State-of-the-art tools to identify druggable protein ligand of SARS-CoV-2

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Abstract

Introduction: The SARS-CoV-2 (previously 2019-nCoV) outbreak in Wuhan, China and other parts of the world affects people and spreads coronavirus disease 2019 (COVID-19) through human-to-human contact, with a mortality rate of > 2%. There are no approved drugs or vaccines yet available against SARS-CoV-2.

Material and methods: State-of-the-art tools based on in-silico methods are a cost-effective initial approach for identifying appropriate ligands against SARS-CoV-2. The present study developed the 3D structure of the envelope and nucleocapsid phosphoprotein of SARS-CoV-2, and molecular docking analysis was done against various ligands.

Results: The highest log octanol/water partition coefficient, high number of hydrogen bond donors and acceptors, lowest non-bonded interaction energy between the receptor and the ligand, and high binding affinity were considered for the best ligand for the envelope (mycophenolic acid: log *P* = 3.00; $\Delta G = -10.2567$ kcal/mol; p*Ki* = 7.713 µM) and nucleocapsid phosphoprotein (1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid: log *P* = 2.901; $\Delta G = -12.2112$ kcal/mol; p*Ki* = 7.885 µM) of SARS-CoV-2.

Conclusions: The study identifies the most potent compounds against the SARS-CoV-2 envelope and nucleocapsid phosphoprotein through state-of-the-art tools based on an in-silico approach. A combination of these two ligands could be the best option to consider for further detailed studies to develop a drug for treating patients infected with SARS-CoV-2, COVID-19.

Key words: COVID-19, SARS-CoV-2, druggable protein, ligand, nucleocapsid phosphoprotein, molecular docking, envelope protein, phylogenetic tree.

Introduction

In December 2019, an unknown pneumonia spread amongst a group of people in Wuhan, China, now termed as coronavirus disease 2019

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(COVID-19). COVID-19 patients were reported with a cluster of acute respiratory illness and higher interleukin 2 (IL-2), IL-7, IL-10, granulocyte colony-stimulating factor (GCSF), interferon gamma-induced protein 10 (IP10), monocyte chemoattractant protein 1 (MCP1), macrophage inflammatory protein 1α (MIP1A), and tumor necrosis factor α (TNF- α) in plasma [1, 2]. It was caused by an unknown beta coronavirus, initially called as 2019-nCoV; later the unknown beta coronavirus was named SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), which formed a clade within the subgenus Sarbecovirus [2, 3]. Apart from the well-known MERS-CoV (Middle East respiratory syndrome coronavirus) and SARS-CoV (severe acute respiratory syndrome coronavirus), the SARS-CoV-2 is the seventh member of the coronavirus family that infects humans [4]. The genome of SARS-CoV-2 has 89% and 82% nucleotide similarity with bat SARS-like-CoVZXC21 and of human SARS-CoV, respectively. The phylogenetic trees of spike, membrane, envelope, orf1a/b, and nucleoprotein from SARS-CoV-2 are clustered closely with those of the bat, civet, and human SARS-CoV. The external subdomain of the spike's receptor of SARS-CoV-2 has 40% amino acid similarity with other SARS-related CoV [5]. The entire orf3b of SARS-CoV-2 encodes a novel short protein. Moreover, new orf8 of SARS-CoV-2 probably encodes a secreted protein with an α -helix, a β -sheet(s) having six strands [5]. The phylogenetic analysis of the complete viral genome (29,903 nucleotides) revealed that WH-Human-1 coronavirus (WHCV) or SARS-CoV-2 was most closely related (89.1% nucleotide similarity) to a group of SARS-like coronaviruses (genus Betacoronavirus, subgenus Sarbecovirus) that were previously sampled from bats in China and that have a history of genomic recombination [6]. A recent study confirmed that the SARS-CoV-2 uses the ACE2 cell entry receptor, similar to SARS-CoV [7].

Considering the outbreak and the high need for treatment strategies, we have carried out an in-silico approach to identify the best ligand against the SARS-CoV-2 envelope and nucleocapsid phosphoprotein.

Material and methods

Sequence retrieval and secondary structure prediction

The amino acid sequence of the Wuhan seafood market pneumonia virus envelope protein (Accession no QHD43418.1), nucleocapsid phosphoprotein (Accession no QHD43423.2), were retrieved from the NCBI database on 28th Jan 2020. Wuhan seafood, SARS (severe acute respiratory syndrome), MERS (Middle East respiratory syndrome), and porcine reproductive and respiratory syndrome and other sequences were retrieved from NCBI, and sequence alignment was done by MAFFT software [8] for both envelop and nucleocapsid phosphoprotein, and phylogeny was constructed using MEGA7 [9–11].

Homology modelling

The sequences of envelope protein and nucleocapsid phosphoprotein were searched against the protein database using BLAST-P [12]. The proteins having PDB Id: 1ssk.1.A for nucleocapsid phosphoprotein [13] and 5x29.1.A for envelope protein [https://swissmodel.expasy.org/repository/uniprot/A3EX99] were selected for use as a template for 3D modelling of the envelope protein and nucleocapsid phosphoproteins of SARS-CoV-2. FASTA sequences were obtained for target and template selection.

3D structure prediction and validation

Homology modelling structure prediction was carried out using the Automated SWISS MODEL server [14]. The modelled PDB file was visualised using PyMOL and validated using PROCHECK [15]. 3D models were validated on the basis of Ramachandran plot [16] statistics using the RAMPAGE server as described earlier [17] and ERRAT2 [18]. From the generated models, the one with highest number of residues in the allowed region and minimum number of residues in the disallowed region were considered as a suitable model for envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2 and then used for further analysis. The active site was predicted using the MOE (Molecular Operating Environment) tool site finder [19]. The two predicted models of 3D atomic coordinates of the receptor were used for computations to verify potential sites for ligand binding and docking.

Preparation of ligand for docking analysis

Chemical compounds were taken from the National Centre for Biotechnology Information (NCBI) Pub-Chem database. All the ligands involved in our report were accumulated from the ones available in the literature [20–23], and others are listed in Table I. The ligands for envelop protein (1175, 2CBU, 2AAC, 1JR1) and nucleocapsid phosphoprotein (4UCE, 4UCC, 4UCD, 4UC8) were downloaded from a protein databank in Structure Data File (SDF) format and later converted to Protein Data Bank (PDB) coordinate files using Marvin space software, and ligands were saved in .mol format with the aim of opening these files in MOE software. Energy minimisation was done using

| Protein | Ligand | Number of bonds | HbA | HbD | Log P | ∆G [kcal/mol] | p <i>Ki</i> [μM] |
|---------------------------------------|--------|--------------------|-----|-----|--------|---------------|------------------|
| Envelope - | E1 | 5 | 5 | 4 | -2.194 | -7.1939 | 5.509 |
| | E2 | 5 | 5 | 2 | 3.00* | -10.2567 | 7.713 |
| | E3 | 6 | 4 | 5 | -3.899 | -7.9052 | 8.105 |
| - | E4 | 6 | 4 | 5 | -3993 | -6.7359 | 8.761 |
| Nucleocapsid phosphoprotein - - | N1 | 4 | 5 | 2 | 1.733 | -10.3805 | 7.067 |
| | N2 | 2 | 5 | 2 | 2.901* | -12.2112 | 7.885 |
| | N3 | 3 | 5 | 2 | 2.248 | -9.3889 | 7.284 |
| | N4 | 1 | 2 | 1 | -1.411 | -8.6312 | 5.725 |

 Table I. The properties of the ligands in the active site of envelope protein and nucleocapsid phosphoprotein of Wuhan coronavirus, 2019-nCoV

*Significant druggable protein ligand; HbA – hydrogen bond acceptors, HbD – hydrogen bond donors, log P – The log octanol/water partition coefficient, pKi – estimated binding affinity, E1 – β -D fucose, E2 – mycophenolic acid, E3 – castanospermine, E4 – deoxynojirimycinls, N1 – M72: 1-[(4-fluorophenyl)methyl]pyrazole-3,5-dicarboxylic acid, N2 – M76: 1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid, N2 – M76: 1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid, N4 – P1: phenylalanine.

