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Structure-function relationships among selected human coronaviruses

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Supplementary Data

Table S1 — Virus families that infect humans their genome information

Name	Genome	Envelope
Adenoviridae	dsDNA	Naked
Arenaviridae	ssRNA	Enveloped
Astroviridae	ssRNA	Naked
Bornaviridae	ssRNA	Enveloped
Bunyaviridae	ssRNA	Enveloped
Caliciviridae	ssRNA	Naked
Circoviridae	ssDNA	Naked
Coronaviridae	ssRNA	Enveloped
Filoviridae	ssRNA	Enveloped
Flaviviridae	ssRNA	Enveloped
Hepadnaviridae	partially ssDNA	Enveloped
Hepeviridae	ssRNA	Naked
Herpesviridae	dsDNA	Enveloped
Orthomyxoviridae	ssRNA	Enveloped
Papillomaviridae	dsRNA	Naked
Polyomaviridae	dsDNA	Naked
Paramyxoviridae	ssRNA	Enveloped
Parvoviridae	ssDNA	Naked
Picornaviridae	ssRNA	Naked
Poxviridae	dsDNA	Variable
Reoviridae	dsRNA	Naked
Retroviridae	ssRNA	Enveloped
Rhabdoviridae	ssRNA	Enveloped
Togaviridae	ssRNA	Enveloped
Delta*	ssRNA	Enveloped

#ds, double stranded; ss, single stranded. *Floating genus, which is not currently assigned to any viral family. It has some similarities to viroid pathogens of plants.Source: Siegel RD et al., 2008

Table S2 — The protein PDB ID and sequence reference number of the proteins NSP3, NSP5, NSP12, NSP14, NSP15, NSP16 and Spike protein of the seven coronaviruses which were selected for the study based on their structure and sequence availability

Proteins	ID	Coronavirus						
		SARS-CoV2	SARS-CoV	MERS-CoV	HCoV-HKU1	HCoV-NL63	HCoV-229E	HCoV-OC43
NSP3	Protein PDB ID	7LOS	5Y3Q	4RNA	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009742610.1	YP_009944368.1	YP_009047215.1	YP_009944271.1	QED88024.1	AGT21366.1	YP_009924321.1
NSP5	Protein PDB ID	6LU7	3SN8	4YOI	3TLO	3D23	27U2	Modelled
	Sequence ID	YP_009725301.1	YP_009944370.1	YP_009047217.1	YP_009944273.1	QED88024.1	NP_073550.1	YP_009924323.1
NSP12	Protein PDB ID	7AAP	6NUR	Modelled	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009725307.1	NC_004718.3	YP_009047223.1	AXT92494.1	AIW52809.1	QNT54713.1	ANZ78850.1
NSP13	Protein PDB ID	6XEZ	6JYT	5WWP	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009725308.1	NP_828849.7	YP_009047224.1	YP_459942.1	QED88024.1	NP_835353.1	YP_009555238.1
NSP14	Protein PDB ID	7EIZ	5C8S	Modelled	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009725309.1	NP_828849.7	YP_009047225.1	YP_460021.1	QED88024.1	AGT21366.1	YP_009555238.1
NSP15	Protein PDB ID	6VWW	2OZK	5YVD	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009725310.1	NP_828849.7	YP_009047226.1	YP_460022.1	AVL25592.1	AGT21366.1	YP_009555238.1
NSP16	Protein PDB ID	6W4H	3R24	5YN5	Modelled	Modelled	Modelled	Modelled
	Sequence ID	YP_009725311.1	NP_828849.7	YP_009047227.1	YP_460023.1	AVL25592.1	AGT21366.1	AAT84351.1
Spike	Protein PDB ID	6M0J	7LM9	5YY5	3KBH	5GNB	6U7F	Modelled
	Sequence ID	YP_009724390.1	YP_009825051.1	YP_009047204.1	YP_173238.1	YP_003767.1	BDB58082.1	QEG03814.1

Table S3 — Mutational analysis of residue in wild type SARS-CoV and SARS-CoV2 indicating the residues that are neutral and deleterious. The predicted residues were analysed using PredictSNP which consist of a collection of mutation prediction tools and servers

Protein	Wild residue SARS-CoV-2	Position	Target residue SARS-CoV-2	Predict SNP prediction	MAPP prediction	PhD-SNP prediction	PolyPhen-1 prediction	PolyPhen-2 prediction	SIFT prediction	SNAP prediction
NSP3	T	15	I	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	V	49	N	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	E	78	P	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Deleterious
	G	100	N	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Neutral	Neutral
	S	115	A	Deleterious	Deleterious	Neutral	Neutral	Deleterious	Deleterious	Deleterious
	A	120	T	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	A	130	P	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Neutral	Neutral
	E	135	D	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	S	156	C	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Deleterious	Deleterious
	H	172	Y	Neutral	Deleterious	Neutral	Neutral	Deleterious	Neutral	Neutral
	K	196	Q	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	T	201	K	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	N	216	Q	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Neutral
	L	217	F	Neutral	Deleterious	Neutral	Neutral	Deleterious	Neutral	Neutral
	T	219	K	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral
	S	222	Q	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Deleterious
	R	229	K	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	Q	233	K	Neutral	Neutral	Neutral	Deleterious	Neutral	Neutral	Neutral
	A	250	P	Neutral	Deleterious	Neutral	Deleterious	Neutral	Neutral	Neutral
	E	251	Q	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral

