Supplementary Methods

Repeat Protein Scaffolds. Repeat proteins, comprised of recurring 20-50 residue stretches, are ideal for use in protein-based material design due to their high stability and capability to have altered lengths and curvatures by varying the number of repeating modules. Listed below are the RCSB Protein Data Bank entries for scaffolds used in this study. An additional set of scaffolds is provided in which experimental small-angle X-ray scattering data agreed with the computational model[1].

X-ray Structures (PDB ID)	SAXS Validated Models
1na0 (1NA0)	tpr1
3ltj (3LTJ)	HR00
2fo7 (2FO7)	
HR04 (5CWB)	
HR07 (5CWD)	
HR10 (5CWG)	

Protein Expression and Purification from E. coli. Synthetic genes for designed proteins were optimized for *E. coli* expression and assembled from purchased genes (Genscript or Gen9) ligated into the pET21-NESG (designed trimers) or pET28b-NESG (designed nanoparticles) vector at restriction sites NdeI and XhoI or NcoI and XhoI respectively. A second ribosome-binding site was inserted between the open-reading frames of individual components of nanoparticle designs ("AGAAGGAGATATCAT"), such that the two proteins would be co-expressed and screened for co-elution by SDS-PAGE. Plasmids were cloned into BL21 or Lemo21 (DE3) *E. coli* competent cells. Transformants were inoculated and grown in 5 mL of either LB or TB medium with either 100 mg/L carbenicillin or 100 μg/L kanamycin at 37 °C overnight. Subsequently, liquid cultures were inoculated 1:100 (v:v) and grown at 37 °C until an OD_{600} of 0.5-0.8. Isopropyl-thio-β-D-

galactopyranoside (IPTG) was then added at a concentration of 0.5-1 mM and growth temperature was reduced to 18 °C to induce protein expression, or cultures were left at 37 °C and auto-induced by virtue of the media-included galactose according to the Studier protocols[2]. Expression proceeded for 20 hours until the cell cultures were harvested by centrifugation. Cell pellets were resuspended in 25 mM Tris, 150 mM NaCl, 5mM imidazole, DNase, EDTA-free protease inhibitors (Pierce), pH 8.0. and lysed by sonication or microfluidization. Each protein was then purified from lysate by Ni^{2+} immobilized metal affinity chromatography (IMAC) with Ni-NTA Superflow resin (Qiagen or GE). Resin with bound cell lysate was washed with 15 column volumes of 25 mM Tris, 150 mM NaCl, 40 mM imidazole, pH 8.0. Proteins were eluted with 5 column volumes of 25 mM Tris, 150 mM NaCl, 400 mM imidazole, pH 8.0 for further purification by size exclusion chromatography.

Size-Exclusion Chromatography. Elution samples for each designed protein were concentrated down using a 10,000 MWCO protein concentrator (Novagen) and fractionated by size on an AKTA pure chromatography system using a Superdex 200 or Superose 6 10/300 GL gel filtration column (GE Life Sciences) in 25 mM Tris, 150 mM NaCl, pH 8.0 (TBS). Sizing profiles were noted based on absorption at 220 nm and 280 nm wavelength light for each fraction. Molecular weights for predominant species in each protein trace were estimated by comparison to the corresponding monomeric profile.

Analytical Size-Exclusion Chromatography on Sephacryl S-500. Purified HA-bearing nanoparticles or trimers were applied to a Sephacryl S-500 column pre-equilibrated with

25 mM Tris, 2 M NaCl, 5% glycerol, pH 8.0 . Sizing profiles were recorded based on absorption at 280 nm wavelength light.

Size-Exclusion Chromatography with Multi-Angle Light Scattering. Fractions containing single predominant species from the initial round of size exclusion chromatography were concentrated down with 10,000 MWCO protein concentrators (Novagen) to a concentration of 1.0-2.0 mg/mL and run through a high-performance liquid chromatography system (Agilent) using a Superdex 200 or Superose 6 10/300 GL gel filtration column (GE Life Sciences) in TBS buffer. These fractionation runs were coupled to a multi-angle light scattering detector (Wyatt) in order to determine the absolute molecular weights for each designed protein complex.

Small-Angle X-ray Scattering. Designed proteins that predominantly formed the target oligomeric species were re-expressed and purified for low-resolution solution structure determination by small-angle X-ray scattering (SAXS) at the SIBYLS High Throughput SAXS Advanced Light Source in Berkeley, California[3]. A beam exposure time of between 0.3-10 seconds was used to obtain averaged diffraction data (SAXS FrameSlice Application), which are represented in plots of log intensity (I) vs. q. A 11kEV/1.125A X-ray beam was used with a 2 m beamstop.

Crystallization Conditions. Design 1na0C3_2 was found to crystallize in 1 M LiCl, 100 mM citrate, 20% w/v PEG 6000, pH 4, and was frozen using 25% glycerol as cryoprotectant. Design 3ltjC3_1 crystallized in 1 mM DL-glutamic acid monohydrate, 100

mM DL-alanine, 100 mM glycine, 100 mM DL-lysine monohydrochloride, 100 mM DL-serine; 100 mM Tris, 100 mM BICINE, 20% v/v ethylene glycol, 10% w/v PEG 8000, pH 8.5. Diffraction data for each of these designs were collected at the Advanced Light Source (Beamline 8.2.1) at Lawrence Berkeley National Laboratory in Berkeley, California. Both trimer designs contained uncleaved C terminal His_6-tags in crystallized conditions.

Data collection, structure determination and refinement. Diffraction data for 3ltjC3_1 was collected on beamline 5.0.1 at the Advanced Light Source (Berkeley, CA) and 1na0C3_2 on beamline 8.2.1, both using an ADSC Q315R CCD area detector. Both datasets were scaled and merged in HKL2000[4]. The structures were phased by molecular replacement, with the computational design as the search model, using the program PHASER[5] in the PHENIX software suite[6]. Iterative rounds of manual model building and refinement were conducted in Coot[7] and Phenix.refine[8], respectively for both structures. Hydrogens were added for all refinement runs. The geometric quality of the final model was assessed using the Molprobity server[9]. Resolution cutoff was determined by monitoring the refinement statistics in the context of the reflection data completeness and the $CC^{1/2}$ and I/σI values[10].

I53_dn5 *in vitro* Assembly. The ability of the two nanoparticle components of I53_dn5 to be separately purified and then mixed to achieve nanoparticle assembly was assessed. Genes for the individual oligomeric components were cloned into expression vectors and expressed independently in *E. coli*. The His_6-tagged proteins were purified following the

purification protocol described above for the designed trimers. Initial size-exclusion chromatograms for the components were obtained on a Superdex 200 10/300 GL column, and predominant peak species were stoichiometrically mixed in TBS buffer for 20 minutes at 25 °C. A secondary size-exclusion step was performed on a Superose 6 10/300GL column to assess assembly of the intended particle based on expected retention volume.

Nanoparticle Structural Model Building and Refinement from CryoEM data. Post-processed maps from Relion were used to relax and refine nanoparticle models. Rosetta relaxed refinement[11] was performed for all datasets using the Rosetta design models of T33_dn10, O43_dn18, and I53_dn5 nanoparticles as inputs. Appropriate symmetry was enforced during model refinement. EMRinger[12] and Molprobity[12,13] scores were used to evaluate the output structures. The best models for each nanoparticle were then manually inspected and edited in Coot v0.9-pre[7]. For T33_dn10 and O43_dn18 datasets this procedure was repeated 2 more times to generate the final structures. The resulting models have been deposited to the PDB database with the IDs: 6VFH (T33_dn10), 6VFI (O43_dn18), and 6VFJ (I53_dn5). Model refinement statistics is shown in Supplementary Table 5.

Production and Purification of BG505 SOSIP–T33_dn2A, BG505 SOSIP–T33_dn10A, and BG505 SOSIP–I53_dn5B. Synthetic genes were optimized for mammalian expression and subcloned into pPPI4 vector. BamHI and NheI restriction sites were used for insertion of different nanoparticle assembly components to the C-

terminus of BG505 SOSIP. Quick Ligation kit, BamHI-HF, and NheI-HF restriction enzymes were purchased from New England Biolabs (NEB). BG505 SOSIP variant used for all early optimizations steps was engineered with a combination of v5.2[14] (mutations: E64K, A73C, A316W, A561C) and MD3D[14,15] (mutations: M271I, A318Y, R585H, L568D, V570H, R304V, F519S) stabilizing mutations, and had glycosylation sites introduced at positions 241 and 289 (mutations: P240T, S241N, F288L, T290E, P291S). This construct was termed BG505 SOSIP.v5.2(7S). For epitope-accessibility experiments (by surface plasmon resonance), a version of this construct was designed without the 241 and 289 glycans. Protein sequences of different constructs used here are shown in Supplementary Table 9. HEK 293F cells were grown in suspension using FreeStyle 293 Expression Medium (Thermo Fisher Scientific) at 135 RPM, 8% CO_2, 80% humidity, 37 °C. At confluency of ~1×10^{-6} cells/ml, the cells were co-transfected with pPPI4 DNA vectors encoding the appropriate fusion component (250 µg per 1 L of cells) and furin protease (80 µg per 1 L of cells). Polyethyleneimine (Polysciences Inc) used as transfection reagent (1 mg per 1 L of cells). Cells were incubated for 6 days, after which they were spun down by centrifugation (7,000 RPM, 1 hour, 4 C) and the protein-containing supernatant was further clarified by vacuum-filtration (0.45 µm, Millipore Sigma). For immuno-affinity chromatography steps, Sepharose 4B columns with immobilized PGT145 IgG were used. Fusion components were eluted with 3 M magnesium chloride, 250 mM L-Arginine buffer, pH 7.2 into an equal volume of gel filtration buffer (25 mM Tris, 250 mM L-Arginine, 500 mM NaCl, 5 % glycerol, pH 7.4). Eluates were concentrated and buffer exchanged into gel filtration buffer. A Sephacryl S200 16/600 column was used for subsequent gel filtration.

Production and Purification of HA–I53_dn5B. Synthetic genes were optimized for mammalian expression and subcloned into the CMV/R vector (VRC 8400)[16]. XbaI and AvrII restriction sites were used for insertion of I53_dn5B component to the C terminus of the H1 HA ectodomain (residues 1-676 from A/Michigan/45/2015) which also contained a Y98F mutation to prevent sialic-acid binding and self-aggregation during expression[17]. Gene synthesis and cloning was performed by Genscript. The protein sequence of HA–I53_dn5B is shown in Supplementary Table 8. HEK 293F cells were grown in suspension using Expi293 Expression Medium (Thermo Fisher Scientific) at 150 RPM, 8% CO_2, 70% humidity, 37 °C. At confluency of ~2.5×10^{-6} cells/mL, the cells were co-transfected with the vector encoding HA–I53_dn5B (1000 µg per 1 L of cells). Expifectamine was used as transfection reagent according to the manufacturer's protocol. Cells were incubated for 96 hours, after which they were spun down by centrifugation (4,000 RPM, 20 min, 4 °C) and the protein-containing supernatant was further clarified by vacuum-filtration (0.45 µm, Millipore Sigma). For nickel-affinity chromatography steps, a background of 50 mM Tris, 350 mM NaCl, pH 8.0 was added to clarified supernatant. For each liter of supernatant, 4 mL of Ni Sepharose excel resin (GE) was rinsed into phosphate-buffered saline (PBS) using a gravity column and then added to the supernatant, followed by overnight shaking at 4 °C. After 16-24 hours, resin was collected and separated from the mixture and washed twice with 50 mM Tris, 500 mM NaCl, 30 mM imidazole, pH 8.0 prior to elution of desired protein with 50 mM Tris, 500 mM NaCl, 300 mM imidazole, pH 8.0. Eluates were concentrated and applied to a HiLoad 16/600 Superdex 200 pg column pre-equilibrated with PBS for gel filtration.

Production and Purification of DS-Cav1–Fusion Nanoparticles. Gene synthesis and cloning was performed by Genscript. The protein sequence for DS-Cav1–I53_dn5b is shown in Supplementary Table 8. HEK 293F cells were grown in suspension using Expi293 expression medium (Thermo Fisher Scientific) at 150 RPM, 8% CO_2, 70% humidity, 37 °C. At confluency of ~2.5 to 3×10^6 cells/ml, the cells were transiently transfected with the vector encoding DS-Cav1–I53_dn5B (1 mg per 1 L of cells). Expifectamine was used as transfection reagent according to the manufacturer's protocol. Cells were incubated for 96 hours and spun down by centrifugation (4,000 RPM for 20 minutes at 4 °C). Supernatant was vacuum-filtered (0.45 μm, Millipore Sigma) and 50 mM Tris, 350 mM NaCl, pH 8.0 was added for nickel-affinity chromatography. Ni Sepharose resin (GE) was washed three times with PBS by centrifugation (2,000 RPM for 5 minutes at 4 °C) and added to the supernatant. Nickel-supernatant was incubated either overnight at 4 °C or for 2 hours at room temperature. Resin was collected and separated from the mixture and washed twice with 50 mM Tris, 500 mM NaCl, 30 mM imidazole, pH 8.0 prior to elution of desired protein with 50 mM Tris, 500 mM NaCl, 300 mM imidazole, pH 8.0. Eluates were concentrated and applied to a HiLoad 10/300 Superdex 200 Increase GL column pre-equilibrated with PBS size exclusion chromatography.

