

## Supplementary Information

### **Impact of SARS-CoV-2 spike stability and RBD exposure on antigenicity and immunogenicity**

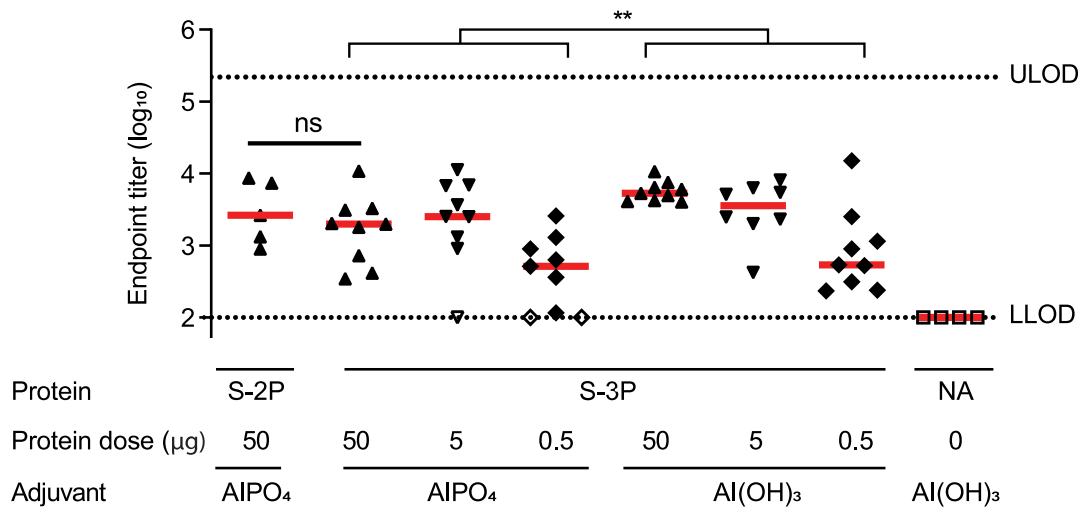
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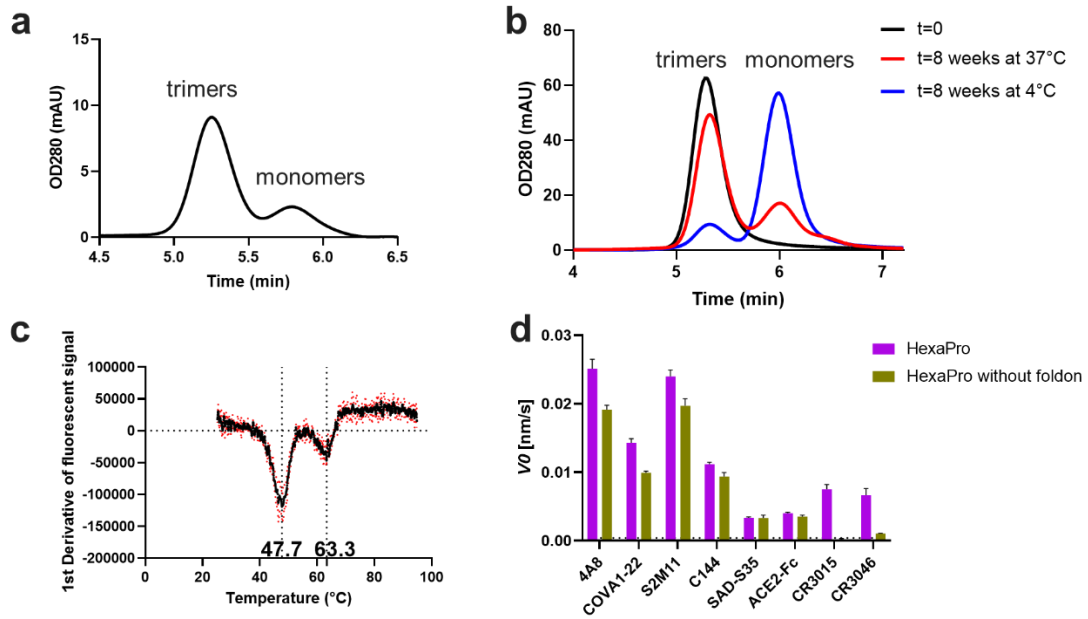
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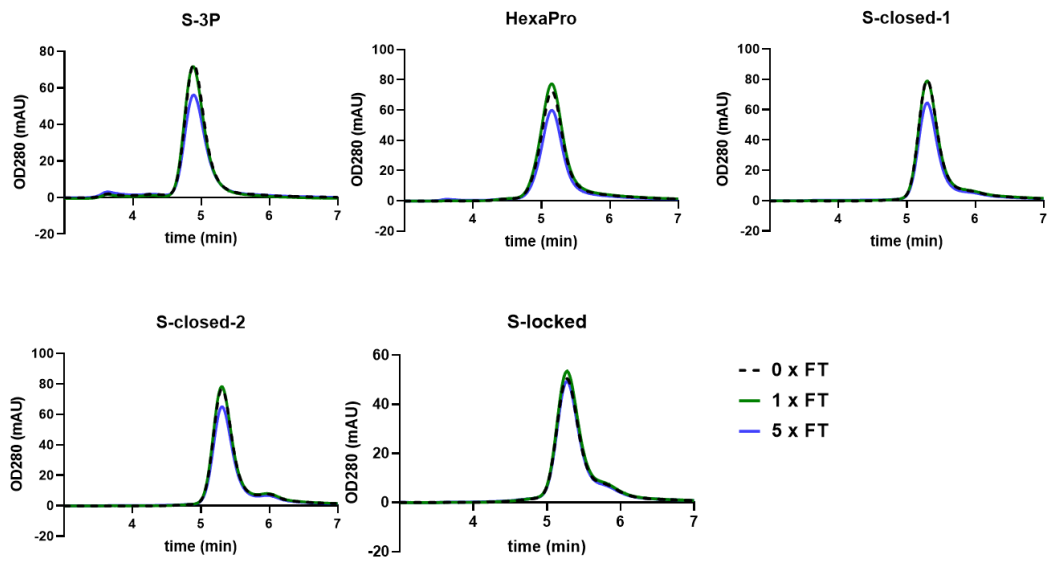
**Supplementary Figure S1. Immunogenicity of S-3P with Al(OH)<sub>3</sub> and Al(PO)<sub>4</sub>.** Mice were immunized at day 0 with 0.5, 5 or 50 µg S-3P adjuvanted with 100 µg Al(OH)<sub>3</sub> or AIPO<sub>4</sub> or 50 µg S-2P with 100 µg AIPO<sub>4</sub>. Spike-binding antibody titers were evaluated with ELISA at day 55. Red horizontal bars indicate the median response per group and the dotted lines indicates the upper and lower limits of detection (U/LLOD). Open symbols indicate response is at U/LLOD. 50 µg S-2P and S-3P adjuvanted with AIPO<sub>4</sub> were compared by a t-test. Differences between Al(OH)<sub>3</sub> and AIPO<sub>4</sub> were analyzed by a pairwise comparison across doses with a z-test from Tobit ANOVA. ns, not significant; \*\*, p<0.01.

