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## Structure-function relationships among selected human coronaviruses

Esther Jamir<sup>1,2</sup>, Kikrusenuo Kiewhuo<sup>1,2</sup>, Lipsa Priyadarsinee<sup>1,2</sup>, Himakshi Sarma<sup>1</sup>, Selvaraman Nagamani<sup>1,2</sup> & G Narahari Sastry<sup>1,2</sup>\*

<sup>1</sup>Advanced Computation and Data Sciences Division, CSIR-North East Institute of Science and Technology, Jorhat-785 006, Assam, India <sup>2</sup>Academy of Scientific and Innovative Research (AcSIR), Ghaziabad-201 002, Uttar Pradesh, India

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## **Supplementary Data**

HCoV-NL63	LKITEDGINVKDVVVESSKSLGKOLGVVSDGVDSPEGVLPINTDTVLSVAP	51
HEoV-229E	- FARVETTRATEDGY/MURVEWEDDESE FOOVGVEDDEDEDI SGAVESDI NEGELLEKAT	59
HEOV-OC42	ELDEWATH LTWORNET NOEWENGES EGEST GNASCOSVINTEL POTING (CVS 2020)	50
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MEDG C.M	<ul> <li>A STATE AND A REAL AND A STATE AND A STAT</li></ul>	27
PIER2-COV		20
SARS-Cov2	KEAKLTKALLIADNTUTULUI ÖAADA2HLIAÖÖÖLENI ATDEMOALKTKAUN2HEEKLI-AATS	60
SARS-CoV	REAKLTEAALLADM INFHUŐFADMZVLLAGÓÓ ARLLAFDAYDA LETENHANHEGK LENAT	66
HCoV-NL63	EVD/VAFYG-FEKAALFASLDVKPYGYPNDFVGGFRVLGTTDNNCNVNATCI	102
HCOV-229E	DADMAFibAGHEDGAJ EWLADH28H8A5289AA0G7EATEATEAD000CMA08AC7	336
HEOM OF 49	NUSSEDU STAVESSEN- POOKELL AXYNYL YNC EKNOVEMURYET EKONNING PARIVEC	118
DOM: ACHINE DI	NEAL ADDRAWO338 (L-DDDDOLL ANOTHER TYC- VIAMAAM/RETERING BOSINER/CARMACI	448
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PIERO-COV	NETADE INFERENCE TOPOPTIFEMENTSERAMANIGUENESCONDERESONNETENRATIV	110
SARS-COV2	NDDTCR0-EMPEYYHTTDPSFLORVASMENHTSXWKYPQVIdETS3KMADNIQCYLMTMLL	118
SARS COV	SDDTLRS EAPEYYHTLDESFLORYMSALNHTRXWKFPQVGGLTSIKNADNNCYLSSVLL	119
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HEOV-NERT	TEOXI - CRITERSENI NVI MNCEVI ONVORESSEI VETTINSSCOORD SEEVI NEI SEYI T	1611
HCoV-229F	ALOYS-SPHETSORI DAAWNSEVLODVETEVAEVYYVABL VKODNOLAPDTLNKL SKYLA	169
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P1282-420W	TEDELADISPOTPALQNAPHANAGOSTOPTALLNASGNCTPGAPOTRSHLLNTOLASAS	1/0
SARS-COV2	TLOOT-BLKPNPPALODAYYRARAGBAANFCALTLAYCNRTVGBLGLWRBTMSYLPOHAN	178
SARS-CoV	ALQQL-EVKPNAPALQEAYYRARADDAANFCALTLAYSNKTVOELOCVKETNTHLLQHAN	178
HCoV-NL68	SOSIVILEQYSTCDDCKSTVVEVKSAVVCASVL\$DOCDVGPCPHRHKLRSRV	213
HCoV-229E	WEAQVQLEHYSSCVECDAKFKNSVTSINSAIVCASVHRDGVQVGYCVHGIHYYSRV	225
HEOV-OC43	LT-GATCDEETA-CICGVKOEO-RTGLDAV/IHEGTLSREDLETGYTVDCSCGKILTH-CV	233
HEOV-HKUT	S-GATTELETT-COORTOES-ENANDAMILENTTAKTELENAVETNENEAMILTKH-CT	2805
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SMRS-COV	EE-SARRACHV9CRICEORTTT-ET9VER9MINGTESTUNERT9V5EPCVCBRDATOTEV	220
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HCAVE NIL 63	PENNERAATTMACENTECOCKIIME TANTTECC COMONAAATAANM MAA	365
HCOV-NLOS	KEYING KEYI ING GELI SURSKELINGIATI INSG-SEDUKAN VETVANNA	200
HCOV-228C	A SYNCHWITT SOUCH FLOOR LESS VALLA SO-FVOLUNT IV FULADA - SYN	477
MCOV-OC43	NPDY-PPLICSNIPASVRLPR0YOSPNIPIODRVOHYVHVRCEQS-YQLY	281
HCoV-HKU1	KLWY-PFLICSNTPLSKDLPDDWVAANMPMGVGVGNYTHLKC66P-YQNY	278
MERS-CoV	SHTT-PWILLESTPNEKLYTSTAPDFWAFNMFQGISTAVGHYWHARLKGGLILKF	292
SARS-COV2	QQ2S-PFVVVSAPPAQYELEH0TPTCASEVT0-NYQC3HYEHITSEET-LYCI	286
SARS-OVV	0025-SFVPMSAPPAEYKL000TPLCANENTO-NYQCOMYTHITAKET-LYRI	266
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HEOV-NL63	DG48L P&SDL	
NC:M-229E	1902 Mill 284	
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INCOVERAGE STREET	DESIVERY IDVIGEDUCTE 302	
IN OV INVE	DRESSER TIS VOALLINCLY 200	
PIERS-COV	DSGIUSEISDNEERVINGLAVGURYSSDEN 522	
SARS-O/V2	DGALLTRSSEYRGPITDVPYRENSYTTTIK 316	
SARS-CoV	DGAHLTKM5CYKGFVTDVFYKETSYTTTIK 316	
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"\*" Fully conserved ":" Conservation between groups of amino acids with strongly similar properties "." Conservation between groups of amino acids with weakly similar properties "\*" Fully conserved ":" Conservation between groups of amino acids with strongly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with

**Figure S1(a)**. Multiple sequence alignment of NSP3 (Pl-pro) protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

	*	
HCoV-NL63	SGLKKMA0PSGCVERCVVRVCYGSTVLNGVvDGDTVTCPRHVIAPSTT-VLIDYDHAYST	59
HCoV-229E	AGLRKMAOPSGFYEKCVVRVCYGNTVLNGLWLGDIVYCPRHVIASNTT-SAIDYDHEYSI	59
SARS-CoV2	SGFRKNAFPSGKVEGCNVOVTCGTTTLNGLWLDDVVYCPRHVICTSEONLNPNYEDLLIR	60
SARS-CoV	SGFRKNAFPSGKVEGCNVOVTCGTTFLNGLWLDDTVYCPRHVICTAEONLNPNYEDLLIR	60
MERS-CoV	SGLVKNSHPSGDVEACNVOVTCGSMFLNGLWLDNTVWCPRHVMCPADQLSDPNVDALLTS	60
HCoV-0C43	SGTVERMNPTSKVERCVVSVTVGNMELNGLM DDKVVCPRHVTCSASDNTN2DYTNLLCR	60
HCoV-HKU1	SGTVKWVSPTSKTERCTVSVTYGSMFLNGLMLDDKVYCPRHVTCSSSNNNEPDYSALLCR	60
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HCoV-NL63	MRLHNPSVSHNGVPLGVVGVTMHGSVLRIKVSOSNVHTPKHVFKTLPGDSFNILAC	116
HCoV-229E	NRLHNFSITSGTAFLGVVGATMHGVTLKIKVSOTNNHTPRHSFRTLHSGEGFNILAC	116
SARS-CoV2	KSNHNFLVOAGNVOLEVIGHS//ONCVLKLK//DTANPKTPKYKFVBI/PGOTFS//LAC	117
SARS-CoV	ESNESELVOAGNVOLEVTGESMONCLE BLEVDTSNPETPKYK EVETOPSOTESVLAC	117
MERS-COV	NTNHSESVOKHTGAPANI EVVGHAMOGTI I KI TVDVANPSTPAYTETTV PSAAESVI AC	120
HCoV-0C43	VTSSDETVLEDRLSLTW9SY0/8GCMLVLTVTL0/ISBTP/CYTEGV/V-PGETETVLAA	117
HCoV-HKU1	YTI GDETTINSGRINSI TW/SYONOGCOLYLTVSI ONPYTRIXTEGNM PSETETYL AA	117
	a	
	* * * * * * * * * * * *	
HCoV-NL63	YEGIASGYFGYNLRINFTIKGSFINGAEGSPGYNVRNDGIVEFCYLHOIELGSGAHVGSD	176
HCoV-229E	YD6CA0GVF6VNNRTNWTIR6SFINGACGSPGYNLKN-GEVEFVYMHOIELGSGSHV65S	175
SARS-CoV2	YNGSPSGVYOCANRPNFTIK6SFLNGSIGSVGFNIDY-DCVSFCYMHHNELPTGVHAGTD	176
SARS-CoV	YNGSPSGYYOCANRPNHTIK6SFLNGS GSVGFNIDY-DCVSFCYMHHNELPTGVHAGTD	176
MERS-COV	YNGRFTGTFTVVNRRNYTEKGSFLCGSGGSVGYTKEG-3VINFCYMHONELANGTHTGSA	179
HCoV_OC43	YNGKROGARMYTNRSSYTTKØSFLCBSTGSVGYVTNG-DCVKRVYMHOLFLSTGCHTGTD	176
HCoV HKU1	YNG BROGARHYTNESSYTTERSELCES GSVGYVLTG-DSVKRVYMHOLELSTGCHTGTD	176
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HCoV-NLOS	PT0SVY0NR0DQPSLOVESANL/PLSONVVAPLYAALLN0CPWULCSTRVNV00PWENAMA	256
HCoV-229E	PD6VMYGGREDOPNLOVESANOMLTVNVVAFLYAATLNGCTWULKGEKLEVEHYNENAOA	235
SARS-CoV2	LEGNEYGERVDROTAGAAGTDTTITVNVLAWLYAAVINGDRWELNRETTTLNDRNLVAMK	256
SARS-CoV	LECKFYGPFYDROTAGAACTDTTITLNVLAWLYAAVINGDRWFLNRFTTTLNDPNLVAMK	256
MERS-COV	PD0T/YGANDK0VHOVOLTDKYCS/NVVANLYAATLN0CAMPVKPNRTS/V/SPNENALA	259
HCoV-OC43	PNODEYOFMODARYVOLLEODYTOS/NEVANLYAATLINICINAEVOSDICS/EDPINYNALS	256
HCoV-HKU1	PTONEYOPHRDAOWYOLRYRDYVOTVNVTAULYAATLINICAUEVONDVCSTEDENVNAMA	256
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HEoV-NL63	NGYTSVSSVECYSTLAAKTGVSVEQLLASTQ-HLHESFGGKWILGYSSLCDEFTLAEV	293
HEOV-229E	NGFTARNGEDAFSTLAARTGVCVERLLHATQ-VLNNSFGGRQTLGYSSLNDEFSTWEV	292
SARS-CoV2	ANAS METODHADTERMERY OLD TWATTACTOR CONTRACTOR OF A CONTRACT OF	298
SARS-CoV	YNYEPLTODHWDELGPLS/AOTGI/WEDMCWALSEELEONSNNSHTELGS/TEEDEF/PPOV	298
MERS-COV	NOPTEPVOTOSVDPLAWKTGVATEOLLYATO-OLYTOPOGKOTLGSTPLEDEFTPEDV	296
HEOV-OC43	NGPSDVESOL VIDALASMIGVSLETLLAAIX-RLENSPOGROIMGSCSPEDELTPSOV	283
HEOV-HKU1	NGFSOVKADLVLDALASNTGVSTETLLAATK-RLYNSFOGROTLGSCTFEDELARSDV	293
	1	
IEOV-NL63	VKRMACAMER 303	
HEoV-229E	VRQMFGVNLQ 302	
SARS-CoV2	VRQCSCVT FQ 306	
SARS-CoV	VRQCSGVT FQ 306	
MERS-CoV	NNOIMGVVNO 306	
HEOV-OC43	YOULAGINLO 503	
HEOV-HKUI	AOOPWARED 283	
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**Figure S1(b).** Multiple sequence alignment of NSP5 (Cl-pro) protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