Assembly and Purification of Antigen-Fused Nanoparticles. Several reactions containing 5-10 μg of the purified fusion component and an equimolar amount of the counter bare assembly component were prepared and incubated under different conditions (varying temperature and assembly buffer) for 24 hours. Native PAGE Bis-Tris

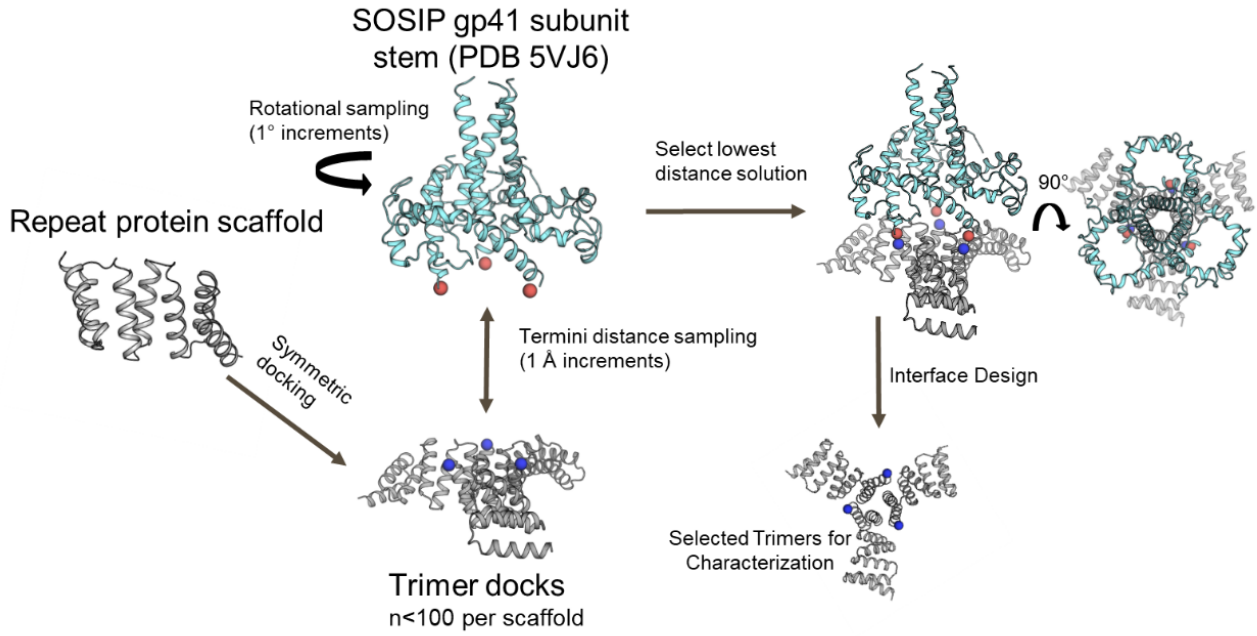
gels (Thermo Fisher Scientific) and negative stain electron microscopy was used for detection of assembly efficacy. Following the identification of optimal assembly conditions, milligram quantities of particles were assembled and purified using gel filtration chromatography (Superose 6 or Sepharose 500 column) with TBS as the running buffer. Fractions corresponding to the fusion component were pooled and concentrated (Amicon Ultra Centrifugal Filter Units, Millipore Sigma).

Biolayer Interferometry on HA–I53_dn5. To produce biotin-labeled antibodies specific to the H1 HA head, 5J8 monoclonal antibody (mAb)[18] in PBS was mixed with a 20× molar excess (relative to complete antibodies) of EZ-Link™ NHS-LC-Biotin (Thermo Fisher Scientific) and allowed to sit for 2 hours at 4 °C, followed by two rounds of overnight dialysis against PBS at 4 °C to remove excess biotinylation reagent. All biosensors were hydrated in assay buffer (25 mM Tris, 150 mM NaCl, 0.5% bovine serum albumin, 0.01% TWEEN 20, pH 8.0) before use. Biotinylated 5J8 (0.02 mg/mL in assay buffer) was immobilized on SA biosensors, then briefly dipped in assay buffer prior to exposure to designed H1 HA fusions (500 nM per asymmetric unit, in assay buffer). The biosensor was again dipped in assay buffer and then exposed to the stem-specific CR6261 mAb[19].

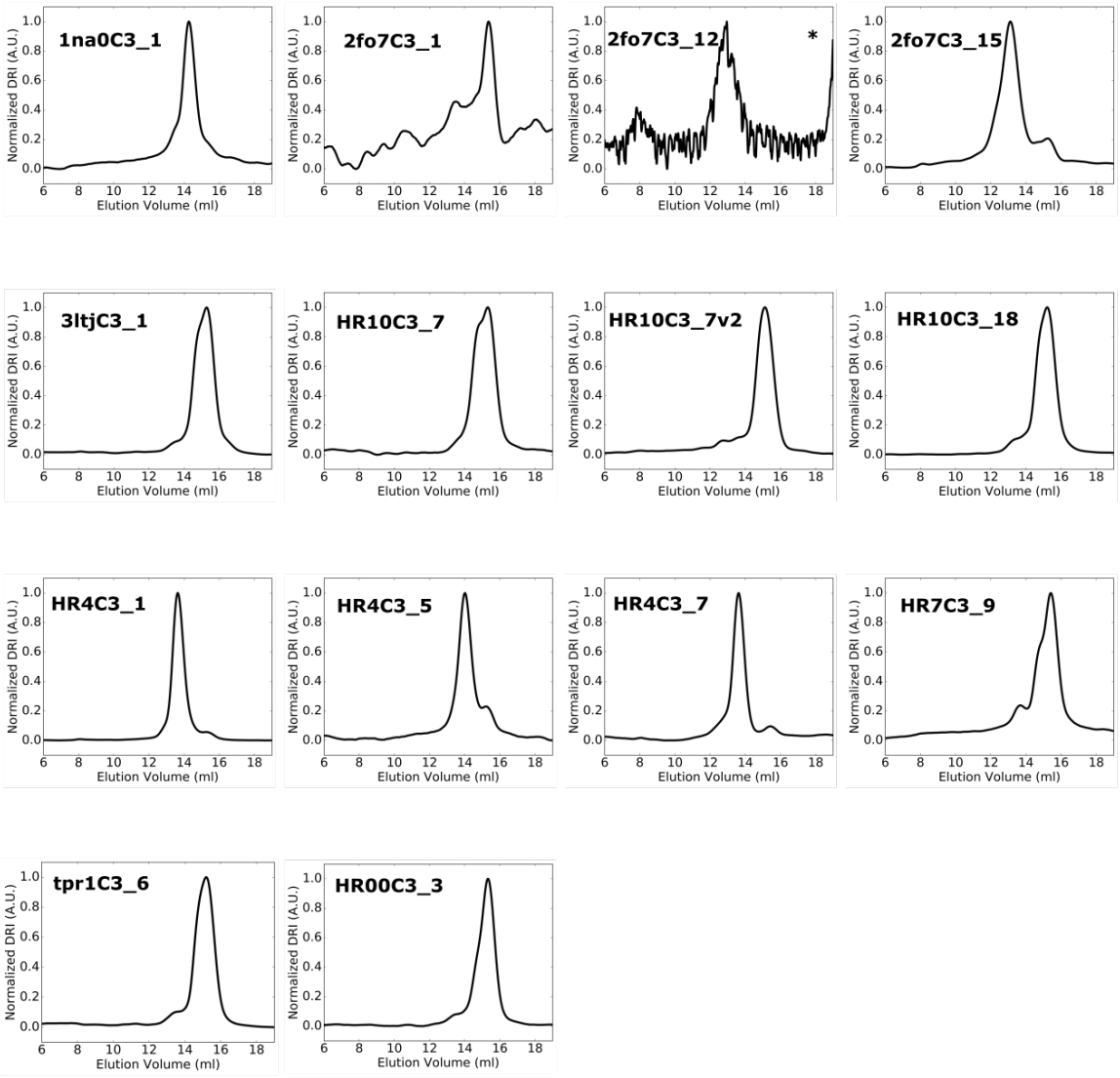
ELISA Assays on DS-Cav1–I53_dn5. ELISA was used to measure binding kinetics of DS-Cav1–I53_dn5 to RSV F-specific mAbs D25, Motavizumab, and AM14. D25 is a pre-fusion specific mAb that binds site Ø[20]. Motavizumab binds site II of the pre and post-fusion conformations. AM14 is trimer-specific binding across protomers of pre-F. 96-well enzyme-linked immunosorbent assay (ELISA) plates were coated with 2 μg/mL DS-

Cav1/H1 HA nanoparticles. Plates were incubated at 4 °C overnight and blocked with PBS containing 5% skim milk at 37 °C for 30 minutes. mAbs listed above serially diluted in fourfold steps, were then added and the plates incubated at 37 °C for 45 minutes. Horseradish peroxidase (HRP)-conjugated anti-human IgG (Southern Biotech., Birmingham, AL) was added and incubated at 37 °C for 30 minutes, followed by 3,3′,5′,5-Tetramethylbenzidine (TMB; Sigma-Aldrich, St. Louis, MO) HRP substrate, and yellow color that developed after the addition of 1 M H_2SO_4 was measured by absorbance at 450 nm.

Supplementary Figures

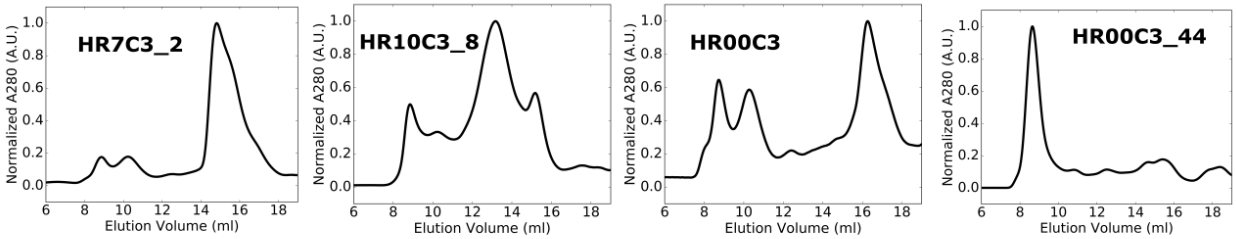


Supplementary Figure 1. *In silico* trimer docking and antigen targeting strategy. Designs for C3-symmetric trimers (N terminal residue labeled in blue) capable of scaffolding target antigens shown in gray. BG505 SOSIP (C terminal residue 664 labeled in red) trimeric glycoprotein subunit gp41 shown in cyan for illustration of targeting strategy.

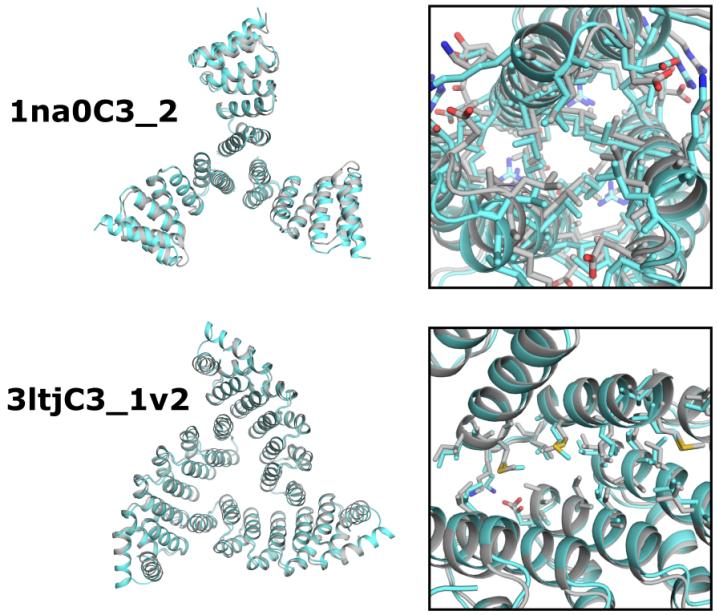


*Chromatogram obtained on Superdex 75 10/300 GL gel filtration column.