S-3P	MFVFLVLLPLVSSQC	VNLLTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTFWFAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSN	100			
HexaPro			100			
S-closed-1			100			
S-closed-2			100			
S-locked			100			
S-3P	IRGWIFGTLLD	SKTQSLIVNNA	TNVKVFCEPFCNDPFLGVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLR	200		
HexaPro			200			
S-closed-1			200			
S-closed-2			200			
S-locked			200			
S-3P	FKIYSKHTPINL	VRDLPQGFSALEPLVDLP	IGINITRFQTLALHRSYLT	PGDSSSGWTAGAAAYVGYLQ	PRTFLKYNENGTITDAVDCALDPLSETK	300
HexaPro						300
S-closed-1						300
S-closed-2						300
S-locked						300
S-3P	CTLKSFTEKGI	YQTSNFRVQPTESIVRFP	NI	NLC	PFGEVFNATRFASVYAWNRKRIS	400
HexaPro						400
S-closed-1						400
S-closed-2						400
S-locked						400
S-3P	VIRGDEV	RQIAPQGTQKIADYNYKLPDD	FTGCVIANN	SNL	SKVGGNYNYLRLFRKSNL	500
HexaPro						500
S-closed-1						500
S-closed-2						500
S-locked						500
S-3P	NGVGYQ	PVVRVLLFPELLHAPATVCGPKK	SNL	VNFK	NVFNGLTGTGVL	600
HexaPro						600
S-closed-1						600
S-closed-2						600
S-locked						600
S-3P	GNISQ	NQAVLYQDVNCTEVPVAH	ADQLTPTWRVYSTG	SNV	FQTRAGCL	700
HexaPro						700
S-closed-1						700
S-closed-2						700
S-locked						700
S-3P	AENSVAYS	SNNSIAIPTNFTISV	TTTEILFVSMKTS	VDCTMYICGDST	EC	800
HexaPro						800
S-closed-1						800
S-closed-2						800
S-locked						800
S-3P	NFSQIL	PDPSKPSKRSFIEDLL	FNKVTLADAGFIK	YGDCLG	DI	900
HexaPro						900
S-closed-1						900
S-closed-2						900
S-locked						900
S-3P	QMA	YRNGIGV	TQNVLYENKLIAN	QFN	SAIGKI	1000
HexaPro						1000
S-closed-1						1000
S-closed-2						1000
S-locked						1000
S-3P	LQSLQ	TYVTQQLIRAAEIRAS	ANLAATRMSECVL	GGSKRVDF	CGKGYH	1100
HexaPro						1100
S-closed-1						1100
S-closed-2						1100
S-locked						1100
S-3P	HWFV	TQRNFYEQIIT	TDNTFVSGNCD	VVIGIVN	NTVYDPLQPEL	1200
HexaPro						1200
S-closed-1						1200
S-closed-2						1200
S-locked						1200
S-3P	QELG	YEQSSGYI	PEAPRDGQAYVR	KDGEWLL	STFLLPATGGSEPEA	1248
HexaPro						1248
S-closed-1						1208
S-closed-2						1208
S-locked						1208

