SARS-CoV-2 whole-genome classification analysis, protein homology modelling and elucidation of associated protein functions

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ABSTRACT

The most recent whole-genome sequence of SARS-CoV-2 was published on NCBI on 13th March 2020, with accession no. NC_045512. The protein products, genetic features, sequence length, NCBI reference sequence, protein structures (published/ homology modelling) and functions are discussed and analysed in this paper. Multiple sequence alignment is performed and Phylogenetic tree is prepared for the 4 closely related coronavirus species. This study provides the whole genome analysis with protein homology structures and elucidates functions of structurally similar proteins for further exploration and contributes to the search for anti-SARS-CoV-2 drugs. The application of this data in new vaccine development techniques such as Rapid-Response Platform and a possibility of a recombinant SARS-CoV-2 are discussed in this paper.

Keywords: SARS-CoV-2; COVID-19; SARS-CoV; Protein structures; Protein functions; Homology modelling; BLAST; Whole-genome sequence; Rapid-Response Platform vaccines; Recombinant SARS-CoV-2

INTRODUCTION

The zoonotic virus of coronavirus (CoV) family, later named as Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in Wuhan, Hubei province in China in 31 December 2019¹. On January 7, 2020 scientist identified it as *coronavirus*, same as which was *emerged* in China in 2002 and MERS which infected people in 2012. The next step was to understanding the sequence of the genome to find out the unique order of nucleotides. The COVID-19 genome is approximately ~30kbp, which is the largest group on the RNA virus genome. On January 13, 2020 scientist from Shanghai, China, sequenced the whole genome of SARS-CoV-2 by samples collected from the patients diagnosed with COVID-19. Compared with the SARS virus studied in November 2002 and MERS virus in April 2003, after this analysis scientist had declared it as new coronavirus. Furthermore, scientist of Shanghai, China has sequenced more than 24 samples with COVID-19 to confirm the new virus

genome. As the SARS-CoV-2 was sequenced, scientist around the world copies the viral gene for further study. This would help in drug and vaccine development against COVID-19.

The disease caused by this virus is named as COVID-19 and it is categorized as a pandemic by WHO on 15th March 2020 (19:14 GMT), 167757 cases, 6456 deaths of COVID-19 were recorded by more than 150 counties, 50.35 % (80849) cases are reported from China and 49.65% (79714) cases are reported by the rest of the world. Currently, COVID -19 is quickly transmitting throughout the world and the number of countries affecting in several areas, therefore, immediate preventive measure needs to be applied. Previous reviews on the COVID-19 were based on information from the specific problem. There is no vaccine specifically available for COVID-19.

The Coalition for Epidemic Preparedness Innovations (CEPI) is a global alliance financing and coordinating the development of vaccines against emerging infectious diseases (<https://cepi.net/>). CEPI is providing funding support for vaccine development process. The objective is to advance development of vaccine technology platforms that enable a rapid response to immunize at-risk populations against emerging infectious diseases.

Biotechnology companies such as Twist Bioscience, a San Francisco, California based company, manufacture customized DNA for clients. Such technology is very useful is new type of vaccine development method known as Rapid-Response vaccines.

Understating the genomic composition of this virus is the primary step to reveal the virus-host interaction mechanism and disease propagation which will be helpful to develop an effective treatment against SARS-CoV-2.

Many SARS-CoV-2 sequences are currently available in GenBank and the Sequence Read Archive (SRA). The database is continuously updated when any new sequence is reported.

METHODS AND MATERIALS

1. Multiple sequence alignment

The whole genome of SARS-CoV-2 with accession no. NC_045512.2 and SARS-CoV with accession no. NC_004718 was downloaded from the NCBI nucleotide database. The individual protein sequences were aligned for both the datasets using BLASTp to search for homology viral genomes and structural similarity parameter. Which is performed by using The Smith-Waterman algorithm is used to calculate the local alignment of two whole-genome sequences

from EMBOSS online tool as shown below -
(https://www.ebi.ac.uk/Tools/psa/emboss_water/).

```
#=====
# Aligned_sequence: 2
# 1: SARS-CoV-2 (NC_045512.2)
# 2: SARS-CoV (NC_004718)
# Matrix: EDNAFULL
# Gap penalty: 10.0
# Extend penalty: 0.5
#
# Length: 21620
# Identity: 17251/21620 (79.8%)
# Similarity: 17251/21620 (79.8%)
# Gaps: 729/21620 ( 3.4%)
# Score: 68746.5
Alignment results showing Length, Identity, Similarity, Gaps
```

DNAfull matrix was used with Gap penalty 10 and Extended penalty 0.5. The two genome shows a 79.8% similarity as well as identity.