HCOV-NL63 HCOV-229E		53
HCoV-229E		
MC 0Y-223C	CHERNEL AND	1000
	SP055TENRVING-SSARREDPEN-GIDIDTEVINAPOVTNRDASPIERNERSNEWR	2.2
HEOV-DE43	SKDTNFLNRVRGRSVDARLVPCASGLSTDVQLNAFDIYNASVRGIGLHLKVNCCR	55
HCOV-HKUR	SUDINFINEWROTS-WARLYPCASOLSTDVOLRAFDICNTNR&GDOLYYUVNCCK	55
MHINK CONC	OPPENDENT NEW YORK OF A CARLEND YOUR OF A CARLEND AND A CARLEND	10.00
PIE K2 - C.9 V	SLDSMFLNK4KSSIGWARIEPCSSGLSIDVVPRAPDICNTLARAPBIGKTTKINICK	27
SARS-CoV2	SADAQSFLNRVCG-VSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCR	55
SARS=CoV	NGSADAST FLNRVCG-VSAARLTPCGTGTSTDX/VYRAFD1YNEKVAGFAKFLKTNCCR	57
	1 1500 5 5 No. 5 5 5 5 5 10 10 1 1 1 1 5 5 5 5	
DOM: NO OT	PROVIDENT LICENSING TRANSPORTED AND LICENSING AND ADDRESS AND ADDRESS TAXABLE ADDRESS ADDR	0.00
THE OVER NEEDS	PRIMADEXDOMPVERKCTRSVPEHEOSHYNELINFSGALAEHDFF TWRDGRWEYGWWS	1064
HCoV-229E	FRNWD\$DDAFYIWRCIRSWNDHEQSNYNLLRGCNAWARHDFFTWHEGRTIYGNWS	1015
HEOV-DE413	POSYDEMEDIC DOFEWARETRI TTYNERMCCYPEWARCERWARHDEPTPDWRASSARHTY	115
LIC AVE LIVE M	CONTRODOMY DIVERSALING WANTER TAKET THE COMMENDED TO TO TO TO THE CONTROL THE	445
HK OV - HKOT	PORTOCOMINE DREP POPULATION CONTINUES TO COMPARENCE POPULACIÓN DE CONTRACTOR DE CONTRACT	113
MERS-COV	PVELDDQBHHLDSYPVVKRHTMENYELEKHCYDLLRDCDAVAPHDPPIPDVDKVKTPHIV	117
SARS-CoV2	PORKDRODNLTDSV PAAKKHTRSNVOHRRTTVNLL KDC SXXXXKHDRRKPSTDGDMVRHTS	118
W/CRM - COVC	DEVELOPMENT AND A DEVELOPMENT	10.10
SANS-COV	POCKDEEGNLLDSTPWYRRTINSWTONEETTTWLWRDCFWWWWIDFPRFRVDGDIWFTLS	116
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HE OLD BUILDER	RELEASE AS AN ADVENUE AND ADVENUES AND ADVENUES AND ADVENUES AND ADVENUES AND ADVENUES AND ADVENUES ADVENUES ADVENUES AND	10.044
MCOV-NEOS	RHINE TRET HAD LEE AARAN DE ONCOVERE DE VET OCCUMSER OSKONEDE VENEDET HAVE	TOP
HCoV-229E	ROULTRYTYMDLCF ALRNFDERDEGYFREILVLTGCCNTDYFEPRNMFDPTENEDIHRWY	168
HCoV-OC43	6K DLTKYTMLDLCYALRHFDRNDCMLLCDTLSTYAGCE0SYFTKKDW/DFVENPDTTNVY	175
HIC ON HIGH D	STALL STATEMENT CALLED CARDONNESS AND CARD CARDON STATEMENT AND A THE TARGET	0.72.00
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MERS-COV	RÖRFLEALMAD FAARTEND ÖF UZEAFRAJ FAKARCODALALENK FINARDEAEND PATRAK	176
5485-CW2	FOR THY TWO I WAS REPROVED THAT WAS CODDWANNER WANTED TO SAY	178
SARS-COV	NORE IN THIS DESTREMANDED IN THE TEST THE COURT PRESENT OF THE PROPERTY IN	176
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HCOV-NUSP	AS LONTANDAM REVENUED AND A DAMAGED AND A DEDUCTION OF THE DAMAGED AND A	990
THE SHE SHE SHE	THE REPORT OF A DESCRIPTION OF A DESCRIP	441
HCOV-229E	ARLIG K.WAMAPILIK CWAF CIDEMWLIKGWYGWLT LIDNQDLINGNFYDF GDFVLC PPGMGIPYCT	228
HCoV-OC43	KILGPTFNRALVSATEFADICLVEVGLVGVLTLDNODLNGKNYDFGDYVTAAPGCGVATAD	235
HC DAG HIGH PI	INTERPORTENDAL ENTYREADTE WAVELING WAVE TERNOOL VOOLANDERDETOTAPOREGAAWAAD	28.8
HCOV-HKOL	KIEGPTPWIMEENI VSFRUTEVIMEENEDINGEFEDINGEFEDINGEFEDING GUTEVIMPERION	200
MERS-COV	HKLGERWROATLNTYKFCDHWYRAGLVGWLTLDNODLNGRNYDFGDFVITOPGSGVAIVD	236
SARS-CoV2	ANL GERMIDIAL LICTVOF CIDAMINIAGEV SWLTLIDNODLINGNAV DEGDIFTOTTPGS SWPV/VD	235
SARS-Cold	AND GEOMORY LIKTYOEY DAMODAGT VICKUT LINNOD I MONUMPE GROMANA OCCAVOTAN	222
SMINS-COV	07	201
HC-ML-NL-C-2	SYNCHIMPTING THELAS STELLED FRANCISCOUTED LIFED THE MICHINE MUSIC COM	300
HCOV-HCO3	STASTPHEINGLINCERSECT VISULINGSOF KIPDLESTOFTERKENETINKTERNINGFOT	243-52
HEOV-229E	SYYAYMIPANGMINCLASECHNESDIHGQDERTEDILKYBETEHKEVLENKYERYMGQDY	289
HCoV-OC43	SYYSYIMPHLIMCHALDCELYVNNAYRLFDLVOYDFTDYKLELFNKYFKHWSMPY	290
HCoV-HKU1	SYNSYMMENI TACHVI DOBLEVNDSYROEDI VOVRETDYKLELENKYEKYMGNKY	298
MEDC C-M	CARCAL AREA CATCOL A A TUDDOOD NEW TOUR TOWN TOWN AND THAT AND THE	0.0.0
PIERS-COV	STISTEMPVESHIDCEAREINNDCOP-INKPETENPETENPETENPETENPETENPETENPETENPET	233
SARS-CoV2	SYYSLLMPILTLTRALTAESHVDTDL-TKPYIKNDLLKYBFTEERLKLPDRYFKYWDQTY	294
SARS-COV	SYYSELMPTETETRALAAFSHIDADE - AKPETKNDEL KYDETEFRECLEDRYFKYMDOTY	296
	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
HCoV-NL63	HPNCSDCYDDMCVIHCANFNTLFATT IPGTAFGPLCRKVFIDGVPLVTTAGYHFKOLGLV	349
HC-M- 220E	HERCYDCHDENCTI HCENENTI FATT TRNTAEGOL CRIVYETROVOVA/ATAGVIEROLGUV	2.40
11000-2250	HP DEVDENDER ETERCSAFIATE PATT TRAFACE CARACTED AVE THAT HE RETAIL AND A	2148 22
MLOV-UL43	HENTADFÖDDHFTTHCHULUTERSHMFHULCHAFFARÖTEARØAKEAARTAUAKEFOTA	226
HCoV-HKU1	HPNTVDWDNBRCIIHCANFNILFSMWLPNTCF6PLVRQIFVBGVPFVVSIGYHYKELGVV	358
MERS-COV	HANCWNCTORRCVI HCANENVI FAMT//PKTCEGETVBKTEV/DGV/PEV//SCGVHV/EFI GLV	355
CARG CAND	LONGVICT DEDCTT LICANCINAL ECTIVEDOT CECOLIVINI TENDOVERIA/CECULERELONAL	25.4
SMR3-COV2	HPHCONCLODERCIERCANPINGERSTOPPOLSEGELORS I PODOPPOVSTOPPEREDOV	22**
SARS-COV	MPHCINCLUDHCIERCANPINVEFSIVPPPISFOFEVRKIPVUOVPFVVSIOYMPRELOVV	220
HC-ML NL GR	LINKOVITUSIADI TTTELLOSVITIDEL TENECIDAL VIDODITE SEVIAL ETGLITINA MIDEN	400
MCOV-NLOS	WINKOWNTHSWHETITELLQFVTDPSLITASSPALVDQHTTCPSVAALSTGLTNQVVKPGH	
HCoV-229E	WNKDWNTHSTRLTITELLOPVTDPTLIVASSPALVDKRTVCPSVAALSTGLTSQTVKPGH	
HEAL OCAR		409
	NNNDVDTHRYRLSLKDLLLYAADPALHVASASALYDLRTCCFSVAATTSGV//FOTV///PGN	409
HCOV-OC43	NNNDVDTHRYRLSLKDLLLYAADPALHVASASALYDLRTCCPSVAATTSGVKFOTVKPGN NNN DVDTHBYRLSLKDLLLYAADPANNHAASASALLDI RTCCSSVAATTSGTVEOD ALBGN	409 410
HCoV-HKU1	NNNDVDTHRYRLSLKDLLLYAADPALHVASASALYDLRTCCPSVAAITSGVKFQTVKPGN NNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCPSVAAITSGIKFQTVKPGN	409 410 410
HCoV-HKU1 MERS-CoV	NNINDVDTHRYRLSLKDLLLYAADPALMVASASALYDLRTCCPSVAAITSGKFOTVFPGN NNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCPSVAAITSGIFOTVFPGN NNINDVSLHHRLSLKELVMYAADPAMHIASSNAFLDLRTSCPSVAAITTGLTFOTVARGN	409 410 410 415
HCoV-HKU1 MERS-CoV SARS-CoV2	NNNDVDTHRYRLSLKDLLLYAADPALHVASASALYDLRTCCFSVAAITSGVKFQTVKPGN NNLDVDTHRYRLSLKDLLLYAADPANHVASASALDDLRTCCFSVAAITSGIXFQTVRFGN NNNDVSLHRHRLSLKELMYYAADPANHASSNAFLDLRTSCFSVAALTGLFFQTVRFGN HNDDVNLHSSRLSFKELLYVAADPANHAASGNLLDCRTTCFSVAALTNNVAFOTVKFGN	409 410 410 415 414
HCoV-HKU1 HCoV-HKU1 MERS-CoV SARS-CoV2 SARS-CoV2	NNINDVDTH SYRLSLKDLLLYAADPAL HWASASALYDLRTCCPSVAATTSGKFOTVFON NNLDVDTH RYRLSLKDLLYAADPAMHWASASALLDLRTCCPSVAATTSGTFOTVFON NNINDVSLHHRLSLKELWYAADPAMHEASSNAFLDLRTSCPSVAATTGLTFOTVARGN HNIDVINLHSSRLSFKELLYVAADPAMHEASGNLLLDCRTTCPSVAALTNNNAFCTVFOGN HNIDVINLHSSRLSFKELLYVAADPAMHEASGNLLLDCRTTCPSVAALTNNNAFCTVFOGN	409 410 410 415 415 414
MCoV-OC43 MCoV-HKU1 MERS-CoV SARS-CoV2 SARS-CoV2	NINDVDTH YYRLSLKOLLLYARDPAL HWASASALYDLRTCCPSVAAITSGKEPTVKPGN NNLDVDTH YYRLSLKOLLLYARDPAMHWASASALLDLRTCCPSVAAITSGIKEPTVKPGN NNMDVSLHHHRLSLKELMYYARDPAMHASSNAFLOLRTSCPSVAAITTGLTPTVAPGN HNQDVNLHSSRLSFKELLVYARDPAMHAASGNLLLDKRTTCPSVAAITNNVAPQTVKPGN HNQDVNLHSSRLSFKELLVYARDPAMHAASGNLLLDKRTTCPSVAAITNNVAPQTVKPGN	409 410 410 415 414 416
MCOV-OC43 MCOV-OKU1 MERS-COV SARS-COV2 SARS-COV2	NNNDVDTH HYRLSLKDLLLYAADPALHVASASALYDLRTCCPSVAATTSGXKFQTVKPGN NNLDVDTH HYRLSLKDLLLYAADPANHVASASALUDLRTCCPSVAATTSGIKFQTVKPGN NNNDVSLHHRLSLKELMYVAADPANHASSNAFLDLRTSCPSVAALTTGLTFQTVRPGN HNQDVNLHSSRLSFKELLVYAADPANHAASGNLLLDKRTTCPSVAALTNNVAFQTVKPGN HNQDVNLHSSRLSFKELLVYAADPANHAASGNLLLDKRTTCPSVAALTNNVAFQTVKPGN 000000000000000000000000000000000000	409 410 410 415 414 416
HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV	NINDVDTHSYRLSLKDLLLYAADPALHWASASALYDLRTCCPSVAAITSGKFOTVKPGN NINDVDTHSYRLSLKDLLYAADPAMHWASASALLDLRTCCPSVAAITSGTKPOTVKPGN NINDVDSLHHRLSLKELWYAADPAMHASSNAFLDLRTSCPSVAALTTGLTFQTVAPGN HNQDVNLHSSRLSFKELLYYAADPAMHAASGNLLLDKRTTCPSVAALTNNVAFQTVKPGN HNQDVNLHSSRLSFKELLYYAADPAMHAASGNLLLDKRTTCPSVAALTNNVAFQTVKPGN ************************************	409 410 410 415 414 416 416
HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63	NINDVOTH YYRLSLKOLLLYAADPAL WASASALYDLRTCCFSVAATTSGKEPOTKFON NINDVOTH YYRLSLKOLLLYAADPANHWASASALLOLRTCCFSVAATTSGKEPOTKFON NINDVSLHHHRLSLKELWYYAADPANHASSNAFLOLRTSCFSVAALTTNGLTPOTAFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCFSVAALTNNAFQTVKPGN HNQDWNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN NINDVNLHSSRLSFKELLYYAADPANHAASGNLLOKRTTCFSVAALTNNAFQTVKPGN	409 410 410 415 414 415 414 416
HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-229E	NINDVDTHRYRLSLKDLLLYAADPALHWASASALYDLRTCCPSVAAITSGKFOTVKPGN NINDVDTHRYRLSLKDLLYAADPAMHWASASALLDLRTCCPSVAAITSGTKPOTVKPGN NINDVDSLHHRLSLKELWYAADPAMHAASSNAFLDLRTSCPSVAALTNOLAFQTVAPGN HNQDVNLHSSRLSFKELLYYAADPAMHAASGNLLLDKRTTCPSVAALTNNNAFQTVKPGN «************************************	409 410 410 415 414 416 469 469
HCoV-OC43 HCoV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-2298 HCoV-0C43	NINDVOTHSYRLSLROLLLYAADPALHWASASALYOLRTCCFSVAATTSGWEGTVEGN NNLDVOTHSYRLSLROLLLYAADPANHWASASALLOLRTCCFSVAATTGGWEGTVEGN NNNDVSLHRHRLSLKELMYYAADPANHIASSNAFLOLRTSCFSVAALTTGLTFGTVRGN HNQDVNLHSSRLSFKELLVYAADPANHAASGNLLLOKRTTCFSVAALTNNVAFGTVFGN NNQDVNLHSSRLSFKELLVYAADPANHAASGNLLLOKRTTCFSVAALTNNVAFGTVFGN NNQDVNLHSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN PNQDVNLHSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN NNQDVNLHSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN PNQDVNLHSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN PNQDVNLHSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN PNQDVPNLSSRLSFKELLVYAADPANHAASGNLLOKRTTCFSVAALTNNVAFGTVFGN PNQDVPNLKLRGFPDEGSELTLKHFFFTQGGNAAXDPDFYRVNKFTILDIGGARVFYG PNQDFYDFVLSKGLKEGSSVDLKHFFFTQGGNAAXDPDNYYYNNFTILDIGGARVAYQ	409 410 415 414 415 414 415 469 469 469 470
HCOV-DL63 HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-2298 HCoV-0C43 HCOV-DC43	NINDVOTHSYRLSLKOLLLYAADPALHWASASALYDLRTCCPSVAAITSGKFOTVKPGN NINDVOTHSYRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAAITSGTKPOTVKPGN NINDVOSLHHRILSLKELWYAADPAHHAASSNAFLOLRTSCPSVAAITTGLTPOTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNVAPQTVKPGN ************************************	409 410 415 414 415 414 416 469 469 470 470
HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-229E HCoV-0C45 HCoV-HKU1 MERS-CoV	NINDVOTHAYRLSLKOLLLYARDPALHWSSASALYOLRTCCPSVAATTSGKFCOTVFGN NNLDVOTHAYRLSLKOLLYARDPANHWSSASALDOLRTCCPSVAATTGGKFCOTVFGN NNNDVSLHRHRLSLKELIWYARDPANHASSALDOLRTSCPSVAALTTGLTFQTVRPGN HNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDOKRTTCPSVAALTTNNNAFQTVKFGN NNDPVNLKEKLKELKKELKKHFFFTQGGNAATTDYNVNNFTILDICQARWAYQ PNQDFVDPVLSKLKEGSSVDLKHFFFTQGGNAATTDYNVYKNLFTNVDIKQLLFVLE PNQDFVEFWSKLFKEGSSTVDLKHFFFTQGGNAATTDYNVYKNLFTNVDIKQLLFVLE PNQDFVEFWSKSKLFKEGSSTVDLKHFFFTQGNAATTDYNVYKNLFTNVDIKQLLFVLE	409 410 415 414 415 414 416 469 469 470 470 470
HCOV-OC43 HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-2298 HCoV-OC43 HCOV-OC43 HCOV-OC43	NINDVOTHSYRLSLKOLLLYAADPALHWASASALYOLRTCCPSVAAITSGKEPTKEPR NINDVOTHSYRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAAITSGKEPTKEPR NINDVSLHHRILSLKELWYAADPAHHASSNAFLOLRTSCPSVAAITTGLTPGTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLYYAADPAHHAASGNLLOKRTTCPSVAALTNNAFQTVKPGN CONTUNESSINSFKELLKHPPFFQQGDAATTOYNYYKNLETNVDIRQULFVLE PNQDFYDFVLSKGLKEGSSVDLKHPFFFTQDGHAATTOYNYYKNLETNVDIRQULFVLE PNQDFYDFVSKGFFKEGSSVLKHPFFFTQDGHAATTOYNYYKNLETNVDIRQULFVLE PNQDFYDFVSKGFFKEGSSVLKHPFFFQQGHAATTOYNYYKNLETNCDIKQKLFCVE	409 410 415 415 414 416 469 469 470 470 470
HCOV-DK43 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-DL63 HCoV-0C45 HCoV-0K45 HCoV-HKU1 MERS-CoV SARS-CoV2	NINDVOTHAYRLSLKOLLLYAROPALHWSSASALYOLRTCCPSVAATTSGKFOTVKPGN NNLDVOTHAYRLSLKOLLYAROPANHWSSASALOLRTSCPSVAATTGGKFOTVKPGN NNNDVSLHRHRLSLKELWYAROPANHASSALOLRTSCPSVAALTTGLTPGTVRPGN HNQDVNLHSSRLSFKELLVYAROPANHARSGNLLOCKTTCPSVAALTTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYAROPANHARSGNLLOCKTTCPSVAALTTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYAROPANHARSGNLLOCKTTCPSVAALTTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYAROPANHARSGNLLOCKTTCPSVAALTTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVKARPFPTQGGNAATTOYNYNNRFTILDICQARWAYQ PNQEFVDFLKLRGSFCDGSELTLKHPFPTQGGNAATTOYNYNNRFTILDICQARWAYQ PNQDFVDFVLSKLRKEGSSTVCLKHPFFTQGGNAATTOYNYNYNLPTNVDIKQLLFVLE PNQDFVSFWSKSFKEGSSVTLKHPFFTQGGNAATTOYNYNSNLPTNCDIKQWLFCME PNQDFYDPVSKGFFKEGSSVTLKHPFFTQGGNAATTOYNYNSNLPTNCDIKQWLFCME	409 410 415 414 415 414 416 469 469 470 470 475 474
HCOV-HKU1 MERS-COV SARS-COV SARS-COV HCOV-NL63 HCOV-229E HCOV-OC43 HCOV-HKU1 MERS-COV SARS-COV	NINDVOTHSYRLSLKOLLLYAADPALHWASASALYOLRTCCPSVAAITSGKEPTVERGN NINDVOTHSYRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAAITSGKEPTVERGN NINDVOSLHHRLSLKELWYAADPAHHAASSNAFLOLRTSCPSVAAITTGLTPGTVARGN HNQDVNLHSSRLSFKELLVYAADPAHHAASGNLLLOKRTTCPSVAALTNNNAFQTVERGN HNQDVNLHSSRLSFKELLVYAADPAHHAASGNLLLOKRTTCPSVAALTNNNAFQTVERGN """"""""""""""""""""""""""""""""""""	409 410 415 414 415 414 416 469 469 470 470 470 475 474 476
HCOV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-229E HCoV-0C43 HCoV-0C43 HCoV-MKU1 MERS-CoV SARS-CoV SARS-CoV	NINDVDTHYYRLSLKDLLLYAADPALHWASASALYDLRTCCPSVAAITSGKEPTVKPGN NINDVDTHYYRLSLKDLLYAADPAHWASASALLDLRTCCPSVAAITSGKEPTVKPGN NINDVDSLHHRLSLKELWYAADPAHHAASSNAFLDLRTSCPSVAAITTGIFPTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLDKRTTCPSVAAITNNAFQTVKPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLDKRTTCPSVAAITNNAFQTVKPGN "*** *********************************	409 410 415 414 416 469 469 470 470 475 476 475
HCOV-UKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-0C45 HCoV-0C45 HCoV-0KU1 MERS-CoV SARS-CoV2 SARS-CoV2	NINDVOTHAYRLSLKOLLLYARDPALHWSSASALYOLRTCCPSVAATTSGKFCOTKPGN NNLDVOTHAYRLSLKOLLLYARDPANHWSSASALOLRTCCPSVAATTSGKFCOTKPGN NNNDVSLHRHRLSLKELLWYARDPANHASSALOLRTSCPSVAATTGLTPGTVAPGN HNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDCKTTCPSVAATTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDCKTTCPSVAATTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDCKTTCPSVAATTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDCKTTCPSVAATTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDCKTTCPSVAATTNNNAPGTVKPGN NNQDVNLHSSRLSFKELLVKARPFPTQGGNAATCPNYAYNNRFTILDICQARWAYQ PNNEFVDPLKSQGFPDEGSELTLKHPPFTQGGNAATCPNYAYNNRFTILDICQARWAYQ PNNDFVDPVLSKGLKEGSSVCLKHPFFTQGGNAATTDYNYYYNLDFNVDIKQLLFVLE PNNDFVDPVLSKGFKEGSSVTLKHPFFTQGGNAATTDYNYYSYNLPTNCDIKQMLFVKE PNNDFYDFAWSKGFFKEGSSVTLKHPFFTQDGNAATDYNYYSYNLPTNCDIKQMLFVKE PNNDFYDFAWSKGFFKEGSSVELKHPFFAQDGNAATSDYDYYYNNLPTNCDIKQULFVKE PNNDFYDFAWSKGFFKEGSSVELKHPFFAQDGNAATSDYDYYYNNLPTNCDIKQULFVKE PNNDFYDFAWSKGFFKEGSSVELKHFFFAQDGNAATSDYDYYYNNLPTNCDIKQULFVKE	409 410 415 415 414 416 469 469 470 470 470 475 474 476
