Research Article

# Reveal the molecular principle of coronavirus disease 2019 (COVID-19)

Lin Fang1, Xinlei Wang4, Zhongyuan Lai1,2, Dongdong Zhang1, Mengqu Wu1, Zhirui Pan1, Li Wang1, Kun Tang1, Dahong Qian1,3, Zhende Huang1,3, Xudong Wang1*, Haibo Chen4*, and Kuo-Chen Chou

1Deepblue Academy of Sciences, Deepblue Technology (Shanghai) Co., Ltd, 369 Weining Rd, Shanghai 200050, China.
2Department of Physics, Fudan University, Shanghai 200433, China.
3School of Biomedical Engineering, Shanghai Jiao Tong University, Shanghai 200240, China.
4Deepblue Technology (Shanghai) Co., Ltd, 369 Weining Rd, Shanghai 200050, China.

***Corresponding Author: Dr. Kuo-Chen Chou** *, 4Gordonlife Science Institute, Boston. MA 02418, USA

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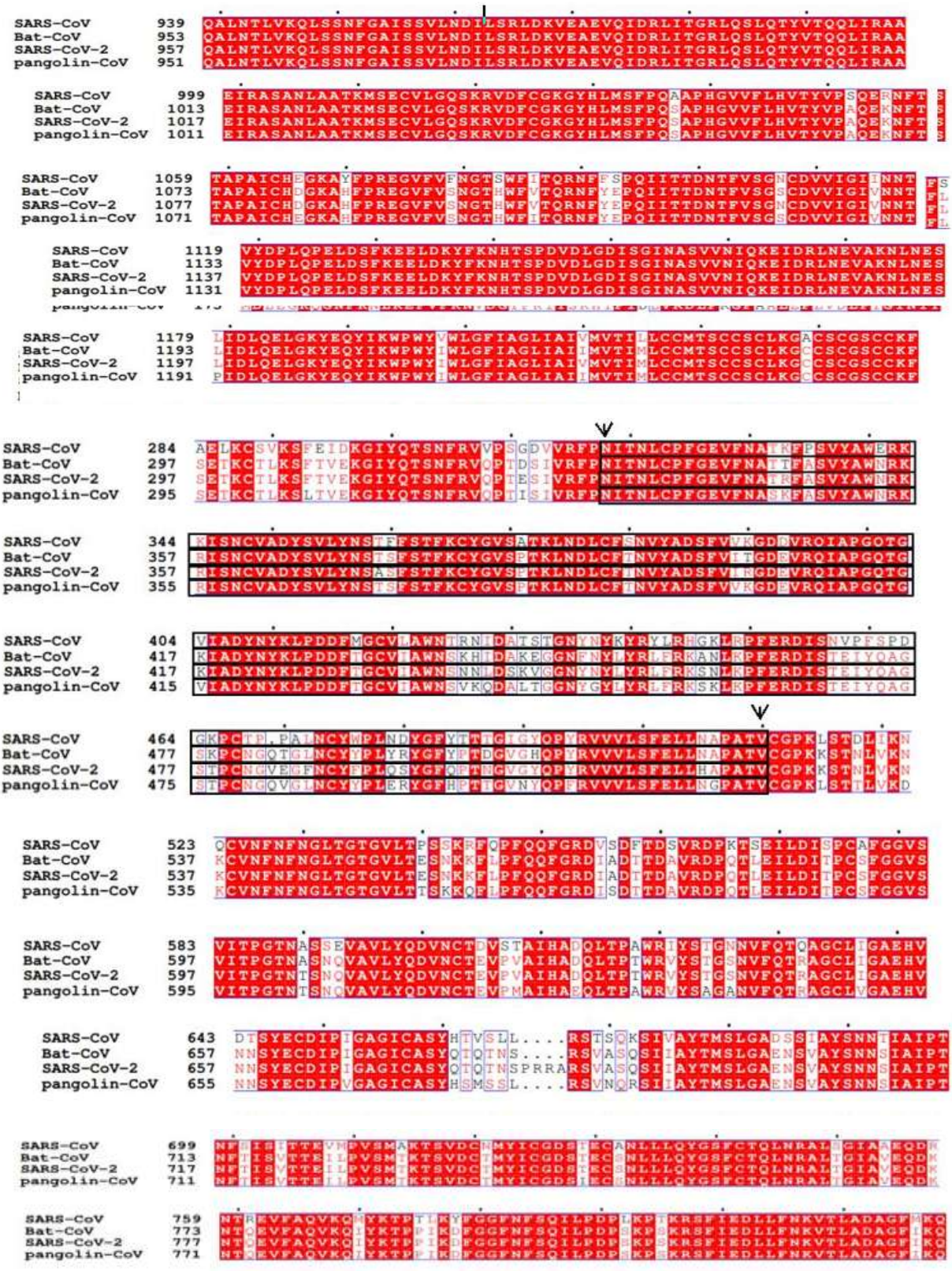
**Figure 1:** The Alignment of the Amino Acid Sequences of the S Proteins from 4 Coronaviruses and The Phylogenetic Tree of the Genes of the Receptor Binding proteins from 8 Different Single Strand RNA Viruses with the MEGA software.