MOE tools to first protonate the structure by using default parameters pH 7 and temp 300°C. The selected ligand molecules were passed through a Lipinski filter.

Molecular docking

For molecular docking the two modelled structures of selected antiviral molecules with envelope protein and nucleocapsid phosphoprotein were 3D protonated, and then docking was performed; we selected ligand (β-D-fucose; mycophenolic acid; castanospermine; deoxynojiri-1-[(4-fluorophenyl)methyl]pyrazole-3,5mycin; dicarboxylic acid; 1-[(2,4-dichlorophenyl)methyl] pyrazole-3,5-dicarboxylic acid; 1-[(2 chlorophenyl) methyl]pyrazole-3,5-dicarboxylic acid, and the PHENYLALANINE atom. Settings were selected in MOE software as rescoring1 at London dG and rescoring2 at GBVI/WSA dG, and the ligand interaction was performed with protein [24]. Four ligands were used for envelope protein, and another four ligands were used for nucleocapsid phosphoprotein. Energy minimisation was done for both ligands and proteins. Envelope protein before energy minimisation E: 5471.98, RMS: 14.93, and after energy minimisation E: 2433.49, RMS: G = 0.0709512, E: 2489.62, RMS G = 0.0700238, E: 2477.92, RMS: G = 0.0713067, and E: 2562.35, RMS: G = 0.124056 with β -D-fucose, mycophenolic acid, castanospermine, and deoxynojirimycinls ligands, respectively. For nucleocapsid phosphoprotein before energy minimisation: E: 2673.4, RMS: G = 17.3825, and after energy minimisation E:475.537, RMS G = 0.0875944, E:428.511, RMS G = 0.0805305, E: 372.844, RMS G = 0.0508421, and E: 390.26, RMS G = 0.0939766 with M72, M76, M81, and P1 ligands, respectively.

Results

The amino acid sequences of envelope protein and nucleocapsid phosphoprotein were blasted against the PDB-BLAST database to identify an appropriate template for homology modelling. The protein having PDB Id: 1ssk.1.A (seq. identity 92.37, seq. similarity 0.61) and 5x29.1.A (seq. identity 91.38, seq. similarity 0.54) were selected as a template for 3D modelling of the envelope protein and nucleocapsid phosphoprotein. The SWISS MODEL server was used to predict the 3D structure of the envelope protein and nucleocapsid phosphoprotein. Models were built based on target-template alignment using ProMod3 in the SWISS MODEL server. The best models of envelope protein and nucleocapsid phosphoprotein were selected based on the best QMEAN score (0.01) and highest resolution 2.48Å, and were validated using the RAMPAGE sever.

The protein structure's stereochemical stability was calculated with the help of a Ramachandran plot. The Ramachandran plot explained the 3D structure of the envelope protein and nucleocapsid phosphoprotein, showing 84% and 90.4% amino acid residue of predicted structure are in the favoured region for the nucleocapsid phosphoprotein and envelope protein, respectively. Also, amino acid residues in the allowed region were 6.1% (nucleocapsid phosphoprotein) and 13.3% (envelope protein), and the remaining number of residues in the outlier region was 3.6% (nucleocapsid phosphoprotein; Figure 1 B) and 2.2% (envelope protein; Figure 1 B). The overall guality factors for nucleocapsid phosphoprotein and envelope protein of the predicted models at ERRAT2 were 94 and 87, respectively.



Figure 1. A, **B** – Ramachandran plot from RAMPAGE of Wuhan coronavirus, SARS-CoV-2 protein. **A** – Envelope protein. **B** – Nucleocapsid phosphoprotein. The phi (ϕ) values of amino acid residues are on the *x*-axis. The psi (ψ) values are on the *y*-axis. **C**, **D** – 3D structure of envelope protein (**C**) and nucleocapsid phosphoprotein (**D**) after homology modelling

Molecular docking

Envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2 were prepared for molecular docking and were analysed by MOE software initially by 3D protonation, energy minimisation, and prediction of active site for the eight ligands by keeping the parameters at their defaults. Then the ligands (E1 to E4 and N1 to N4) were docked separately with the envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2 (Figures 2, 3) using MOE software. The results from molecular docking suggested that the E2: mycophenolic acid (log P =3.00; $\Delta G = -10.2567$ kcal/mol; pKi = 7.713 μ M) was the most potent druggable protein ligand of the SARS-CoV-2 envelope protein (Figures 2 A, B), while N2, 1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid (Log P = 2.901; $\Delta G = -12.2112$

kcal/mol; $pKi = 7.885 \mu$ M) was the most potent druggable protein ligand of SARS-CoV-2 nucleo-capsid phosphoprotein protein (Table I, Figure 2).

Discussion

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a global pandemic health threat. SARS-CoV-2 was identified as a new strain of the Beta-CoVs genera, and is a member of the zoonotic origin coronavirus group. It causes coronavirus disease-2019 (COVID-19), which is the greatest concern in all the countries involved in the outbreak for health and economy reasons. SARS-CoV-2 is distinct from the severe acute respiratory syndrome virus [2, 3, 25–27]. However, the phylogenetic analysis of the envelope protein and nucleocapsid phosphoprotein revealed





Figure 2. Significant druggable protein ligand complex of envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2. E2 ligand has five hydrogen bonds: one with Asn_64, two with lys_63, one with val_49, and one with ILE_46. N2 has two hydrogen bonds: one with Thr 49, and the other with Tyr112, in addition to one arene-arene interaction with Tyr 109

that these proteins are close to the nucleocapsid phosphoprotein of bat coronavirus and severe acute respiratory syndrome-related coronavirus (Figures 4-6). Hence, the study was designed to predict potent ligands against druggable envelope and nucleocapsid phosphoprotein of SARS-CoV-2. The 3D models of the envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2 were predicted, validated, and used for docking studies. The docking studies help in the prediction of the preferred orientation of a ligand with the binding site on a protein and are used for conformation of various chemical compounds at the target site of the protein. The most potent identified compounds for envelope protein, mycophenolic acid and nucleocapsid phosphoprotein, 1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid) with highest log octanol/water partition coefficient (Log P), high number of hydrogen bond donors and acceptors, lowest non-bonded interaction energy (ΔG) between the receptor and the ligand, and high binding affinity (pKi), indicate that they are the most potent compounds against the SARS-CoV-2 envelope and nucleocapsid phosphoprotein.

The coronavirus nucleocapsid phosphoprotein is a multifunctional structural protein; during virion assembly it interacts with the viral membrane and forms complexes with genomic RNA. The coronavirus nucleocapsid phosphoprotein plays an important role in coronavirus transcription and assembly as well as the coronavirus lifecycle [28–34]. The most potent identified compound, 1-[(2,4-dichlorophenyl)methyl]pyrazole-3,5-dicarboxylic acid], may inhibit any of its multifarious activities and functions during virion assembly; however, detailed studies are needed on the inhibitory effect of these compounds on the interaction of nucleocapsid phosphoprotein with the viral membrane, and formation of complexes with genomic RNA during SARS-CoV-2 transcription and virion assembly.