HCOV-NL63 HCOV-NL63 HCOV-NL63 HCOV-229E HCOV-229E HCOV-0C43 HCOV-MKU1 MERS-COV SARS-COV SARS-COV HCOV-NL63	NINDVOTHYYRLSLKOLLLYAADPALHWASASALYOLRTCCPSVAAITSGWEPOTWEPGN NINDVOTHYYRLSLKOLLLYAADPAMHWASASALLOLRTCCPSVAAITSGWEPOTWEPGN NINDVOSLHHHRLSLKELWYAADPAMHAASGNLLLOKRTTCPSVAALTNNWAFQTVKPGN HNQDVNLHSSRLSFKELLYYAADPAMHAASGNLLLOKRTTCPSVAALTNNWAFQTVKPGN """"""""""""""""""""""""""""""""""""	409 410 415 415 414 416 469 470 470 470 470 475 475 529
HCoV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-229E HCoV-OC43 HCoV-HKU1 MERS-CoV SARS-CoV SARS-CoV HCoV-NL63 HCoV-NL63 HCoV-NL63	NINDVOTHSYRLSLKOLLLYAADPALHVASASALYOLRTCCPSVAATTSGKFOTVFGN NINDVOSLHHNRLSLKOLLLYAADPANHVASASALLOLRTCCPSVAATTSGKFOTVFGN NINDVOSLHHNRLSLKELMYAADPANHAASSNAFLOLRTSCPSVAALTNOLAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCPSVAALTNNNAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCPSVAALTNNNAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLLOKRTTCPSVAALTNNNAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLDOKRTTCPSVAALTNNNAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLDOKRTTCPSVAALTNNNAFOTVFGN HNQDVNLHSSRLSFKELLYYAADPANHAASGNLLDOKRTTCPSVAALTNNNAFOTVFGN PNDEFYNPLRLRGFPDEGSELTLKHPPFTQGDAAXIDFDFYRYNRPTILDICQARWAYQ PNDEFYDPULKLKEGSSVLKHPPFTQGDIAAITDYNYYNNFPTNVDIKQLLFVLE PNDDFYBPVSKGLFKEGSSTVLKHPPFTQDGNAAITDYNYYNNFPTNVDIKQLLFVLE PNDDFYDFVSKGLFKEGSSVLKHPFFTQDGNAAITDYNYYNNLPTNCDIKQLLFVLE PNDDFYDFWSKGFFKEGSSVELKHPFFFQDGNAAISDYNYYNNLPTNCDIKQLLFVE PNNDFYDFWSKGFFKEGSSVELKHPFFFQDGNAAISDYNYYNNLPTNCDIKQLLFVE SNILFSFKEGSSVELKHPFFFQDGNAAISDYNYYNLDFNCDIKQLLFVE SNILFSFKEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLLFVE SNILFSFKEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLLFVE SNILFSFKEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLLFVE SNILFSFKEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLLFVE SNILFSFKFEGSSVELKHFFFFAQDGNAAISDYNYYSNLDFNCDIKQLLFVE SNILFSFKFEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLFFVE SNILFSFKFEGSSVELKHFFFFAQDGNAAISDYNYYNLDFNCDIKQLFFVE	409 410 415 415 414 415 469 470 470 470 470 470 470 470 529 529 725
HCOV-NKU1 MERS-COV SARS-COV SARS-COV HCOV-NL63 HCOV-229E HCOV-0C43 HCOV-0C43 HCOV-MKU1 MERS-COV SARS-COV SARS-COV SARS-COV HCOV-NL63 HCOV-NL63 HCOV-0C43	NINDVOTHYYRLSLKOLLLYAADPALHWSASALYOLRTCCPSVAATTSGWEPOTWEPGN NINDVOTHYYRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAATTSGWEPOTWEPGN NINDVOSLHHHRLSLKELWYAADPAHHAASSNAFLOLRTSCPSVAATTTGLTPOTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNVAFQTVKPGN ************************************	409 410 410 415 414 415 409 409 470 470 470 475 475 475 475 529 529 529 529
HC0V-UK43 MERS-C0V SARS-C0V SARS-C0V HC0V-NL63 HC0V-229E HC0V-0C43 HC0V-HKU1 MERS-C0V SARS-C0V SARS-C0V HC0V-NL63 HC0V-NL63 HC0V-0C43 HC0V-0C43	NNINDVOTHSYRLSLKOLLLYAADPAALMYSASALYOLRTCCPSVAATTSGIKEOTVERGN NNLDVOTHSYRLSLKOLLLYAADPAAHMYSASALLOLRTCCPSVAATTSGIKEOTVERGN NNINDVSLHHHRLSLKELMYAADPAAHAASSNAFLOLRTSCPSVAALTNOLRTOTVERGN HNQDVNLHSSRLSFKELLYYAADPAAHAASSNAFLOLRTSCPSVAALTNONAFOTVERGN HNQDVNLHSSRLSFKELLYYAADPAAHAASGNLLLDCRTTCPSVAALTNONAFOTVERGN """"""""""""""""""""""""""""""""""""	409 410 412 415 414 415 409 470 470 470 470 470 475 474 475 529 530
HC0V-UKU1 MERS-C0V SARS-C0V SARS-C0V HC0V-129E HC0V-229E HC0V-0C43 HC0V-0C43 HC0V-MKU1 MERS-C0V SARS-C0V SARS-C0V SARS-C0V HC0V-NL63 HC0V-229E HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-0C43	NINDVOTHYRLSLKOLLLYAADPALHWSASALYOLRTCCPSVAATTSGKEOTKPGN NINDVOTHRYRLSLKOLLLYAADPAHWSASALLOLRTCCPSVAATTSGKEOTKPGN NINDVOSLHHRLSLKELWYAADPAHHASSNAFLOLRTSCPSVAATTGLTFQTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHASSNAFLOLRTSCPSVAATTNNAFQTVKPGN """"""""""""""""""""""""""""""""""""	409 410 410 415 414 415 409 409 470 470 470 475 475 475 475 529 529 520
HC0V-UKU3 MERS-C0V SARS-C0V SARS-C0V HC0V-NL63 HC0V-229E HC0V-0C43 HC0V-HKU1 MERS-C0V SARS-C0V HC0V-NL63 HC0V-NL63 HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-0C43	NINDVOTHSYRLSLKOLLLYAADPALHVASASALYOLRTCCPSVAATTSGKFOTVFGN NINDVOSLHHIRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAATTSGKFOTVFGN NINDVOSLHHIRLSLKELWYAADPAHHAASSNAFLOLRTSCPSVAATTGUTFGTVAPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNNAFQTVKPGN HNQDVNLHSSRLSFKELLYYAADPAHHAASGNLLLOKRTTCPSVAALTNNNAFQTVKPGN """"""""""""""""""""""""""""""""""""	409 410 415 415 416 415 416 416 470 470 470 470 475 475 475 529 538 538 535
HC0V-UKU1 MERS-C0V SARS-C0V SARS-C0V HC0V-1298 HC0V-2298 HC0V-0C43 HC0V-0C43 HC0V-0C43 HC0V-1KU1 MERS-C0V SARS-C0V2 SARS-C0V2 SARS-C0V2 HC0V-1KU1 HC0V-0C43	NINDVDTHYRLSLROLLLYARDPALHWSSASALDDLRTCCPSVAATTSGWEGTVERGN NNLDVDTHYRLSLROLLLYARDPANHWSSASALDDLRTCCPSVAATTGGWEGTVERGN NNNDVSLHRHRLSLKELLWARDPANHAASGNLLDDRTTCPSVAALTTGLTFQTVRGN HNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDDRTTCPSVAALTTNNAFQTVLPGN HNQDVNLHSSRLSFKELLVYARDPANHAASGNLLDDRTTCPSVAALTTNNAFQTVLPGN NNDPVSLHRHRLSLKELLWARDPANHAASGNLLDDRTTCPSVAALTTNNAFQTVLPGN NNDPVDFLRLRGFPDEGSELTLKHPFPFQGBAAITDPNYYNNRPTILDICQARWTYC PNNEFYNPLRLRGFPDEGSELTLKHPFPFQGBAAITDPNYYNNRPTILDICQARWTYC PNNEFYNPLRLRGFPDEGSELTLKHPFPFQGBAAITDPNYYNNRPTILDICQARWTYC PNNEFYNPLRLRGFPDEGSELTLKHPFPFQGBAAITDPNYYNNRPTILDICQARWTYC PNNEFYDPVLSKGLRKEGSSVELKHPFFTQGBIAAITDYNYYNNLPTNVDIRQLLFVLE PNNDPVPVSKGFFKEGSSVELKHPFFTQGBIAAITDYNYYNNLPTNCDIRQLFVLE PNNDPVDFWSKGFFKEGSSVELKHPFFAQDBIAAITDYNYYNNLPTNCDIRQLFVLE PNNDPVDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFVLE FNNDFYDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFVUE FNNDFYDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFVUE FNNDFYDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFVUE FNNDFYDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFFVUE FNNDFYDFWSKGFFKEGSSVELKHPFFAQDBIAAISDYBYYRYNLPTNCDIRQLFFVUE FNNDFYDFYEGGCIRACEVVYNLNNYGSGACHYFTRICIRKGLYYESISVEEDDAIFLTTRM WARMYTDCYUQGCITSRCWYNNLNYGSGACHYFTRICIRKGLYYESISVEEDDAIFLTTRM WARMYTDCYUQGCITSRCWYNNLDISGACHYFTRICIRKGLYYESISVEEDDAIFLTTRM WARMYTDCYUQGCITSRCWYNNLDISGACHYFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHYFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHYFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHYFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHYFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHFFTRICIRKGLYYEALSFEEDDEITAYTTRM WARKYFDCYUCUGCITSRCWYNNLDISGACHFFTRICIRKGLYYEALSFEEDDRICHAFATRM	409 410 410 415 414 415 416 409 409 470 470 470 470 476 520 520 525 535 535
HC0V-UK43 MERS-C0V SARS-C0V SARS-C0V SARS-C0V HC0V-NL63 HC0V-0C43 HC0V-0C43 HC0V-HKU1 MERS-C0V SARS-C0V HC0V-NL63 HC0V-0C43 HC	NINDVOTHYRLSLKOLLLYAADPALHYASASALYOLRTCCPSVAATTSGWEPGTVERGN NINDVOTHYRLSLKOLLLYAADPAHWASASALLOLRTCCPSVAATTSGWEPGTVERGN NINDVOSLHHHRLSLKELWYAADPAHHASSNAFLOLRTSCPSVAATTTGLTPGTVARGN HNQDVNLHSSRLSFKELLYYAADPAHHASSNAFLOLRTSCPSVAATTTGLTPGTVARGN HNQDVNLHSSRLSFKELLYYAADPAHHASSNAFLOLRTSCPSVAATTTNNVAFQTVERGN """"""""""""""""""""""""""""""""""""	409 410 415 414 415 416 416 409 470 470 470 475 475 475 529 525 530 525 530 525 530 525 530 525 530 525 530
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**Figure S1(c)**. Multiple sequence alignment of NSP12 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.



