# Spike proteins of SARS-CoV and SARS-CoV-2 utilize different mechanisms to bind with human ACE2

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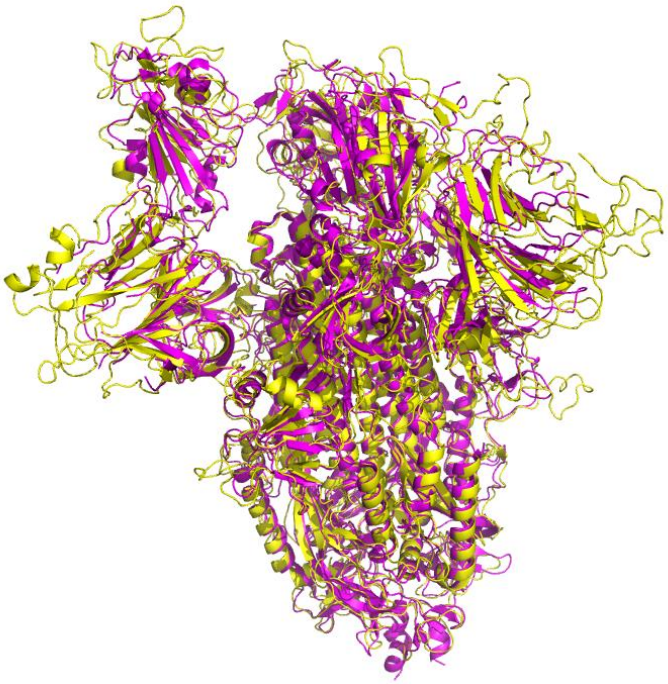

**Figure S1**. The structural comparison of modeled SARS-COV-2 and its template (6ACG). The template structure is shown in magenta, and the modeled structure is shown in yellow.

```
SARS_CoV        MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL 60
SARS_CoV-2      ------------------CVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFL 42
                                  *..:        :  .*  *******::***..*: ******

SARS_CoV        PFYSNVTGFHTIN-------HTFGNPVIPFKDGIYFAATEKSNVVRGWVFGSTMNNKSQS 113
SARS_CoV-2      PFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQS 102
                **:**** **:*:       : *.***:**:**:***:*****::***:**:*::.*:**

SARS_CoV        VIIINNSTNVVIRACNFELCDNPFFAVSKPMGT----QTHTMIFDNAFNCTFEYISDAFS 169
SARS_CoV-2      LLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFL 162
                ::*:**:*****:.*:*::*::**:.*    ..    ::.  ::..* ******:*: *

SARS_CoV        LDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIFKLPLGINIT 229
SARS_CoV-2      MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINIT 222
                :*:. *.****:******** **:: :*. : **::*****.**.:*:*:..**:*****

SARS_CoV        NFRAILTAFS------PAQDIWGTSAAAYFVGYLKPTTFMLKYDENGTITDAVDCSQNPL 283
SARS_CoV-2      RFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCALDPL 282
                .*:::*: .        :.. * :.****:****:* **:***:***********: :**

SARS_CoV        AELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERK 343
SARS_CoV-2      SETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRK 342
                :* **::*** ::*********** *: .:*******************:* *****:**

SARS_CoV        KISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG 403
SARS_CoV-2      RISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTG 402
                :***************: ********** ********:********::**:**********