Whole-genome sequencing of SARS-CoV-2 has uncovered varied dimensions for research and brought us one more step closer to understand the epidemiology of COVID-19. The actual source of viral outburst is still ambiguous, but the novel virus which was collected in Yunnan province, China has 96.2% similarity to a bat SARS-related coronavirus (SARSr-CoV; RaTG13), 79% similarity to SARS-Cov and 50% similarity to MERS-CoV², as previously reported.

Despite lesser genomic similarity, SARS-CoV-2 and SARS-CoV spike proteins share a 76.5% identity a high degree of homology^{3,4}.

2. Phylogenic Tree

MEGA software with version 7.0.26 is used to perform alignment and build phylogenic tree for the genome sequences of SARS-Cov-2 (MN908947), SARS-CoV (NC_004718), SARS-CoV BJ01 (AY278488) and MERS-CoV (NC_019843).

89 The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree
90 with the sum of branch length = 1.62357032 is shown in this analysis. The analysis involved 4
91 nucleotide sequences.

92
93 **Fig 1: Evolutionary relationships of taxa**
94

95 Phylogenetic analysis suggests that SARS-CoV and SARS-CoV-2 are closely related. The
96 close relation between SARS-CoV and SARS-CoV-2 is helpful to the inhibitor drugs
97 preparation, vaccine development, homology modelling and protein functions estimation.

98 3. Genetic features

99 The reported whole-genome sequence of SARS-CoV-2 has the size of 29903 nucleotides, from
100 which the number of adenine (A), guanine (G) are, thymine (T), cytosine (C) is 8954, 9594,
101 5863, 5492 nucleotides respectively as shown in figure 2.

Nucleotide Frequencies
Sites Used: All selected
All frequencies are given in percent.
Domain: Data

	T (U)	C	A	G	Total
MN908947_SARS-CoV-2	32.1	18.4	29.9	19.6	29903
NC_004718_SARS-CoV	30.8	19.5	28.4	21.3	21221
AY278488_SARS-CoV_BJ01	30.7	20.0	28.5	20.8	29725
NC_019843_MERS-CoV	32.5	20.3	26.2	20.9	30119
Avg.	31.6	19.5	28.3	20.6	27742

Fig 2: Nucleotide frequencies in all 4 genome sequences

The whole-genome sequence is comprised of a 5' UTR (265 aa), 3' UTR (229 aa), 12 CDS, 16 Mature peptides and 5 Stem-Loops.

Table 1: Protein name, range, sequence length and NCBI reference for UTRs, CDS and Mature peptides present in the whole genome sequence

S.N.	Protein	Gene range (5'-3')	Sequence length (aa)	NCBI Reference Sequence
1	5' UTR	1-265	265	-
2	ORF1AB polyprotein	266-13468, 13468- 21555	7096	YP_009724389.1
3	Leader protein	266-805	180	YP_009725297.1
4	NSP2	806-2719	638	YP_009725298.1
5	NSP3	2720-8554	1945	YP_009725299.1
6	NSP4	8555-10054	500	YP_009725300.1
7	3CL-like protease	10055- 10972	306	YP_009725301.1
8	NSP6	10973- 11842	290	YP_009725302.1
9	NSP7	11843- 12091	83	YP_009725303.1
10	NSP8	12092- 12685	198	YP_009725304.1