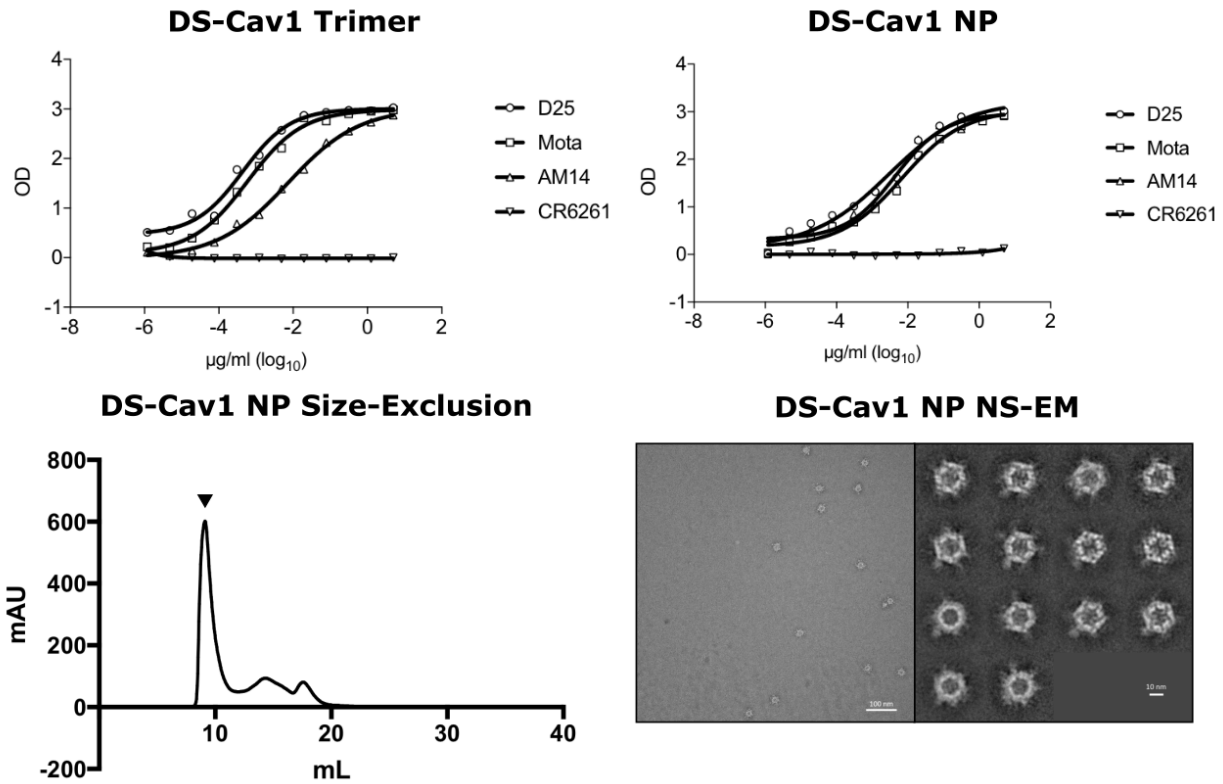
Supplementary Figure 2. SEC-MALS chromatograms for failed designs, occupying an unintended oligomeric configuration. Predominant oligomeric species for each design were collected by fractionation from a primary size exclusion run, and 14 sizing profiles are presented here from the subsequent round of high-performance size exclusion chromatography from a Superdex 200 gel filtration column.



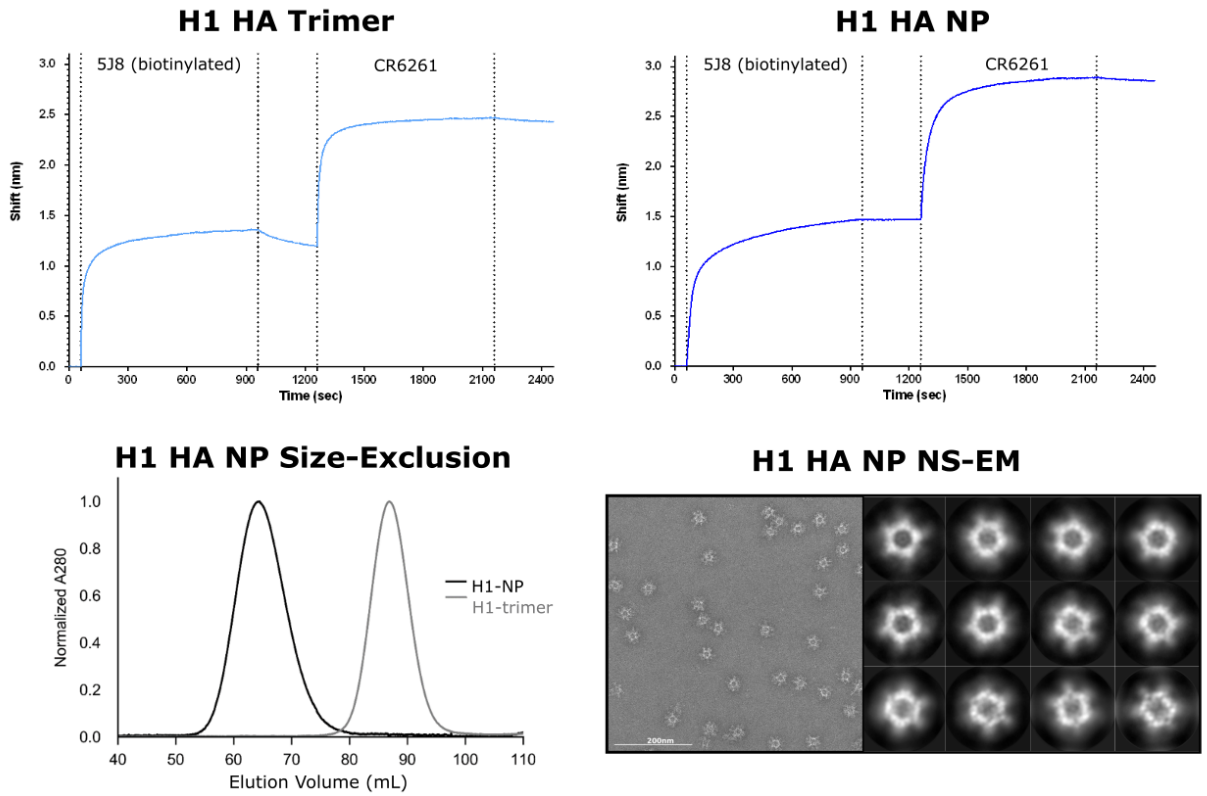
Supplementary Figure 3. SEC chromatograms for trimers with off-target retention volumes after Ni^{2+} IMAC. Primary size exclusion chromatograms obtained from a Superdex 200 gel filtration column for soluble proteins directly after purification by Ni^{2+} IMAC. 2 designs displayed polydisperse profiles indicating formation of off-target oligomers, whereas 4 designs formed soluble aggregate.



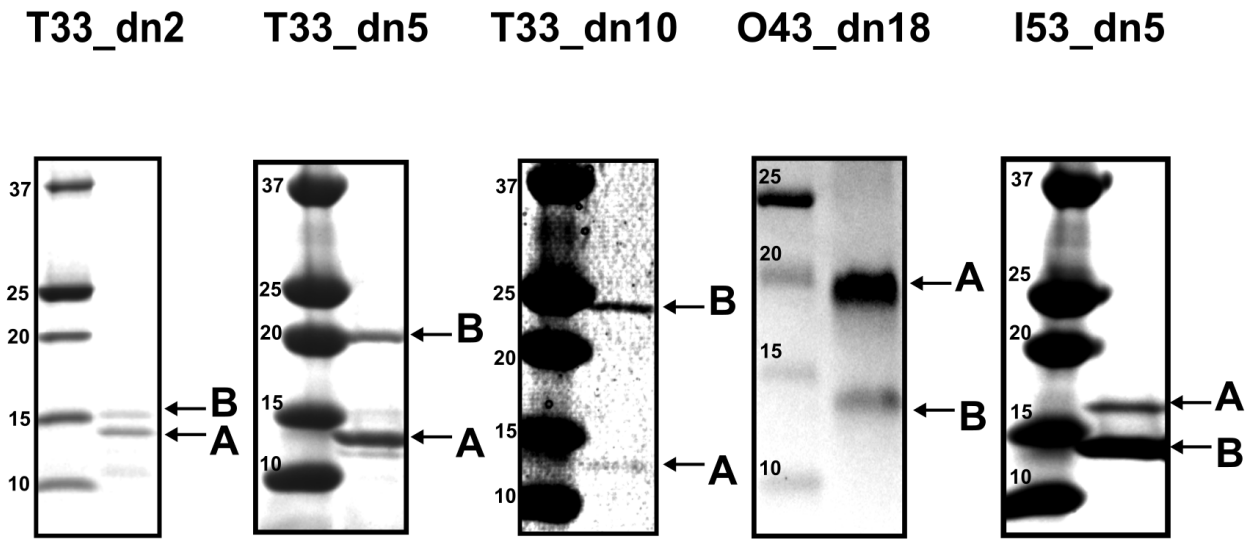
Supplementary Figure 4. Comparison between the experimentally determined crystal structures and corresponding models of designed trimers. A full model and crystal structure superposition is displayed, with crystal structures shown in cyan and models in gray. Magnified view illustrates the side chains at the designed interface.



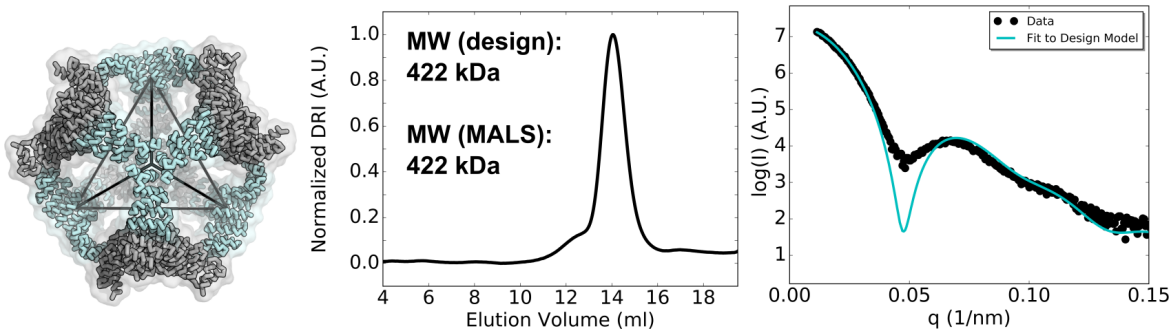
Supplementary Figure 5. Top panel: ELISA using anti-DS-Cav1 antibodies bound to DS-Cav1 trimer with foldon or designed nanoparticle I53_dn5. Fluorescence signal is plotted as a function of binding to purified trimer and nanoparticle. Bottom panel: size-exclusion profile of DS-Cav1–I53_dn5 particle assembly on a Superose 6 column and negative stain electron micrograph field image and 2D class averages of purified particle.