	K	253	Y	Neutral	Neutral	Neutral	Deleterious	Neutral	Deleterious	Neutral
	Q	255	K	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	Q	256	H	Neutral	Neutral	Neutral	Deleterious	Neutral	Deleterious	Neutral
	N	263	S	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Neutral	Deleterious
	T	275	K	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious
	A	279	S	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	R	285	C	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Deleterious	Deleterious
	H	290	L	Neutral	Deleterious	Neutral	Deleterious	Neutral	Neutral	Neutral
	M	294	S	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral
	T	309	N	Deleterious	Deleterious	Neutral	Deleterious	Neutral	Deleterious	Deleterious
NSP5	H	134	F	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	T	285	A	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
NSP12	G	65	D	Neutral	-	Deleterious	Neutral	Neutral	Neutral	Neutral
	M	79	F	Neutral	-	Neutral	Neutral	Neutral	Deleterious	Deleterious
	D	200	N	Neutral	-	Neutral	Neutral	Neutral	Deleterious	Neutral
	A	254	T	Neutral	-	Neutral	Deleterious	Deleterious	Neutral	Neutral
	C	283	K	Neutral	-	Neutral	Deleterious	Neutral	Neutral	Neutral
	I	301	V	Neutral	-	Neutral	Neutral	Neutral	Neutral	Neutral
	T	613	N	Neutral	-	Neutral	Deleterious	Neutral	Neutral	Neutral
	Y	768	F	Deleterious	-	Deleterious	Neutral	Deleterious	Deleterious	Deleterious
NSP13	I	570	V	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
NSP14	I	31	T	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	D	90	E	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious
	E	128	P	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious
	E	132	D	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	N	228	H	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	S	307	A	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Deleterious
	A	396	S	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral	Neutral
	T	437	V	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	Q	493	L	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Neutral
NSP15	A	19	Q	Neutral	Neutral	Neutral	Deleterious	Deleterious	Neutral	Neutral
	A	22	V	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	A	30	T	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Neutral
	I	42	L	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	S	118	P	Neutral	Deleterious	Neutral	Neutral	Deleterious	Neutral	Deleterious
	L	122	F	Deleterious	Deleterious	Neutral	Deleterious	Neutral	Deleterious	Deleterious
	T	152	Q	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral
	K	155	V	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Neutral
	I	186	V	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	D	202	E	Neutral	Deleterious	Neutral	Neutral	Neutral	Deleterious	Neutral
	T	211	I	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	S	258	F	Neutral	Neutral	Neutral	Deleterious	Deleterious	Neutral	Deleterious
	L	263	F	Neutral	Deleterious	Neutral	Neutral	Deleterious	Neutral	Neutral
	K	264	E	Neutral	Deleterious	Neutral	Neutral	Deleterious	Neutral	Neutral
	I	314	V	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral
	A	325	T	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
NSP16	A	1	S	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral	Neutral
	E	32	D	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	K	158	Q	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral
	A	209	C	Deleterious	Neutral	Neutral	Deleterious	Deleterious	Deleterious	Deleterious
	V	290	I	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious

SPIKE	A	67	V	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	T	95	I	Deleterious	Neutral	Neutral	Deleterious	Deleterious	Deleterious	Deleterious
	Y	145	D	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Deleterious
	G	339	D	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	S	375	F	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	K	417	N	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious	Neutral
	N	440	K	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Neutral
	T	478	K	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Deleterious
	Q	493	R	Neutral	-	Neutral	Neutral	Neutral	Neutral	Deleterious
	G	496	S	Neutral	-	Neutral	Neutral	Deleterious	Deleterious	Neutral
	Q	498	R	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral	Deleterious
	N	501	Y	Neutral	Neutral	Neutral	Deleterious	Deleterious	Deleterious	Neutral
	Y	505	H	Deleterious	Neutral	Neutral	Deleterious	Deleterious	Deleterious	Deleterious
	H	655	Y	Neutral	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral
	P	681	H	Neutral		Neutral	Neutral	Neutral	Neutral	Deleterious
	N	764	K	Deleterious	Neutral	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious
	D	796	Y	Neutral	Neutral	Deleterious	Neutral	Neutral	Neutral	Neutral
	N	856	K	Deleterious	Deleterious	Deleterious	Neutral	Deleterious	Deleterious	Deleterious
	Q	954	H	Neutral	Neutral	Neutral	Neutral	Neutral	Neutral	Deleterious
	N	969	K	Deleterious	Deleterious	Deleterious	Neutral	Deleterious	Neutral	Deleterious

Table S4 — Solvent accessible surface areas, atomic solvation energies and their gradients for NSP3, NSP5, NSP12, NSP13, NSP14, NSP15, NSP16, and Spike (RBD) for 7 Coronaviruses