11	NSP9	12686- 13024	113	YP_009725305.1
12	NSP10	13025- 13441	139	YP_009725306.1
13	NSP11	13442- 13480	13	YP_009725312.1
14	RNA-dependent RNA polymerase (NSP12)	13442- 16236	932	YP_009725307.1
15	Helicase (NSP13)	16237- 18039	601	YP_009725308.1
16	3'-to-5' exonuclease (NSP14)	18040- 19620	527	YP_009725309.1
17	endoRNAse (NSP15)	19621- 20658	346	YP_009725310.1
18	2'-O-ribose methyltransferase (NSP16)	20659- 21552	298	YP_009725311.1
19	ORF1A polyprotein	266-13483	4405	YP_009725295.1
20	Surface glycoprotein	21563- 25384	1237	YP_009724390.1
21	ORF3a protein	25393- 26220	275	YP_009724391.1
22	Envelope protein	26245- 26472	75	YP_009724392.1
23	Membrane glycoprotein	26523- 27191	222	YP_009724393.1
24	ORF6 protein	27202- 27387	61	YP_009724394.1
25	ORF7a protein	27394- 27759	121	YP_009724395.1
26	ORF7b	27756- 27887	43	YP_009725318.1
27	ORF8 protein	27894- 28259	121	YP_009724396.1

28	Nucleocapsid phosphoprotein	28274-29533	419	YP_009724397.2
29	ORF10 protein	29558-29674	38	YP_009725255.1
30	3' UTR	29675-29903	229	-

4. Protein structures and functions

Fig 3: SARS-CoV-2 spike (S), membrane (M) and Envelope (E) proteins and enlarged structure of spike protein (PDB ID: 6VSB)

The individual protein structures are searched for existing models in RCSB PDB (<http://www.rcsb.org/>) database. When experimentally determined structures are not found for most of the proteins, then homology modelling approach is used to model protein structure.

SWISS-MODEL (<https://swissmodel.expasy.org/>) server is used to predict 3D homology models. UCSF Chimera (<http://www.cgl.ucsf.edu/chimera>) software is used to visualise the homology models. UniProtKB (<https://www.uniprot.org/uniprot/>), DrugBank (<https://www.drugbank.ca/>), NCBI (<https://www.ncbi.nlm.nih.gov/>) and available literature is used to compile the different function of the proteins.

124 **ORF1AB polyprotein**

125
126 **Fig 4:** The 3D structure of ORF1AB polyprotein is available on PDB ID: 3R24

127 **Function:** ORF1AB polyprotein has 95.55% identity with non-structural polyprotein 1ab [Bat
128 SARS-like coronavirus] (Accession no. AVP78030.1).

129 Its general function is Zinc ion binding but it can also inhibit host translation by interacting
130 with the 40S ribosomal subunit.

131 ORF1ab proteins is a multifunctional protein involved in virus pathogenesis distinct from or in
132 addition to functions directly involved in the transcription and replication of viral RNAs.
133 Recent reverse genetic studies have confirmed that proteins of ORF1ab may be involved in
134 cellular signalling and modification of cellular gene expression, as well as virulence by
135 mechanisms yet to be determined (Graham et al., 2007).

136 **Leader protein (NSP1)**

137

138 **Fig 5:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
139 PDB ID: 2HSX was having a maximum sequence identity of 86.09%

140 **Function:** SARS coronavirus NSP1 plays an important role in CCL5, CXCL10, and CCL3
141 expression in human lung epithelial cells via the activation of NF- κ B (Law et al., 2006).

142

143 **NSP2**

144

145 **Fig 6:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
146 PDB ID: 4V7E was having a maximum sequence identity of 19.67%

147 **Function:** NSP2 of SARS-CoV is dispensable for viral replication in the host cell. Deletion of
148 the nsp2 coding sequence attenuates viral growth and RNA synthesis. (Graham et al., 2005).

149 **NSP3**

150

151 **Fig 7:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
152 PDB ID: 6VXS was having a maximum sequence identity of 100%

153 **Function:** NSP3 along with other NSPs is required for RNA transcription and genome
154 replication as large polyprotein. These proteins are proteolytically processed by virus-encoded
155 proteinases to produce mature replicase proteins (Prentice et al., 2004).

156

157 **NSP4**

158

159 **Fig 8:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
160 PDB ID: 3VCB was having a maximum sequence identity of 61.36%

161 **Function:** H120 & F121 in the luminal loop in NSP4 are essential for binding to NSP3.
162 Interaction with NSP3 through H120 & F121 in NSP4 is crucial for viral propagation. H120 &
163 F121 substitutions in NSP4 cause defect in membrane rearrangement function. Although,
164 NSP3-NSP4 interaction is not sufficient to induce membrane rearrangement (Sakai et al.,
165 2017).