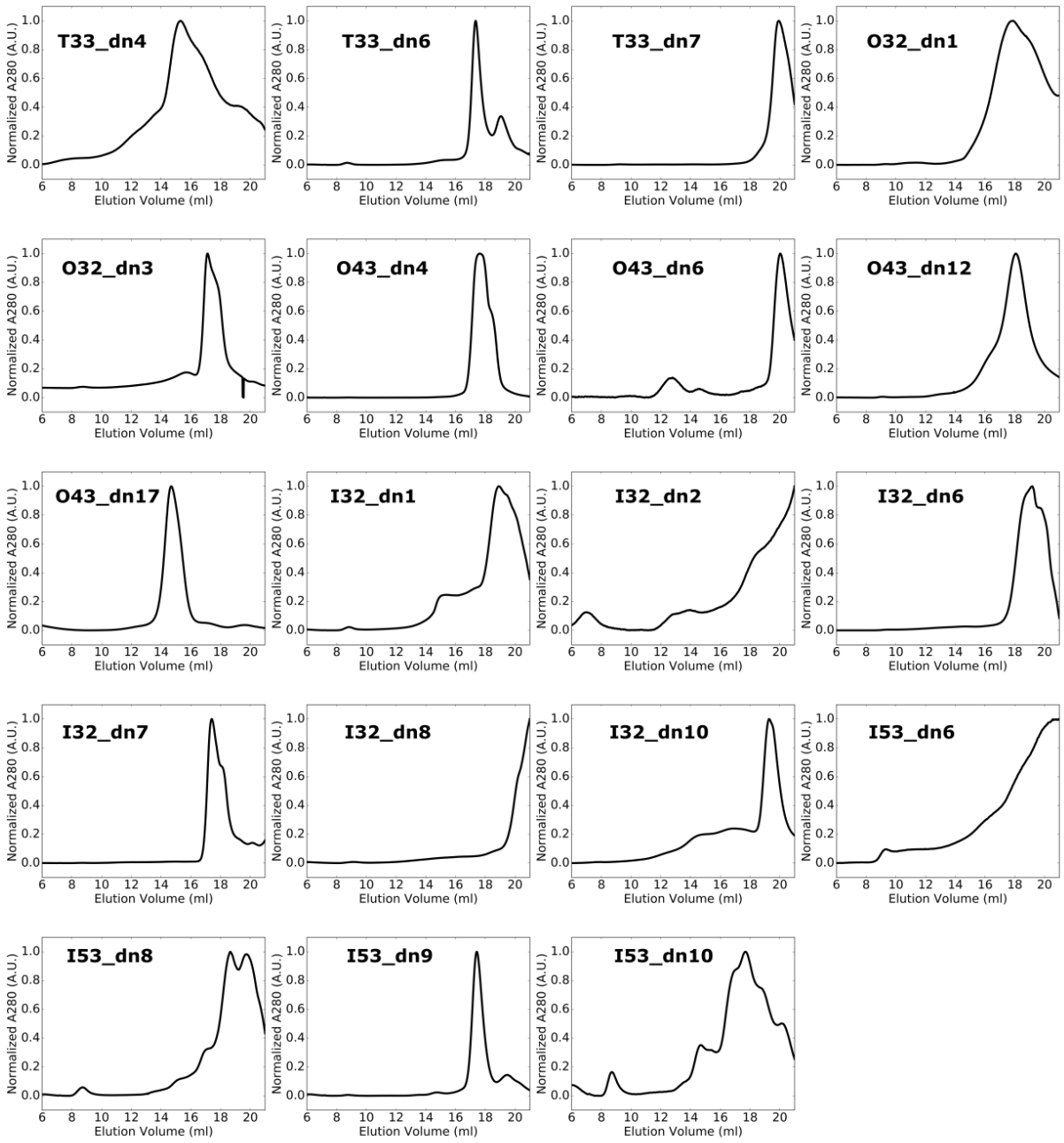
Supplementary Figure 6. Top panel: Octet bio-layer interferometry using plate-coated head-directed H1 HA mAb (5J8) for antigen capture, and subsequent stem-directed H1 HA mAb (CR6261) addition to both HA–I53_dn5 (NP) and corresponding trimeric component HA–I53_dn5B (trimer). Bottom panel: size-exclusion profile of HA–I53_dn5 assembled particle and corresponding trimer HA–dn5B assembly on a Sephacryl S-500 column, and negative stain electron micrograph field image and 2D class averages of purified particle.



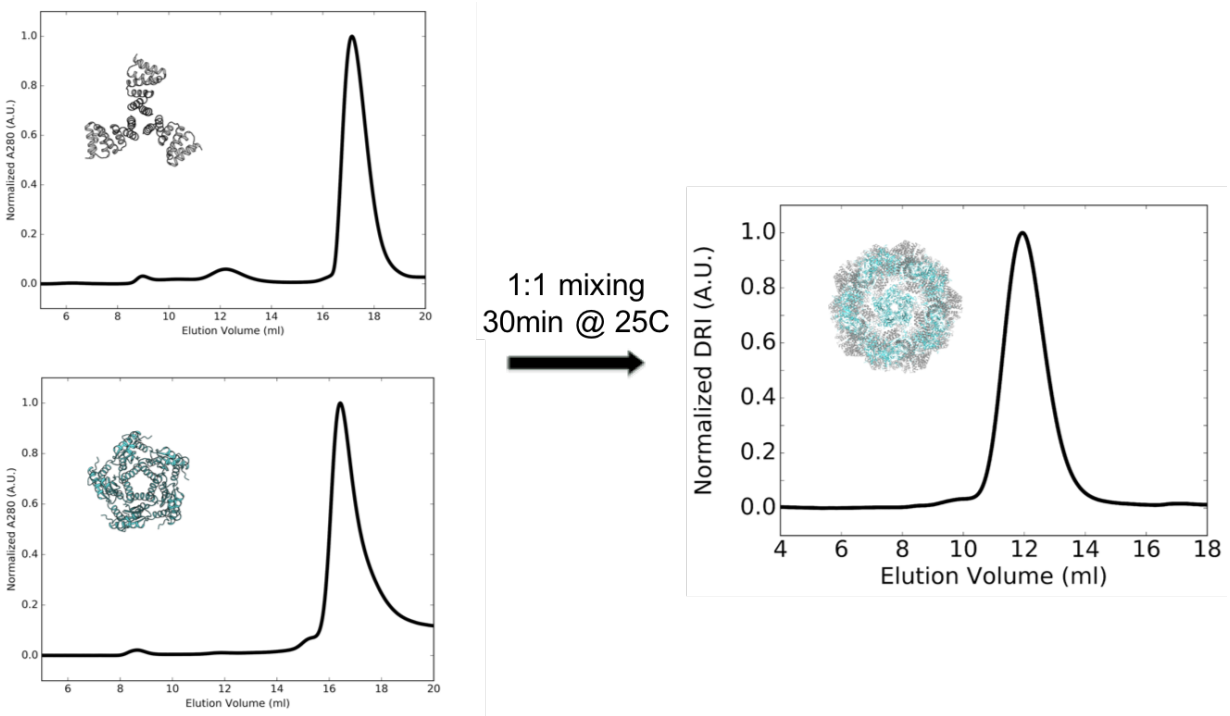
Supplementary Figure 7. SDS-PAGE of bicistronically-expressed de novo nanoparticle eluted from Ni^{2+} IMAC. For each designed nanoparticle: Left - protein standard (Precision Plus Dual Xtra, Bio-Rad). Right - labeled bands corresponding to the expected size of each component.



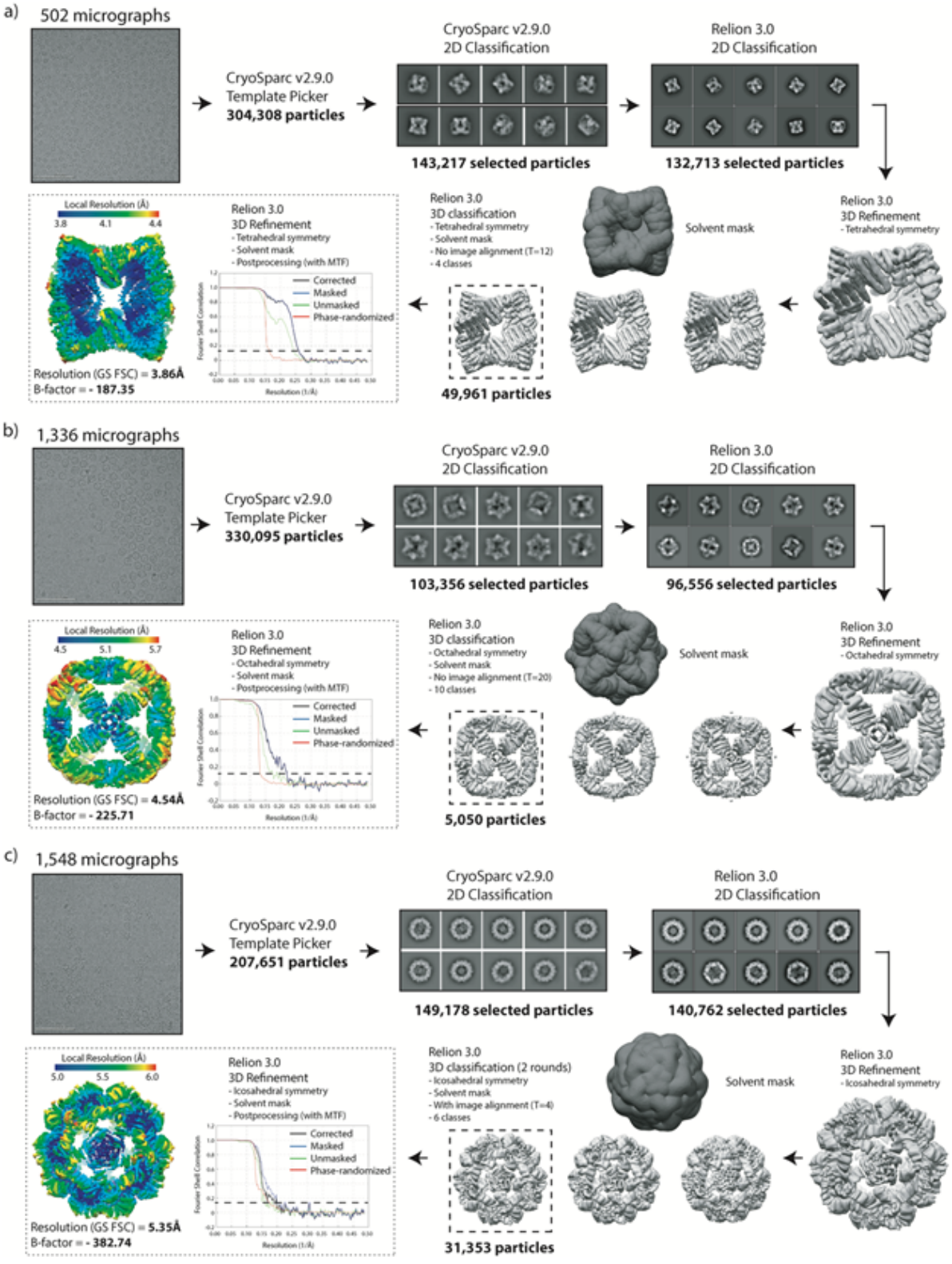
Supplementary Figure 8. Biophysical Characterization of T33_dn5. Left - designed model. Middle - size-exclusion chromatograms and calculated molecular weights from multi-angle light scattering. Right - small-angle X-ray scattering comparisons between experimental data and profile computed from model.



Supplementary Figure 9. SEC profiles for two-component nanoparticles that failed to co-assemble as predicted by Rosetta. Primary size exclusion chromatograms obtained from a Superose 6 gel filtration column for soluble proteins directly after purification by Ni^{2+} IMAC. Designs presented here appear to form off-target assemblies based on retention volume or occupy polydisperse complex states.



Supplementary Figure 10. Size-exclusion chromatogram of individual components I53_dn5A (pentamer) and I53_dn5B (trimer) and assembly run on a Superose 6 10/300 GL column.



Supplementary Figure 11. Cryo-electron microscopy data processing workflow and relevant statistics for a) T33_dn10, b) O43_dn18, and c) I53_dn5.

Supplementary Tables

Design	Targeted Antigens	Experimental Molecular Weight (kDa)	Target Molecular Weight (kDa)	SAXS *X* value	Resolution, r.m.s.d. structure (Å, Å)
1na0C3_2	HA, SOSIP, DS-Cav1	48	45	1.4	2.6, 1.4
3ltjC3_1v2	SOSIP, DS-Cav1	56	63	1.1	2.3, 0.8
3ltjC3_11	SOSIP, DS-Cav1	50	66	1.6	--
HR04C3_5v2	SOSIP	71	69	1.5	--
T33_dn2	HA, SOSIP, DS-Cav1	397	345	4.8	--
T33_dn5	HA, SOSIP, DS-Cav1	422	422	1.7	--
T33_dn10	HA, SOSIP, DS-Cav1	546	556	2.3	3.9, 0.65
O43_dn18	HA,SOSIP, DS-Cav1	810	876	2.9	4.5, 0.98
I53_dn5	HA, SOSIP, DS-Cav1	2000	1960	1.2	5.3, 1.30

Supplementary Table 1. Summary of the experimental results from characterization of the antigen-tailored symmetric homotrimeric proteins and subsequent two-component nanoparticles. 1na0C3_2 and 3ltjC3_1v2 structures determined by X-ray crystallography and T33_dn10, O43_dn18, and I53_dn5 determined by cryo-electron microscopy.

Design	Target Molecular Weight (kDa)	Experimental Molecular Weight (kDa)	Approximate Oligomerization State
1na0C3_1	44	43	3
2fo7C3_1	51	20	1
2fo7C3_12	50	106	6
2fo7C3_15	51	70	4
3ltjC3_1	63	37	2
HR10C3_7	67	47	2
HR10C3_7v2	67	38	2
HR10C3_18	67	35	2
HR4C3_1	69	75	3
HR4C3_5	69	61	3
HR4C3_7	68	65	3
HR7C3_9	56	30	2
tpr1C3_6	48	28	2
HR00C3_3	94	37	1

Supplementary Table 2. SEC-MALS data for designs intended to be homotrimeric with C3 symmetry.