**Figure S1(d)**. Multiple sequence alignment of NSP13 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

HCoV-NLG3	CGLPHNCTRTPLNLPPTHANTPLGLGBOPHTTGDLAWQIGSNN-VCTYEHVISPNG	55
HCoV-229E	SESSCGLFKDCARNPIDLPPSHATTYLSLSDRFKTSGDLAWDIGNNN-VCTYEHVISYNG	59
HCoV-0C43	CSTNLFKBCSKSYSGYHPAH2PSFLAVDDKYKATGDLAVCLGTGDSAVTYSPLISLVG	58
HEOVERKUN	CTTNLPROCSESCLIGYHPAH205PL AVDREVEMENT AWU NTCESKLTYSHITSLING	58
MEDS-CoM	CONTROL EXPECTED CONVERTING ACCORDING TO ALL IN DALLING ACCOUNTS	59
CARC-C-MO	SYSTEM CONCINENT OF A CONTRACT OF A CONCINENT OF A CONCINENT OF A CONCINENT OF A CONCENTRAL OF	23
SANS-COV2	ABMETGEPRICERCETTEENE TOAPTHESEDTRIK TEGECODERGEPREDUT FRACTSHING	2.5
SARS-CoV	AENVTGLFRDCSK11TGLHPTQAPTHLSVDIRFRTEGLCVDIPGIPR-DNTYRRLISNNG	59
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110 - N. 81 - 65		
HEOV-NEGA	FHFOISIPOSHSLFCIRDFAIRWARGNLGHDWESAHACODALGINAFLQWGFSASAAFW	115
HCuV-229E	PRPOVSMPDSH&LFCTRDPAMRHVRdNLGMDW2DAHVTDDNXDTNVPLQVdPSNOVDPVA	119
HCoV-0C43	FKLOVTLDGYCKLFITKEEAVKRVRANVGFDAEGAHATRDSIGTNFPLQLGFSTGIDFVV	118
HCoV-IIKU1	PREDETEDGYSKEFITKDEAIKSVRGNVGFDVEGAHATRENEGTNFPLOIGPSTGVDPVV	118
MERS-CoV	FKLDATVPGYPKLFITREEAVR0VRSNIGFDVEGAHASRNALGTNVPLOLGFSTSVNFVV	119
SARS-CoV2	FRANKOWNGYPRIMETTREEAT DHYPANTGEDWESCHAT REAVGTNL PLOUGESTS/NL VA	119
SARS-COM	BUNNYOAMSYRNMETTERBATCHYGONTGEDWRICHOT SDAWSTNI, PLOLORSTRAMI WO	110
2010/2010/2010		
HEOV-NI 63	OTESCASTNEGDATKRACAKSREGEOFERI ARI LEKGORALTVERETVOMTSDALSNI SD	175
HEoV-329E	OPESCAL INCOMMENDADADADEGEOSTHING LICEGODISM DICTIONITADELAGSSD	179
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LIC AND DECEM	CHILDLE MARKED 21 NEWWOOD COUNTER COMPANY OF ALWARD CALLS 2	170
NCOV-INCL	CRIDERACHULTIFICIUM APPE EXTENEIPERS COMPENSIONE VERTEUR	170
MERS-COV	6hA2AADI EMONNE LOTWARAAAGEGAEREAAENAKOWAANAALAKAKI AKAKI AGAEPOLEDKE 2D	175
SARS-CoV2	VPTSYVDTPNNTDFSRVSAKPPPGDQFKHLTPLWYKGLPWNVVRTKIVQWLSDTLKNLSD	179
SARS-O/V	VPTOYVDTENNTEFTRVNAKPPPODOFKHLIPLPYKOLPWNYVRIKIVOPLSDTLKOLSD	179
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HEOV-NL03	II AAAIWAQATATI MIKAHAKINATIK-ACAGAMAMI CAMAANIGAKHATAGOAAAMA	259
HCoV-229E	VEVPVEWAGELEETTWKYPVKDS/WK-HCQCGTV/ATCYNSVSND/CCRKH/ALGCD/VV/NP	238
HEOV-0043	CVVLVTUAANPPLTCLEYPASVORTSCRVCTSCATVYNSETGYYSCNEHSVTCDYLYNP	258
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SAKS-COV2	KVVPVLWARKPELTSVKTPVKT8PEKTCCLCOKRATCPSTRSDT7AC0PHSTGPD7VTNP	2.58
SARS COV	RAALAAHQEETZXXXAAAGEETZXXXAAAGEEXICCTCCCCCCCXXXAACCE21Z2201AACWAHQAGEDAAAAM	236
HCoV-NL63	YAPDIQQUGYVGSLSQNHMTFCNIHKNEHDASGDAVIYTRCLAWHDCPWKNVDWTVTYPPI	294
HCoV-229F	YVIDTOOMGYVSSI STNHHATCAVHENEHVASEDATIYT BCLAVYDCEVKNVDUSTTY PMT	298
HE oV-DE43	LTADTOOLGYTSEL SSNHDLYCSYHDGAHVAS SDATWTRCLAWADCECUNTNUMSYRTT	20.9
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HERC COM		230
PIEKS-5.9V	PPODOQQWARVANLAIMMDHYCSVHQAMIQASALVIIII KCLAIMSCPICHVOWDICYPYI	288
5AK3-4.0V2	FNIDAGÓNG FLAUFÓSNIHDE A CÓAHAUMHANS COMTA LA USCHARMACHAR A COMTE A MET	235
SARS-CoV	FMIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIYTRCLAWHECFWCRVDWSVEYPII	299
	'alasesi s's su' s'is ' a ss usissastell'se i lis i as s	
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HCOV-428E	ANCIALINEGGRIZUGSHIPRAAISLIYNPERIHDIGNPEGIRCAVI-DARWYCYDANPINSN	257
HEOV-DE43	SNELSINTSCHVLQHVILSAAMLCNRYTLCYDIGAPRAIACVHDF0FHFYD2QPIVHS	356
HCoV-HKU1	SNEVSINTSCRLLQRWALKAAMLCNRYNLCYDIGNPNGLACVWDYEPWPYDAFPVAWS	356
MERS-CoV	SHEKKLNSCCRIVERNV/RAALLAGSFDKVYDIGNPKGIPI/DDPV/WHYFDAQPLTRK	359
SARS-CoV2	GDELKINAACRKVQHRWWKAALLADKFPYLHDIGNPKAIKCVPQADVEWNFYDAQPCSDK	359
SARS-CoV	GDEL BYNSAC REVOHWYWSALL ADKEPYL HDIGNPKATEC/POAEVEWEFYD40PC SDK	359
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HCoV-NL63	VKLLDYDYATHGQLDGLCLFWNCNVDWYPBFSIVCRFDTRTRSVFWLECVNGGSL	408
HCoV-229E	VKTLEYDYMTHOQNEOLCLFWNCRVDWYPEPSIVCRPDTRTRSTLNLECVWOOSL	412
HEOVE-DE413	VKTLLYSFEAHKRSFEDGLONFUNCTIVDKYPPNAWACBEDTRALINULUL RECUGES	413
LIK OVE LIKE M	WKOLDVWDWUKENERDGLONDUNCUVDUNGTWERDTENNING BURGERE	412
MBDS-CoV	WOOLEVE_EDWARDENDELENDENDENDENDENDENDENDENDENDENDENDENDENDE	442
CLENS-LOV	VETERVENT I EDURANTAVOLULITVINUNTSTYNINALVURTURISETVURGETVURGUNAL	410
5//K2-6.0V2	WTALCELP TO TWITTSERPT DOWLLPWINLINDHYPWINSLUCHPDTHINLONLINLPGCDGGSL	419
SARS-COV	AYNIBELFYSYATHHERFTDØWCLFWINCINDRYPANAIVCR*DTRVLSNLNLFGCDØØSL	419
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HC-M-NLC2		463
NEOV-NEO3	T WWWIRKEN I PROVINCE WAL APPENDIC DUDUC DUVU	492
HEOV-328E	Y WINNER I REVUSIONARIA SIMPERY YOUGS CEWH DOWNY VPL RATICITIES	467
HCOV-NC43	Y WARREN I DE FARARE EN LEF IPPP YY SUTECYPIU- UNDARQADY APLES ATCT TRON	472
HCoV-HKUI	YVNKHAFHTNPFTRTVFENLKPMPFFYYSDTPCVYVD-GLESKQVDYVPLRSATCITRCN	472
MERS-COV	YVNKMAPNTPAYDVSAPROLKPLPPPYYSTTPCEVHONOSPIEDIDYVPLKSAWCITACN	475
SARS-CoV2	YVNKHAFHTPAFDKSAFVNLKQLPFFYYSDSPCESHGKQ-V/SDTDYYPLKSATCITRCN	478
SARS-CoV	YVNKHAFHTPAFDKSAFTNLKOLPFFYYSDSPCESHGKO-W/SDTDYVPLKSATCITECN	478
	648-64464 + 48 6484 - 86484 - + + + + + + +	