		229E	HKU1	MERS CoV	NL63	OC43	SARS CoV	SARS CoV2
NSP3	POLAR	6227.26	5691.64	6148.66	5601.25	6106.84	5783.05	6219.6
	APOLAR	10247.91	9446	9908.05	9878.34	9620.05	9464.92	9066.04
	TOTAL	16475.17	15137.64	16056.7	15479.59	15726.89	15247.97	15285.64
NSP5	POLAR	5518.92	5148.36	5076.21	5320.85	4371.34	5586.34	5528.38
	APOLAR	8727.78	8727	9043.2	8810.86	8956.31	8899.28	8498.64
	TOTAL	14246.71	13875.36	14119.41	14131.71	13327.65	14485.63	14027.02
NSP12	POLAR	15154.89	15354.83	14885.77	16344.86	14905.25	19268.66	14447.69
	APOLAR	22077.37	23867.79	23616.13	24337.7	22917.55	24435.26	22607.76
	TOTAL	37232.27	39222.61	38501.9	40682.56	37822.81	43703.92	37055.45
NSP13	POLAR	10287.32	10421.24	8415.18	9802.14	10286.49	11019.12	9524.98
	APOLAR	16811.61	16774.76	14136.14	16621.52	16677.71	18012.93	19203.37
	TOTAL	27098.92	27196	22551.32	26423.66	26964.2	29032.05	28728.34
NSP14	POLAR	28728.34	10221.18	10237.8	9971.95	9771.09	9487.63	9790.74
	APOLAR	16086.79	16863.97	17352.45	16028.67	17250.98	16342	18702.23
	TOTAL	26599.52	27085.15	27590.26	26000.62	27022.06	25829.63	28492.97
NSP15	POLAR	6310.61	7058.96	6379.9	6205.29	7058.96	5740.68	6823.03
	APOLAR	10119.98	10281.78	10466.97	10507.37	10281.78	9980.56	10303.68
	TOTAL	16430.58	17340.74	16846.86	16712.66	17340.74	15721.24	17126.71
NSP16	POLAR	5214.17	5017.82	4588.78	5258.17	4524.28	5393.02	4968.31
	APOLAR	9272.04	8936.27	8318.46	9250.97	9110.57	8686.01	8432
	TOTAL	14486.2	13954.09	12907.25	14509.13	13634.86	14079.03	13400.31
SPIKE (RBD)	POLAR	2625.73	6837.38	3791.92	2635.73	7105.6	3677.93	3767.74
	APOLAR	4234.64	10942.49	6513.44	4400.91	10602.12	6287.38	6234.48
	TOTAL	6860.37	17779.88	10305.36	7036.64	17707.72	9965.31	10002.22

Table S5 — Protein structure alignment and comparison of NSP3, NSP5, NSP12, NSP13, NSP14, NSP15, NSP16 and Spike proteins of SARS-CoV2 Vs SARS-CoV, MERS-CoV, HCoV-NL63, HCoV-229E, HCoV-OC43 and HCoV-HKU1 along with RMSD and TM scores of the superimposed structures generated from TM-align server

Protein	Reference coronavirus	Coronavirus	RMSD	TM Score
NSP3	SARS-CoV2	HCoV-HKU1	1.41	0.967 (0.964)

		HCoV-229E	2.78	0.860 (0.852)
		HCoV-OC43	1.11	0.817 (0.935)
		SARS-CoV	3.05	0.770 (0.807)
		HCoV-NL63	3.05	0.761 (0.805)
		MERS-CoV	2.99	0.680 (0.753)
NSP5	SARS-CoV2	SARS-CoV	0.87	0.972 (0.972)
		HCoV-229E	1.31	0.948 (0.964)
		MERS-CoV	1.27	0.948 (0.948)
		HCoV-NL63	1.58	0.937 (0.949)
		HCoV-HKU1	1.50	0.935 (0.950)
		HCoV-OC43	1.62	0.928 (0.943)
NSP12	SARS-CoV2	HCoV-229E	0.60	0.996 (0.979)
		MERS-CoV	0.59	0.995 (0.976)
		HCoV-OC43	0.61	0.992 (0.978)
		HCoV-HKU1	0.62	0.992 (0.978)
		HCoV-NL63	0.80	0.988 (0.976)
		SARS-CoV	0.78	0.865 (0.993)
NSP13	SARS-CoV2	HCoV-OC43	3.05	0.881 (0.888)
		HCoV-229E	3.15	0.881 (0.887)
		HCoV-NL63	2.85	0.880 (0.904)
		HCoV-HKU1	3.20	0.877 (0.884)
		SARS-CoV	3.64	0.851 (0.860)
		MERS-CoV	2.87	0.776 (0.888)
NSP14	SARS-CoV2	SARS-CoV	0.79	0.945 (0.961)
		MERS-CoV	0.86	0.938 (0.940)
		HCoV-229E	0.85	0.934 (0.950)
		HCoV-OC43	0.82	0.928 (0.940)
		HCoV-HKU1	0.81	0.926 (0.938)
		HCoV-NL63	0.83	0.919 (0.947)
NSP15	SARS-CoV2	HCoV-229E	0.44	0.992 (0.995)
		MERS-CoV	1.18	0.944 (0.963)
		HCoV-OC43	1.30	0.934 (0.934)
		HCoV-HKU1	1.30	0.934 (0.934)
		HCoV-NL63	1.92	0.900 (0.918)
		SARS-CoV	2.32	0.792 (0.895)
NSP16	SARS-CoV2	HCoV-NL63	0.55	0.986 (0.986)
		HCoV-229E	0.52	0.984 (0.987)
		SARS-CoV	0.89	0.958 (0.981)
		MERS-CoV	0.79	0.952 (0.985)
		HCoV-OC43	1.52	0.942 (0.954)
		HCoV-HKU1	1.52	0.942 (0.954)
Spike	SARS-CoV2	SARS-CoV	1.31	0.955 (0.955)
		HCoV-HKU1	3.27	0.753 (0.430)
		MERS-CoV	3.17	0.713 (0.669)
		HCoV-OC43	3.42	0.555 (0.378)
		HCoV-NL63	4.18	0.303 (0.433)
		HCoV-229E	4.82	0.232 (0.332)