Top: The Alignment of the Amino Acid Sequences of the S Proteins from 4 coronaviruses, namely Bat Coronavirus RaTG13, Pangolin CoV(GX), SARS-CoV (NC_004718) and SARS-CoV-2 (NC_045512). Receptor Binding Domain (RBD) are labeled with the color boxes and the black arrows indicate the beginning and the end of RBD.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Bat-CoV 953 QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
SARS-CoV-2 957 QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
pangolin-CoV 951 QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
SARS-CoV 999 EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPSQERNFTT
Bat-CoV 1013 EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTS
SARS-CoV-2 1017 EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTS
pangolin-CoV 1011 EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQEKNFTS
SARS-CoV 1059 TAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNT
Bat-CoV 1073 TAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGSCDVVIGIVNNT
SARS-CoV-2 1077 TAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNT
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SARS-CoV 1119 VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES
Bat-CoV 1133 VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES
SARS-CoV-2 1137 VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES
pangolin-CoV 1131 VYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES
SARS-CoV 1179 LIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKF
Bat-CoV 1193 LIDLQELGKYEQYIKWPWYIWLGFIAGLIAIIMVTIMLCCMTSCCSCLKGCCSCGSCCKF
SARS-CoV-2 1197 LIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKF
pangolin-CoV 1191 PIDLQELGKYEQYIKWPWYIWLGFIAGLIAIIMVTIMLCCMTSCCSCLKGCCSCGSCCKF
SARS-CoV 284 AELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERK
Bat-CoV 297 SETKCTLKSFTVEKGIYQTSNFRVQPTDSIVRFPNITNLCPFGEVFNATTFASVYAWNRK
SARS-CoV-2 297 SETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRK
pangolin-CoV 295 SETKCTLKSLTVEKGIYQTSNFRVQPTISIVRFPNITNLCPFGEVFNASKFASVYAWNRK
SARS-CoV 344 KISNCVADYSVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG
Bat-CoV 357 RISNCVADYSVLYNSTSFSTFKCYGVSPTKLNDLCFTNVYADSFVIKGDEVRQIAPGQTG