The coronavirus envelope protein plays a crucial role for the lifecycle of the virus. The small integral membrane protein, the coronavirus envelope protein, is important for the development of the disease in the host through viral assembly, to exit the host cell by viral budding, viral propagation, envelope formation by taking portions of the host cell membranes, and the release of infectious virus from the host cell [33-35]. Hence, the SARS-CoV-2 envelope protein was considered for the docking study to identify the most potent compound; the study revealed that mycophenolic acid may an appropriate druggable protein ligand of SARS-CoV-2 to inhibit the development of a COVID-19 by blocking the viral assembly. Complete wet lab analysis is needed to elucidate the impact of the mycophenolic acid on the virus' exit



Figure 3. 2D and 3D protein-ligand interaction of envelope protein and nucleocapsid phosphoprotein of SARS-CoV-2

State-of-the-art tools to identify druggable protein ligand of SARS-CoV-2



Figure 4. Phylogenetic analysis of the nucleocapsid phosphoprotein of SARS-CoV-2 by Maximum Likelihood method. "The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model [11]. The bootstrap consensus tree inferred from 500 replicates [10] is taken to represent the evolutionary history of the taxa analysed [10]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. Initial tree(s) for the heuristic search were obtained automatically by applying neighbour-joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The analysis involved 78 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 43 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [9]." Nucleocapsid phosphoprotein sequence used for constructing the phylogenetic tree: MSDNGPQNQRNAPRITFGGPSDSTGSNQNGERSGARSKQRRPQGLPNNTASWFTALTQHGKEDLK-FPRGQGVPINTNSSPDDQIGYYRRATRRIRGGDGKMKDLSPRWYFYYLGTGPEAGLPYGANKDGIIWVATEGALNTPKDHIGTRNPANNAAIVLQLPQGTTLPKGFYAEGSRGGSQASSRSSRSRNSTPGSSRGTSPARMAGNGGDAALALLLDRLNQLE-SKMSGKGQQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYKHWPQIAQFAPSAS-AFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLL-PAADLDDFSKQLQQSMSSADSTQA