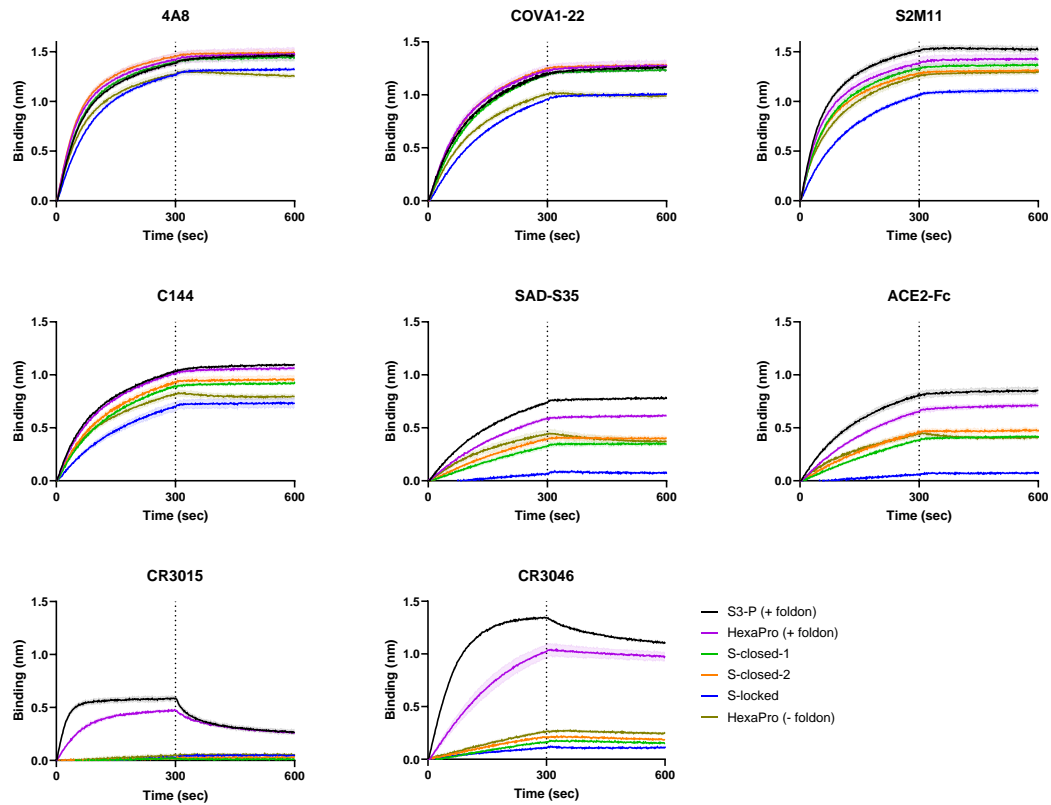
**Supplementary Figure S2. Protein sequence alignment of five stabilized spikes.** The signal peptide is indicated with a green background. The foldon trimerization domain followed by a sortase A tag and C-tag is indicated with a cyan background. All substitutions compared to the ectodomain sequence of the Wuhan-Hu-1 spike are indicated with a yellow background. A dot indicates that the amino acid is the same as in the first sequence and a dash indicates that the residue is missing compared to the first sequence.