166 **3CL-like protease (NSP5)**

167

168 **Fig 9:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
169 PDB ID: 6Y2G was having a maximum sequence identity of 100%

170 **Function:** NSP5 is essential for virus replication. Its activity is extensively regulated by intra-
171 and intermolecular interactions. NSP5 exhibits a conserved three-domain structure containing
172 a chymotrypsin-like fold formed by domains 1 and 2 as well as the third domain of unclear
173 function but which likely is important for the required dimerization of NSP5 (Stobart et al.,
174 2013).

175

176 **NSP6**

177

178 **Fig 10:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
179 PDB ID: 5LC5 was having a maximum sequence identity of 18.52%

180 **Function:** NSP6 has multiple transmembrane domain NSP6 of SARS-CoV is reported to
181 induce the formation of DMVs in the transfected cells (Angelini et al., 2013).

182 *NSP7*

183

184 **Fig 11:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
185 PDB ID: 1YSY was having a maximum sequence identity of 98.80%

186 **Function:** NSP7 is an all- α -helical protein. The hexadecameric NSP7–NSP8 supercomplex
187 implying that its role is to confer processivity on RNA-dependent RNA polymerase (Zhai et
188 al., 2005).

189

190 *NSP8*

191

192 **Fig 12:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
193 PDB ID: 2AHM was having a maximum sequence identity of 97.47%

194 **Function:** NSP8 octamer makes NSP7+NSP8 complex with eight nsp7 molecules. This
195 complex is reported as a unique multimeric RNA polymerase capable of both de novo initiation
196 and primer extension. (Zhai et al., 2005), (te Velhuis et al., 2012), (Imbert et al., 2006).

197 **NSP9**

198

199 **Fig 13:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
200 PDB ID: 1QZ8 was having a maximum sequence identity of 97.35%

201 **Function:** NSP9 is a dimeric protein which has no designated function but is most likely
202 involved with viral RNA synthesis. NSP9 binds to RNA and interacts with nsp8. (Sutton et al.,
203 2004).

204

205 **NSP10**

206

207 **Fig 14:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
208 PDB ID: 5NFY was having a maximum sequence identity of 98.47%

209 **Function:** Interaction between NSP10 and NSP14 or NSP16 has important implication for the
210 mechanisms of replication/transcription complex assembly (Pan et al., 2008).

211 **NSP11**

212 **NOTE:** Protein sequence is very small, hence cannot be modelled

213 **Function:** Nsp15 play an important role in virus RNA synthesis (Wu et al., 2020).

214 ***RNA-dependent RNA polymerase (NSP12)***

215

216 **Fig 15:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
217 PDB ID: 6NUR was having a maximum sequence identity of 96.35%

218 **Function:** RNA-dependent RNA polymerase (RdRp) in SARS-CoV showed both primer
219 dependent and primer-independent RNA synthesis activities using homopolymeric RNA
220 templates. It can initiate de novo RNA synthesis from the 3'-ends of both the plus- and minus-
221 strand genome of SARS-CoV, using the 3'-terminal 36- and 37-nt RNA, respectively (Ahn et
222 al., 2012), (Imbert et al., 2006).

223

224 ***Helicase (NSP13)***

225

226 **Fig 16:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
227 PDB ID: 6JYT was having a maximum sequence identity of 99.83%

228 **Function:** Helicases are multifunctional proteins that are involved in diverse processes such as
229 genome replication, subgenomic mRNA transcription, and 5' cap formation. RNA and DNA
230 duplex-unwinding activities of NSP13 in SARS-CoV have also been reported (Ivanov et al.,
231 2004).

232 **3'-to-5' exonuclease (NSP14)**

233

234 **Fig 17:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
235 PDB ID: 5NFY was having a maximum sequence identity of 94.88%

236 **Function:** 3'-to-5' exonuclease (ExoN) shows proofreading activity in SARS-CoV which may
237 enhance the fidelity of RNA synthesis by correcting nucleotide incorporation errors made by
238 the RNA-dependent RNA polymerase (Ogando et al., 2019).

239

240 **endoRNase (NSP15)**

241

242 **Fig 18:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
243 PDB ID: 6W01 was having a maximum sequence identity of 100%

244 **Function:** Nsp15 has endoribonuclease activity and plays an important role in the virus RNA
245 synthesis (Wu et al., 2020).