SARS_CoV        VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPD 463
SARS_CoV-2      KIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG 462
                 ************ ***:***:.*:*:.  ***** ** :*:.:*:*******.  :. .

SARS_CoV        GKPCTP-PALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKN 522
SARS_CoV-2      STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKN 522
                ..**.   .:***:**:.***  *.*:****************:********* **:*:**

SARS_CoV        QCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVS 582
SARS_CoV-2      KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS 582
                :**************** *.*:* *******::* **:****:* *****:********

SARS_CoV        VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV 642
SARS_CoV-2      VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV 642
                *******:*.:***********:* .*********:**:****.*****:**********

SARS_CoV        DTSYECDIPIGAGICASYHTVSL----LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT 698
SARS_CoV-2      NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT 702
                :.****************:* :      **.:.:**:********:.*:*****:*****

SARS_CoV        NFSISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDR 758
SARS_CoV-2      NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK 762
                **:**:***::****:******.**********:******************:***.***:

SARS_CoV        NTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQ 818
SARS_CoV-2      NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ 822
                **:********:**** :* ************* **:********************:**

SARS_CoV        YGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQI 878
SARS_CoV-2      YGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQI 882
                **:***** **********************:*** **:**::** *:************

SARS_CoV        PFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNA 938
SARS_CoV-2      PFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNA 942
                ************************* ******.**.:**:**::*::*************

SARS_CoV        QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA 998
SARS_CoV-2      QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
      1002
                ************************************************************

SARS_CoV        EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFT 1058
SARS_CoV-2      EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFT 1062
                ***************************************:**************:**:***

SARS_CoV        TAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT 1118
SARS_CoV-2      TAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNT 1122
                *******:***:******** *** **:*****:.*********************:***

SARS_CoV        VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES 1178
SARS_CoV-2      V------------------------------------------------------------ 1123
                *

SARS_CoV        LIDLQELGKYEQYIKWPWSHPQFEK 1203
SARS_CoV-2      ------------------------- 1123
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**Figure S2.** Genome sequence alignment of SARS-CoV and SARS-CoV-2 S protein RBDs

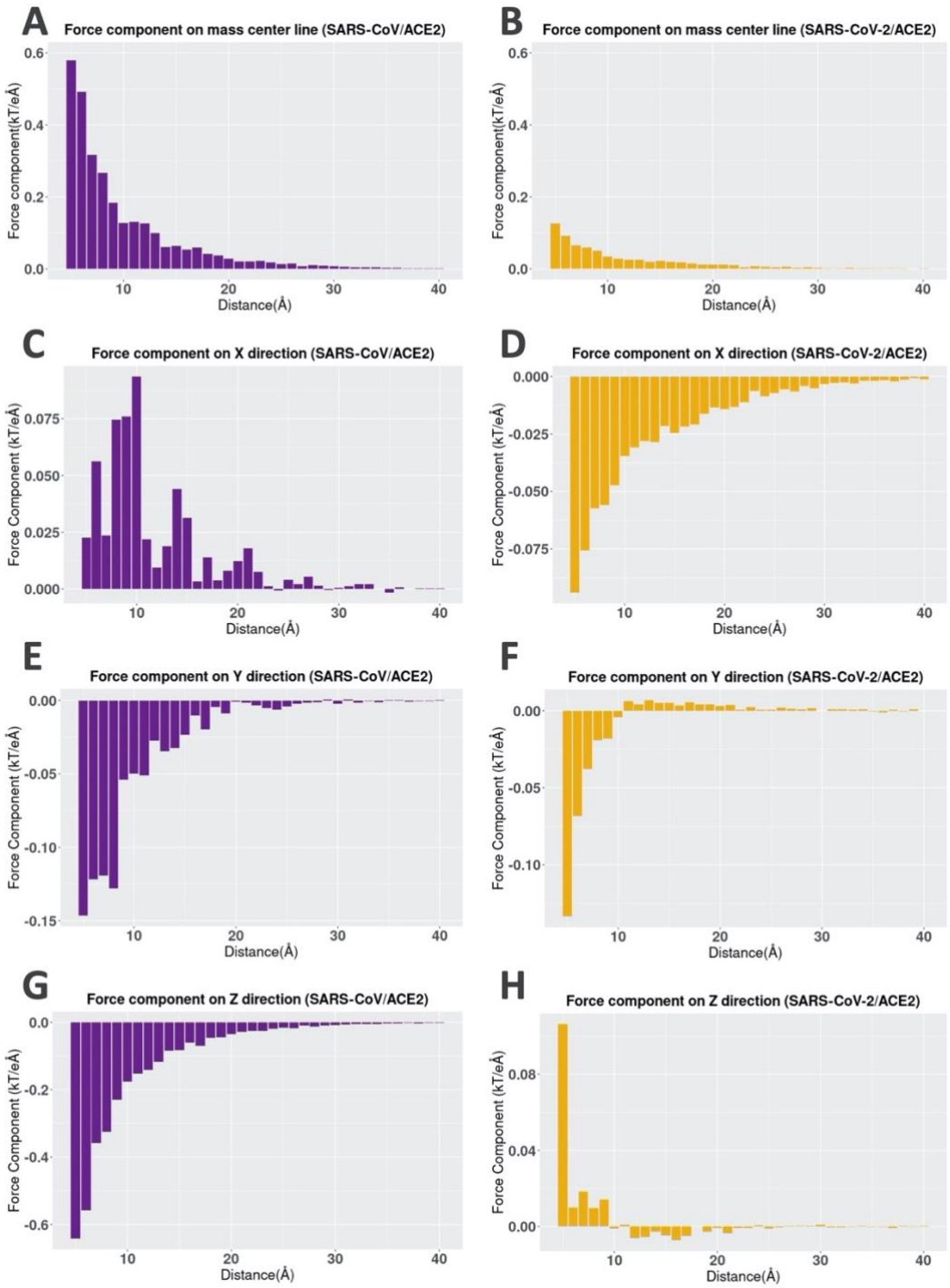