Design	MW A (kDa)	MW B (kDa)	MW model (kDa)	MW exp (kDa)	Rg model (Å)	Rg exp (Å)	Dmax model (Å)	Dmax exp (Å)	*X*	qmax (1/nm)
1na0C3_2	14.99	-	44.97	48	26.4	29.5	84	86	1.4	0.23
3ltjC3_1v2	20.90	-	62.69	56	27.7	31.3	88	94	1.1	0.18
3ltjC3_11	22.21	-	66.62	50	28.3	30.3	87	92	1.6	0.20
HR04C3_5v2	23.05	-	69.14	71	25.9	28.6	82	86	1.5	0.25
T33_dn2	13.82	14.88	344.45	397	61.4	64.7	169	169	4.8	0.17
T33_dn5	13.72	21.49	422.42	422	66.7	69.4	177	193	1.7	0.16
T33_dn10	14.07	31.42	545.88	556	62.3	60.1	169	170	2.3	0.20
O43_dn18	22.69	13.82	876.26	810	80.6	81.3	217	221	2.9	0.28
I53_dn5	17.19	15.33	1951.57	2000	95.9	97.1	241	243	1.2	0.21

Supplementary Table 3. Biophysical properties of designed trimers (top) and two-component nanoparticles (bottom). Experimentally-measured data (exp) is compared to predicted design data (model). Molecular weights (MW) were obtained using the ASTRA software. R_g and D_{max} calculations performed in Scatter3 SAXS analysis software with the determined q_{max} values. *X* values computed from the FoXS online SAXS web server between the designed model and the experimental scattering data.

	1na0C3_2 (PDB ID X)	3ltjC3_1v2 (PDB ID Y)
Data Acquisition		
Space group	P 1 21 1	R 3 :H
Cell dimensions a, b, c (Å) α , β , γ (°)	 69.47, 64.91, 99.03 90, 106.33, 90	 88.182, 88.182, 65.244 90, 90, 120
R_{merge}	0.1427 (0.8023)	0.1189 (1.041)
$CC_{1/2}$	0.994	0.997 (0.623)
$<I/\sigma_I>$	9.5 (2.16)	9.35 (1.30)
Completeness (%)	99.86	91.51 (77.88)
Multiplicity	4.6 (4.6)	5.6 (5.1)
Wilson B-factor ($Å^2$)	37.11	40.43
Refinement		
Resolution range (Å)	38.87 - 2.53 (2.60 - 2.53)	44.09 - 2.303 (2.386 - 2.303)
No. of reflections for refinement	27066 (2030)	8361 (655)
No. of reflections for R_{free}	1442 (103)	756 (62)
R_{work}(%)/R_{free}(%)	0.1859 (0.195) / 0.2316 (0.240)	0.2021 (0.2555) / 0.2261 (0.2240)
Water count	110	25
Residue count	711	180

Average B-factors (Å^2) Protein Water	 47.40 46.01	 49.36 50.80
r.m.s.d. deviations Bond length (Å) Bond angles (°)	 0.68 0.78	 0.002 0.44
Ramachandran favored (%)	98.00	100.00
Ramachandran allowed (%)	1.00	0.00
Ramachandran outliers (%)	1.00	0.00
Rotamer outliers (%)	3.00	0.00

Supplementary Table 4. Crystallography data collection and refinement statistics for constructs 1na0C3_2 and 3ltjC3_1v2. Statistics for the highest-resolution shell are shown in parentheses.

	T33_dn10	O43_dn18	I53_dn5
Microscope	Titan Krios	Titan Krios	Titan Krios
Voltage (kV)	300	300	300
Detector	Gatan K2 Summit	Gatan K2 Summit	Gatan K2 Summit
Recording mode	Counting	Counting	Counting
Magnification	29,000 X	29,000 X	29,000 X
Movie micrograph pixel size	1.03	1.03	1.03
Dose rate ($e^-/Å^2/s$)	5.04	5.04	4.46
No. of frames per movie micrograph	40	40	45
Frame exposure time (ms)	250	250	250
Movie micrograph exposure time (s)	10.00	10.00	11.25
Total dose ($e^-/Å^2$)	50.4	50.4	50.2
Under focus range (μm)	0.6 - 1.6	0.6 - 1.6	0.6 - 1.6
Number of movie micrographs	502	1,336	1,548

Supplementary Table 5. Cryo-electron microscopy data acquisition metrics for nanoparticle constructs T33_dn10, O43_dn18, and I53_dn5.

	T33_dn10	O43_dn18	I53_dn5
PDB	6VFH	6VFI	6VFJ
Residues	4,752	7,560	16,320
Amino-acids	4,752	7,560	16,320
Carbohydrates	0	0	0
RMSD Bonds	0.019	0.018	0.020
RMSD Angles	1.389	1.484	1.648
Ramachandran			
Favored (%)	99.13	98.71	98.88
Allowed (%)	0.87	1.29	1.12
Outliers (%)	0.00	0.00	0.00
Rotamer outliers	0.00	0.00	0.00
Clash score	0.32	0.41	0.27
Molprobity score	0.62	0.65	0.60
EMRinger score	2.12	0.68	0.69

Supplementary Table 6. Cryo-electron microscopy model building and refinement statistics for nanoparticle designs T33_dn10, O43_dn18, and I53_dn5.

Design	Sequence
1na0C3_1 (SEC-MALS)	**MNIAEAAYRVGNKAYKKGRYELAILAYILAILLDPNNAEAWYNLGNAYYKEG EYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGLEHHHHHH**
1na0C3_2 (SEC-MALS, SAXS)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGLEHHHHHH**
2fo7C3_1 (SEC-MALS)	**MAERLYKLGNKAYKRGEYILALIAYVVALRDDPRSAEAWYNLGNAAYKSGE YDEAIEYYQKALELDPRSAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPR SAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPRSLEHHHHHH**
2fo7C3_12 (SEC-MALS)	**MAEKAYNIGNAAYKEGEYRVAILAYMLALLADPRSAEALYNLGNAAYKEGD YKVAIAAYLLALDLDPRSAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPR SAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPRSLEHHHHHH**
2fo7C3_15 (SEC-MALS)	**MALRWLLLGILAMLLGAEELAIEAYQKALELEPRSAMAWLALGAAYYKEGD YDEAIEYYQKALELDPRSAAAWALLGNAYYKQGDYDEAIEYYQKALENRPR SARAWYNLGNAYYKQGDYDEAIEYYQKALELDPRSLEHHHHHH**
3ltjC3_1 (SEC-MALS)	**MTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRA AAADALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDERAVEPLIKAL KDERDLVRVAAAVALGRIGDERAVEPLIKALKDEEGEVREAAAIALGSIGGE RVRAAMEKLAETGTGFARKVAVNYLETHKLEHHHHHH**
3ltjC3_1v2 (SEC-MALS, SAXS)	**MTDPMKVILYIAMLELEKYIMRAAAAYALGKIGDERAVEPLIKALKDEDAIVR AAAADALGQIGDERAVEPLIKALKDEDGAVRVSAAVALGQIGDERAVEPLIK ALKDEDAVVRVAAAIALGLIGDERAVEPLIKALKDEKGKVREAAALALGAIG GERVRAAMEKLAETGTGFARKVAVNYLETHKLEHHHHHH**
3ltjC3_11 (SEC-MALS, SAXS)	**MRREETDPLAVVMYRLNLRDDSYYVRRAAAYALGKIGDERAVEPLIKALKD EDAWVRRAAADALGQIGDERAVEPLIKALKDEDGWVRQSAAVALGQIGDE RAVEPLIKALKDEDWFVRAAAAAALGRIGDERAVEPLIKALKDEDEMVREIA ALALGMIGGERVRAAMEKLAETGTGFARKVAVNYLETHKLEHHHHHH**
HR4C3_1 (SEC-MALS)	**MDICELEARLVALLVLLAKRAGADEDLIAELVAVMIMIVILRLKKSGSSYEVIC ECVARIVAEIVEALKRSGTSEDEIAEIVARVISEVIRALKRSGSSYEVICECVAR IVAEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSSYEVIKECVQRIVEEIV EALKRSGTSEDEINEIVRRVKSEVERTLKESGSLEHHHHHH**
HR4C3_5 (SEC-MALS)	**MDECEEKARRVAEKVERLKRSGTSEDEIAEEVAREISEVIRTLKESGSEYKVI CRCVARIVAEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSKYKIICICVAII VAEIVAALKRSGTSEDEIAEIVARVISEVIRTLKESGSSYEVIKQCVQAIVQAIIL ALMKSGTEVEEILLIVLRVEEEVERTLKESGSLEHHHHHH**
HR4C3_5v2 (SEC-MALS, SAXS)	**MDECEEKARRVAEKVERLKRSGTSEDEIAEEVAREISEVIRTLKESGSEYKVI CRCVARIVAEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSDYLIICVCVAII VAEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSSYEVIKECVQIIVLAIILA LMKSGTEVEEILLILLRVKTEVRRTLKESGSLEHHHHHH**
HR4C3_7 (SEC-MALS)	**MDECEKKARLVAILVIVAKALGAEEKLIALLVALEIVVVIIELKASGSSYEVICE CVARIVAEIVEALKRSGTSEDEIAEIVAKVIAAVIIVLKELGSSYEVICECVARIV**

	AEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSSYEVIKECVQRIVEEIVEA LKRSGTSEDEINEIVRRVKSEVERTLKESGSLEHHHHHH
HR7C3_2 (SEC)	**MEKRIARELCELAAERAAESNDEREARIAAIECLLVAERAGMPTKEAARSFC EAAARAAAESNDEEVAKIAAKACLEVAKQAGMPTKEAARSFCEAAARAAA ESNDEEVAKIAAKACLEVAKQAGMPTKEAARSFCEAAKRAAKESNDEEVE KIAKKACKEVAKQAGMPLEHHHHHH**
HR7C3_8	MTEEDAARTCKKAARKAAESNDEEVAKQAAKDCLEVAKQAGMPTTIAAAIFCL AAARAAAESNDEEVAKIAAKACLEVAKQAGMPTKAAAIAFCIAAAMAAAESRD EEVAKIAAKACLEVAKQAGMPTKTAAALFMIAAIAAALRSEDEVVLAIAALAIAE VLKQAGMPLEHHHHHH
HR7C3_9 (SEC-MALS*update)	**MTKEMAAVLCMVLALKAAESNDEEKAKKAAKLCLIMADEAGMPTKEAARS FCEAAAIAAAVSEDEEVAKIAAKACLEVAKQAGMPTKEAARSFCEAAASAA AILNEEEVAKIAAKACLEVAKQAGMPTKEAARSFCEAAKRAAKRSNDEEVE KIAKKACKEVAKQAGMPLEHHHHHH**
HR10C3_7 (SEC-MALS)	**MSSEKEELRELLVAIVAVAAEDKGDDTEEAREAAREAFELVREAAERAGIDS SEVLTLAILLILIVVLIAADAGYDISEAARAAAEAFKRVAEAAKRAGITSSEVLE LAIRLIKEVVVNAAIRGYDISEAARAAAEAFKRVAEAAKRAGITSSKILKMAIIL IRVMVKMAKERGKDISEAARQAAEIFRKAAERMRGSLEHHHHHH**
HR10C3_7v2 (SEC-MALS)	**MSSEKEELRKMLVALVVVAAKEKGDDTEEAREAAREAFELVREAAERAGID SSVVLALAILLILLVVLAAQMAGYDISEAARAAAEAFKRVAEAAKRAGITSSE VLELAIRLIKRVVLNAQIRGYDISEAARAAAEAFKRVAEAAKRAGITSSLLLK MAIVLIRVLVELAQESGADISEAARKAAEIMRRAAEDMRGSLEHHHHHH**
HR10C3_8 (SEC)	**MDECEEKARRVAEKVERLKRSGTSEDEIAEEVAREISEVIRTLKESGSEEVEI CACVARIVAEIVEALKRSGTSEDEIAEIVARVISEVIRTLKESGSSYLVICMCVA LIVAQIVEALKRSGTSRKEIAEIVARVISEVIRTLKESGSSYEVIKECVERIVRAI VLALRESGTRITEIMAIVLAVLKEVLRTLKESGSLEHHHHHH**
HR10C3_18 (SEC-MALS)	**MKREKMELAKRLLKIVVENAKRKGDEEALAALAALLAFALVREAAERAGID SSEVLELAIRLIKEVVENAQREGYRIALAALVAAMAFAVVAEAAKEAGITSSE VLELAIRLIKEVVENAQREGYEIVDAAMAAALAFARVAEAAKRAGITSSETLK RAIEEIRKRVEEAQREGNDISEAAEQAAEEFRKKAEELKLEHHHHHH**
HR00C3 (SEC)	**MKEEKIAKLISLLAELSKKLIEIVARAADNKTTEEAVDIAILLIAIIARLAIRLIEML AKNLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDIRMLKAILAIAELAAE AIKAIADLAKNHTTEEFMARAISAIAELAKKAIEAIYRLADNHTTDLFMAIAIMA IAVLALLAIMAIADLAKNHTTEEFMAKAISAIAELAKKAIEAIYRLADNHTSPDL IELAILAIEIIALAAIIAIEELAENITTEEYKEKAKSAIDEIREKAKEAIKRLEDNRT LEHHHHHH**
HR00C3_3 (SEC-MALS)	**MKERLIAKLISVLAEASKILIRIAAKAADKLEREAAVILAIVLIAVAAIAAIAAIAL LAANLASEEFMARAISAIAELAKKAIEAIYRLADNHTEDEAMALAIEIIAILALL AIVAIALLAANHTTEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMAKAIEA IAELAKEAIKAIAELAKNHTTEEFMAKAISAIAELAKKAIEAIYRLADNHTSPTY IEKAIEAIEKIARTAIKAIEDLAKNITTEEYKEKAKSAIDEIREKAKEAIKRLEDN RTLEHHHHHH**
HR00C3_44 (SEC)	**MTEEKIAKEISRIAEESKKRIEELARKADNKTREAVVALAIAKIALLAREAIKRI EDLAKNLASEEFMARAISAIAELAKKAIEAIYRLADNHTKDVLMLVAIVAIAEL AKEAIKAIADLAKNHTTEEFMARAISAIAELAKKAIEAIYRLADNHRLVAAMLL**