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| 2. APO40661.1:1-76_E_protein_Severe_acute_respiratory_syndrome-related_coronavirus | MYSFYSEETDTLIVHSYLLFLAFYYFLLVTLAILTALRLCAYCOMIYMYSLVKPSFYIYSRYKHLMSSOGI- |
| 8. AGZ48809.1 1-76_envelope_protein_Bat_SARS-like_coronavirus_RsSHC014 | MYSFYSEETGELLYMSYLLFLAFYYFLLYTLAILELALRLCAYCCHIYMYSLYKPEYYYXSSYKMLMSSOGY. |
| L QDF43816.1:1-76_smail_envelope_protein_Coronavirus_BIRI-BetaCoV/9C2018 | N入器とへ器数を実施器に1人構築へてたとなどとなんとして人間にかして置くて近くなどの時1人類人類へんだ法案1人人が開始した時に構造器を読み、 |
| 5. NP_828854.1:1-76_protein_E_Severe_acuts_respiratory_syndrome-related_coronavirus | 利太陽と大量電気重要用「人物酸入口下と「ヤモハ入と「こん」「ヤ」「血ヤ」がついていたので利用人酸「人物酸素」人人の含素の大物の細胞素を含み、 |
| ADE34767.1:1-76_small_memorane_protein_Bat_SARS_coronavirus_HKU3-7 | 明治語とな習慣医正認識でした性感なしたというとなったものであっていた。「そうなどのなど」と聞きなどのなどのなどが必要が必要的などので、 |
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| AAP51230.1.1-76_envelope_protein_E_SARS_coronavirus_GD01 | MYSFYSEETCTLIVNSVLLFLAFMVFLLVTLAILTALRLCAVCCNIVNVSLVKPTVVVVSRVKNLNSSEGV- |
| AAA62312.1:1-76_smail_envelope_protein_BIRs-BetaCoV/HuB2013 | NYSEVEREESSELLYNE VILLEVAEVVELLYNE ALLENALBICAVCCHIVNYSELVEPEVVYSERVENI MEREESY. |
| 10. ACB69908.1:1-76_envelope_protein_E_SARS_coronavirus_BJ182-12 | |
| 1. ACZ72023.1.1-76_envelope_protein_SARS_coronavirus_ExoN1 | |
| 11. AU2/2023-1.1-r6_envelope_protein_SARS_coronavirus_EXXV1 (2. YP_003858586.1:1-76_envelope_protein_Bat_coronavirus_BM46-31/8GR/2008 | AFSTYSEELOTLIVESVLLFLATVYFLLVLLATLIALKLUATCONTYNYSUVAFEVTVISKVANLHSSERV. |
| 2 YP_003858586.111-76_envelope_protein_8at_coronavirus_8148-31/8GR/2008 | NYSFYBEETERLIVNSVLLFLAFYYFLLYTLAILELCAYCONIYNYSLYAPFFYYYSRYASLMBEDEY. |
| 3. Q0C473.1:1-76_RecName:_Full_Envelope_small_membrane_protein_Bat_CoV_279/2005 | HYSEVELETERLIVESVLLFFAFVVFLLVELAILELCAVCOMIVEVVYVXSRVKHLMBSERV- |
| 14. ADC35514.1.1-76_envelope_protein_SARS_coronavirus_HKU-39849 | NASEASEE重整要で1人構築AFEとでやたAAEFCA、電「マルドの型やに低けなど人のCMEIAMAASEAAAASEAAAMETMESSEESA- |
| 5 ADE34768.1:1-76_smail_membrane_protein_Bat_SARS_coronavirus_HKU3-8 | HYBEVEETETLIVHEVILFLAFVVFLLVTIAILELCAYCOMIVHVELVKFTVVVVERVKHLHEEEV- |
| 6. AKZ19089.1:1-76_envelope_protein_Bat_SARS-like_coronavirus_YNLF_34C | NYRFYBEETHTLIVNEVLLFLKFVVFLLVALAILMALHLCAVCCHIVNVSLVKPTVVVVSRVKNLMBBEERV- |
| 7. AHX37660.1: 1-76_envelope_protein_Rhinolophus_affinis_coronavirus | MYREVER FERTILIVES VILLELAFYVELLUT ALLEALELCAVCCHIVEVELVER VXVX SEVENLESSEV. |
| I8. ACZ72198.1 1-76_envelope_protein_SARS_coronavirus_ExoN1 | |
| | |
| 9. AAR23255.1 1-76_envelope_protein_SARS_coronavirus_Sino3-11 | MISFFEELENLIVESVLLFLATVFLLVELATLEALKLCATCCHIVEVSLVATVIVISKVALHSSEAV. |
| 0. ABD75313.1:1-76_envelope_protein_Bat_SARS_CoV_Rf1/2004 | NAMEAABEEEDUICIAMBACCEAAEAAECCAECAECAECAECAECAECAECAECAECA |
| 1. AlA62280.1:1-76_smail_envelope_protein_BIRF-BetsCoVUL2012 | 四人間と人間を登載したした後期の人口でとんせたかたところ、国人に広くていたのでは人間へ気でんだも可んれんである人を強い強迫を見知る。 |
| 2. AGC74167.1:1-76_envelope_protein_Bat_coronavirus_Rp/Shaanvi2011 | NAX あとA 単名単加加工「IA 種類A FFE ととA A EFF A EF |
| 3 AC272243.1:1-76_envelope_protein_SARS_coronavirus_MA16_Exot/1 | MYSFYSEETSTLIVNSVLLFLAFVYFLLVTLAILSALRLCAYCCNIVNVSLVXFTVVVVSRVKNLNSFESV- |
| 4. AUA62302.1:1-76_small_envelope_protein_BIRF.BetaCoV/SX2013 | MYREVERETONILLYNEVILLEVAEVVELLYN ALLENALBICAVCCHLYNYSEVVEVERVENUSSECV |
| 5. ABM92862.1:1-76_smail_envelope_protein_SAR3_coronavirus_TJ01 | |
| 5. ABM22892.1:1-75_smail_envelope_protein_SARS_coronavirus_L301 6. AC272257.1:1-75_envelope_protein_SARS_coronavirus_ExoN1 | |
| to AUC/2201.1.1+ro_etheliope_protein_SARS_coronawrus_Exote1 | MERCYREE WAYLERCAPYFLEY BLAILEALKLEACED IYNYELYKEEYYYYY SEYKMLMESERY. |
| 7. ATO96184.1.1-76_small_envelope_protein_Bal_SARS-like_coronavirus | WARKARE ARE AND A CONTRACTOR AND AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND A CONTRACTOR AND AND A CONTRACTOR AND A |
| 8 AAS44718.1:1-75_small_envelope_E_protein_SARS_coronavirus_TW-GD1 | 市工器を本語目目は配置に1・構築AFFEでをためたとしてA型でを1・加量を下述でであるの時1を置きる低いまたのである。 |
| 9 AV4A96030.1:1-76_envelope_protein_Bat_coronavirus | MCEFYEEEIIIIIIIVWEVLLFVAFVVFLLVILLAILIIALRLCAYCOMIVWVELVKMEVVXERVKWELWEAEIIV |
| A 44P32247 1 1 76 employe protein SLPS constraint Singl 11 | MYSEVSEETUTII. HSVLLFLAFVVFLLVTLAILTALRLCAYCCYIVHVSLVXFTVVVSRVXHLHSSEDV. |
| 1. AAS48454.1:1-76_small_envelope_protein_SAR8_coronavirus_EJ01 | NYREVEETETLIVESVLPFLAFVVFLLAILAILAILALELCAYCCHIVEVSLVXETVVVERVVERVVEL |
| 2. ACZ72168.1:1-75_envelope_protein_SARS_coronavirus_ExoN1 | NYSEVERETENT LIVESVILE LAFYXELLVELAILEAL BIGING STUDIES VERSUS VERSUS |
| 2.AC2/2168.1.1-/5_envelope_protein_SARS_coronavirus_extern 3.5X29_A20-81_Chain_A_Envelope_smail_membrane_protein_SARS-related_coronavirus | |
| a. 57.29_r.29/61_Chain_r_Enverope_smail_memotiane_protein_SARS-related_cotonavitus | THE FIRST CLARK VECTOR CALLEAL ANALY BUY SUVER VERVEY SERVER |
| 4.21884_A:1-56_Chain_A_Envelope_small_membrane_protein_SARS-related_coronavirus | |
| 5. ADY17913.1.1-77_putative_envelope_protein_Zaria_bat_coronavirus | 四人達と大変な影し部国にした時1人と「1と聞こんんた「1人ヤヤツ国に同じに図ったのに、1人間の部に人がも聞えた人大変が「ない」 |
| 8. YP_009072442.1:1-71_envelope_protein_Bat_Hp-betacoronovirus/2hejlang2013 | MY当FY国位新聞前でVIV税AVF1LV設FVAULIVALAILTCCRECATCCMILDDG高VVRPTRVVELDATFYMRLDP |
| 7. 0004EB 1 1-75_Envelope_smail_memorane_protein_Bat_coronavirus_(BtCoV/133/2005) | HUPFYHERINETIIVEFFILEVYCAITLLVCLAVLTAIRLCVCCABEVHTLLFVPAFYIVETERMAYFEFE |
| 8. YP_001039958.1:1-75_smail_membrane_protein_Tylonycleria_bat_coronavirus_HKU4 | HIS COMPANY AND IN THE CALL BUTCH IN THE REPORT AND AND INCOMENTS OF THE REPORT OF THE |
| 9. AV4495044 1 1-54_envelope_protein_Bat_coronavirus | |
| 8 Avavasou44 1 1-64_envelope_proteat_Bat_coronawites | NUCE VIEW IN TIVEFFILE VICATELVICLATE ATSLEVICASE VALUE VEAFETING |
| 0. VP_009513016.1:1-76_E_Betacoronavieus_Eninaceus/VMC/DEU/2012 | NTSEAHDOTESEIAMEELLEAACVALLTANNAILEACSTCAACTERAMETTAASAYAAAMEHBAAAAAAME |
| 1. ASL68947.1.1-75_envelope_protein_Hypsugo_bat_coronavirus_HKU25 | NTSとん器を注意値とした語ととした更んでないまででんのかとし至り回転でない語んが見着してん語らかした人気料理器と高くたんだと語言。 |
| 2. QCC20719.1:1-76_E_Hedgehog_coronavirus_1_Hedgehog_coronavirus_1 | いた多をな日間間に開始とした様をとうと思いないとしたのでは、日本の出行の人間にも認識を確認してないためのでは、「「「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないでは、「」」のないないできた。 |
| 3. ASL68958 1:1-59_envelope_protein_Hypsugo_bat_coronavirus_HKU25 | MUREVERINEFIVEFIFEVACAI TUUCHAFUTATELCHECAI EVMTUUVEAI YVY |
| 4. AHY61342.1.1-75_small_envelope_protein_BtVs-BetaCoV/9C2013 | HEREYORG LENGING THEFT FT VACATILLY CHAFTER AND LOVE A THE HALLY OPATIVE THERE VY VERICE. |
| 45. BBJ36013.1:1-75_small_envelope_protein_Bat_coronavisus | |
| 6 VP_009361862.1:1-75_small_envelope_protein_Bat_coronavirus | NEETINEN INGELINEETINGELINE VOOR SEARCHAR VOOR SE |
| | |
| | |
| ie. YP_DUVS51062_11-75_smail_envelope_protein_Bat_Coronaerus 17. QGA70697.1;1-60_envelope_protein_Eninaceus_hedgehog_coronaeirus_HKU31 | NLEFYDOUL AFFIYN FFIFTYACAYILLYCNAFLTATRLCYDCITDYNTLLYD PAYNYNTARDYYY FFE- Nlefyn Goverfiyn Ffiftyacayilyycarltayrlcygaartru Lybeatyyy |
| | |
| 17. QGA70097.11-60_envelope_protein_Ennaceus_hedgehog_coronavirus_HKU31 | |
| 7. QG470697.1;1-60_envelope_protein_Ennaceus_hedgehog_coronavirus_HKU31 | MLPEYHQYWBFIYNFFIFBYACAYILYYCAAILBAYRLCYQCAABFNELLYDFAIWYN Ymaan Klodad merwdy ilwrh garmefraftarwd - wrac adergalag alfarwdd y gllefaad udfar gargo bosu ymaa i clodad af yn y llwrh garmefraftarwd - wrac adergalag ac yn |
| 7. 03470097.11-80_envelope_protein_Ennaceus_hedgehog_coronavius_HKUS1 2019-nDyV 2019-nDyV 2019-000724397.21-418_nucleocapsid_phosphoprotein_Vknam_seato-d_markst_presmorea_vkna | |
| 7. QGA20007.11-00_anvelope_protein_Einaceus_hedgehog_coronarius_J4KU31 2019-00/ 195.000238172-1419_pudoscopert_phosphoprotein_Vunan_seatoo_manst_preumona_vusa 0002884.11-111_pudoscopert_phosphoprotein_Vunan_seatoo_manst_preumona_vusa | NLPFYHQQYBJFIYNFFIFBYACAYILYYCAAILBAYRLCYQCAABFNBLLYQFATYYNB YRBAINLDBHOPNFHCQYILLNHHIDAYNTFPFTBFHND YRBAINLDBHOPNFHCQYILLNHHIDAYNTFFTTBFHND YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTBFHND YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTFFTBFHND YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTFFTBFHND YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTFFTBFHND YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTFFTBFTHPHND YRBAINLDBHOPNFHCQXILDBHOPNC YRBAINLDBHOPNFHCQXILDBHOPNC YRBAINLDBHOPNFHCQXILBANGANAAN YRBAINLDBHOPNFHCQXILLNHHIDAYNTFFTTFTFTFTFTFTFTFTFTFTFTFTHFTHFTHTTTTTT |
| OGA70697 1:1-60_envelope_protein_Einaceus_hedgehog_coronaxivus_HKU31 2019ex0pi YP_00972397 2:1-415_mudescapsir_prosphoprotein_TWinam_seabod_mantat_preumosa_wus GH02864 1:1-1-13_mudescapsir_prosphoprotein_UMInam_seabod_mantat_preumosa_wus GH02864 1:1-1-13_mudescapsir_prosphoprotein_UMInam_seabod_mantat_preumosa_wus GH02864 1:1-1-13_mudescapsir_prosphoprotein_UMInam_seabod_mantat_preumosa_wus | |