SARS-CoV-2 357 KISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIKGDEVRQIAPGQTG
pangolin-CoV 355 RISNCVADYSVLYNSTSFSTFKCYGVSPTKLNDLCFTNVYADSFVVKGDEVRQIAPGQTG
SARS-CoV 404 VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPD
Bat-CoV 417 KIADYNYKLPDDFTGCVIAWNSKHIDAKEGGNFNYLYRLFRKANLKPFERDISTEIYQAG
SARS-CoV-2 417 KIADYNYKLPDDFTGCVIAWNSNNIDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG
pangolin-CoV 415 VIADYNYKLPDDFTGCVIAWNSVKQDALTGGNYGYLYRLFRKSKLKPFERDISTEIYQAG
SARS-CoV 464 GKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKN
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SARS-CoV-2 477 STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKN
pangolin-CoV 475 STPCNGQVGLNCYYPLERYGFHPTTGVNYQPFRVVVLSFELLNGPATVCGPKLSTTLVKD
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Bat-CoV 537 KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS
SARS-CoV-2 537 KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS
pangolin-CoV 535 KCVNFNFNGLTGTGVLTTSKKQFLPFQQFGRDISDTTDAVRDPQTLEILDITPCSFGGVS
SARS-CoV 583 VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV
Bat-CoV 597 VITPGTNASNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
SARS-CoV-2 597 VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
pangolin-CoV 595 VITPGTNTSNQVAVLYQDVNCTEVPMAIHAPQLTPAWRVYSAGANVFQTRAGCLVGAEHV
SARS-CoV 643 DTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT
Bat-CoV 657 NNSYECDIPIGAGICASYQTQTNSRSVASQSIIAYTMSLGAENSVAYSNNSIAIPT
SARS-CoV-2 657 NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT
pangolin-CoV 655 NNSYECDIPVGAGICASYHSMSSLRSVNQRSIIAYTMSLGAENSVAYSNNSIAIPT
SARS-CoV 699 NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
Bat-CoV 713 NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
SARS-CoV-2 717 NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
pangolin-CoV 711 NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
SARS-CoV 759 NTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQ
Bat-CoV 773 NTSEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ
SARS-CoV-2 777 NTSEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ
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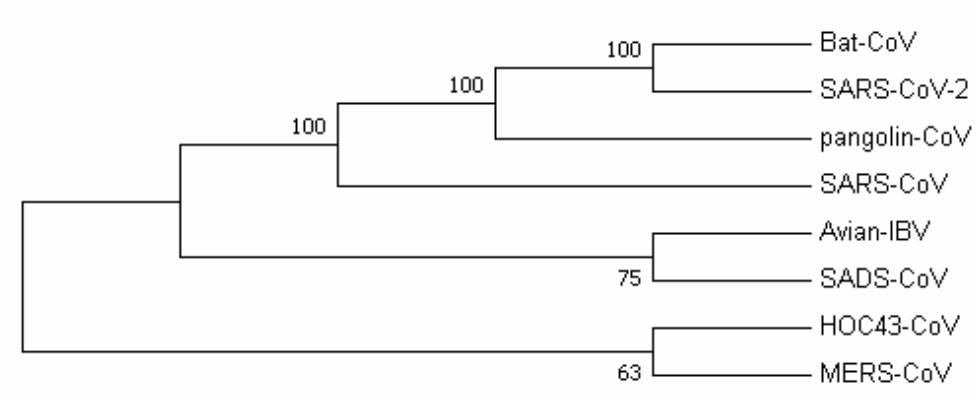
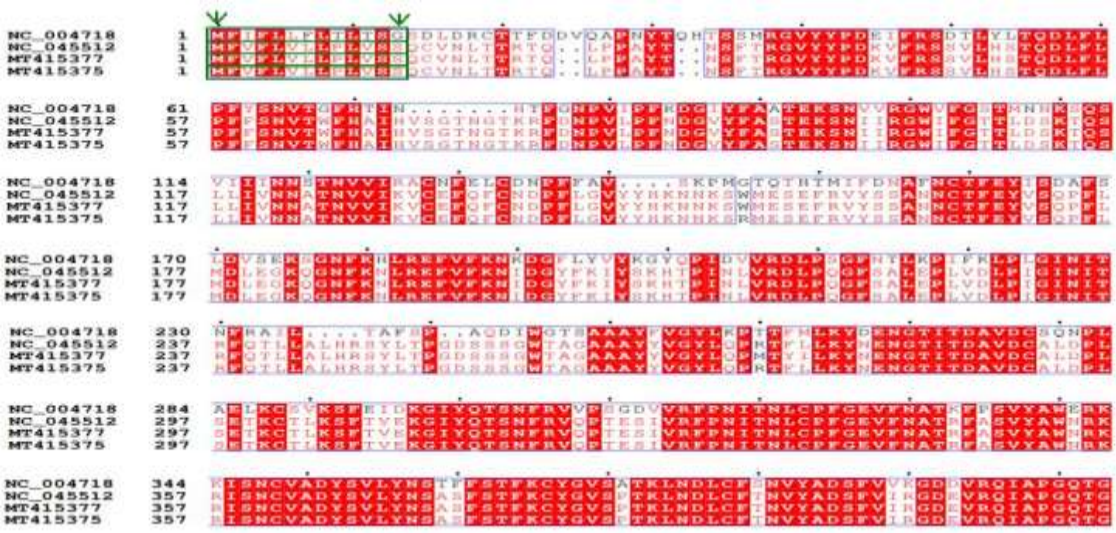
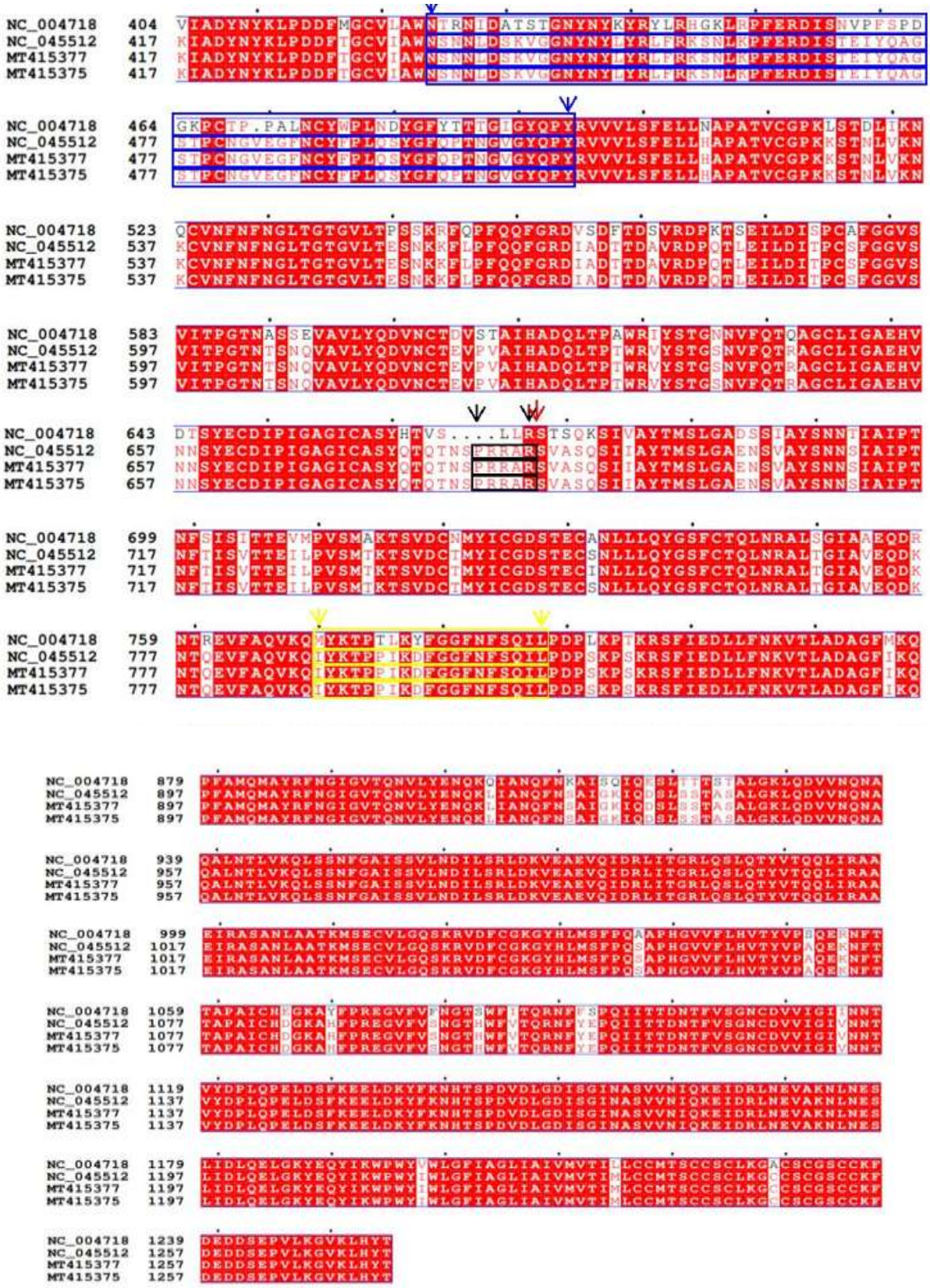