**Figure S3.** The binding force components on different directions.

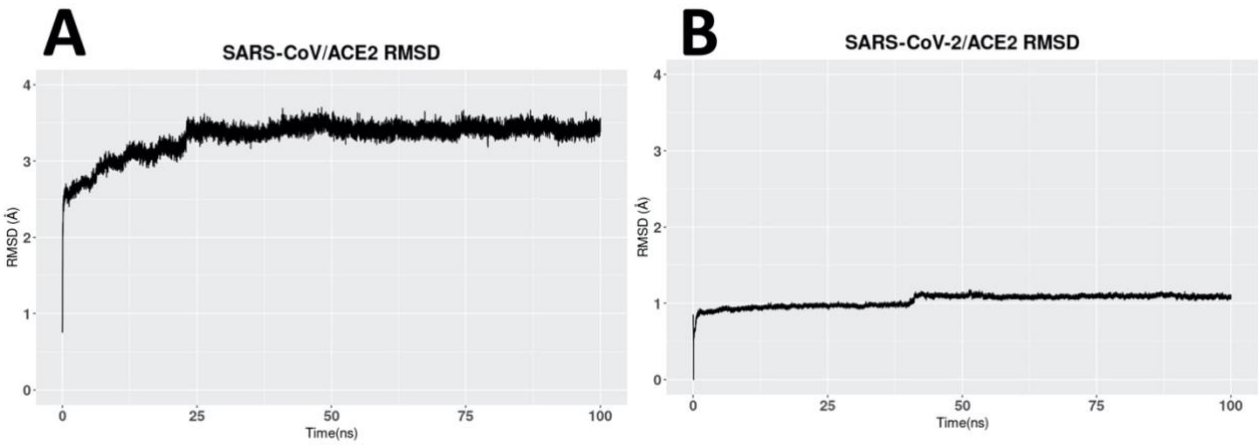


**Figure S4.** RMSD comparison of SARS-CoV/ACE2 and SARS-CoV-2/ACE2 complex structure

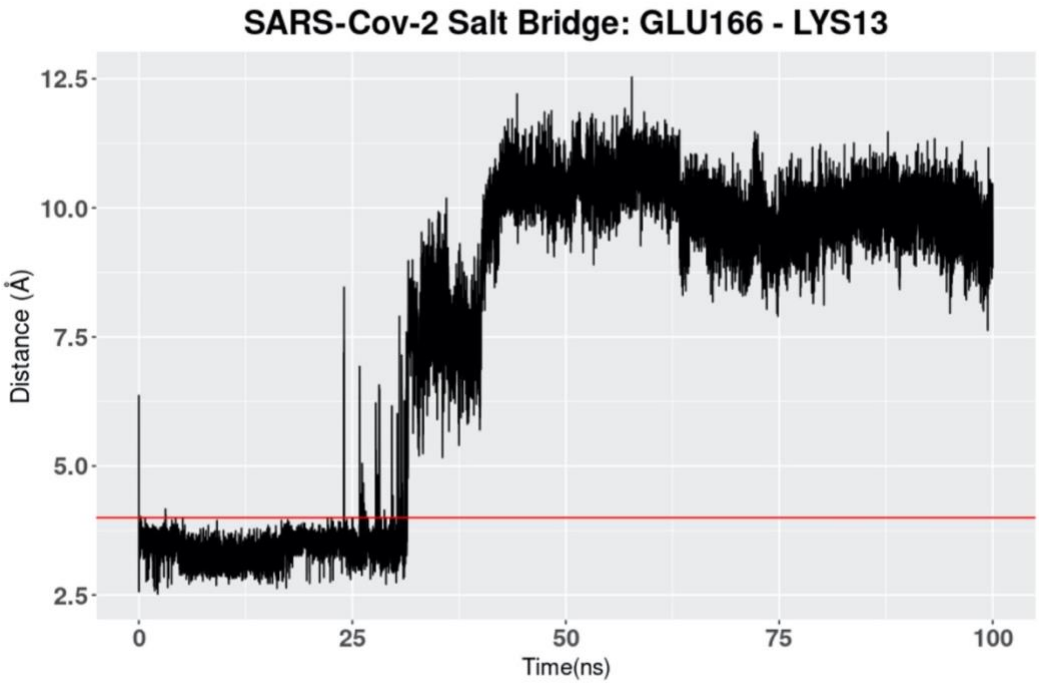


**Figure S5.** A special salt bridge in SARS-CoV-2 RBD

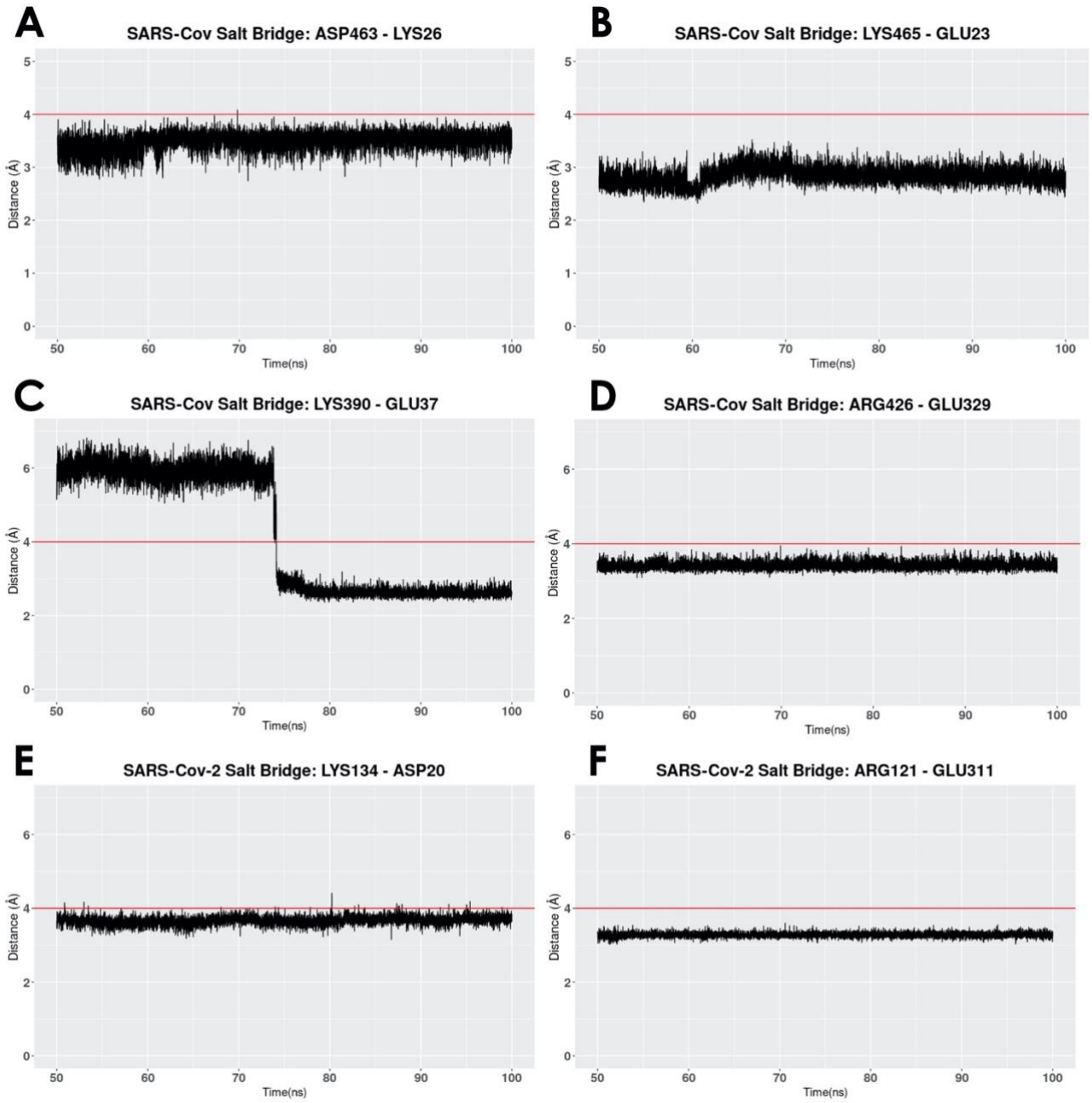


**Figure S6.** Key residues forming salt bridges at interfaces of S protein RBDs and ACE2 protein binding domain. Red line is the cutoff value of 4 Å which is chosen when calculating the salt bridge. (A) Distance of the ASP463 – LYS26 salt bridge found on the interface of SARS-CoV and ACE2; (B) Distance of the GLU23 – LYS465 salt bridge found on the interface of SARS-CoV and ACE2, (C) Distance of the GLU37 – LYS390 salt bridges found on the interface of SARS-CoV and ACE2; (D) Distance of the GLU329 – ARG426 salt bridges found on the interface of SARS-CoV and ACE2; (E) Distance of the ASP20 - LYS134 salt bridge found on the interface of SARS-CoV-2 and

ACE2; (F) Distance of the GLU311 – ARG121 salt bridges found on the interface of SARS-CoV-2 and ACE2.

**Movies:**

Movie1: SARS-CoV simulation (100ns)

Movie2: SARS-CoV-2 simulation (100ns)

Movie3: ACE2 electrostatic surface

Movie4: SARS electrostatic surface

Movie5: SARS2 electrostatic surface