*The threshold value forTM-score >0.5, RMSD < 5.0Å. The >0.5 TM score and RMSD < 5.0 depicts the similar structure among two proteins

Table S6 — List of interacting residues at protein-protein interacting interface of SARS-CoV-2 Spike RBD (chain E) and ACE2 (chain A). The interface hotspot residues are predicted using three servers i.e., KFC server, SpotON server and Robetta server. The KFC server and SpotOn server predicts binding hotspot while the Robetta server predicts hotspot with a binding energy between the residues in kcal/mol

(Chain E) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)	(Chain A) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)
ARG403E	-	-	-	SER19A	-	-	-
LYS417E	-	-	0.62	GLN24A	-	-	2.2
VAL445E	-	-	-	THR27A	HS	-	0.66
GLY446E	-	-	-	PHE28A	HS	-	0.25
TYR449E	-	-	1.61	ASP30A	-	-	0.52
TYR453E	-	-	0.2	LYS31A	HS	HS	0.5
LEU455E	HS	-	1.21	HIS34A	HS	-	0.7
PHE456E	HS	-	1.64	GLU35A	-	-	-0.13
TYR473E	-	-	-	GLU37A	-	-	1.07
ALA475E	-	-	-	ASP38A	-	-	0.69
GLY476E	-	-	-	TYR41A	HS	-	4.69
SER477E	-	-	-	GLN42A	-	-	2.25
GLU484E	-	-	-	LEU45A	-	-	0.45
GLY485E	-	-	-	LEU79A	-	-	0.54
PHE486E	-	HS	2.06	MET82A	-	-	0.21
ASN487E	-	-	4.38	TYR83A	-	-	2.9
TYR489E	HS	-	2.27	THR324A	-	-	-
PHE490E	-	-	-	GLN325A	-	-	-
GLN493E	-	-	0.51	GLY326A	-	-	-
GLY496E	-	-	-	ASN330A	-	HS	0.19
GLN498E	HS	HS	1.15	LYS353A	HS	HS	0.26
THR500E	HS	HS	0.69	GLY354A	-	-	-
ASN501E	HS	-	1.18	ASP355A	-	-	3.63
GLY502E	-	-	-	ARG357A	-	-	2.12
VAL503E	-	-	0.07	ALA386A	-	-	-
TYR505E	HS	-	2.47	ARG393A	-	-	-

*HS: Hotspot. The common predicted hotspots by three the servers are highlighted in boldface

Table S7 — List of interacting residues at protein-protein interacting interface of SARS-CoV Spike RBD (chain E) and ACE2 (chain A). The interface hotspot residues are predicted using three servers i.e., KFC server, SpotON server and Robetta server. The KFC server and SpotOn server predicts binding hotspot while the Robetta server predicts hotspot with a binding energy between the residues in kcal/mol.

(Chain E) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)	(ChainA) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)
ARG393E	-	-	-	SER19A	-	-	0.57
LYS390E	-	-	-0.1	GLN24A	-	-	0.64
ARG426E	-	-	1.05	THR27A	HS	HS	0.54
SER432E	-	-	-	PHE28A	-	-	0.18
THR433E	-	-	-	ASP30A	-	-	-0.09
TYR436E	-	-	0.3	LYS31A	-	-	0.47
TYR440E	-	-	0.22	HIS34A	-	-	0.28
PHE442E	-	HS	1.25	GLU37A	-	-	0.08
LEU443E	-	-	0.47	ASP38A	-	-	0.45
PHE460E	-	-	-	TYR41A	HS	-	4.34
PRO462E	-	-	-	GLN42A	-	HS	2
ASP463E	-	-	-	LEU45A	-	-	0.71