**Figure 2:**

The Alignment of the Spike（S）Protein of 3 strains of SARS-CoV-2 and 1 Strain of SARS-CoV (NC_004718.3), SARS-CoV-2（NC_045512）, MT415375 and MT415377. Important functional regions, such as the signal peptide (SP), Receptor Binding Motif (RBM), Fusion Peptide (FP) and the inserted amino acid (amino acids PRRA)/host protease recognition site and cleavage site (amino acids RRAR)/cleavage site (between amino acids 685R and 686S) have been marked on the CA pictures.

SP: green Box (the green arrows showing the beginning and end of the SP); RBM: blue box (the blue arrows showing the beginning and end of the RBM); PRRAR: black box (the black arrows showing the beginning and end of the inserted/host protease recognition amino acid sites; the red arrow showing the host protease cleavage site between amino acids 685R and 686S) （T. Meng, et al.）; FP: yellow box.

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MT415375 417 KIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAG
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NC_045512 537 KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS
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MT415375 537 KCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS
NC_004718 583 VITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHV
NC_045512 597 VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
MT415377 597 VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
MT415375 597 VITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHV
NC_004718 643 DTSYECDIPIGAGICASYHTVS....LLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT
NC_045512 657 NNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT
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NC_045512 717 NFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDK
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MT415375 777 NTQEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQ
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NC_004718 1239 DEDDSEPVLKGVKLHYT
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MT415377 1257 DEDDSEPVLKGVKLHYT
MT415375 1257 DEDDSEPVLKGVKLHYT

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