

Table SI. Multiple alignment using ExPASy. Alignment score, identity and similarity of RNA polymerase DNA sequences of COVID-19 RdRp (GenBank accession no. MT042778.1), SARS RNA polymerase (GenBank accession no. AY340092.1), influenza A PB1 (GenBank accession no. AJ620348.2), hepatitis C NS5B (GenBank accession no. AJ608785.1), calcivirus RNA polymerase (GenBank accession no. Y13703.1) and T7 bacteriophage RNA-polymerase (GenBank accession no. M38308.1).

Sequences	Alignment core	Identity	Similarity
1:2	0.88	0.81	0.84
1:3	0.39	0.54	0.54
1:4	0.39	0.46	0.56
1:5	0.38	0.57	0.57
1:6	0.39	0.53	0.53
2:3	0.37	0.47	0.51
2:4	0.38	0.47	0.49
2:5	0.37	0.50	0.51
2:6	0.39	0.51	0.51
3:4	0.37	0.47	0.51
3:5	0.38	0.47	0.50
3:6	0.19	0.49	0.49
4:5	0.36	0.52	0.52
4:6	0.37	0.52	0.52
5:6	0.40	0.52	0.52

Sequence 1, COVID-19\_294 bp; Sequence 2, SARS\_368 bp; Sequence 3, Influenza A\_2336 bp; Sequence 4, HCV\_384 bp; COVID-19, coronavirus disease 2019; SARS, severe acute respiratory syndrome.

Table SII. Multiple alignment using ExPASy. Alignment score, identity and similarity of RNA polymerase amino acid sequences of COVID-19 nsp 12 (GenBank accession no. YP\_009725307.1), SARS rep (UniProtKB accession no. R1AB\_CVHSA), influenza A PB1 (GenBank accession no. AAK18013.1) and T7 bacteriophage PHA (PDB accession no. 4RNP\_C).

Sequences	Alignment score	Identity	Similarity
1:2	0.96	0.96	0.99
1:3	0.10	0.62	0.67
1:4	0.90	0.38	0.67
2:3	0.11	0.20	0.52
2:4	0.11	0.25	0.54
3:4	0.95	0.18	0.65

Sequence 1, COVID-19\_ 932 aa; Sequence 2, SARS\_ 7073 aa; Sequence 3, Influenza \_757 aa; Sequence 4, T7\_ 883 aa; COVID-19, coronavirus disease 2019; SARS, severe acute respiratory syndrome.

Table SIII. Multiple 3C-like protease DNA sequence alignment using ExPASy. Alignment score, identity and similarity of COVID-19 nsp5A\_3CLpro and nsp5B\_3CLpro (NCBI Reference Sequence accession no. YP\_009742612.1), SARS Peptidase\_C30 (PDB accession no. 3F9G\_A), YHV Peptidase\_C62 (GenBank accession no. ABL96309.1), black queen cell virus 3C-like protease (GenBank accession no. AIW60925.1) and European brown hare syndrome virus (NCBI Reference Sequence accession no NP\_786901.1).

Sequences	Alignment score	Identity	Similarity
1:2	0.82	0.81	0.83
1:3	0.10	0.15	0.17
1:4	0.41	0.34	0.41
1:5	0.60	0.24	0.26
2:3	0.30	0.36	0.42
2:4	0.42	0.42	0.46
2:5	0.05	0.24	0.35
3:4	0.02	0.31	0.37
3:5	0.03	0.28	0.34
4:5	0.04	0.37	0.43

Sequence 1, SARS\_948 bp; Sequence 2, COVID-19\_29903 bp; Sequence 3, YHV\_1005 bp; Sequence 4, IBV\_921 bp; Sequence 5, KM232906.1\_535 bp; COVID-19, coronavirus disease 2019; SARS, severe acute respiratory syndrome; YHV, yellow head virus.

Table SIV. Multiple 3C-like protease amino acid sequence alignment using ExPASy. Alignment score, identity and similarity of COVID-19 nsp5A\_3CLpro and nsp5B\_3CLpro (NCBI Reference Sequence accession no. YP\_009742612.1), SARS Peptidase\_C30 (PDB accession no. 3F9G\_A), YHV Peptidase\_C62 (GenBank accession no. ABL96309.1), black queen cell virus 3C-like protease (GenBank accession no. AIW60925.1) and European brown hare syndrome virus (NCBI Reference Sequence accession no. NP\_786901.1).

Sequences	Alignment score	Identity	Similarity
1:2	0.95	0.96	0.96
1:3	0.12	0.24	0.25
1:4	0.08	0.34	0.41
1:5	0.13	0.24	0.26
2:3	0.12	0.36	0.42
2:4	0.11	0.42	0.46
2:5	0.08	0.24	0.35
3:4	0.07	0.31	0.37
3:5	0.07	0.28	0.34
4:5	0.15	0.37	0.43

Sequence 1, COVID-2\_306 aa; Sequence 2, SARS\_303 aa; Sequence 3, YHV\_343 aa; Sequence 4, BQV\_178 aa; Sequence 5, EBHV\_143 aa; COVID-19, coronavirus disease 2019; SARS, severe acute respiratory syndrome; YHV, yellow head virus.