HCoV-NL63	ISGAVCSKH4DSYQKYVEAYNTFTQXGFNINVPHSFDYYNLNQIF1E	510
HCoV-229E	IGGAVCSKHANLYRAYVESYNIFTQAGFNINVPTTFDCYNLNOTF1DVNLQ	518
HCu¥-QC43	LOGAVCLEHAEEYREYLESYNTATTAGFTFWYYKTFDFYNLWNTFTKL	520
HCoV-HKU1	LGGANCSKHAEEYCNYLESYNIVTTAGFTFNWYKNFDFYNLWNTFTTLQ	521
MERS-CoV	LGGAVCRXHATEYREYNEAYNLVSASGFRLNCYRTFDCYNLHSTFTRVQ	524
SARS-CoV2	LGGAVCRHIANEYRLYLDAYWPPTSAGFSLWYYKQFDTYWLWNTFTRLQ	527
SARS-CoV	LOGAVERHMANEYROYLDAYNMMISAGFSLNIYKOPDTYNLWNTPTR	525
	Taxasaa Tana a a 111 axa taxa ta	

**Figure S1(e)**. Multiple sequence alignment of NSP14 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

HCoV-NL63 HCoV-2298 HCoV-0C43 HCoV-CHU1 MERS-CoV SARS-CoV2 SARS-CoV2 SARS-CoV2	SLENIAFNYWRKGCFTGYDGELPYAYYNDKYFYRYGDYDDLYFTNKTTLPTNYAFELFAK GLENIAFNYWRGSFYGADDELFYAISGDKYFYHDGNIDNLYFYNKTSLPINIAFELFAK SLENYYNLYNGGHTGGACEMPCAIINDKYYAKIDKEDWYFINNTYPTNYAYELFAK GLENIAFNYWRGHFIGYEGELPYAYWNDKIFTKSGYNDIONFERKTTLPTNIAFELYAK SLENYAFNYWRGHFIGYEGELPYAYWNDKIFTKSGYNDIONFERKTTLPTNIAFELYAK SLENYAFNYWRGHFIGYEGELPYAYWNDKIFTKSGYNDIONFERKTTLPTNIAFELYAK SLENYAYNYWNKGHFIGYEGELPYASIINNYYTKYDGIDYEIFENKTTLPYNWAFELWAK SLENYAYNYWNKGHFIGHAGEAFYSIINNYYTKYDGIDYEIFENKTTLPYNWAFELWAK	60 60 60 60 60 60
HCoV-NL63 HCoV-2298 HCoV-0C43 HCoV-CHU1 MER3-COV SARS-COV2 SARS-COV2 SARS-COV2	RKNGLTPPLSTLKNLGVWATYKFVLWDYEAERPFTSYTKSVCKYTDFNEDVC RKVGLTPPLCTLKNLGVWATYKFVLWDYEAERPLTSFTKSVCGYTDFAEDVC RSVRHHPELKLFRNLNIDVCWKHVINDYARESIFCSNTYGVCKYTDLKFTENLN RSIRHHPELKTLRNLUNDIDCWKHVLWDYVKDSLFCSSTYGVCKYTDLKFTENLN RAVKSHFUFXLLHNLGVDIARNTVINDYKRDAPAHISTIGVCSYTDIAKSPTETICAPLT RNIKFVFEIKTLNNLGVDIARNTVINDYKRDAPAHISTIGVCSYTDIAKSPTETICAPLT RNIKFVFEIKTLNNLGVDIARNTVINDYKRDAPAHISTIGVCTYYDIAKSPTETICAPLT 8 : 8 : :::00 : 00:000	112 112 114 114 116 128 128
HCoV-NL63 HCoV-229E HCoV-0C49 HCoV-CHU1 MCRS-CoV SARS-CoV2 SARS-CoV2 SARS-CoV2	VCFDNSIQGSYERFTLTTNAWLFSTWIKNLTPTKLNFGMLNGMPVSSIKGDKGVE TCYDNSIQGSYERFTLSTNAWLFSATAWKTGGNSLPAIKLNFGMLNGNAIATVKSEDGNI VLFDGRDUGALEAFNKSNIQVYISTTKKNSLSNINGFPRAELNGVYUDKVGDTI ILFDGRDUGALEAFNKARNGVFISTEKLSRLSNINGFQRAELNGVYUDKVGELK FDIRDNCSLEKFNSTPNAIFISDRVIKKYFCMVCFDYAYFNGAIDBSDVWK VFFDGRVDGQVDLFRNARNGVLITEGSVKGLQFSVGPKQASLNGVTLIGEAVK- VLFDGRVEGQVDLFRNARNGVLITEGSVKGLTPSNGPAQASLNGVTLIGESVK- I <sup>#</sup> I <sup>®</sup> I <sup>®</sup> I <sup>®</sup> I <sup>®</sup> I <sup>1</sup>	168 172 168 168 169 173
HCoV-NL65 HCoV-229E HCoV-0C43 HCoV-CHU1 MERS-CoV SARS-CoV SARS-CoV SARS-CoV	KLVNWYIYWR	194 198 226 225 194 197 197
HCoVV-NL63 HCoVV-229E HCoVV-0C43 HCoVV-KHU1 MERS-CVV SARS-C0V2 SARS-C0V	RNLSDFTPRSDMECDFLNNDMGVFINKYGLEDFNFEHWVYGDVSKTTLGGLHLLISOFRL RNLODFLPRSTMEEDFLNNDIGVFINKYGLEDFNFEHWVYGDVSKTTLGGLHLLISOVNL RVISSPTCHIDMEKDMIALDQDVFIDRVGLEDYAPEMIVYGNMVQKIIGGLHLLIGLYHK RVLSSFEPRSDLERDFIDNDDNLFIAKYGLEDYAPEMIVYGDPSHTUGGLHLLIGLYHK RNLQFKPRSQMEIDFLELAMDGFIERYKLEGYAPEMIVYGDPSHTUGGLHLLIGLAKR RDLEDFKPRSQMEIDFLELAMDGFIDRYKLEGYAPEMIVYGDFSHQUGGLHLLIGLAKR	254 258 285 254 257 257
HCOV-NL63 HCOV-229E HCOV-0C43 HCOV-KHU1 MERS-CoV SARS-CoV SARS-CoV	SKINGVLKADDPVTASDTTLRCCTVTYLNELSSKVVCTYNDLLLDDFVTILKSLDLGVTSK SKINGILKAEEPVAASDTTLRCCTVTYLNDPSSKTVCTYNDLLLDDFVSLLKSLDLTVVSK QOTSNLVVGEPVSYD-SSIHSYFITDEKSGSSNSVCTVIDILLDDFVALVKSLNLNCVSK KXKSNLLGEFLQVD-SSIHSYFITDECGGSSNSVCTVIDILLDDFVSIVKSLNLSCVSK QOEGHIINEEMLKGS-STIHNYFITDALIGSSNCVCSVIDLLLDDFVSIXSDLSVVSK SQDSPLKLEDFIPVD-STVKNYFITDALIGSSNCVCSVIDLLLDDFVEITXSQDLSVVSK	514 318 345 344 313 516 316
HCoV-NL63 HCoV-229E HCoV-0C43 HCoV-CHU1 MERS-CoV SARS-CoV2 SARS-CoV2 SARS-CoV2	VHEVIIDNKPYRWMLNCKDNHLSTFYPOLQ 344 VHEVIIDNKPMRWMLNCKDNAVATFYPOLQ 348 VVNVNVDFKDFQSFOLNCNDEKVMTFYPELQ 375 VVNLNVDFKDFQSFOLNCKDEKVMTFYPELQ 374 VVNVTIDYTEISFMLNCKDGVGTFYPELQ 343 VVKVTIDYTEISFMLNCKDGVMCTFYPELQ 346 VVKVTIDYAEISFMLNCKDGHVCTFYPELQ 346 VVKVTIDYAEISFMLNCKDGHVCTFYPELQ 345	