The endoribonucleolytic activity of NSP15 is reported for the orthologous protein from another coronavirus, implying that the endoribonuclease activity of Nsp15 may be common to coronaviruses (Bhardwaj et al., 2004).

2'-O-ribose methyltransferase (NSP16)

Fig 19: The 3D structure of the protein is modelled from the Swiss Model server. Template - PDB ID: 2XYR was having a maximum sequence identity of 93.49%

Function: Nsp16 in SARS-CoV requires NSP10 as a stimulatory factor to execute its MTase activity and the NSP16/NSP10 complex bound with methyl donor SAM. NSP16/NSP10 interface may represent a better drug target than the viral MTase (Chen et al., 2011).

ORF1A polyprotein

Fig 20: The 3D structure of the protein is modelled from the Swiss Model server. Template - PDB ID: 2AHM was having a maximum sequence identity of 97.47%

Function: Involved in the activation of host autophagy [GO:0039520].

263 **Surface glycoprotein**

264

265 **Fig 21:** The 3D structure of surface glycoprotein is available on PDB ID: 6VSB

266 **Function:** Spike proteins which are present on the surface of virus shared a 76.5% identity and
267 a high degree of homology with of SARS-CoV's spike protein structure (Xu et al., 2020).

268 The human ACE2 receptor (lysine 31) can recognize the SARS-CoV-2 receptor-binding
269 domain (RBD) (glutamine 394) (Wan et al., 2020). The spike protein interaction with the ACE2
270 receptor and TMPRSS2 pave the way for the virus to enter into the host cell.

271

272 **ORF3a protein**

273

274 **Fig 22:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
275 PDB ID: 2M6N was having a maximum sequence identity of 35.71%

276 **Function:** ORF3a protein in SARS-CoV activates the NLRP3 inflammasome by promoting
277 TNF receptor-associated factor 3 (TRAF3)-mediated ubiquitination of apoptosis-associated
278 speck-like protein containing a caspase recruitment domain (ASC). It also activates pro-IL-1b
279 gene expression and IL-1b secretion (Siu et al., 2020).

280 *Envelope protein*

281

282 **Fig 23:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
283 PDB ID: 5X29 was having a maximum sequence identity of 91.38%

284 **Function:** E protein down-regulate the signalling pathway inositol-requiring enzyme 1 (IRE-
285 1) of the unfolded protein response, but not the PKR-like ER kinase (PERK). It activates the
286 transcription factor 6 (ATF-6) pathways and also found to be involved in cell apoptosis. The
287 protein also facilitates the ion-conductive pore in the membrane (DeDiego et al., 2011).

288

289 *Membrane glycoprotein*

290

291 **Fig 24:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
292 PDB ID: 6QPK was having a maximum sequence identity of 20%

293 **Function:** Membrane glycoprotein of SARS-CoV can interact with nucleocapsid (N) protein
294 in-vitro and in-vivo (He et al., 2004). M protein suppresses NF-kB activity through interaction
295 with IKK β which results in lower Cox-2 expression which contributes to SARS pathogenesis
296 (Fang et al., 2007).

297 M protein has also reported containing highly conserved glycosylated sequences and its
298 glycosylation helps to facilitate a viral-host interaction (de Haan et al., 1998).

299 **ORF6 protein**

300

301 **Fig 25:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
302 PDB ID: 5VYJ was having a maximum sequence identity of 25%

303 **Function:** ORF6 protein can induce intracellular membrane rearrangements which results in a
304 vesicular population in the infected cell.

305 It has been reported that a putative diacidic motif in the ORF6 protein influences its subcellular
306 localization and ability to suppress the expression of co-transfected expression constructs
307 (Gunalan et al., 2011).

308

309 **ORF7a protein**

310

311 **Fig 26:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
312 PDB ID: 1YO4 was having a maximum sequence identity of 91.57%

313 **Function:** ORF7a localize in the rER/Golgi apparatus and encodes a proapoptotic activity.
314 Overexpression of ORF7a induces apoptosis via a caspase-dependent pathway (Tan et al.,
315 2004).

316 **ORF7b**

317

318 **Fig 27:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
319 PDB ID: 5DOQ was having a maximum sequence identity of 30%

320 **Function:** ORF7b protein is a structural component of SARS-CoV virions an integral
321 membrane protein. It localizes to the Golgi apparatus and has its C terminus exposed to the
322 cytoplasm (Schaecher et al., 2007).

