-0.09	-0.28	0.106
320	Glu	9	123.84	0.01	0.02	0.011
323	His	7.68	112.72	-0.02	0.35	0.073
324	Gly	7.96	108.75	-0.06	-0.06	0.061
325	Thr	6.7	106.95	0.01	0.06	0.016
326	Val	8.89	116.76	-0.02	-0.24	0.052
328	Val	8.67	121.4	0.08	-0.33	0.104
331	Gln	9.12	120.9	0.01	-0.79	0.158
332	Tyr	9.17	126.18	-0.02	0.62	0.126
333	Ala	8.09	128.83	0.02	0.33	0.069
335	Thr	8.15	106.46	-0.04	-0.2	0.057
336	Asp	9.39	119.33	-0.04	-0.05	0.041
337	Gly	8.61	108.52	0	0	0.000
339	Cys	8.44	117.17	-0.02	-0.04	0.022
340	Lys	9.04	121.45	-0.02	-0.03	0.021
341	Val	8.62	129.67	-0.01	0.08	0.019
343	Ala	7.73	128.49	-0.01	-0.02	0.011
344	Gln	8.65	115.81	-0.03	-0.13	0.040
345	Met	8.85	116.3	0.06	0.19	0.071
346	Ala	9.34	123.03	-0.02	-0.01	0.020
347	Val	9.37	116.61	-0.11	0.52	0.151

Table S2, related to Figure 3. Chemical shift perturbation (CSP) values for assigned residues in rsZDIII-2.39 compared to ZDIII-WT (5OMZ; BMRB 34167).

352	Leu	8.24	119.02	-0.03	-0.29	0.065
355	Val	7.67	116.01	-0.03	0.21	0.052
356	Gly	8.6	107.35	-0.03	0.08	0.034
359	lle	8.62	127.21	-0.05	0.04	0.051
360	Thr	7.23	115.35	-0.03	0.02	0.030
361	Ala	8.3	129.67	-0.03	0.05	0.032
362	Asn	8.6	115.13	-0.01	-0.11	0.024
364	Val	8.04	124.26	-0.04	0.06	0.042
365	lle	8.55	127.08	-0.04	-0.05	0.041
366	Thr	8.39	116.64	0	-0.09	0.018
367	Glu	7.72	120.12	-0.05	-0.03	0.050
368	Ser	8.58	114.76	-0.01	0.03	0.012
369	Thr	7.18	112.31	-0.04	0.08	0.043
370	Glu	8.8	122.19	0.04	0.32	0.075
371	Asn	8.08	116.98	0.03	-0.24	0.057
372	Ser	8.72	116.14	0.02	0.16	0.038
377	Glu	8.38	121.17	0.62	1.96	0.734
378	Leu	9.27	126.87	0.01	-0.21	0.043
379	Asp	9.2	122.15	-0.04	0.08	0.043
382	Phe	8.31	117.7	-0.02	-0.08	0.026
383	Gly	8.9	111.03	0	0.11	0.022
384	Asp	8.95	125.66	-0.05	-0.17	0.060
385	Ser	9.09	116.57	0	-0.09	0.018
386	Tyr	9.23	114.83	-0.04	-0.16	0.051
387	lle	9.3	123.75	-0.01	0	0.010
388	Val	8.98	127.27	0	0.02	0.004
389	lle	8.88	128.82	0	0.1	0.020
390	Gly	8.48	112.68	-0.04	-0.18	0.054
391	Val	8.39	112.2	-0.03	-0.02	0.030
392	Gly	8.81	111.06	-0.03	-0.11	0.037
393	Glu	8.98	122.36	-0.02	-0.08	0.026
394	Lys	8	116.04	0	0.1	0.020
395	Lys	7.19	120.4	-0.02	-0.04	0.022
396	lle	9	118.38	-0.02	-0.12	0.031
397	Thr	8.46	111.7	-0.01	-0.21	0.043
400	Trp	9.19	129.52	0.01	0.24	0.049

401	His	6.44	123.45	-0.01	-0.06	0.016
402	Arg	8.16	127.72	0	0.01	0.002
403	Ser	9.18	125.11	-0.06	-0.07	0.062
404	Gly	8.56	110.16	-0.01	0.01	0.010
405	Ser	8.11	114.77	-0.01	0.03	0.012
406	Thr	8.22	115.85	-0.02	0.14	0.034
407	lle	8.07	122.87	-0.01	0	0.010
408	Gly	8.47	113.01	-0.02	0.55	0.112