PRO470E	-	-	-	GLU75A	-	-	-
PHE472E	-	-	0.87	THR78A	-	-	-
ASN473E	-	-	1.13	LEU79A	-	-	-
TYR475E	HS	HS	1.89	MET82A	-	-	0.44
ASN479E	-	-	0.14	TYR83A	-	-	0.67
ASP480E	-	-	-0.01	THR324A	-	-	0.03
TYR481E	-	-	-	GLN325A	-	-	0.14
GLY482E	-	-	-	GLY326A	-	-	-
TYR484E	HS	-	3.27	GLU329A	-	-	1.08
THR486E	HS	HS	1.28	ASN330A	-	-	0.16
THR487E	HS	-	0.33	LYS353A	HS	-	2.09
GLY488E	-	-	-	GLY354A	-	-	-
ILE489E	-	-	0.41	ASP355A	-	-	1.78
TYR491E	HS	-	1.65	ARG357A	-	-	0.08

*HS: Hotspot. The common predicted hotspots by three the servers are highlighted in boldface

Table S8 — List of interacting residues at protein-protein interacting interface of MERS-CoV Spike RBD (chain B) and DDP4 (chain A). The interface hotspot residues are predicted using three servers i.e., KFC server, SpotON server and Robetta server. The KFC server and SpotOn server predicts binding hotspot while the Robetta server predicts hotspot with a binding energy between the residues in kcal/mol

(Chain B) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)	(Chain A) Residue	KFC	SpotOn	Robetta ΔΔG (kcal/mol)
SER451B	-	-	-0.01	THR188A	-	-	-
MET452B	-	-	-	THR265A	-	-	0.05
SER454B	-	-	-0.03	VAL266A	-	-	-
ASP455B	-	-	-0.11	LYS267A	HS	-	0.91
SER460B	-	-	-	PHE269A	-	-	0.26
ALA461B	-	-	-	ASN281A	-	-	-
GLY462B	-	-	-	THR283A	-	-	0.02
PRO463B	-	-	-	SER284A	-	-	-
GLN466B	-	-	-	GLN286A	HS	-	0.43
TYR499B	-	-	0.36	THR288A	HS	-	0.27
ASN501B	HS	-	1.49	ALA289A	-	-	-
LYS502B	HS	-	3.78	PRO290A	HS	-	-
SER504B	-	-	1.15	ALA291A	HS	-	-
ARG505B	-	-	-	SER292A	HS	-	0.47
LEU506B	HS	-	1.38	LEU294A	HS	-	1.56
ASP510B	-	-	0.14	ILE295A	HS	-	1.36
ARG511B	HS	-	0.32	GLY296A	-	-	-
THR512B	-	-	0.03	ASP297A	-	-	-
GLU513B	HS	-	7.44	HIS298A	-	-	0.31
PRO515B	-	-	-	ARG317A	-	-	0.24
GLU536B	-	-	-0.18	TYR322A	-	-	1.17
ASP537B	-	-	0.29	ASP331A	-	-	-0.09
GLY538B	-	HS	-	SER333A	-	-	0.41
ASP539B	-	-	0.58	SER334A	-	-	-0.06
TYR540B	HS	-	1.71	ARG336A	HS	HS	0.54
TYR541B	-	-	-	ASN338A	-	-	-
ARG542B	-	-	0.87	VAL341A	-	-	0.8
TRP553B	-	-	1.51	GLN344A	-	-	2.03
VAL555B	HS	-	1.01	ILE346A	-	-	0.64

ALA556B	HS	-	-	MET348A	-	-	-
SER557B	HS	-	1.29	LYS392A	-	-	0.03
SER559B	-	-	0.62				
ALA562B	-	-	-				

*HS: Hotspot. The common predicted hotspots by three the servers are highlighted in boldface

Table S9 — List of interacting residues at protein-protein interacting interface of HCoV-NL63 Spike RBD (chain E) and ACE2 (chain A). The interface hotspot residues are predicted using three servers i.e., KFC server, SpotON server and Robetta server. The KFC server and SpotOn server predicts binding hotspot while the Robetta server predicts hotspot with a binding energy between the residues in kcal/mol

(Chain E) Residue	KFC	SpotON	Robetta ΔΔG (kcal/mol)	(Chain A) Residue	KFC	SpotON	Robetta ΔΔG (kcal/mol)
PHE493E	-	-	-	ASP30A	-	-	0.36
GLY494E	-	-	-	LYS31A	-	-	-
GLY495E	-	-	-	ASN33A	-	-	0.02
SER496E	-	-	0.28	HIS34A	-	-	0.71
CYS497E	-	-	-0.1	GLU37A	HS	-	2.68
TYR498E	HS	-	2.61	ASP38A	-	-	-0.09
VAL499E	HS	-	0.53	TYR41A	-	-	0.64
CYS500E	-	-	-	LEU45A	-	-	-
HIS503E	-	-	0.1	PRO321A	-	-	-
SER533E	-	-	1.03	ASN322A	-	-	-
GLY534E	-	-	-	MET323A	-	-	-
SER535E	-	-	0.79	THR324A	HS	-	1.22
PRO536E	-	-	-	GLN325A	-	-	1.03
GLY537E	-	-	-	GLY326A	-	-	-
SER539E	-	-	0.32	ASN330A	-	-	0.17
SER540E	-	-	1.15	LYS353A	HS	-	0.4
TRP585E	HS	-	1.49	GLY354A	HS	HS	-
HIS586E	-	-	1.1	ASP355A	-	-	-0.11
THR588E	-	-	0.18	PHE356A	HS	-	0.46
SER589E	-	-	-	ARG357A	-	-	-
				MET383A	-	-	-
				ALA384A	-	-	-
				ALA386A	-	-	-
				ALA387A	-	-	-
				PRO389A	-	-	-
				PHE390A	-	-	-
				ARG393A	-	-	1.89
				PHE555A	-	-	-