	AIEAIAELAKEAIKAIADLAKNHTTEEFMAKAISAIAELAKKAIEAIYRLADNHR LPAAILLAALAILLIAVTAILAILILALNITTEEYKEKALSAIEEIVEKAEEAIDRLE DNLTLEHHHHHH
tpr1C3_6 (SEC-MALS)	**MAEAWKELGKVLEKLGRLEEAAVAYLLAVIDDPNDAEAWKELGKVLEKLG ELDAAAVAYEAAIELDPNDAEAWKELGKVLEKLGRLRRAALAYIKAIALDPN DAEAWKELGKVAEKLGRLKIAARIYKKAIELDPNDLEHHHHHH**
ank1C2_1*	**MHHHHHHGSWGSSELGKRLIEAAENGNKDRVKDLIENGADVNASDSDGRT PLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLL KGADVNAKDSDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDL AREHGNEEVVKALEKQ**
ank3C2_1*	**MSELGKRLIEAAENGNKDRVKDLLENGADVNASDSDGKTPLHLAAENGHA KVVLLLLEQGADPNAKDSDGKTPLHLAAENGHAVVVALLLMHGADPNAKD SDGKTPLHLAAENGHEEVVILLLAMGADPNTSDSDGRTPLDLAREHGNEEV VKVLEDHGGWLEHHHHHH**
1na0C3_3*	**MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKK GEYDEAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELD PNNAEAKQNLGNAKQKQGLEHHHHHH**
1na0C3_7*	**MNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQ GDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELD PNNAEAKQNLGNAKQKQGLEHHHHHH**
HR00C3_2*	**MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLI EALAKNLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANL AVTAILAIAALASNHTTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAA AIEAIALLATLAILAIALLASNHTTEEFMAKAISAIAELAKKAIEAIYRLADNHTS PTYIEKAIEAIEKIARKAIKAIEMLAKNITTEEYKEKAKSAIDEIREKAKEAIKRL EDNRTLEHHHHHH**
1na0C4_1*	**MTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQG DYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDP NNAEAKQNLGNAKQKQGLEHHHHHH**
HR04C4_1*	**MHHHHHHGSWGSDECEEKARRVAEKVERLKRSGTSEDEIAEEVAREISEVI RTLKESGSSYEVICECVARIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKE SGSSYEVICECVARIVAEIVEALKRSGTSAAIIALIVALVISEVIRTLKESGSSFE VILECVIRIVLEIIEALKRSGTSEQDVMLIVMAVLLVVLATLQLSGS**
2JFB (PDB ID)*	**MAVKGLGEVDQKYDGSKLRIGILHARWNRKIIDALVAGAVKRLQEFGVKEEN IIIETVPGSFELPYGSKLFVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTH QLMKLNFELGIPVIFGVLTCLTDEQAEARAGLIEGKMHNHGEDWGAAAVEM ATKFN**
2OBX (PDB ID)*	**MNQHSHKDYETVRIAVVRARWHADIVDQCVSAFEAEMADIGGDRFAVDVFD VPGAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQ LSTGVPVLSAVLTPHNYHDSAEHHRFFFEHFTVKGKEAARACVEILAAREKI AA**
2B98 (PDB ID)*	**MTKKVGIVDTTFARVDMASIAIKKLKELSPNIKIIRKTVPGIKDLPVACKKLLEE EGCDIVMALGMPGKAEKDKVCAHEASLGLMLAQLMTNKHIIEVFVHEDEAK DDKELDWLAKRRAEEHAENVYYLLFKPEYLTRMAGKGLRQGFEDAGPARE**

Supplementary Table 7. List of all designed homotrimers and pre-validated components tested with their corresponding amino acid sequences including initiating methionine and His_6-tag. Designs that expressed solubly are denoted in bold and under their name are the experimental methods used for characterization.
*Components from previously described designed homo-oligomers[1] or the Protein Data Bank (PDB IDs).

Design	Sequence
T33_dn1A (1na0C3_3)	MGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDE AIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYERALELDPENAEAALNLLE AKEKQG
T33_dn2B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYREAIK YYAKALTLDPKNAEAWYNLGNAVYKQGDYRIAILFYRAALKLDPNNAEAKQNLGNAKQ KQGLEHHHHHH
T33_dn2A (1na0C3_3)	**MGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYD EAIEAYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYKKALRLDPRNVDAIEN LIEAEEKQG**
T33_dn2B (1na0C3_2)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYRE AIRYYLRALKLDPENAEAWYNLGNALYKQGKYDLAIIAYQAALEEDPNNAEAKQNL GNAKQKQGLEHHHHHH**
T33_dn3A (1na0C3_7)	MGNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYKE AILYYIRALQLDPNNAEAWYNLGNAFYKKGDYRVAIILYRMALKLDPNNAEAKQNLGNA KQKQGDIHHHHHH
T33_dn3B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQGDYEEAILYYLEALDLDPNNAEAAENLLNAV KKDE
T33_dn4A (1na0C3_7)	**MGNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDY DEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYEKALELDPRNAEALK NLLEAKAKQD**
T33_dn4B (3ltjC3_1)	**MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAA AADALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDERAVRPLIKALADERDL VRVAAAVALGRIGDERAVKPLIIVLLDEEGEVREAAAIALGSIGGERVRAAMEKLAER GRGFARKVAVNYLETHKLEHHHHHH**
T33_dn5A 1na0C3_7	**MGNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDY DEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYEKALELDPNNAEALK NLLEAIAEQD**
T33_dn5B (3ltjC3_1)	**MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAA AADALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDERAVQPLIKALTDERDL VRVAAAVALGRIGDEKAVRPLIIVLKDEEGEVREAAAIALGSIGGERVRAAMEKLAER GTGFARKVAVNYLETHKLEHHHHHH**
T33_dn6A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALDEDPDNAEAWYNLGNAYYKQGDYR EAILYYQMALRLDPNNAEAWYNLGNAYYKQGDYDRAIEYYQKALELDPNNAEAKQ NLGNAKQKQGDIHHHHHH**
T33_dn6B (3ltjC3_1)	**MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAA AADALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDKRAVRPLIRALKDERDL VREAAAVALGRIGDELAVEPLIKALKDEEGEVREAAAIALGSIGGEIVRMMMDKLAE TGTGFARKVAVNYLETHK**

T33_dn7A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYRKALELDPENEEALEN LLNAKQKQGDIHHHHHH**
T33_dn7B (3ltjC3_1)	**MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAA AADALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDERAVEPLIKALKDERDL VRVAAAVALGRIGDERAVEPLIKALKDEEGEVREAAAIALGSIGGKRVRLAMLKLAL EGTGFARKVAVNYLETHK**
T33_dn8A (1na0C3_2)	MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEA IEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYRKALELDPENLEALLNLLNA KDKRG
T33_dn8B (HR00C3_2)	MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAKNL ASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAALASNH TTEEFMARAIRAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIALLASNHT TERFMAKAILAIAVLAKKAIEAIYRLADNHTSPTYIEKAIEAIEKIARKAIKAIEMLAKNITTE EYKEEAKSAIEIIRELARIAIRRLEDNRTLEHHHHHH
T33_dn9A (1na0C3_2)	MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEA IEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPENLEAILNLGEA KLKQG
T33_dn9B (HR00C3_2)	MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAKNL ASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAALASNH TTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIALLASNHT TEKFMAEAIIVIALLAVLAIMAIYRLADNHTSPTYIEKAIEAIEKIARKAIKAIEMLAKNITTEE YKEKAKSAIDLIRQLADIIIRKLEDNRTLEHHHHHH
T33_dn10A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYEKALELDPENLEALQN LLNAMDKQG**
T33_dn10B (HR00C3_2)	**MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAK NLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAAL ASNHTTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIA LLASNHTTEKFMARAIMAIAILAAKAIEAIYRLADNHTSPTYIEKAIEAIEKIARKAIKAIE MLAKNITTEEYKEKAKKIIDIIRKLAKMAIKKLEDNRTLEHHHHHH**
T33_dn11A (1na0C3_2)	MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEA IEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYRKALELDKENIEALLNLLNAK EKQD
T33_dn11B (HR00C3_2)	MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAKNL ASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAALASNH TTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIALLASNHT TERFMAKAILAIAILAAKAIEAIYRLADNHTSPTYIEKAIEAIEKIARKAIKAIEMLAKNITTEE YKEEAKSAIEIIRLLAKAVIKRLQDNRTLEHHHHHH
O32_dn1A (1na0C3_3)	**MGELAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYD EAIVAYVEALELDPNNAEAWYNLGNAYYKQGDYEEAIEYYQKALELDPNNAEAKQN LGNAKQKQG**
O32_dn1B (ank1C2_1)	

	MSRRGRLLIIAAENGNKDRVKDLIQRGADVNASDRRGRTPLHHAAENGHAEVVALLI EKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAE NGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQLEHHHHHH
O32_dn2A (1na0C3_2)	MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEA IEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEARKNLIIA DLKQEDIHHHHHH
O32_dn2B (ank1C2_1)	MSELGEALILAAERGKKDRVKDLIEEGADVNASDSDGRTPLHHAAENGHAEVVALLIE KGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAENGH KRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQ
O32_dn3A (3ltjC3_1)	**MGHHHHHHGWHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKAL KDEDALVRAAAADALGQIGDERAVEPLIEALEDEEGLVRASAAIALGQIGDERAVEP LILALADERDLVRVAAAVALGRIGDERAVEPLIVMLRDEEGEVREAAAIALGSIGGER VRAAMEELAERGRGFARKVAVNYLETHK**
O32_dn3B (ank1C2_1)	**MSELGKRLIEAAENGNKKRVKDLIENGADVNASDSDGRTPLHHAAENGHAEVVALL IEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAE NGHKRVVLVLILAGADVNTKDEEGDTPLALALEHGNREVIKALLKQ**
O43_dn1A (1na0C4_1)	MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYLLAIVYYAKALILDPNNAEAKQNLGNAI QKQD
O43_dn1B (1na0C3_3)	MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAI EAYQKALELDPNNAEAWYNLGNAYYKQGDYLEAIAYYAKALLLDPNNAEARQNLGNA MQKSELEHHHHHH
O43_dn2A (1na0C4_1)	MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAILYYVKALVLDPNNAEAKQNLGNA RQKQG
O43_dn2B (1na0C3_3)	MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAI EAYQKALELDPNNAEAWYNLGNAYYKQGDYLEAILYYVKALKLDPNNAEAKQNLGNA EQKKDLEHHHHHH
O43_dn3A (1na0C4_1)	MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDEAI KYYQKALELDPNNAEAWYNLGNAYYKQGDYVIAIALYQLALELDPNNAEAKQNLGNA EQKEGDIHHHHHH
O43_dn3B (1na0C3_7)	MNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYLEAIEYYIKALELDPNNEEARQNLLNAA KKIE
O43_dn4A (1na0C4_1)	**MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAWYNLGNAYYKQGDYEEAIEYYLKALELDPNNAEARQNL RNAMQKEG**
O43_dn4B (1na0C3_7)	**MNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYLAAIIYYRRALELDPNNAEAKQN LGNAEQKEGLEHHHHHH**