**Figure S1(f)**. Multiple sequence alignment of NSP15 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

	* *	
HCoV-NL63	<ul> <li>SABUKCOYAMPOTYKLORMCLEPCNLYNYGAOTKLPSOTMLMAVRYTOLCOYLNSTTWC</li> </ul>	59
11CoV-228E	- SACWIK COYSINFO SYNTOKING L CIPCUL YNYGAO LIKLFEOD SIN WYNYD L COYTUS TT L C	52
HEOVE OF 418	4480-HKRAYRMENT YRYT NSEMBENST HNYGRENTT STOCKNMASKMEDT COVENTITE A	60
HC oV HK10	ATKIDLIK BAYAMBAL MANI NARI REVOLUNIYA BYAR MANIAA MANIA MANIA MANIA	60
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HERS SOV	WOWENER A WARRANT AND A CONTRACT THE WARRANT AND A CONTRACT OF	00
SARS COV2	A 2004MONO AND MULTIC RECOLOUVED AND TAKEN MANAANI A COATULET FW	60
SARS COV	ASQAMQFGVAMFNLYKNORMLLEKCOLONYGENAVTFKGIWNVKAHYFQLCQYLNTLTLA	60
	i e la e la la la la e e e e e e e e e e	
HCOX-NL68	VORMONA HYDROGODIA WARATTYI KOMI BADATTTININI WARAADBATTADCATYYI	446
HCoV DOOR	TELEVISION AND A REPORT AND THE ALL CONTINUES FOR TAXABLE AND A REPORT OF A DESCRIPTION AND A REPORT OF THE ADD	100
IN WY ACRE	YP PHYTRYCH LLARA DY TRYWY YH WY LLARY LPHYMLY YW HUY YW TRYCHWY TO Y HUY AN Y FL	112
NOV UCH S	AA AMAMAATUTOWOOG KAAMA AAMAATUWATAMATITAANAATUAATAANAI IIAADATITAA	120
HEOV HKUI	VPVNYRVEHLOADSDREVAPOSAWLKOWLPBOSTLVDNDLNPPVBOSLVTYPODCNTLPF	120
MERS COV	VPANYRVIHPGAGSDKØTAPGTSVLKOWLFTDATITDNDLNEPVSDADITLPGDCVTVRV	120
SARS CoV2	VPYNYRVIHPOADSDKØVAPOTAVLKOWLPTOT LLVDSDLNDPVSDADSTLICDCATVHT	120
SARS-CoV	VPYNYRWTHPOADSDKOVAPOTAWLKOWLFTOTILLYDSDLNDPVSDADSTLTODCATVHT	120
	68 7678 8 7678 1676 168 168 111 8 8 168 1 868 8	
INTERVAL MILLORE		0.000
NOV-NLOS	CONTRELESSION AND ALTER COMENY SNUMPETER INCOMENTATION AND AN AND A SAME TO THE AND A SAME AND A SAME AND A SAME	1/1
HCOV 2291	EDKADLETSDAMDORIEKSTDOENASKEOPPTYTNOPTCEREATOOSTRIKATEYSMAKKE	179
HCoV-OC43	DCONDLITSDVYDPITKNIGBYWYSKDOPFTYTCHMIRDKLALGGSVAIHITEPSWNAEL	180
HCoV-HKU1	DCHNDLTTSDVYDPLTKNIGDYWYSKDOPPTYTCHLTRDKLSLOGSVAIKITEPSWNADL	180
MERS-CoV	GOONDLVISDVINDPTTKNWTGSNESKALPPTYLICALINANILALGGSVAIKITENSWSVEL	180
SARS-CoV2	ANENDI TTREWNORFTENNT CENDRE OFFICERTOOSI AL GORVATHITTENSHNADI	180
MARN FOX	2000 NOT THE DRIVEN BELLET AND AND AND AND AND A STREET AND A ST	180
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HEOV NLOS	YELTOR APARTLECTS VITISS SEAPLINING PTOOPTION FTAON FOR WYTH WANT TWO	258
HCoV-229E	YELVOR SPUTMPCTSVMTSSSBAPVVOINYLODPAQOPPIDONIIHANYVPURNSTVMS	239
HCoV-OC43	YKLMOYFARWTVPCTNANASSSBOPLTOTNYLCKPKVBTDONVMHANYLRWRNSTVNN	238
HCoV-HKU1	YELMSC APATYPCTNVMASSSB0PLTOTNYLOESS BTDONVMHANYLPARNSTTAN	238
MERS-CoV	YELMOK FANATVPCTNANASSSEGFLLOINYLOTIX ENIDOGAMHANYIPWRNSTPVN	238
SARS CoV2	YELMON PANJTARY INVIASES BAR TOCHYLORER. BOTDOWNINAWY TRURNTNETO	288
SARS-COV	VALMAN BALLTORWINKNASSSBARLTORAVVLAURA ROTHAVTOLANVTRUANTNETO	288
and a set of a		621
	alal allas s'allalanastella sus con lasastasasti t	
HCOV-NLOB	LSYNSYLDLSKF2CKHNATYVYTLKDSDYNDVMLSL1KSGRLLLRANGRPOOFSNHLVST	29.9
HCoV-229E	LSYNSVLDLSH FNCKHKATVVVOLKDSDINDVMLSLVRSGKLLVRGNGKCLSFSNHLVST	289
HEOV OF 4 B	GRAYST FOMARERENT AGTAVTNE RADOTIND/WYSELFISHELLTROTING VEVODSTVIW	29.8
HC of the HK1PI	AGAVST FRATER VI AGTAVANI DOOM NOT VVRT 19 20 VI TAVATOR'S 19 VORT VINT	29.8
MID C COV	NORTH PERFECTION PERFECTION OF A DESCRIPTION OF A DESCRIP	00.9
		289
SAKS COV2	LSAYALFDWARFPLRLKUTAWIALREDGINDWILALLARMRLIIRENWRWVIAADWLWNN	240
SARS COV	LSSYSLFOWSKIPLKLKGTAWASLKENCTNDWTYSLLEKGRLTTRENNKWWYSSDTLVNN	298
	' ellelise e 's si el 'lisili sul sisile '	
HCoV-NL63	S 300	
HCoV-2298	K 388	
HCoV-0C43	289	
HEOVERKUM	289	
MBP 8 CoV	V 281 8 9(3) 9	
CARG-COVO		
DAND OV2	200	
SARS COV		
1		

"\*" Fully conserved ":" Conservation between groups of amino acids with strongly similar properties "." Conservation between groups of amino acids with weakly similar properties "\*" Fully conserved ":" Conservation between groups of amino acids with strongly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with weakly similar properties "." Conservation between groups of amino acids with

**Figure S1(g)**. Multiple sequence alignment of NSP16 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

HCoV-NL63 HCoV-2298 HCoV-0C45 HCoV-CHU1 MERS-CoV SARS-CoV SARS-CoV SARS-CoV	SLENIAFNVVKKGCFTGVDGELPVAVWNDKVFVRYGDVDNLVFTNKTTLPTNVAFELFAK GLENIAFNVVNKGSFVGADGELPVAISGDKVFVRDGNTDNLVFVNKTSLPTNIAFELFAK SLENVYNLVKTGNYTGGAGENFCAIINDKVVVKIDNEDVVIFINNTTYFTNAVELFAK GLENIAFNVVNGGNFDGELPCAINNDKVVKINNVDTVIFKNNTSPTNIAVELFAK GLENIAFNVVNGGNFDGVGGELPVAVNDKIFTKSVVDDICMFENKTTLPTNIAFELVAK SLENVAFNVVNGHFDGQGGEVPVSIINNVYTKVDGVDVELFENKTTLPVNVAFELMAK SLENVAYNVVNKGHFDGHAGEAPVSIINNVYTKVDGIDVEIFENKTTLPVNVAFELMAK	60 60 60 60 60 60 60
HCuV-NL03 HCoV-229E HCoV-0C43 HCoV-KHU1 MERS-CoV SAR3-CoV SAR3-CoV SAR5-CoV	RKMGLTFPLSTLKNLGVVATYKFVLWDYEAERPFTSYTKSVCKYTDPNEDVC RKVGLTPPLCTLKNLGVVATYKFVLWDYEAERPLTSFTKSVCGYTDPAEDVC RSVRHHPELKILFNLNDVCVKHVDUDYRESITFCSVTVGVCKYTDLKFTERLN RSJRHHPELKTLHNLQVDICVKFVLWDYERSNIYGTATIGVCKYTDLKFTERLN RAVRSHPPRILLHNLQVDICVKFVLWDYERSNIYGTATIGVCKYTDIAKFTETICAPLT RNIKFYPEVKILINNLGVDIAANTVDWDYKRDAPAHISTIGVCSYTDIAKKFTETICAPLT RNIKFYPEVKILINNLGVDIAANTVDWDYKRDAPAHISTIGVCTYTDIAKKFTETICAPLT RNIKFYPEXLINNLGVDIAANTVDWDYKREAPAHISTIGVCTYTDIAKKFTETICAPLT	112 112 114 114 116 120 120
HCoV-NL63 HCoV-2298 HCoV-0C43 HCoV-CHU1 MERS-CoV SARS-CoV2 SARS-CoV2	VCFDNSIQGSYERFTLTTNAVLFSTVVIKNLTPIKLNFGMLNGMPVSSINGDKGVE TCYDNSIQGSYERFTLSTNAVLFSATAVKTGGKSLPAIKLNFGMLNGNAIATVKSEDGNI VLFDGRDNGALEAFKRENNGVYISTTKVKSLSNIDNGFPRAELNGVVVDKVGDTD ILFDGRDTGALEAFRKARNGVFISTEKLSRLSNIDNGFQRAELNGVVVDKVGLK FDIRDNCSLEKFMSTPNAIFISDRKIKKYPCVWGFDYAYFNGAIDDSVVK VFFDGRVDGQVDLFRNARNGVLITEGSVKGLTPSNGPAQASKNGVTLIGEANK- VLFDGRVEGQVDLFRNARNGVLITEGSVKGLTPSNGPAQASKNGVTLIGESVK- 1* 1* 1* 1* 1* 1	168 172 168 168 168 173 173
HCoV-NL63 HCoV-229E HCoV-0C43 HCoV-KHU1 MERS-CoV SARS-CoV SARS-CoV2 SARS-CoV2	KLVNWYIYWR	194 198 226 225 194 197 197
HCoV-NL63 HCoV-229E HCoV-QC43 HCoV-KHU1 MERS-CoV SARS-CoV SARS-CoV	:	254 258 286 265 254 257 257
HCoV-NLGR HCoV-2288 HCoV-0C43 HCoV-KHU1 MBRS-CoV SARS-CoV SARS-CoV SARS-CoV	SKMGVLKAODFVTASDTTLRCCTVTYLNELSEN VVCTYMDLLLDDFVTILKSLDLGVISK SKMGILKAEEFVAASDITLKCCTVTYLNDFSSNTVCTYMDLLLDDFVSILKSLDLGVISK QQTSNLWQEFVSYD-SSIHSYFITDEKSGGSNSVCTMIDILLDDFVSIVKSLNLNCVSK NNKSNLLIQEFLQVD-SSIHSYFITDECGSSSSVCTMIDILLDDFVSIVKSLNLSCVSK QQEMIIMEEPLK0S-STIHNYFITDAGCGSSSSVCTMIDILLDDFVSIVKSLNLSCVSK SQDSFLKLEDFIPMO-STVKNYFITDAGTGSSNCVCFMIDILLDDFVEITXSQDLSVVSK SQDSFLKLEDFIPMO-STVKNYFITDAGTGSSNCVCFMIDILLDDFVEITXSQDLSVVSK	314 310 345 344 313 316 316
HCoV-NL63 HCoV-2298 HCoV-0C49 HCoV-KHU2 MERS-CoV SARS-CoV SARS-CoV	VHEVIIDNKPYRMMLNCKDNHLSTFYPQLQ 344 VHEVIIDNKPYRMMLNCKDNHASTFYPQLQ 346 VWWYNWDFKDFQFMLNCNDNKIMFYPHDQ 374 VWNINVDFKDFQFMLNCNDNKIMFYPHDQ 374 VWNFIDLINIEFMLNCKDQQVGFYPHDQ 345 VWKVFIDTHEFFNLNCKDQHVEFFYPHQ 346 VWKVFIDYFEISFMLNCKDGHVEFFYPHLQ 346 VWKVFIDYFEISFMLNCKDGHVEFFYPHLQ 346 VWKVFIDYFEISFMLNCKDGHVEFFYPHLQ 345	