323

324 **ORF8 protein**

325

326 **Fig 28:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
327 PDB ID: 1XAK was having a maximum sequence identity of 21.57%

328 **Function:** ORF8 protein sequence of SARS-CoV-2 ORF8 shared very low similarity with
329 sequences in SARS-CoV. It is functionally uncategorized.

330 ***Nucleocapsid phosphoprotein***

331

332 **Fig 29:** The 3D structure of the protein is modelled from the Swiss Model server. Template -
333 PDB ID: 2JW8 was having a maximum sequence identity of 95.76%

334 **Function:** Nucleocapsid (N) phosphoprotein binds the viral RNA to form the helical core
335 structure (Davies et al., 1981). Functions such as viral packaging, viral core formation, and
336 signal transduction have been reported to the coronavirus nucleocapsid (Hiscox et al., 2001),
337 (He et al., 2004).

338

339 ***ORF10 protein***

340 **NOTE:** No matches were found for the target sequence for homology modelling

341 **Function:** ORF10 had a premature stop codon in both SARS-CoV. Its homology structure
342 cannot be modelled due to no template matching.

343 **RESULTS AND DISCUSSION**

344 The whole-genome sequence of the novel coronavirus – SARS-CoV-2 is analysed. The local
345 alignment was performed for the closely related 2 virus species (SARS-CoV and SARS-CoV-
346 2) by the Smith-Waterman algorithm. Bioinformatics software MEGA is used to perform MSA
347 on closely related four virus species and then the phylogenetic tree is prepared by the neighbour-
348 joining method.

349 Homology modelling is performed and their structure identity noted for all the proteins whose
350 PDB structures are not reported yet (as on March 16 2020).

Functions for all the proteins are documented from the literature. As our local alignment results show that SARS-CoV and SARS-CoV-2 have 79.8% similarity as well as the identity, hence most of the functions for proteins in SARS-CoV is been reported here because their exact function in SARS-CoV-2 is not known yet. Some protein functions of SARS-CoV-2 are recently in research focus such as spike protein, but further research is needed to reveal the role of all SARS-CoV-2 proteins and their mechanisms.

The predicted homologues proteins and their attenuated functions in this paper can be used as a preliminary step towards the exploration of exact protein functions in SARS-CoV-2. The homologues structures are prepared and sorted based on structural similarity with SARS-CoV proteins. This can ease the process of function detection in SARS-CoV-2 rather than a de novo approach.

Once the structure and the function of the protein are known, it will be easier to develop anti-viral vaccines against COVID-19. Presently, spike proteins are under extreme research. It is reported that spike proteins interact with lysine 31 on the human ACE2 and TMPRSS2 on the host cell membrane. This interaction leads to the entry of SARS-CoV-2 inside the host cell.

Our analysis suggests that there may be other drug targets as well. NSPs such NSP10/NSP16 or NSP14 complex has importance in replication/transcription assembly. NSPs can be targeted to halt the viral transcription inside the host cell of a sever infected person.

Similarly, membrane protein and nucleocapsid protein may be targeted to limit the virus-host interaction. ORF proteins are not much explored in SARS-CoV-2. ORF10 does not match any template and hence is not modelled. Its function is also very less explored.

Researchers around the world are using a new technique for fast vaccine development known as Rapid Response Platform. Rather than sending the antigens in the body, as traditional method, RRP vaccines send RNA/DNA directly into the cells in order to manufacture response antigen inside the host cell. This method of vaccine development is less time consuming and more specific as compared to the traditional method.

Other advantage to this technique is that when the RNA/DNA used to make antigens against one type of virus is developed, it can easily be manipulated to make antigens against other strads of viruses. Knowing the whole-genome sequence and the function each protein performs may add up to the RRP vaccine development process.

Exploring the structural and functional characteristics of SARS-CoV-2 whole genome may enable us to create recombinant SARS-CoV-2 vectors with desired and limited capabilities. The protein machinery of recombinant SARS-CoV-2 even can be used to deliver anti-viral drug or RNA to create specific antibodies. We present a complied record as a preliminary step to understand the lesser-explored proteins of SARS-CoV-2 and contribute to the process of anti-viral drug development.

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