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Supplemental Information

Structural and Functional Basis of SARS-CoV-2 Entry by Using Human ACE2

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Table S1. Comparison of hACE2 binding to SARS-CoV-2-CTD and SARS-RBD. Related to Figures 2 and 3 and Table 2.

Residues	**K417/V404**[a]	**N439/R426**	**G446/T433**	**Y449/Y436**	**Y453/Y440**	**L455/Y442**	**F456/I443**	**Y473/F460**
Contacts	4(1)/0[b]	0/8(1)	4/0	13(2)/14(3)	5(1)/5(1)	13/9	14/3	1/0
Residues	**A475/P462**	**G476/D463**	**E484/P470**	**F486/I472**	**N487/N473**	**Y489/Y475**	**F490/W476**	**Q493/N479**
Contacts	9(1)/1	9/0	1/0	22/6	23(2)/14(3)	21/20	2/0	17/4
Residues	**G496/G482**	**Q498/Y484**	**T500/T486**	**N501/T487**	**G502/G488**	**V503/I489**	**Y505/Y491**	
Contacts	21(1)/4	20(3)/18	27(2)/32(2)	19(1)/22	12(1)/17(1)	0/2	40/33	

[a] The former residue indicates the one in SARS-CoV-2-CTD, and the latter indicates its equivalent in SARS-RBD.

[b] The number represent the counts of van der Waals contacts, which the indicated residues conferred. The number in the parentheses suggest the potential H-bond between the pair of residues. In this table, van der Waals contact was analyzed at the cutoff of 4.5 Å and the H-bonds at the cutoff of 3.5 Å. Residues in red are in the β1'/β2' loop.