*HS: Hotspot

Table S10 — List of interacting residues at protein-protein interacting interface of HCoV-229E Spike RBD (chain E) and APN (chain B). The interface hotspot residues are predicted using three servers *i.e.*, KFC server, SpotON server and Robetta server. The KFC server and SpotOn server predicts binding hotspot while the Robetta server predicts hotspot with a binding energy between the residues in kcal/mol

(Chain E) Residue	KFC	SpotON	Robetta ΔΔG (kcal/mol)	(Chain B) Residue	KFC	SpotON	Robetta ΔΔG (kcal/mol)
SER312E	-	-	-0.03	ASP242B	-	-	-
GLY313E	-	-	-	THR244B	-	-	0.01
GLY314E	-	-	-	GLU286B	-	-	-0.02

GLY315E	-	HS	-	PHE287B	-	-	-
LYS316E	-	-	-	ASP288B	HS	-	1.87
CYS317E	HS	HS	-0.12	TYR289B	-	-	1.46
PHE318E	HS	-	1.62	VAL290B	HS	-	0.85
ASN319E	HS	HS	0.2	GLU291B	-	-	-0.15
CYS320E	-	-	-0.1	LYS292B	-	-	0.59
VAL357E	-	-	-	TRP303B	-	-	-
GLY358E	-	-	-	PRO306B	-	-	-
ARG359E	-	-	0.5	ILE309B	HS	-	0.37
TRP404E	HS	-	1.51	ALA310B	-	-	-
ALA405E	-	-	-	ALA311B	-	-	-
SER407E	-	-	0.66	GLY312B	-	-	-
LYS408E	-	-	0.31	ASP315B	-	-	0.05
				LEU318B	-	-	0.44

*HS: Hotspot. The common predicted hotspots by three the servers are highlighted in boldface

Table S11 — Theper residue energy calculation of the complexes SARS-CoV2 with ACE2, SARS-CoV with ACE2, MERS-CoV with DDP4, HCoV-NL63 with ACE2 and HCoV-229E with APN. The electrostatic, solvation, van der Waals energy and pyDock total energy is calculated for each residue contributing of the protein-protein interaction

Complex	Residue	ele (kcal/mol)	solv (kcal/mol)	vdw (kcal/mol)	Total (kcal/mol)
SARS-CoV2 and ACE2	E.LYS.417	-4.92839	2.33736	-1.39523	-2.73055
	E.GLY.446	-0.0203	0.1277	-1.45266	-0.03787
	E.TYR.449	0.33148	2.65759	-1.03873	2.88519
	E.TYR.453	-0.0409	-2.5827	-0.03898	-2.6275
	E.LEU.455	-0.93251	0.62541	-5.85977	-0.89308
	E.PHE.456	-0.08618	-6.42077	-4.57836	-6.96478
	E.ALA.475	-1.23856	0.42373	-3.04302	-1.11913
	E.PHE.486	-0.42636	-10.8933	-7.48157	-12.0678
	E.ASN.487	-0.32872	2.19183	-3.37819	1.52529
	E.TYR.489	0.08867	-4.62367	-8.6467	-5.39967
	E.GLN.493	0.73959	4.52071	-3.08951	4.95135
	E.GLY.496	-0.31004	3.38586	-2.09003	2.86681
	E.GLN.498	-0.16944	-0.8504	-5.68142	-1.58798
	E.THR.500	0.52844	2.30085	-7.95479	2.03381
	E.ASN.501	-0.74903	-0.07062	-7.92897	-1.61254
	E.GLY.502	-0.49386	0.40743	-2.2631	-0.31274
	E.TYR.505	-0.54268	-4.71266	-9.83448	-6.23878
	A.GLN.24	-0.73366	1.23105	-4.44449	0.05294
	A.THR.27	0.05818	-7.17397	-6.56842	-7.77262
	A.PHE.28	-0.24835	-0.00753	-3.46241	-0.60212
	A.ASP.30	-4.91536	2.31782	-3.42407	-2.93994
	A.LYS.31	0.46392	0.52814	-6.96378	0.29568
	A.HIS.34	-0.37223	-2.06548	-4.70932	-2.90863
	A.GLU.35	-1.15145	0.3609	-1.9626	-0.98681
	A.GLU.37	-2.32317	1.68236	-2.45023	-0.88584
	A.ASP.38	-3.07567	1.20229	-2.6734	-2.14072
	A.TYR.41	0.46671	-0.1412	-6.61164	-0.33565
	A.GLN.42	1.65749	2.8475	-1.79922	4.32507
	A.LEU.79	-0.13612	-0.73033	-1.91359	-1.05781
	A.MET.82	-0.03018	-2.90649	-2.25182	-3.16184

