



Supplementary Materials:

Peptide-based Vaccine against SARS-CoV-2: Peptide Antigen Discovery and Screening of Adjuvant Systems

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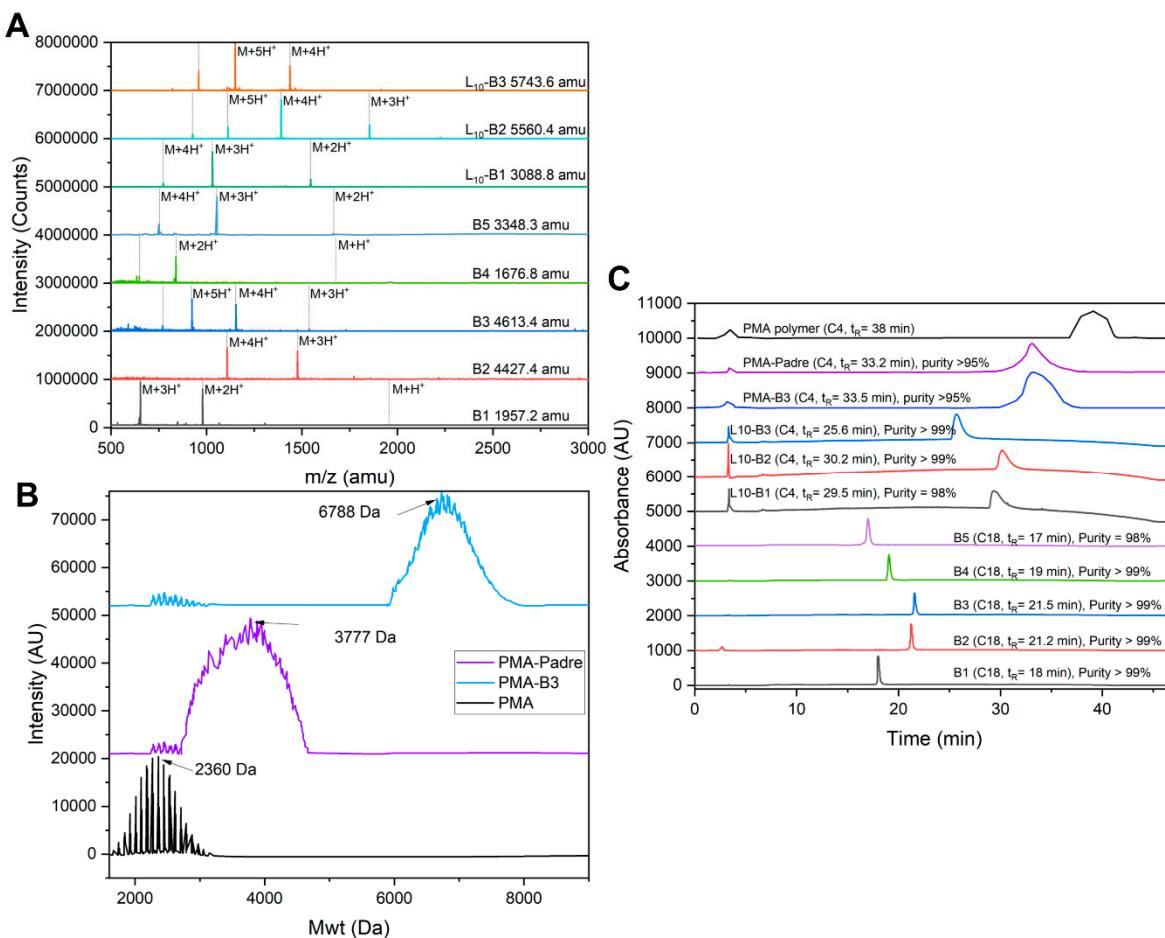


Figure S1. Characterization results of synthesized peptides and peptide conjugates by MS-ESI (A), MALDI-ToF (B), and RP-HPLC (C).

320 330 340 350
RV QPTESIVRFP NITNLCPFGE VFNATRFASV
 360 370 380 390 400
YAWNKRKISN CVADYSVLYN SASFSTFKCY GVSPTKLNDL CFTNVYADSF
 -----**B5** ($S^{366}-S^{395}$)-----
 410 420 430 440 450
VIRGDEVRQI APGQTGKIA D YNYKLPDDFT GCVIAWNSNN LDSKVGGNYN

 460 470 480 490 500
YLYRLFRKSN LKPFERDIST EIYQAGSTPC NGVEGFNCYF PLQSYGFQPT
 -----**B3** ($S^{444}-S^{483}$)-----**B2** ($S^{469}-S^{508}$)-----
 510 520 530 540 550
NGVGYQPYRV VVLSFELLHA PATVCGPKKS TNLVKNKCVN FNFNGLTGTG

