Supplemental information

Binding and molecular basis of the bat coronavirus

RaTG13 virus to ACE2 in humans and other species

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Supplementary tables:

Table S1. The coding genes of 25 ACE2 orthologs, Related to Figure 2

Species of ACE2	Organism	Database	Code
Human	*Homo sapiens*	NCBI Reference Sequence	NP_001358344.1
Macaca	*Macaca fascicularis*	NCBI Reference Sequence	XP_005593094.1
Rabbit	*Oryctolagus cuniculus*	NCBI Reference Sequence	XP_002719891.1
Mouse	*Mus musculus*	NCBI Reference Sequence	NP_001123985.1
Rat	*Rattus norvegicus*	NCBI Reference Sequence	NP_001012006.1
Malayan pangolin	*Manis javanica*	NCBI Reference Sequence	XP_017505746.1
Cat	*Lynx canadensis*	NCBI Reference Sequence	XP_030160839.1
Civet	*Paguma larvata*	NCBI Reference Sequence	Q56NL1.1
Fox	*Vulpes vulpes*	NCBI Reference Sequence	XP_025842512.1
Dog	*Canis lupus familiaris*	NCBI Reference Sequence	XP_005641049.1
Raccon Dog	*Nyctereutes procyonoides*	GenBank	ABW16956.1
Horse	*Equus caballus*	NCBI Reference Sequence	XP_001490241.1
Pig	*Sus scrofa*	NCBI Reference Sequence	XP_020935033.1
Wild bactrian camel	*Camelus ferus*	NCBI Reference Sequence	XP_006194263.1
Alpaca	*Vicugna pacos*	NCBI Reference Sequence	XP_006212709.1
Bovine	*Bos taurus*	NCBI Reference Sequence	XP_005228486.1
Goat	*Capra hircus*	NCBI Reference Sequence	XP_005701129.2
Sheep	*Ovis aries*	NCBI Reference Sequence	XP_011961657.1
Intermediate horseshoe bat	*Rhinolophus affinis*	GenBank	QMQ39222.1
Little brown bat	*Myotis lucifugus*	NCBI Reference Sequence	XP_023609439.1
Fulvous fruit bat	*Rousettus leschenaultii*	GenBank	ADJ19219.1
Greater horseshoe bat	*Rhinolophus ferrumequinum*	NCBI Reference Sequence	BAH02663.1
Least horseshoe bat	*Rhinolophus pusillus*	GenBank	ADN93477.1
Big-eared horseshoe bat	*Rhinolophus macrotis*	GenBank	ADN93471.1
Lesser hedgehog tenrec	*Echinops telfairi*	NCBI Reference Sequence	XP_004710002.1

Table S3. The binding affinities between ACE2s and SARS-CoV-2 RBD, RaTG13 RBD or RaTG13 RBD mutants, Related to Figure 3

	Binding affinity（μM）								
Species	SARS-CoV-2 RBD	RaTG13-CoV RBD	F449Y	L486F	Y493Q	Y498Q	D501N	H505Y	6-mutant
Human	0.015 ± 0.001^{1}	3.86 ± 1.1	1.43 ± 0.36	0.88 ± 0.16	9.78 ± 0.46	$--^{2}$	0.34 ± 0.03	0.7 ± 0.03	0.028 ± 0.001
Mouse	--	2.55 ± 0.01	1.02 ± 0.41	6.65 ± 3.7	--	--	35.6 ± 10.5	0.6 ± 0.05	--
Horse	0.056 ± 0.006	0.69 ± 0.1	0.48 ± 0.15	1.21 ± 0.43	0.33 ± 0.07	9.39 ± 3.14	0.25 ± 0.04	0.15 ± 0.009	0.111 ± 0.001
Intermediate horseshoe bat	0.382 ± 0.054	42.3 ± 15.4	--	21.4 ± 9.9	--	--	0.59 ± 0.11	5.82 ± 0.74	0.179 ± 0.04

[1] The binding affinities between ACE2s and RaTG13 RBD or RaTG13 RBD mutants are shown with the means ± SD of three independent experiments.

2 "--" means no detectable binding.

Table S4. The capture level of the indicated MAb and concentrations of the indicated RBD, together with the calculated K_D in the SPR assay were listed, Related to Figure 5.

MAbs	Capture level (RU)	Solution	Concentrations of Solutions (nM)	K_D
H4	662.3 ± 4.97	SARS-CoV-2 RBD	6.25 12.5 25 50 100	1.72 ± 0.11nM
B38	776.3 ± 12.55	SARS-CoV-2 RBD	50 100 200 400 800	10.9 ± 0.85nM
CB6	744.1 ± 4.01	SARS-CoV-2 RBD	6.25 12.5 25 50 100	1.95 ± 0.17nM
S2H14	575.1 ± 2.80	SARS-CoV-2 RBD	50 100 200 400 800	3.98 ± 0.462nM
REGN10933	495.7 ± 4.69	SARS-CoV-2 RBD	1.5625 3.125 6.25 12.5 25	0.223 ± 0.0018nM
REGN10987	701.2 ± 9.03	SARS-CoV-2 RBD	6.25 12.5 25 50 100	1.66 ± 0.13nM
C110	398.8 ± 9.90	SARS-CoV-2 RBD	6.25 12.5 25 50 100	0.122 ± 0.007nM
H4	662.2 ± 4.88	RaTG13 RBD	200 400 800 1600 3200	--
B38	757.1 ± 3.95	RaTG13 RBD	200 400 800 1600 3200	963 ± 16.9nM
CB6	744.2 ± 5.49	RaTG13 RBD	50 100 200 400 800	39.0 ± 0.45nM
S2H14	571.7 ± 2.17	RaTG13 RBD	200 400 800 1600 3200	--
REGN10933	492.7 ± 5.02	RaTG13 RBD	200 400 800 1600 3200	551 ± 20.2nM
REGN10987	696.5 ± 11.82	RaTG13 RBD	200 400 800 1600 3200	5930 ± 381nM
C110	391.2 ± 24.53	RaTG13 RBD	200 400 800 1600 3200	1100 ± 59.3nM

[1] The binding affinities between ACE2s and RaTG13 RBD or RaTG13 RBD mutants are shown with the means ± SD of three independent experiments.

2 "--" means no detectable binding.

Table S5. The information of donors, Related to Figure 5

Donors	Gender	Age	Developmental stage
1	Male	50	Convalescent
2	Male	51	Convalescent
3	Male	56	Convalescent
4	Male	20	Convalescent
5	Male	28	Convalescent
6	Female	61	Convalescent
7	Male	30	Healthy
8	Female	27	Healthy
9	Male	24	Healthy