	A.TYR.83	-0.167	-6.12236	-4.16448	-6.70581
	A.ARG.393	0.76567	0.7381	-0.72364	1.43141
SARS-CoV2 and ACE2	E.ARG.426	-5.77801	4.06848	-2.31736	-1.94127
	E.TYR.436	-0.23988	1.5576	-1.04817	1.2129
	E.PHE.442	0.07003	-6.80749	-3.69468	-7.10694
	E.LEU.443	-0.00471	-1.48236	-2.0217	-1.68923
	E.PRO.462	-1.41296	1.57606	-3.69255	-0.20615
	E.PHE.472	-0.34529	-7.73865	-5.20636	-8.60457
	E.ASN.473	1.35653	2.71268	-3.33746	3.73546
	E.TYR.475	0.36802	-5.70233	-6.91307	-6.02561
	E.TYR.481	0.24549	4.38999	-1.19294	4.51618
	E.GLY.482	-0.61516	0.26003	-1.62445	-0.51757
	E.TYR.484	-0.90681	-7.3596	-8.04373	-9.07079
	E.THR.486	-0.44841	3.08442	-6.99593	1.93641
	E.THR.487	-0.28625	-1.13322	-7.67071	-2.18653
	E.GLY.488	-0.45501	0.22874	-3.17303	-0.54357
	E.ILE.489	0.00138	-0.20872	-2.40571	-0.44791
	E.TYR.491	-0.20879	-5.38891	-10.1701	-6.61471
	A.SER.19	-2.60137	1.69866	-2.32981	-1.1357
	A.GLN.24	-0.02945	0.46954	-3.03727	0.13636
	A.THR.27	0.16721	-6.38234	-5.04773	-6.7199
	A.PHE.28	0.21423	-0.7133	-2.84563	-0.78363
	A.ASP.30	-1.34172	-1.48185	-1.92405	-3.01598
	A.LYS.31	1.40872	-7.2503	-3.83078	-6.22466
	A.GLU.37	-1.6435	1.46415	-1.98747	-0.3781
	A.ASP.38	-0.40831	0.10589	-2.15211	-0.51763
	A.TYR.41	-0.56799	-1.56053	-6.08896	-2.73741
	A.GLN.42	-0.31524	1.34465	-2.60316	0.76909
	A.LEU.45	-0.27424	-3.80429	-3.00057	-4.37859
	A.MET.82	0.13218	-6.8173	-2.68572	-6.95369
	A.TYR.83	0.48335	2.91173	-2.34476	3.1606
	A.GLN.325	-1.14014	-0.1576	-2.29679	-1.52742
	A.GLU.329	-4.39255	3.99531	-2.23445	-0.62068
	A.ASN.330	-0.52071	0.50616	-2.61238	-0.27579
	A.LYS.353	-0.36365	-0.6893	-11.355	-2.18845
	A.GLY.354	-0.25778	-1.99437	-3.92266	-2.64442
	A.ASP.355	-1.8544	-0.17975	-3.88865	-2.42301
	A.ARG.357	1.83615	0.52153	-1.44954	2.21273
MERS-CoV and DDP4	B.SER.454	-0.55813	1.15937	-1.92915	0.40833
	B.ASP.455	-2.07094	1.1039	-2.94216	-1.26125
	B.PRO.463	0.35916	0.60922	-2.88649	0.67973
	B.TYR.499	0.55695	3.14943	-1.08998	3.59738
	B.ASN.501	-0.51701	-0.16929	-2.13321	-0.89963
	B.LYS.502	-2.22827	0.7806	-6.93759	-2.14143
	B.LEU.506	-0.35561	-1.30474	-5.51663	-2.21201
	B.ASP.510	-2.61581	3.29363	-4.5479	0.22303
	B.ARG.511	3.03216	7.13137	-9.10422	9.25311
	B.GLU.513	-1.52599	0.63321	-8.07601	-1.70038
	B.ASP.537	-1.53136	-0.54324	-2.94466	-2.36906
	B.GLY.538	0.97008	-0.53604	-2.42087	0.19195
	B.ASP.539	-2.72575	6.57577	-1.6731	3.68272