 560 570 580 590 600
VLTESNKKFL PFQQFGRDIA DTDAVRDPQ TLEILDITPC SFGGVSVITP
 --**B4** ($S^{559}-S^{572}$)---
 610 620 630 640
GTNTSNQVAV LYQDVNCTEV PVAIHADQLT PTWRVYSTGS
 ---**B1** ($S^{623}-S^{639}$)---

Figure S2. Peptide antigen sequences B1-B5 (bolded) and their locations on the original Wuhan-1 strain SARS-CoV-2 spike protein sequence with RBD amino acid sequence coloured in blue. The italicized sequence “*STEIYQAGSTPCNGV*” is a part of both B2 and B3 sequences.

Table S1. Secondary structural content of screened and candidate peptide B-cell epitopes.

<i>Peptide</i>	<i>Experimental</i>			<i>i-tasser predicted</i> ^a			<i>Native (Cryo-EM)</i> ^a		
	Helix	Strand	Random Coil	Helix	Strand	Random Coil	Helix	Strand	Random Coil
<i>B1</i>	%	%	%	%	%	%	--	--	--
<i>B2</i>	28.5	2.5	69.0	47.0	0.0	53.0	0.0	10.0	90.0
<i>B3</i>	18.0	20.5	61.5	7.5	22.5	70.0	0.0	10.0	90.0
<i>B4</i>	29.0	0.0	71.0	59.0	0.0	41.0	0.0	10.0	90.0
<i>B5</i>	27.0	0.0	73.0	43.0	0.0	57.0	0.0	17.5	82.5
<i>L₁₀-B1</i>	0.0	59.5	40.5	10.0	20.0	70.0	13.0	13.0	74.0
<i>L₁₀-B2</i>	18.0	82.0	0.0	35.0	23.5	41.5	Non-native		
<i>L₁₀-B3</i>	95.0	0.0	5.0	22.5	0.0	77.5	Non-native		
	61.0	23.0	16.0	59.0	0.0	41.0	Non-native		

^a Predicted percentage results were calculated by summing the amino acid residues of a specific secondary structure, then dividing that by the total number of residues in the peptide [1,70].

The L10-conjugated peptide antigens were self-assembled in PBS, resulting in micro-particles (Figure S2). L10-B1, L10-B2, and L10-B3 self-assembled into particles with sizes of: $1.42 \pm 0.12 \mu\text{m}$, $1.32 \pm 0.08 \mu\text{m}$, and $1.38 \pm 0.17 \mu\text{m}$, respectively, with relatively small polydispersity indices (PDIs) for aggregating, self-assembled particles (PDI = 0.302 ± 0.072 , 0.265 ± 0.078 , and 0.398 ± 0.022 , respectively).

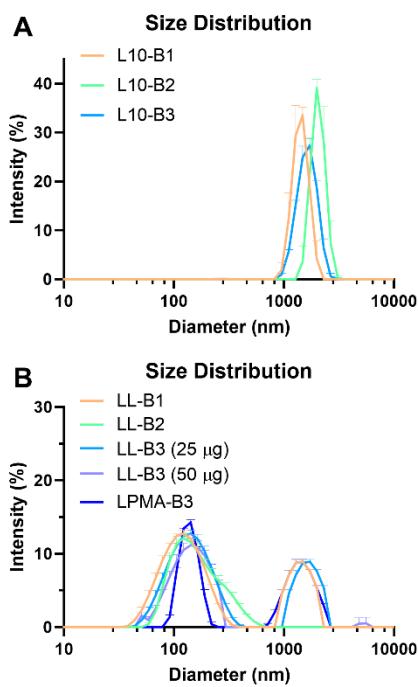


Figure S3. Size distribution of (A) self-assembled peptide antigens, and (B) liposomal formulations of polyleucine-, or PMA- conjugated peptides.