| 7. QBA20097.11-60, anvelope_protein_Einaceus_hedgehog_protoasivus_HKU31 2019-00/ 19. 000224972-1-19. puccescapert_prosphore/set_Ukraw_sest0od_manet_presentes_vess Cend2884.11-14.75, puccescapert_prosphore/settes_Ukraw_sest00.75, punct_presentesity_was Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa | MLPFYHQQYBFIYNFFFFTBYACAYILYYCAAILBAYRLCYQCAABFMBLLYQFATYYNB YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTBFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTFFTFFHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFFTFTFFTHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFTFTFFTHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFTFTFTFFTHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFTFTFTFTHND YRBAINLDDHOFNFKODYILLNKHIDAYNFFTFTTFTFTHND YRBAINLDDHOFNFKONYILLNKHIDAYNFFTTTFTTTNHKO YRBAINLDDHOFNFKONYILLNKHIDAYNFFTTTTNHKO YRBAINLDDHOFNFKONYILLNKHIDAYNFFTTTTNHKO YRBAINLDDHOFNFTND YRBAINLDDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFNFTND YRBAINLDHOFN < |
| 7. QBA20097.11-60, anvelope_protein_Einaceus_hedgehog_protoasivus_HKU31 2019-00/ 19. 000224972-1-19. puccescapert_prosphore/set_Ukraw_sest0od_manet_presentes_vess Cend2884.11-14.75, puccescapert_prosphore/settes_Ukraw_sest00.75, punct_presentesity_was Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa Cend2884.11-14.75, puccescapert_press_B4_protoasiwa | |
| 7. QBA20097.11-60, envelope, protein, Erinarceur, hedgehog, promaelrus, JekU31 2018-00/ 19. 000728472-1-11, juuciscoppint, prinsphoreien, Jivinan, seatoor, manst, preumois, juus Con20184.11-147, juuciscoppint, prinsphoreien, Jivinan, seatoor, manst, preumois, juus Con20184.11-147, juuciscoppint, prinsphoreien, Jivinan, seatoor, manst, preumois, juus Cherd Stabit, 1-147, juuciscoppint, prinsphoreien, Jivinan, seatoor, manst, preumois, juus AMP2004.11-147, juuciscoppint, prinsphoreien, prinsphoreie | NLEFYHQUYEFIYN YCACAYILYYCAAILEN AV KUCYUCAALEN AV KUCYUCAAF YEBAIKUCDK YEBAIKUCYU YEBAIKUCYU YEBAIKUCU YEBAIKUCYU YEBAIKUCYU YEBAIKUCU YEBAIKUCU YEBAIKUCU YEBAIKUCU YEBAIKUCU YEBAIKUCUU |
| 7. QGA20097 1:1-00, envelope_protein_Erinaceus_hedgehog_coronaelrus_HKU21 2018-cov 19. 0007288 1:1-11 guidecoperi, prosphorotein_TVuhan_seabod_manst_preumosa_was 0007288 1:1-12 guidecoperi, prosphorotein_TVuhan_seabod_manst_preumosa_was 0007288 1:1-12 guidecoperi, protectual (2010) 0007281 1:1-12 guid | |
| 7. QBA20097.11-60, anwelope, protein, Erinasceur, Inedgehog, poronanivus, Jeku21 2018-00/ 19. 000724972-11-19, publicaceasti, prosphornien, Jivinan, seatood, mariet, preumora, juna Contesti 11-19, publicaceasti, prosphornien, Jivinan, seatood, mariet, preumora, juna Contesti 11-19, publicaceasti, provin, BL, potomalen AP70004.11-119, publicaceasti, previn, BL, SPSS-III, potomalen AP7004.11-119, publicaceasti, previn, BL, SPSS-III, potomalen AP70404.11-119, publicaceasti, previn, BL, SPSS-III, potomalen AP70404.11-110, publicaceasti, previn, BL, SPSS-III, potomalen AP70404.11-110, publicaceasti, previn, BL, SPSS-III, potomalen AU310071.11-121, publicaceasti, previn, BL, SPSS-III, potomalen AU310071.11-121, publicaceasti, previn, BL, SPSS-III, potomalen | NL H F VHQU V BU F I V M F F I F BV ACA VIL VVCAAIL BAV KLCVQCAA BF MELLYQ CAA BF MELLYQ PAIA VVYM YTEAIK K CON HON F K CON ILL MAH ID XX M F F F F F F F F F F F F K KA CONTO ALP BR M K CONT VIL F A CLCOF F M CL CONTUN YTEAIK K CON HON F K CON ILL MAH ID XX M F F F F F F F F F F F F F F F F F |
| 7. QGA20097.11-00, envelope_protein_Einaceus_hedgehog_coronaelrus_HKU21 2018-cov 19. 00072847.21-418_uudeocqesir_prinsphonolein_Tikinan_teatbod_mantet_preumosa_ves 0x072846.11-418_uudeocqesir_protein_Ulvahan_teatbod_mantet_preumosa_ves 0x072846.11-418_uudeocqesir_protein_BL_ADOches_proteinae x0772846.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0772846.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0772846.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0772846.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0772847.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0747284.11-418_uudeocqesir_previn_BL_ADOches_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOches_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOches_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOChes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOChes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOChes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOChes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocqesir_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocquer_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocquer_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocquer_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocquer_previn_BL_ADOCHes_proteinae x0747284.11-428_uudeocquer_previn_BL_ADOCHes_proteinae x074784.11-428_uudeocquer_previn_BL_ADOCHes_previn_BL_ADOCHes_proteinae x074784.11-428_uudeocquer_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHes_previn_BL_ADOCHEs_previn_BL_ADOCHEs_previn_BL_ADOCHEs_previn_BL_ADOCHEs_previn_BL_ADOCHEs_previn_ | |
| C.Q&A70007.11-00, anwelope, protein, Einacose, Jedgehog, coronanius, JekU31 2018-00/ Yo, 000224072-1-118, undercopert, phosphoreler, Jivana, selbod, manet, preumore, jess Cond2084.11-1478, undercopert, phosphoreler, Jivana, selbod, manet, preumore, jess Cond2084.11-1478, undercopert, physika, 20450-14, phosphore, selbod, manet, phosphore, jess Cond2084.11-1478, undercopert, physika, 20450-14, phosphore, selbod, manet, phosphore, jess Cond2084.11-1478, undercopert, physika, 20450-14, physika, selbod, manet, phosphore, jess Kond2084.11-1478, undercopert, physika, 20450-14, physika, selbod, manet, physika, selbod, manet, physika, selbod, manet, physika, selbod, physika, 20450, physika, selbod, physika, 20450, physika, selbod, physika, 20450, | NL H F VHQU V BU F I V M F F I F U VACA VIL VVCAAIL U AV KUCVQCAA B F MILLVQ CAA B F MILLVQ PAINOV VIII AI K LOD K P M F KOD VIL LUKH I DAXK T F F T T P K KO - KKK A DE TO ALF D R M KOD T VIL F A D LOG F M C LOG U M VIII AI K LOD K P M F KOD VIL LUKH I DAXK T F F T T P K KO - KKK A DE TO ALF D R M KOD T VIL F A D LOG F M C LOG U M VIII AI K LOD K P M F KOD VIL LUKH I DAXK T F F T T P K KO - KKK A DE TO ALF D R M KOD T VIL F A D LOG F M C LOG U M VIII AI K LOD K P M F KOD VILL K H I DAXK T F F T F F M K M A D KO ALF D R K C D T VIL F A D LOG F M C LOG U M VIII AI K LOD K P M F KOD VILL K H I DAXK T F F T F M K M A LOK A D K C A D K M C D T VIL F A D LOG F M C LOG U M VIII AI K LOD K P M F K KOVIL K K H DAXK T F F T F M K M A LOK A D K C A D K M C D T VIL F A A D LOG F M C A D C G U M VIII AI K LOD K M M F K K VIL K K H DAXK T F F T T M K M A LOK A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K A D K K K K |
| CQA20097.11-00_envelope_protein_fileActing_hedgehog_coronaelrus_HKU21 2018-cov Y0_000723397 2-1-11_puddecopsir_princephopotein_fileAna_seabod_mantet_preumora_ves GeA20084.11-11_puddecopsir_princephopotein_fileAna_seabod_mantet_preumora_ves GeA20084.11-11_puddecopsir_princephopotein_fileAna_seabod_mantet_preumora_ves GeA20084.11-11_puddecopsir_princephag_A2554es_coronaelrus AV70905.11-112_puddecopsir_princephag_A2554es_coronaelrus AV70905.11-112_puddecopsir_princephag_A2554es_coronaelrus AV70905.11-112_puddecopsir_princephag_A2554es_coronaelrus AV20100.11-112_puddecopsir_princephag_A2554es_coronaelrus AV20100.11-112_puddecopsir_princephag_A554es_coronaelrus AV20100.11-112_puddecopsir_princephag_A554es_coron | |
| 7. QBA20097.11-00, envelope, protein, Erinasceur, hedgehog, promaelius, JekU31 2019-00/ 19. 09072472.1-118, puddecasetar, princednomini, Tutorian, seatood, martet, preumonis, jesis GoodBall 1-1147, puddecasetar, prince, Ball 2007-billio, promaini Condestituti 1-147, puddecasetar, prince, Ball 2007-billio, promaini AMP2004.1-1418, puddecasetar, prince, Ball 2007-billio, promainia AMP2004.1-1418, puddecasetar, prince, Ball 2007-billio, promainia AMD2005.1-1421, puddecasetar, prince, Ball 2007-billio, promainia AMD2005.1-1422, puddecasetar, prince, Ball 2007-billio, promainia AMD2005.1-1422, puddecasetar, prince, Ball 2005-billio, commania AMD2005.1-1422, puddecasetar, prince, Ball 2005-billio, puddecasetar, perince and AMD2005.1-1422, puddecasetar, prince, Ball-2005, puddecasetar, perince and AMD2005.1-1422, puddecasetar, prince, Ballio, and puddecasetar, perince and AMD2005.1-1422, puddecasetar, prince, Ballio, and puddecasetar, perince and AMD2005.1-1422, puddecasetar, perince and puddecasetar, perince and AMD2005.1-1422, puddecasetar, perince and AMD2005.1-1422, puddecasetar, perince and AMD2005.1-1422, puddecasetar, perince and AMD2005.1-1422, puddecasetar, perince and AMD2005. | NL H F VH QQ V BU F I V M F F I F W VACA VIL VVCAAIL X A V KUVQ CAA B F M L L VQ CAA B F M L L VQ P A I VVYM VIII A I K L Q P A D M F K G M VIL L M H I D A X M T F P T M M K M L V CAAIL X A V KUVQ CAA B F M L L VQ CAA B F M L L VQ P A I V VYM VIII A I K L Q P A D M F K G M VIL L M H I D A X M T F P T M M K M L V CAAIL X A L VQ F A K A D M D A L P F A L VQ F A L V CAAUL X A L L Q F M K Q V L L M H L D A X M T F P T M M K M L X A L VQ F A L V Q CAA B F M L V Q V L V A A L L Q F M K Q V L L M H L D A X M T F P T M M K M L X A L VQ F A L VQ F M K Q V L L M H L D A X M T F P T M M K M L X K A D M Q A L Q F M K Q V L L M H L D A X M T F P T M M K M L X A L VQ F A L Q F M K Q V L L M H L D A X M T F P T M M K M L X K A D M Q A L Q F M K Q V L L M H L D A X M T F P T M M K M L X K A D M Q A L Q F M K Q A L Q D F M Q A L Q D F M Q A L Q D F M Q A L Q D F M Q A L Q D F M Q A L Q D F M Q A L Q Q F M Q A L Q D F M Q A L Q M M M M M M M M M M M M M M M M M M |