	B.TYR.540	-0.37068	-7.1706	-8.76723	-8.41801
	B.ARG.542	-4.19377	1.53689	-5.6669	-3.22357
	B.TRP.553	0.0785	-4.3326	-6.6913	-4.92323
	B.VAL.555	-0.00866	-1.90035	-4.98456	-2.40747
	A.THR.265	0.1624	-0.45074	-1.10572	-0.39891
	A.LYS.267	-3.50065	5.29214	-3.6563	1.42586
	A.PHE.269	-0.08958	-0.72109	-0.32942	-0.84361
	A.GLN.286	-3.90309	1.24418	-6.56737	-3.31565
	A.THR.288	0.42333	-0.4098	-4.5792	-0.44439
	A.ALA.289	-1.47737	0.97239	-1.47944	-0.65293
	A.ALA.291	-0.11783	-1.94288	-8.38131	-2.89884
	A.SER.292	-1.07183	-1.16345	-3.35818	-2.57109
	A.LEU.294	-1.24381	-3.63357	-9.14111	-5.79149
	A.ILE.295	-0.13879	-4.32091	-12.7478	-5.73448
	A.HID.298	-0.42819	-4.30075	-1.98466	-4.9274
	A.ARG.317	-4.27206	2.82074	-2.61407	-1.71272
	A.TYR.322	-0.04554	0.04126	-2.99829	-0.30411
	A.SER.334	-1.25469	2.57788	-3.21369	1.00182
	A.ARG.336	-3.52471	3.34466	-6.72289	-0.85234
	A.VAL.341	-0.18432	-1.18479	-4.29313	-1.79842
	A.GLN.344	-0.73739	2.57838	-1.6937	1.67163
	A.ILE.346	-0.34211	-0.331	-4.4244	-1.11555
	A.LYS.392	4.80093	7.9179	-1.26832	12.592
HCoV-NL63 and ACE2	E.GLY.494	-0.42676	1.42567	-2.03252	0.79566
	E.GLY.495	0.11271	-0.41849	-3.42873	-0.64865
	E.SER.496	-1.46157	0.93312	-7.86498	-1.31495
	E.CYX.497	0.45182	0.79148	-5.05695	0.73761
	E.TYR.498	-0.9745	-1.11126	-7.16016	-2.80177
	E.CYX.500	-0.03617	-0.75253	-1.85202	-0.97391
	E.GLY.534	-0.23725	0.07976	-1.62048	-0.31955
	E.SER.535	-1.01996	-1.24831	-3.53657	-2.62192
	E.PRO.536	-0.45524	-1.09729	-9.44868	-2.4974
	E.GLY.537	-0.52825	-0.2994	-3.34551	-1.16219
	E.SER.540	-0.21879	1.77513	-2.18177	1.33817
	E.TRP.585	-0.3188	-7.49717	-5.9481	-8.41079
	E.HID.586	-1.27535	-0.83162	-5.83924	-2.6909
	A.ASP.30	-2.33667	-0.18965	-2.39945	-2.76626
	A.ASN.33	0.02289	0.53739	-2.14933	0.34534
	A.HID.34	-0.88449	0.4722	-6.15409	-1.0277
	A.TYR.41	-0.75492	-1.28534	-3.346	-2.37487
	A.ASN.322	-0.99549	-1.05392	-0.36784	-2.0862
	A.THR.324	-0.52191	0.70564	-4.53806	-0.27008
	A.GLY.326	-0.0909	-0.90274	-1.91624	-1.18527
	A.ASN.330	0.15413	-0.15409	-1.43155	-0.14312
	A.GLY.354	-0.21634	-2.91628	-6.23444	-3.75606
	A.ASP.355	-1.15328	-0.39478	-4.04673	-1.95273
	A.PHE.356	-0.03752	-5.67535	-1.89154	-5.90203
	A.ALA.387	-0.00401	-0.82106	-2.94271	-1.11934
	A.ARG.393	0.32227	0.75532	-2.29447	0.84815
HCoV-229E and APN	E.SER.312	-1.1567	-0.27086	-2.0269	-1.63025
	E.GLY.313	-0.29159	1.38245	-2.1695	0.87391

	E.GLY.314	-0.54566	-0.46729	-4.58783	-1.47173
	E.GLY.315	-0.97915	1.96469	-3.3188	0.65366
	E.LYS.316	-2.80168	-0.04174	-6.4897	-3.49238
	E.CYX.317	-0.56307	-3.36089	-6.05572	-4.52954
	E.PHE.318	-0.30051	-4.98442	-7.85194	-6.07012
	E.ASN.319	-0.42891	0.61677	-3.29001	-0.14114
	E.CYX.320	0.30753	0.28677	-1.2805	0.46625
	E.ARG.359	-6.32069	1.72731	-2.19631	-4.81301
	E.TRP.404	-0.59485	-7.08312	-3.89697	-8.06767
	E.SER.407	-0.04819	2.61114	-1.66655	2.39629
	E.LYS.408	-2.94054	1.59646	-4.55705	-1.79979
	A.THR.244	0.1014	0.85784	-0.85421	0.87382
	A.GLU.286	-1.42739	-0.10833	-2.71704	-1.80742
	A.PHE.287	-0.15845	-0.08466	0.07357	-0.23575
	A.ASP.288	-4.33786	1.55499	-8.07885	-3.59076
	A.TYR.289	-0.46541	-1.67157	-6.6455	-2.80153
	A.VAL.290	0.94081	-1.93494	-6.75719	-1.66985
	A.GLU.291	-4.57375	3.38288	-3.43029	-1.5339
	A.LYS.292	3.11831	2.2321	-4.20061	4.93036
	A.ILE.309	-0.23579	-1.82185	-3.34289	-2.39193
	A.ASP.315	-7.03806	-1.00797	-1.76479	-8.22251
	A.LEU.318	-0.48258	-4.12121	-0.9329	-4.69708