O43_dn5A (1na0C4_1)	MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYREALRYYIKALKLDPNNAEAKQNLGNA LEKRG
O43_dn5B (1na0C3_7)	MNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYLVAIIYYLEALELDPNNAEAKQNLGNAK QKEGLEHHHHHH
O43_dn6A (1na0C4_1)	**MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAWYNLGNAYYKQGDYQEAIEYYARALRRDRRNKEAIENLI NALQKED**
O43_dn6B (1na0C3_2)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGRYVR ALIYYLRALLLDPENAEAWYNLGNAYYKKGDYDIAIVYYELALEDDPNNAEAKQLLG NAKQKQGLEHHHHHH**
O43_dn7A (1na0C4_1)	MGTLARVAYILGAIAYAQGEYDIAITAYQVALDLDPNNAEAWYNLGNAYYKQGDYDEAI EYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYKKALRLDPNNEEAKQNLMN ALQKQD
O43_dn7B (3ltjC3_1)	MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAAAA DALGQIGDERAVEPLIKALKDEEGLVRASAAIALGQIGDERAVEPLIKALKDERDLVRVA AAVALGRIGDKKAVLPLIKALKDEEGEVREAAAIALGSIGGRLVRAMMELLAETGRGFA RKVAVNYLETHKLEHHHHHH
O43_dn8A (HR04C4_1)	MGDECEEKARLLAELVETLKRSGTSEDEIAEDVARLISEMIRNLKESGSSYEVICECVA RIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKR SGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMA VLLVVLATLQLSGS
O43_dn8B (1na0C3_3)	MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAI EAYQKALELEPNNAEAWYNLGNAYYKQGDYEEAIIYYLKALVLDPRNAEARQNLGNA KQKEGLEHHHHHH
O43_dn9A (HR04C4_1)	MGDECEELARIVAELVEKLKRSGTSEDEIAERVAREISEVIKLLKKSGSSYEVICECVAR IVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKRS GTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAV LLVVLATLQLSGS
O43_dn9B (1na0C3_3)	MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAI EAYQKALELDPENAEAWYNLGNAYYKQGEYLEALLYYLKALILDPNNAEAKQNLGNA RQKQGLEHHHHHH
O43_dn10A (HR04C4_1)	MGDECERKARLVAKIVELLKRSGTSEDEIAEEVARLISLVIKVLKKSGSSYEVICECVAR IVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKRS GTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAV LLVVLATLQLSGS
O43_dn10B (1na0C3_3)	MNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAI EAYQKALELDPENAEAWYNLGNAYYKQGDYAEAMLYYLKALLLDPNNAEAKQNLGN AEQKAGLEHHHHHH
O43_dn11A (HR04C4_1)	MGDECEEKAELVALLVEALKKLGTSEDEIAEEVAKEISRVIRRLKESGSSYEVICECVA RIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKR

	SGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMA VLLVVLATLQLSGS
O43_dn11B (1na0C3_7)	MNSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYDEAI EYYQKALELDPENAEAWYNLGNAYYKQGDYELAIIFYKVALALDPNNAEAKQNLGNAK QKQGLEHHHHHH
O43_dn12A (HR04C4_1)	**MGDRCERRAKLVALKVELLKKDGTSEDEIAEEVAREISEVIRDLRKSGSSYEVICECV ARIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEAL KRSGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLI VMAVLLVVLATLQLSGS**
O43_dn12B (1na0C3_2)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNIKAELNLII AEEKQGLEHHHHHH**
O43_dn13A (HR04C4_1)	MGDECEELARAVALVVEILKRSGTSEDEIAEEVARLISRVIRKLKESGSSYEVICECVAR IVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKRS GTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAV LLVVLATLQLSGS
O43_dn13B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKKGDYLIAILYYLVALTLDPNNAEAKQNLGNAKQ KDGLEHHHHHH
O43_dn14A (HR04C4_1)	MGDKCEEMAELVAQLVELLKESGTSEDEIAEKVARLISKVIRKLKESGSSYEVICECVA RIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKR SGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMA VLLVVLATLQLSGS
O43_dn14B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYMKALKLDPKNAEAWYNLGNAYYKQGDYLLAILIYEMALILDPNNAEAKQNLGNAKQ KEGLEHHHHHH
O43_dn15A (HR04C4_1)	MGRKCELLARLVAMIVELLKESGTSEDEIAEEVAREISEVIRTLKEEGSSYEVICECVAR IVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKRS GTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAV LLVVLATLQLSGS
O43_dn15B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPRNAEAWYNLGNAYYKQGDYLMAILIYQLALMLDPNNAEAKQNLGNAK QKRGLEHHHHHH
O43_dn16A (HR04C4_1)	MGEDCEELAELVAELVERLKRRGTSEDEIAEEVARIISEVIRMLKESGSSYEVICECVA RIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKR SGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMA VLLVVLATLQLSGS
O43_dn16B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYKEAIK YYQKALKLDPNNAEAWYNLGNAYYKKGDYIMAILAYELALEEDPNNAEAKQNLGNAK QKQGLEHHHHHH
O43_dn17A (HR04C4_1)	**MGDECEEKARRVALKVLKLRLRGTSEDEIAEEVAREISKVIETLKESGSSYEVICECV ARIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEAL**

O43_dn17B (1na0C3_2)	**KRSGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAVLLVVLATLQLSGS** **MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNEEAKIVLGLAKEEQELEHHHHHH**
O43_dn18A (HR04C4_1)	**MDRCEELARRIAEVVERAKRAGTSEDEIAESVARVISLVIRALKLSGSSYEVICECVARIVAEIVEALKRSGTSAVEIAKIVARVISEVIRTLKESGSSYEVICECVARIVAEIVEALKRSGTSAAIIALIVALVISEVIRTLKESGSSFEVILECVIRIVLEIIEALKRSGTSEQDVMLIVMAVLLVVLATLQLSGSGGWLEHHHHHH**
O43_dn18B (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPSNLDAAVNLGAATMLTS**
I32_dn1A (1na0C3_3)	**MGNLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELEPENAEALYNLGNAYYKQGEYDEAILYYLIALELDPNNAEAKQNLGNAKQKQGDIHHHHHH**
I32_dn1B (ank1C2_1)	**MSRLGIRLIIAAIEGNKDRVKDLIENGADVNASDSVGRTPLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDRDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQ**
I32_dn2A (1na0C3_3)	**MGDLAEKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYDEAILAYLKALELDPNNAEAWYNLGNAFYKQGDYRMAIKYYQKALELDPNNAEAKQNLGNAKQKQG**
I32_dn2B (ank1C2_1)	**MSELGELLIVAAENGNKKMVRDLIKNGADVNASDEDGRTPLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQLEHHHHHH**
I32_dn3A (1na0C3_3)	MGRLAKKMYKAGNAMYRKGQYTIAIIAYTLALLKDPNNAEAWYNLGNAAYKKGEYAEAIVAYIKALELDPNNAEAWYNLGNALYKLGAYNAAIQVYQKALELDPNNAEAKQNLGNAKQKKG
I32_dn3B (ank1C2_1)	MKILGLALIAAARNGEKERVETLIEAGADVNASDDDGRTPLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQLEHHHHHH
I32_dn4A (1na0C3_7)	MGKSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPKNAEAWYNLGNAAYKQGDYEEAIRYYLKALLLDDNNAEAWYNLGNAYYKQGDYREAIMLYQKALELDPNNAEAKQNLGNAKQKQG
I32_dn4B (ank1C2_1)	MSELGKLLIMAAELGNKRLVKELIENGADVNASDSDGRTPLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAEEGHDEVVLILLLKGADVNAKDSDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQLEHHHHHH
I32_dn5A (1na0C3_7)	MGRSAEAMYKMGNAAYKQGDYILAIIAYLLALEKDPNNAEAWYNLGNAAYKQGDYREAIRYYLKALALDPNNAEAWYNLGNAFYKQGDYNEAIEVYQKALELDPNNAEAKQNLGNAKQKQG
I32_dn5B (ank1C2_1)	MSELGRMLIEAAELGKKEIVKELIENGADVNASDSDGRTPLHHAAENGHAEVVALLIEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAENGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQLEHHHHHH

I32_dn6A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNDEADDN LLNADQKQDDIHHHHHH**
I32_dn6B (ank1C2_1)	**MSRLGKKLIIAAERGNKDRVKDLIENGADVNASDEDGRTPLHHAAENGHAEVVALLI EKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAE NGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQ**
I32_dn7A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPKNMEALLD LGNAKQKQKDIHHHHHH**
I32_dn7B (ank1C2_1)	**MSELGKDLIVAAALGNKDRVKDLIENGADVNASDRRGATPLHMAALNGHAEVVALL IEKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAE NGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQ**
I32_dn8A (1na0C3_2)	**MGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYD EAIEYYQKALELDPNNAEAWYNLGNAYYKQGDYLRAIAYYRKALELDPNNAEAKQN LGNAKQKIE**
I32_dn8B (ank3C2_1)	**MELEGERLIEAAENGNKDRVKDLLENGALVNASDSDGKTPLHLAAENGHAKVVLLL LEQGAKPNAKDSDGKTPLHLAAENGHAVVVALLLMHGADPNAKDSDGKTPLHLAA ENGHEEVVILLLAMGADPNTSDSDGRTPLDLAREHGNEEVVKVLEDHGGWLEHHH HALEHHHHHH**
I32_dn9A (HR00C3_2)	MGIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAKN LASEEFMADAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAALASN HTTEQFMAIAIIAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIALLASNHT TEAFMALAILLIAELAKKAIEAIYRLADNHTSPTYIEKAIEAIEKIARKAIKAIEMLAKNITTE EYKEKARAAILEIREKAKEAIKRLEDNRT
I32_dn9B (ank1C2_1)	MHHHHHHSELGKRLIEAAENGNKKRVLELIENGADVNASDSDGRTPLHHAAENGHAE VVALLIELGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHH AAENGHKRVVLVLILAGADVETSDSRGRTPLMLAVEHGNIEVALALLKQGW
I32_dn10A (HR00C3_2)	**MGHHHHHHWGIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLAT AAIQLIEALAKNLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANL AVTAILAIAALASNHTTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIA LLATLAILAIALLASNHTTEEFMAKAISAIARLAKKAILAIYKLADNHTSPTYIEKAIEAIE KIARKAIKAIEMLAKNITTEEYKEKAKSAIDEIREIAKIAIKTLEDNRT**
I32_dn10B (ank1C2_1)	**MSEIGKRLIEAAENGNKERVKLLIELGADVNASDSDGRTPLHHAAENGHAEVVALLI EKGADVNAKDSDGRTPLHHAAENGHDEVVLILLLKGADVNAKDSDGRTPLHHAAE NGHKRVVLVLILAGADVNTSDSDGRTPLDLAREHGNEEVVKALEKQ**
I53_dn1A (2B98)	MGHHHHHHHKKVGIVDTTFARVDMAIMAIIVLELRPRNIKIIRKTVPGIKDLPVACKKLLEE EGCDIVMALGMPGKAEKDKVCAHEASLGLMLAQLMTNKHIIEVFVHEDEAKDDRELD WLAKRRAEEHAENVYYLLFKPEYLTEMAGKGLRQGFEDAGP
I53_dn1B (HR00C3_2)	MIEEVVAEMIDILAESSKKSIRELAKAAKNKTTEKAVAEAIEEIARLATAAIQLIEALAKNL ASEEFMARAISAIAELAKKAIEAIYRLADKHKTDTFMARAIAAIANLAVTAILAIAALASNH TTEEFMARAISAIAELAKKAIMAILLLALLHTTDKFMAAAIEAIALLATLAILAIALLASNHTT EEFMAKAISAIAELAKKAIEAIYLLADLHTPVLYEDKAIEAIEKIARKAIKAIEMLAKNITTEE YKEKAKSAIDEIREKAKEAIKRLERNRE

