Supplemental Information

A Universal Design of Betacoronavirus Vaccines

against COVID-19, MERS, and SARS

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Table S1. Data collection and refinement statistics for MERS-CoV RBD-dimer, Related to Figure 2.

	MERS-CoV RBD dimer
Data collection	
Space group	$P2_12_12_1$
Wavelength (Å)	0.97891
Unit cell dimensions	
a,b,c (Å)	46.46, 108.79, 125.45
α,β,γ (°)	90, 90, 90
Resolution (Å)	50.00 – 2.90 (3.00 – 2.90)
Observed reflections	14565 (1406)
Completeness (%)	99.9 (100.0)
Redundancy	5.9 (6.0)
Rsym (%)	14.4 (84.7)
Rpim (%)	8.4 (48.0)
I/σ (I)	9.6 (1.8)
Wilson B factor	46
Refinement	
No. reflections	13671
R_{work}/R_{free} (%)	22.93 / 26.04
No. atoms	
Protein	3209
Ligands	0
Water	0
B-factors ($Å^2$)	
Protein	52
Ligands	
Water	
r.m.s. deviation	
Bond lengths (Å)	0.005
Bond angles (°)	0.884
Ramachandran plot	
Favoured (%)	98.05
Allowed (%)	1.95
Outliers (%)	0.00

[a]Values in parentheses are for highest-resolution shell.

Table S2. Binding affinities of hACE2 to SARS-CoV-2 RBDs measured by SPR, Related to Figure 3.

		K_D (nM)	
		Mammalian-expressed hACE2	Baculovirus-expressed hACE2
Mammalian-expressed SARS-CoV-2 RBD	sc-dimer	1.86 (1.98)*	215 (206)
	Monomer	1.20 (1.03)	186 (187)
Baculovirus-expressed SARS-CoV-2 RBD	Monomer	4.04 (4.54)	184 (187)

*Values in parentheses are K_D values by experimental repeat

Table S3. Binding affinities of hACE2 to SARS-CoV RBDs measured by SPR, Related to Figure 4.

		K_D (nM)	
		Mammalian-expressed hACE2	Baculovirus-expressed hACE2
Mammalian-expressed SARS-CoV RBD	sc-dimer	8.75 (8.37)*	2040 (1980)
	Monomer	14.2 (14.3)	2220 (2190)
Baculovirus-expressed SARS-CoV RBD	Monomer	12.3 (12.4)	1370 (1300)

*Values in parentheses are K_D values by experimental repeat