**Supplementary Figure S3. Expression and characterization of HexaPro without a foldon trimerization domain.** (a) Analytical SEC on supernatant, reflecting trimer expression levels. (b) SEC pattern of purified protein at t=0, t=8 weeks at 37°C, and t=8 weeks at 4°C. (c) First derivatives of fluorescent signals measured with differential scanning fluorimetry (DSF) with the black curve showing the average of a technical triplicate. The average of three values of calculated melting temperatures in °C are shown below the valleys in the curves. (d) Biolayer Interferometry (BLI) showing the initial slope  $V_0$  at the start of binding with neutralizing antibodies 4A8 and COVA1-22 that bind to the NTD, and S2M11 and C144 that bind to the RBD irrespective of its position (up or down), and SAD-S35 and the ACE2 receptor that bind to the RBD when it is in the up position, and non-neutralizing antibodies CR3015 and CR3046 that bind epitopes in S2 that are shielded in the prefusion conformation. The lower limit of detection (LLOD) is indicated with a horizontal dotted line. Bars are plotted as average +SD (n=3 technical replicates).



**Supplementary Figure S4. SEC analysis before and after freeze-thawing.** Flash freezing in liquid nitrogen and thawing (freeze-thawing; FT) was performed one and five times.



**Supplementary Figure S5. Bi-layer interferometry using Octet.** Bi-layer interferometry curves of SARS-CoV-2 S proteins binding to ACE2-Fc fusion and diverse antibodies, as indicated above for each panel. The association curves (left of the vertical dotted line) were used to calculate the initial slope  $V_0$  plotted in Figures 2D, 2E, 2F and S3D. Right of the vertical dotted line dissociation is measured. Lines depict average of  $n=3$  technical replicates  $\pm$  standard deviation (shaded area).

**Supplementary Table S1.** SEC-MALS analysis of purified spikes

Protein	Theoretical Mw <sup>a</sup> (kDa) for trimer without glycans	T=0		T=8 weeks at 37°C		T=8 weeks at 4°C			
		Trimer		Trimer		Trimer		Monomer	
		Mw <sup>a</sup> (kDa)	Rh <sup>b</sup> (nm)	Mw <sup>a</sup> (kDa)	Rh <sup>b</sup> (nm)	Mw <sup>a</sup> (kDa)	Rh <sup>b</sup> (nm)	Mw <sup>a</sup> (kDa)	Rh <sup>b</sup> (nm)
S-3P	409.5	466	11.00	464.2	9.8	494.9	10.5	NA <sup>c</sup>	NA <sup>c</sup>
HexaPro	409.5	453.3	9.5	462.5	9.1	454.6	9.7	NA <sup>c</sup>	NA <sup>c</sup>
S-closed-1	397.0	455.6	9.1	466.5	8.8	447.7	8.8	175.3	ND <sup>d</sup>
S-closed-2	396.8	439.5	8.9	454.3	8.7	451.1	8.8	159.3	6.2
S-locked	397.2	462.4	9.2	456.3	8.8	471.4	8.7	NA <sup>c</sup>	NA <sup>c</sup>

<sup>a</sup> Mw stands for molecular weight

<sup>b</sup> Rh stands for hydrodynamic radius

<sup>c</sup> NA stands for not applicable

<sup>d</sup> ND stands for not determined