I53_dn2A (2JFB)	MGRYDGSKLRIGILHARWNRSIILALVLGAIERLLEFGVRAKNIIIETVPGSFELPYGSKL FVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTCLTD EQAEARAGLIDGKMHNHGEDWGAAAVEMATKFN
I53_dn2B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYRRALKLEPENAEAWYNLGNAYYKQGDYKEAIAYYLIALILDPNNAEAKQNLGNAEQ KQDLEHHHHHH
I53_dn3A (2JFB)	MGKYDGSKLRIGILHARWNRAIIIALVLGALKRLLEFGVKAKNIIIETVPGSFELPYGSKL FVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTCLTD EQAEARAGLIKGKMHNHGEDWGAAAVEMATKFN
I53_dn3B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYQEALELDPENAEAWYNLGNAYYKQGDYKEALAYYLLALELDPNNAEAEQNLGNAE QKRDLEHHHHHH
I53_dn4A (2JFB)	MGKYDGSKLRIGILHARWNVKIIIALILGAIKRLREFGVKRENIIIEIVPGSFELPYGSKLFV EKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTCLTDEQ AEARAGLIEGKMHNHGEDWGAAAVEMATKFN
I53_dn4B (1na0C3_2)	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDEAIE YYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNLDAVMNLLEAS LKQELEHHHHHH
I53_dn5A (2JFB)	**MGKYDGSKLRIGILHARWNAEIILALVLGALKRLQEFGVKRENIIIETVPGSFELPYGS KLFVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTC LTDEQAEARAGLIEGKMHNHGEDWGAAAVEMATKFN**
I53_dn5B (1na0C3_2)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGRYRE AIEYYQKALELDPNNAEAWYNLGNAYYERGEYEEAIEYYRKALRLDPNNADAMQNL LNAKMREELEHHHHHH**
I53_dn6A (2JFB)	**MGDYDGSKLRIGILHARKNTEIIVALVIGAVERLEEFGVKRENIIIEIVPGSFELPYGSKL FVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTCLT DEQAEARAGLIEGKMHNHGEDWGAAAVEMATKFN**
I53_dn6B (1na0C3_2)	**MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYKKALRLDPDNAKALLNLI EAILKQKLEHHHHHH**
I53_dn7A (2JFB)	MGKYDGSKLRIGILHARWNRRIILALVIGAIIRLLEFGVKEDNIIIETVPGSFELPYGSKLF VEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFELGIPVIFGVLTCLTDE QAEARAGLIEGKMHNHGEDWGAAAVEMATKFN
I53_dn7B (3ltjC3_1)	MHHHHTDPLAVILYIAILKAEKSIARAKAAEALGKIGDERAVEPLIKALKDEDALVRAAAA DALGQIGDERAVIPLLRALLDKEGLVRASAAIALGQIGDKRAVLILILALEDERDLVRVAA AVALGRIGDEKAVEPLIEALKDEEGEVREAAAIALGSIGGERVRAAMEKLAETGTGFAR KVAVNYLETHKLEHHHHHH
I53_dn8A (2OBX)	**MGHHHHHHHHKDYETVRIAVVRARWHADIVRQCVMAFMKEMMRIGGRRFAVEVFDV PGAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLSTGVP VLSAVLTPHNYHDSAEHHRFFFEHFTVKGKEAARACVEILAARERI**
I53_dn8B (1na0C3_2)	

	MEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGDYDE AIEYYQKALELDPNNAEAWYNLGNAYYKQGDYDEAIEYYQKALELDPENEEAIDNLL EARQKQE
I53_dn9A (2OBX)	**MGHHHHHHHHKDYETVRIAVVRARWHAEIVDVCVLAFEIEMLDIGGDRFAVDVFDVPG AYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLSTGVPVL SAVLTPHNYHDSAEHHEFFFEHFTVKGKEAARACVEILAAREKI**
I53_dn9B (HR00C3_2)	**MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAK NLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAAL ASNHTTEEFMARAISAIAELAKKAIAAIYRLADNHKTDKFMAAAIEAIALLATLAILAIA LLASNHTTEEFMAKAIRAIAKLAKMAILVIYALAIMHTSPTYIEKAIEAIEKIARKAIKAIE MLAKNITTEEYKEKAKSAIDEIREKAKEAIKRLEDKRE**
I53_dn10A (2OBX)	**MGHHHHHHHHKDYETVRIAVVRARWHADIVDLCVIAFELEMLLIGGRRFAVDVFDVPG AYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLSTGVPVL SAVLTPHNYHDSKRHHRFFAMHFIKKGKEAARACVEILAAREKI**
I53_dn10B (HR00C3_2)	**MIEEVVAEMIDILAESSKKSIEELAKAADNKTTEKAVAEAIEEIARLATAAIQLIEALAK NLASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAAL ASNHTTEEFMARAISAIAELAKKAIEAILELALEHETDKFMAAAIEAIALLATLAILAIAL LASNHTTEEFMAKAIEAIAQLAKLAIIAIYLLALLHESPTYIEKAIEAIEKIARKAIKAIEM LAKNITTEEYKEKAKSAIDEIREKAKEAIKRLEDKRE**
I53_dn11A (2OBX)	MGHHHHHHHHKDYETVRIAVVRARWHADIVDQCVSAFEREMAKIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLSTGVPVL SAVLTPHEYHDSEIHHKIFFLLFTEKGKEAARACVEILAAREKI
I53_dn11B (HR00C3_2)	MIEEVVAEMIDILAESSKKSIEELARAADNKTTEKAVAEAIEEIARLATAAIQLIEALAKNL ASEEFMARAISAIAELAKKAIEAIYRLADNHTTDTFMARAIAAIANLAVTAILAIAALASNH TTEEFMARAISAIAELAKKAIEAIYRLADNHTTDKFMAAAIEAIALLATLAILAIALLASNHT TEEFMAKAISAIAELAKKAIEAIYRLADDHTSPTYIEKAIEAIEKIAKKAIKAIEMLAKNITTE EYQEKARKAILEILEKALEAIRRLEDNRR

Supplementary Table 8. List of all designed two-component nanoparticles tested and their corresponding amino acid sequences including initiating methionines and His_6-tags. Designs that expressed solubly and co-eluted from IMAC are denoted in bold. Input oligomers from Supplementary Table 7 are included in parentheses.

Antigen-fused component	Sequence
BG505 SOSIP.v5.2(7S)–T33_dn2A without N241/N289	**MKRGLCCVLLLCGAVFVSPSQEIHARFRRGARAENLWVTVY YGVPVWKDAETTLFCASDAKAYETKKHNVWATHCCVPTDP NPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCV KLTPLCVTLQCTNVTNNITDDMRGELKNCSFNMTTELRDKK QKVYSLFYRLDVVQINENQGNRSNNSNKEYRLINCNTSAITQ ACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCPSVSTV QCTHGIKPVVSTQLLLNGSLAEEEVIIRSENITNNAKNILVQFN TPVQINCTRPNNNTVKSIRIGPGQWFYYTGDIIGDIRQAHCNV SKATWNETLGKVVKQLRKHFGNNTIIRFANSSGGDLEVTTH SFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSITLP CRIKQIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGST NSTTETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCK RRVVGRRRRRRAVGIGAVSLGFLGAAGSTMGAASMTLTVQ ARNLLSGIVQQQSNLLRAPECQQHLLKDTHWGIKQLQARVL AVEHYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEI WDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLEL DKWASLWGSMGNLAEKMYKAGNAMYRKGQYTIAIIAYTLA LLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPN NAEAWYNLGNAYYKQGDYDEAIEYYKKALRLDPRNVDAIEN LIEAEEKQGAS**
BG505 SOSIP.v5.2(7S)–T33_dn2A	**MKRGLCCVLLLCGAVFVSPSQEIHARFRRGARAENLWVTVY YGVPVWKDAETTLFCASDAKAYETKKHNVWATHCCVPTDP NPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCV KLTPLCVTLQCTNVTNNITDDMRGELKNCSFNMTTELRDKK QKVYSLFYRLDVVQINENQGNRSNNSNKEYRLINCNTSAITQ ACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCTNVSTV QCTHGIKPVVSTQLLLNGSLAEEEVIIRSENITNNAKNILVQLN ESVQINCTRPNNNTVKSIRIGPGQWFYYTGDIIGDIRQAHCNV SKATWNETLGKVVKQLRKHFGNNTIIRFANSSGGDLEVTTH SFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSITLP CRIKQIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGST NSTTETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCK RRVVGRRRRRRAVGIGAVSLGFLGAAGSTMGAASMTLTVQ ARNLLSGIVQQQSNLLRAPECQQHLLKDTHWGIKQLQARVL AVEHYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEI WDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQDLLEL DKWASLWGSMGNLAEKMYKAGNAMYRKGQYTIAIIAYTLA LLKDPNNAEAWYNLGNAAYKKGEYDEAIEAYQKALELDPN NAEAWYNLGNAYYKQGDYDEAIEYYKKALRLDPRNVDAIEN LIEAEEKQGAS**
BG505 SOSIP.v5.2(7S)–T33_dn10A	**MKRGLCCVLLLCGAVFVSPSQEIHARFRRGARAENLWVTVY YGVPVWKDAETTLFCASDAKAYETKKHNVWATHCCVPTDP NPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCV KLTPLCVTLQCTNVTNNITDDMRGELKNCSFNMTTELRDKK QKVYSLFYRLDVVQINENQGNRSNNSNKEYRLINCNTSAITQ ACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCTNVSTV QCTHGIKPVVSTQLLLNGSLAEEEVIIRSENITNNAKNILVQLN ESVQINCTRPNNNTVKSIRIGPGQWFYYTGDIIGDIRQAHCNV SKATWNETLGKVVKQLRKHFGNNTIIRFANSSGGDLEVTTH SFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSITLP CRIKQIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGST**

	NSTTETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCK RRVVGRRRRRRAVGIGAVSLGFLGAAGSTMGAASMTLTVQ ARNLLSGIVQQQSNLLRAPECQQHLLKDTHWGIKQLQARVL AVEHYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEI WDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQGSGS GSGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNN AEAWYNLGNAYYKQGDYDEAIEYYQKALELDPNNAEAWYN LGNAYYKQGDYDEAIEYYEKALELDPENLEALQNLLNAMDK QG
BG505 SOSIP.v5.2(7S)–I53_dn5B	**MKRGLCCVLLLCGAVFVSPSQEIHARFRRGARAENLWVTVY YGVPVWKDAETTLFCASDAKAYETKKHNVWATHCCVPTDP NPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCV KLTPLCVTLQCTNVTNNITDDMRGELKNCSFNMTTELRDKK QKVYSLFYRLDVVQINENQGNRSNNSNKEYRLINCNTSAITQ ACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCTNVSTV QCTHGIKPVVSTQLLLNGSLAEEEVIIRSENITNNAKNILVQLN ESVQINCTRPNNNTVKSIRIGPGQWFYYTGDIIGDIRQAHCNV SKATWNETLGKVVKQLRKHFGNNTIIRFANSSGGDLEVTTH SFNCGGEFFYCNTSGLFNSTWISNTSVQGSNSTGSNDSITLP CRIKQIINMWQRIGQAMYAPPIQGVIRCVSNITGLILTRDGGST NSTTETFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTRCK RRVVGRRRRRRAVGIGAVSLGFLGAAGSTMGAASMTLTVQ ARNLLSGIVQQQSNLLRAPECQQHLLKDTHWGIKQLQARVL AVEHYLRDQQLLGIWGCSGKLICCTNVPWNSSWSNRNLSEI WDNMTWLQWDKEISNYTQIIYGLLEESQNQQEKNEQGSGS GSGSGGEEAELAYLLGELAYKLGEYRIAIRAYRIALKRDPNN AEAWYNLGNAYYKQGRYREAIEYYQKALELDPNNAEAWYN LGNAYYERGEYEEAIEYYRKALRLDPNNADAMQNLLNAKM REELEAS**
HA–I53_dn5B	**MKAILVVLLYTFTTANADTLCIGYHANNSTDTVDTVLEKNVTV THSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPEC ESLSTASSWSYIVETSNSDNGTCFPGDFINYEELREQLSSVS SFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIW LVKKGNSYPKLNQSYINDKGKEVLVLWGIHHPSTTADQQSL YQNADAYVFVGTSRYSKKFKPEIATRPKVRDQEGRMNYYW TLVEPGDKITFEATGNLVVPRYAFTMERNAGSGIIISDTPVHD CNTTCQTPEGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATG LRNVPSIQSRGLFGAIAGFIEGGWTGMVDGWYGYHHQNEQ GSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNH LEKRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSN VKNLYEKVRNQLKNNAKEIGNGCFEFYHKCDNTCMESVKN GTYDYPKYSEEAKLNREKIDGVSAEEAELAYLLGELAYKLG EYRIAIRAYRIALKRDPNNAEAWYNLGNAYYKQGRYREAIEY YQKALELDPNNAEAWYNLGNAYYERGEYEEAIEYYRKALRL DPNNADAMQNLLNAKMREEGGWELQHHHHHH**
DS-Cav1–I53_dn5B	**MELLILKANAITTILTAVTFCFASGQNITEEFYQSTCSAVSKG YLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQELDKY KNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTN VTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIK SALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQ SCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTN SELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVL**

	AYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDR GWYCDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEV NLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKC TASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQE GKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR KSDELLSAIGGSAEEAELAYLLGELAYKLGEYRIAIRAYRIAL KRDPNNAEAWYNLGNAYYKQGRYREAIEYYQKALELDPNN AEAWYNLGNAYYERGEYEEAIEYYRKALRLDPNNADAMQN LLNAKMREEGGWELQHHHHHH

Supplementary Table 9. List of all antigen-fused components tested and their corresponding amino acid sequences.

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