**Figure S1(f)**. Multiple sequence alignment of NSP15 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.

	* *	
HCOV-NL63	- SAEMKCOYAPPOTYKLORIACLEPCINLYNYGAOTICLPSOTPLNYVRYFOLCOYLNSTTWC	59
HCoV-228E	- SABWKCOYSMPOIYKTORMCLEPCNLYNYGAOLKLPSOINPWKVNYFOLCOYPNSTTLC	58
HCoV-OC43	AASDWK POYSMPYLYKYLNSPMBKYSLWNYCK PYTLPTOCWNWARNYTOL COYLNTTTLA	60
HCoV-HKU1	ATNOW FOYSPEVLY KYLWYPL BRYSLWNYCH PTNL FTCC/WWARKYTOL COYLNTTTLA	60
MERS-CoV	AS ADWK FEHAMESLEK VON WILLERCELANYKOSTEMEROVHNINEA KYNOL COYLNT CTLA	60
SARS CoV2	88040086VANENLY KNOENLL BECTLONYODSATLEK GTWINKARYTOLCOVENTET A	60
SARS CoV	48040088V408NI VENORNI L BCCTI ONVORMANTEKOTUNNKOSVTOLCOVI NTI TI A	60
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LICE AND ALL OLD		
HOOM BOOM	YP HITTERY HITTERY DY YMP YN YMP YN HYDL HYDDA'R YMWALL LYNWYN MYNWYD DY'N YMD GANTAR Y YD. MEUNWYNW UL GLAGODWGWADAR WYL HYDL HIRUDA'R WWARNWW WWWARWAAR DD GWTGD GATWAAL	110
HOW AZBE	YE FINE WERE AND	110
NOV UCTS	AN ANALYZEN CHARACTER AN ANY CRAMENANT TEADART THAT AND T	120
MCOV MKUT	AA AAAAKAFWI GAGRO KEAAKARARAAKI KOMI KRORI LI ADADI MAAARIRI A LAAADON LI AA	120
MERS COV	AAMULKATHI GAGROKGI MAQLAAFKOMI KI DATTI DUDI UGAARDI LI HADCA LAKA	120
BARS COV2	VPYNYRYTHPOROSOKOVAROTAVLKOMLPTOTILLYDSDLNDPVSDROSTLTODCATVHT	120
SARS COV	VPYNYRYIHPOAOSOKOVAPOTAVLKOHLPTOTILLYDSDLNDPYSOADSTLIODCATVHT	120
	ee vevale veval levellees 'IIIIs'ei ise <mark>s</mark> i i sev vi	
	* *	
HCoV-NL68	EDKROLLISDVINDORTKECDOENVSKDOFF TYLNOVIREKLATOOSVATKITEYSWINKYL	178
HCoV-228E	BOKROLLISDWYDORTKAIDOENVSKEOPPTYINOPICEKLAIOOSIAIKWTEYSWNXKL	179
HCoV-OC43	DCONDLIISDVYDPITKNIGBYWYSKDGPPTYICHMIRDKLALGGSVAIHITEPSWNAEL	180
HCoV-HKU1	DCHNDLITISDYNOPLITKNIGDYNVSKDOPPTYTCHLIRDKLISLOGSVATHITEPSWNADL	180
MERS-CoV	GOOMDLVISD/WDFTTKNWTGSNESKALPFTYLCNLINNNLALGGSVAIHITENSWSVEL	180
SARS CoV2	ANKARI TTSD///DB//TK///TEP/08/20/PFTYTC9/200001 AL 9/98/ATH/TTP//SUNADI	180
SARS CoV	ANKNOL TTROWNDERTKHYT KENDSKERRETYL CRETKOXLAL ROSTANI (TTRHSUNAD)	180
	1 8416866484 10 8 88 68681 8 1141186818181868.88. 8	
HCOX-NIL68	VELTORIARUTI RETEXINTERERARI TOTMU ADRIOGERITAGUTURANY TRUONETTUR	280
HCoM-2298	VELVOOR RELITING TRAINTERS RABAWATUVLADRAOGRATINALTHAUVAHAUSTVUS	280
HColle OCAR	VIET MAKER PERMIT KARANAN ANA ANA ANA ANA ANA ANA ANA ANA A	989
HCOV-HV10	T IN MENNEL FOR THE STORE THAT AND A STORE AND A STORE TO THE STORE TO THE STORE AND A STORE AN	029
MBD 9 - CoV	T IN MENNY FAMILY INTERNATIONAL AND A CONTRACT AND A CO	0.8 9
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RAD C - COV	T IN MINING FRANKLING & LINY DAY SPECIFIC AND DESIDENT ************************************	0.2 9
200.2 3.2 8		420
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HCoV-NL68	LSYNSVLDLSKFECKHKATWWTLKDSDWND/WLSLTKSGRLLLRANGRFØGFSNHLVST	299
HCoV-228E	LSYNSVLDLSKENCKHKATVVVOLKDSDINDVMLSLVRSGKLLVRGNGKCLSESNHLVST	299
HCoV-0C43	GGAYSLEDWAREPLIKLAGTAVINLBADOINDWYSLLEKGKLLIRDINKEVPVGDSLVW	298
HCoV-HKU1	GGAYSLFDWT KESLKLAGTAVYNLRFOCLNDLVYSLTERGKLLVRDTRKETFVGDSLVNT	298
MERS-CoV	LSTYSLFDLSKFOLKLKGTPVLOLKESCINELVISLLSCOKLLIRDNDTLSVSTDVLVNT	288
SARS CoV2	LSSYST FONSKEPLKLKGTAVMSLKEGOTNOWITSLLSKGRLTTRENNKVVTSSOVLVNN	298
SARS CoV	LSSYST FONSKEPLKLKGTAVMSLKENCTNDMTYSTTEREN KAVVSSOTTANN	298
	I sheller is here in the ment sheller in the	
HCoV-NL63	K 300	
HCoV-228E	N 300	
HEOV OF 49	289	
HE OXE HELPI	200	
MBR 8 CoV	VOLT B SOR	
8488-CoV2		
SADS_COV	600 008	
SUUS ANY		
1		

**Figure S1(g)**. Multiple sequence alignment of NSP16 protein of Human coronavirus OC43, Human coronavirus HKU1, Human coronavirus NL63, Human coronavirus 229E, MERS -CoV, SASR-CoV2 and SARS-CoV. The analysis was performed using Clustal Omega. The actives sites residues present in the conserved regions are highlighted in box with star marks.



**Figure S2(a)**. Superimposed structures of NSP3 (Pl-pro) of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2 (b)**. Superimposed structures of NSP5 (3Cl-pro) of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2 (c)**. Superimposed structures of NSP12 of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2 (d)**. Superimposed structures of NSP13 of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.





**Figure S2 (e)**. Superimposed structures of NSP14 of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2 (f)**. Superimposed structures of NSP15 of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2 (g)**. Superimposed structures of NSP16 of i) SARS-CoV2 vs SARS-CoV2 ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera.



**Figure S2(h)**. Superimposed structures of Spike RBD of i) SARS-CoV2 vs SARS-CoV ii) SARS-CoV2 vs MERS-CoV iii) SARS-CoV2 vs HCoV-HKU1 iv) SARS-CoV2 vs HCoV-NL63 v) SARS-CoV2 vs HCoV-229E vi) SARS-CoV2 vs HCoV-OC43 using TM-Align and UCSF Chimera



Figure S3(a). Hydrophobicity map of NSP3 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi)SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity.



**Figure S3 (b).** Hydrophobicity map of NSP5 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity.



**Figure S3(c).** Hydrophobicity map of NSP12 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity



Figure S3(d). Hydrophobicity map of NSP13 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate





Figure S3(e). Hydrophobicity map of NSP 14 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv)

NL63 (v) OC43 (vi) SARS CoV (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity.



**Figure S3(f).** Hydrophobicity map of NSP 15 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity.



**Figure S3(g).** Hydrophobicity map of NSP 16 protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity.



**Figure S3(h):** Hydrophobicity map of Spike protein surface of all 7 types of corona viruses (i) 229E, (ii) HKU1 (iii) MERS CoV (iv) NL63 (v) OC43 (vi) SARS CoV and (vii) SARS CoV2. Red colour regions indicate hydrophobicity and white colour regions indicate hydrophilicity



\*ACE2 (Angiotensin-converting enzyme 2), APN (Aminopeptidase N), DPP4 (Dipeptidyl peptidase 4)

**Figure S4.** The protein-protein interface between the viral spike receptor binding domain and host proteins. The interactions are represented for SARS-CoV2 with ACE2, SARS-CoV with ACE2, MERS-CoV with DPP4, HCoV-NL63 with ACE2, HCoV-229E with APN. The diagrammatic representation indicates the interaction interface between the proteins such as salt bridges, hydrogen bonds and non-bonded contacts.

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