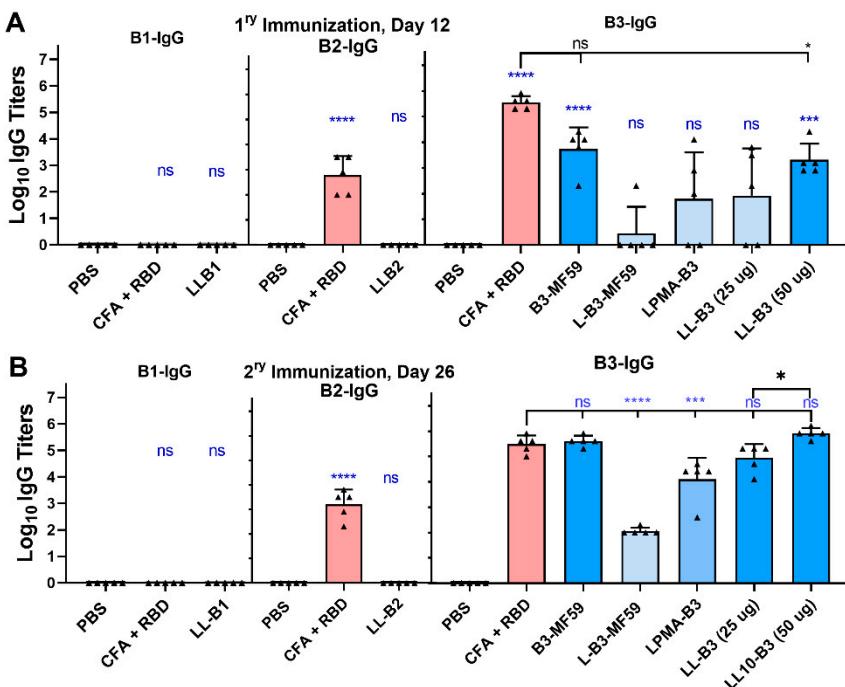


Figure S4. Immunogenicity results from the peptide adjuvant screening study following immunization of C57BL/6 mice. Anti-peptide IgG titers in the serum after primary immunization (A), and anti-peptide IgG titers against self-peptide antigens B1–B3 after secondary immunization (B). Error bars represent standard deviation. Statistical analysis was performed using one-way ANOVA with Dunnett's multiple comparison test. (ns) non-significant, $p > 0.05$; (*) $p < 0.05$; (**) $p < 0.01$; (***) $p < 0.001$, and (****) $p < 0.0001$.

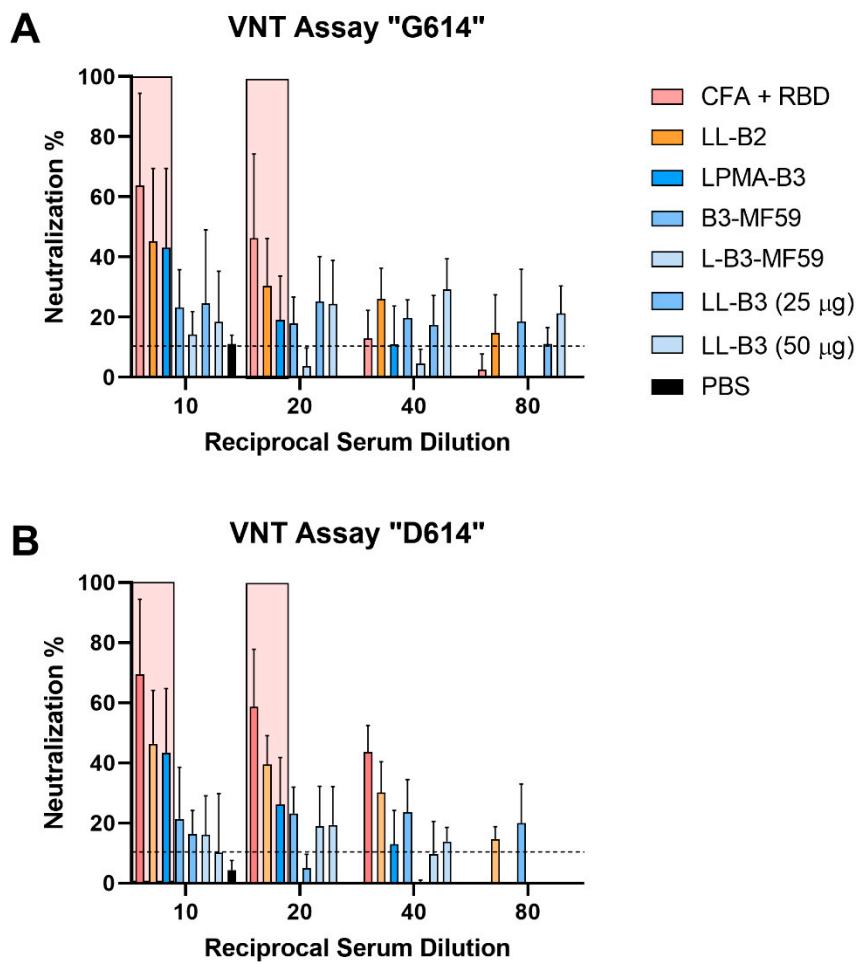


Figure S5. Live virus neutralization assays of mouse serum against the original SARS-CoV-2 Wuhan strain (G614) (A), and the D614 variant (B). Red boxes highlight the most promising neutralizing sera.