| 7. QGA20097.11-00, envelope_protein_timesces_hedgehog_coronaelrus_HKU21 2018-00/ 170, 000728317.21-418_pudecoperin_timescess_hedgehog_coronaelrus_HKU21 2018-00/ 200288.11-1417_pudecoperin_timescess_hedgehom_netst_presentees_aves GMR5305.11-147_pudecoperin_timescess_hedgehom_netstants_presentees_aves AMP2002.11-147_pudecoperint_timescess_hedgehom_netstants_ NMP2002.11-147_pudecoperint_timescess_hedgehom_netstants AMP2002.11-147_pudecoperint_timescess_hedgehom_netstants NMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_metals AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_pudecoperint_timescession_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP2002.11-147_publics AMP20 | |
| CQA20097.11-00, envelope_protein_Einscress_hedgehog_coronavirus_J4KU31 2019-00/ Y0.000224072-1-110, puddecaperi_phosphorein_Uhunas_sealod_mant_phosphorein_jkes GOA20081-11-110, puddecaperi_phosphoreins_hillion, sealod_mant_phosphoreins_kes GOA20081-11-110, puddecaperi_phosphoreins_hillion, sealod_mant_phosphoreins_kes GOA20081-11-110, puddecaperi_phosphoreins_hillion GOA2008-11-120, puddecaperi_phosphoreins GOA2008-11-120, pu | NL H F VH Q V W F I V M F F I F W VACA VIL VVCAAIL X A V KL V CAAFL X A V KL V Q CAAFW F W L L VACAW Y W Y TO AL X C D X D Y D L W H L D X X W T F P T T P T P X Y X Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y |
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| 7. QQA20097.11-00, envelope_protein_Ukran_seatoot_nexture_JHKU21 2019-00/ 19. 000728417.21-418_pudocopert_inter_Ukran_seatoot_manter_preumera_vera GMR530021.11-117_pudocopert_inter_BL_0001abus AM77002.11-117_pudocopert_inter_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_inter_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77002.11-117_pudocopert_protein_BL_9555bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_promains AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-127_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein_BL_955bis_pudocomentality AM77003.11-147_pudocopert_protein | ULEFYHQUYEF!!! UNEFF!!! VACAY!LYVCAA!LEXX UVCAA!LXX UVC |
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| 7. QBA20097.11-00, envelope_protein_Union_setup.hedgehog_coronavirus_UHXU21 2018-00/ 179, 000728372-11-12, modecoperin_Unionsphorebat_Union_setup.commons_unions GMR53021-11-12, modecoperin_Unionsphorebat_Union_setup.commons_unions GMR53021-11-12, modecoperin_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_Union_Union_Union_SetUp.commons AV779203-11-12, modecoperin_Union_Union_Union_Union_SetUp.commons AV7793-11-12, modecoperin_Union_Union_Union_Union_Union_Union_SetUp.commons AV7793-11-12, modecoperin_Union_Union_Union_Union_Union_SetUp.commons AV7793-11-12, modecoperin_Union_Union_Union_Union_Union_Union_Union_Union_AU779- AV7793-11-12, modecoperin_Union_Union_Union_Union_Union_Union_AU779- AV7793-11-12, modecoperin_Union_Union_Union_Union_Union_Union_Union_Union_Union_AU779- AV7793-11-12, modecoperin_Union_Un | ULEFYHQUYERFITWURFTTFTVTVACAYILVYCAATLEAXVELCYQCAATEFHTLLYQ ALPEFYHQUYERFITWURFTTFTVTFVACAYILVYCAATLEAXVELCYQCAATEFHTLLYQ YEGAIWCDENDFUTWUCDENT SCOULAGEFHTLXDENT SCOULAGEFHTLXDENT SCOULAGEFHTLXDENT YEGAIWCDENT SCOULAGEFHTLXDENT SCOULAGEFHTLXDENT |
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| 7. QGA20097, 11-40, envelope_protein_Uturan_seator_martu_preumora_ves 2019-00/ 170, 00072817 2-1418, puddecaperi_princephoneru/Uturan_seator_martu_preumora_ves Genesitati 2-1418, puddecaperi_pretin_BL_0008-bits_containes 201970001, 11-107, puddecaperi_pretin_BL_0008-bits_containes 201970101, 11-107, puddecaperi_pretin_BL_0008-bits_containes 201970101, 11-107, puddecaperi_pretin_BL_0008-bits_containes 201970101, 11-107, puddecaperi_pretin_BL_0008-bits_containes 20197011, 11-107, puddecaperi_pretin_BL_0008-bit | ULEFYHQUYERFITWURFTTFTV VACAYILVYCAATLEXAVELCYQCAATER YEGAIWCDHAFWERGYTLUNKT SUNTYLUNKT YEGAIWCDHAFWERGYTLUNKT SUNTYLUNKT YEGAWCDHAFWERGYTLUNKT SUNTYLUNTUL YEGAWCDHAFWERGYTLUNKT SUNTYLUNTUL |
| 7. QGA20097 1:1-00, envelope_protein_Tkinan_teaboot_contantius_JHKU21 2018-004 79. Q0272817 2:1-11undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst_preumosa_twis GMR53081 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst AV77091 1:1-12undeccepsit_protection_Tkinan_teaboot_mantst AV77091 1:1-12undeccepsit_protection_Tkinan_containing 0.0743081 1:1-22undeccepsit_protection_Tkinan_containing 0.0743081 1:1-22undeccepsit_protection_Tkinan_teaboot_witControl 0.0743081 1:1-22undeccepsit_protection_Tkinan_teaboot_witControl 0.0743081 1:1-22undeccepsit_protection_Tkinan_teaboot_witControl 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_accentaining 0.0743081 1:1-22undeccepsit_protection_United_BMR54000000000000000000000000000000000000 | ULB F VH Q V W F I V M F F I F W VACA VILVY CAATLWAV CUV CAAW F W LLVY W A I VY W VIN A I K CO K A C F F K CO VILL K H I D A X M F F F F M F M X A C F F A C LO K F W VACA VILVY CAATLWAY CUV CUV CAAW F W LLVY W VIN A I K CO K A C F F K CO VILL K H I D A X M F F F M M Y A C A Y L V CAAW F W C F W C F W C C A C LO K F W C A C LO |
| 7. QGA20097.11-00, envelope_protein_Uturan_seator_martu_preumora_ves 2019-00/ 170_000728127.21-410_pudocoperi_protein_Uturan_seator_martu_preumora_ves GA030281.11-817_pudocoperi_protein_Uturan_seator_martu_preumora_ves GA030281.11-817_pudocoperi_protein_BL_ADSD- NO70028.11-817_pudocoperi_protein_BL_ADSD- NO70028.11-817_pudocoperi_protein_BL_ADSD- NO70028.11-817_pudocoperi_protein_BL_ADSD- NO70028.11-817_pudocoperi_protein_BL_ADSD- NO70028.11-827_pudocoperi_protein_BL_ADSD- NO70038.11-827_pudocoperi_protein_BL_ADSD- NO70038.11-827_pudocoperi_protein_BL_ADSD- NO70038.11-827_pudocoperi_protein_BL_ADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NO70038.11-827_pudocoperi_protein_BLADSD- NOF0038 | ULB F VH Q V W F I V M F I F F F W VACA VILVY CAAILWAY KUCY Q CAAW F W L VY Q VIE A I K L D K P M F K GD VILL M KH I D X H W F P F F F F F F F F F K M C A L D K P K K A D K G A L D K P K M V U L K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K G A L D K P K K A D K K A D K G A L D K P K K A D K |
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| 7. QBA20097 1:1-40, envelope_protein_thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_protectory thinan_seabod_mants_preumona_wes 0005284 1:1-41modeccepsic_preum_DB_34054 e.g.contains 0005284 1:1-41modeccepsic_preum_DB_34054 e.g.contains 0005285 1:1-42modeccepsic_preum_DB_34054 e.g.contains 0005285 1:1-42modeccepsic_preum_DB_4504000102019 0005285 1:1-42modeccepsic_preum_DB_4504000102019 0005285 1:1-42modeccepsic_preum_DB_400000000000000000000000000000000000 | ULB F VH QU V BL F I V M F F I F W VACA VILVY CAATLUX AV LLVY CAATLUX AV LLVY QU AA E U DY ULLY AA U LUS F W VY W VIII AI K LOD K P W F K CD VILL W H LOAN W F P F F F F F F F F F F F F F F F F F |
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| 7. QGA20097.11-00, envelope_protein_Ukinan_seatoo_mantus_JHKU21 2019-00/ 17, QGA20097.21-41Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_pressmons_ukes GMC50284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_pressmons_ukes GMC50284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_phosphop AMC70284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_phosphop AMC70284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_phosphop AMC70284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-81Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_mantus_ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo_MS/ AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukinan_seatoo AMC70284.11-82Audoccepsit_phosphoptein_Ukina_conseatus_AMC74 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_AMC74 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphoptein_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosphopteins_Ukina_conseatus_CHAC4010 AMC70384.11-82Audoccepsit_phosph | ULB F VH Q V W F I V M F F I F W VACA VILVY CAATLU AV CAAUL X AV COCAAUF W W A I V V W VIII AI K CO K AU F I V M F F I F W W A CAVILVY CAATLU AV CAAUF W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W W W A AU CO K W W W A AU CO K W W AU C |
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Figure 5. Representative of the multiple protein sequence alignment of envelope protein (A) and nucleocapsid phosphoprotein (B) of Wuhan novel coronavirus, SARS-CoV-2. Envelope protein and nucleocapsid phosphoprotein sequence used for the sequence alignment are available in Figures 4 and 6, respectively

from the host cell by viral budding, the effect on blocking the envelope formation by taking portions of the host cell membranes, as well as its controlling power on release of infectious virus from the host cell.

There is no defined curative treatment for COVID-19 or any approved vaccines against SARS-CoV-2 infection. The WHO recommendation for the management of MERS-CoV is being in practice: initiation of oxygen therapy to keep the oxygen saturation above 90%, with conservative fluid management in the absence of shock, and an empiric antimicrobial regimen that includes antibiotics and a neuraminidase inhibitor for treatment of influenza. All of those supportive treatments are for the prevention of acute respiratory distress syndrome and for the prevention septic shock [2, 3, 36]. Hence, drug development against SARS-CoV-2 is considered urgent in order to fight COVID-19. The present in-silico approach identifies one potent ligand against the envelope protein and one potent ligand against nucleocapsid phosphoprotein of SARS-CoV-2. A combination of these two ligands might be the best option to

State-of-the-art tools to identify druggable protein ligand of SARS-CoV-2



Figure 6. Phylogenetic analysis of the envelope protein of Wuhan coronavirus, SARS-CoV-2 by Maximum Likelihood method. "The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model [11]. The bootstrap consensus tree inferred from 500 replicates [10] is taken to represent the evolutionary history of the taxa analysed [10]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. Initial tree(s) for the heuristic search were obtained automatically by applying neighbour-joining and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The analysis involved 78 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 43 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [9]." Envelope protein sequence used for constructing the phylogenetic tree: MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVSLVKPSFYVYSRVKNLNSSRVPDLLV

consider for further detailed studies in wet laboratories to develop a drug for treating patients infected with SARS-CoV-2.

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Conflict of interest

The authors declare no conflict of interest.

References

- 1. Huang C, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020; 395: 497-506.
- 2. WHO, 2020a. Naming the coronavirus disease (COVID-19) and the virus that causes it, Accessed 23 Mar 2020. https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-thecoronavirus-disease-(covid-2019)-and-the-virus-thatcauses-it
- Cárdenas-Conejo Y, Liñan-Rico A, García-Rodríguez DA, Centeno-Leija S, Serrano-Posada H. An exclusive 42 amino acid signature in pp1ab protein provides insights into the evolutive history of the 2019 novel human-pathogenic coronavirus (SARS-CoV2). J Med Virol 2020; doi: 10.1002/jmv.25758.
- 4. Zhu N, Zhang D, Wang W, et al. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med 2020; 382: 727-33.
- 5. Chan JF, Kok KH, Zhu Z, et al. Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. Emerging Microbes Infections 2020; 9: 221-36.
- Wu F. Zhao S, Yu B, et al. Complete genome characterisation of a novel coronavirus associated with severe human respiratory disease in Wuhan, China. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.24.919183.
- Zhou P, Yang X L, Wang X G, et al. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin. bioRxiv 2020. doi: https://doi.org/10.1101/2020.01.22.914952.
- Katoh K, Standley DM. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol 2013; 30: 772-80.
- Kumar S, Stecher G, Tamura K, MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol 2016; 33: 1870-4.
- Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 1985; 39: 783-91.
- Jones DT, Taylor WR, Thornton JM. The rapid generation of mutation data matrices from protein sequences. Bioinformatics 1992; 8: 275-82.
- 12. Altschul SF, Madden TL, Schäffer AA. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res 1997; 25: 3389-402.

- 13. Huang Q, Yu L, Petros AM, et al. Structure of the N-terminal RNA-binding domain of the SARS CoV nucleocapsid protein. Biochemistry 2004; 43: 6059-63.
- 14. Guex N, Peitsch MC. SWISS-MODEL and the Swiss-Pdb Viewer: an environment for comparative protein modeling. Electrophoresis 1997; 18: 2714-23.
- Laskowski RA, MacArthur MW, Moss DS, et al. PROCHECK: a program to check the stereochemical quality of protein structures. J Appl Crystallogr 1993; 26: 283-91.
- 16. Ramachandran GN, Ramakrishnan C, Sasisekharan V. Stereochemistry of polypeptide chain configurations. J Mol Biol 1963; 7: 95-9.
- 17. Abdulazeez S, Sultana S, Almandi, NB, et al. The rs61742690 (S783N) single nucleotide polymorphism is a suitable target for disrupting BCL11A-mediated foetal-to-adult globin switching. PLoS One 2019; 14: e0212492.
- 18. Colovos C, Yeates TO. Verification of protein structures: patterns of nonbonded atomic interactions. Protein Sci 1993; 2: 1511-9.
- 19. Ouizougun-Oubari M, Pereira N, Tarus B, et al. A druggable pocket at the nucleocapsid/phosphoprotein interaction site of human respiratory syncytial virus. J Virol 2015; 89: 11129-43.
- 20. Galloux M, Tarus B, Blazevic I, et al. Characterization of a viral phosphoprotein binding site on the surface of the respiratory syncytial nucleoprotein. J Virol 2012; 86: 8375-87.
- 21. Tran TL, Castagne N, Bhella D, et al. The nine C-terminal amino acids of the respiratory syncytial virus protein P are necessary and sufficient for binding to ribonucleoprotein complexes in which six ribonucleotides are contacted per N protein protomer. J Gen Virol 2007; 88: 196-206.
- 22. Botta L, Rivara M, Zuliani V, et al. Drug repurposing approaches to fight Dengue virus infection and related diseases. Front Biosci Landmark 2018; 23: 997-1019.
- Benvenuto D, Giovannetti M, Ciccozzi A, et al. The 2019 new coronavirus epidemic: evidence for virus evolution. J Med Virol 2020. https://doi.org/10.1002/jmv.25688.
- 24. Chemical Computing Group ULC .Molecular Operating Environment (MOE) 09. 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2017.
- 25. Hui DS, I Azhar E, Madani TA, et al. The continuing 2019nCoV epidemic threat of novel coronaviruses to global health – the latest 2019 novel coronavirus outbreak in Wuhan, China. Int J Infect Dis 2020; 91: 264-6.
- Wang C, Horby PW, Hayden FG, et al. A novel coronavirus outbreak of global health concern. Lancet 2020; 395: 470-3.
- Surjit M, Kumar R, Mishra RN, et al. The severe acute respiratory syndrome coronavirus nucleocapsid protein is phosphorylated and localizes in the cytoplasm by 14-3-3-mediated translocation. J Virol 2005; 79: 11476-86.
- 28. McBride R, Van Zyl M, Fielding BC. The coronavirus nucleocapsid is a multifunctional protein. Viruses 2014; 6: 2991-3018.
- 29. Chang CK, Hou MH, Chang CF, et al. The SARS coronavirus nucleocapsid protein – forms and functions. Antiviral Res 2014; 103: 39-50.
- 30. Cong Y, Ulasli M, Schepers H, Mauthe M. Nucleocapsid protein recruitment to replication-transcription complexes plays a crucial role in coronaviral life cycle. J Virol 2020; 94: e01925-19.
- Sungsuwan S, Jongkaewwattana A, Jaru-Ampornpan P. Nucleocapsid proteins from other swine enteric coronaviruses differentially modulate PEDV replication. Virology 2020; 540: 45-56.

- Boscarino JA, Logan HL, Lacny JJ, et al. Envelope protein palmitoylations are crucial for murine coronavirus assembly. J Virol 2008; 82: 2989-99.
- 33. Stodola JK, Dubois G, Le Coupanec A et al. The OC43 human coronavirus envelope protein is critical for infectious virus production and propagation in neuronal cells and is a determinant of neurovirulence and CNS pathology. Virology 2018; 515: 134-49.
- 34. Schoeman D, Fielding BC. Coronavirus envelope protein: current knowledge. Virol J 2019; 16: 69.
- 35. Westerbeck JW, Machamer CE. The infectious bronchitis coronavirus envelope protein alters Golgi pH to protect the spike protein and promote the release of infectious virus. J Virol 2019; 93: e00015-19.
- 36. World Health OrganizationWHO, 2019. Clinical management of severe acute respiratory infection when Middle East respiratory syndrome coronavirus (MERS-CoV) infection is suspected: interim guidance (No. WHO/MERS/ Clinical/15.1 Revision 1). World Health Organization.