

✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/CA-CZB-EX00709/2020_complete genome	39316	39316	100%	0.0	100.00%	MT385458.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/USA/CA-CZB-000095/2020_complete genome	39316	39316	100%	0.0	100.00%	MT385430.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/Wuhan_ILME-BJ05/2020_complete genome	39316	39316	100%	0.0	100.00%	MT291835.2
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/HKG/HKU-902a/2020_complete genome	39316	39316	100%	0.0	100.00%	MT114413.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/HKG/HKU-902a/2020_complete genome	39316	39316	100%	0.0	100.00%	MT114412.1
✓	Synthetic construct ORF1ab_spike_ORF3_E_M_ORF6_ORF8_and_N_genes_complete cds	39316	39316	100%	0.0	100.00%	MT108784.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/IME-HZ01/2020_complete genome	39316	39316	100%	0.0	100.00%	MT039874.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/Wuhan_ILME-WH05/2019_complete genome	39316	39316	100%	0.0	100.00%	MT291830.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/Wuhan_ILME-WH04/2019_complete genome	39316	39316	100%	0.0	100.00%	MT291829.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/Wuhan_ILME-WH03/2019_complete genome	39316	39316	100%	0.0	100.00%	MT291828.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/Wuhan_ILME-WH02/2019_complete genome	39316	39316	100%	0.0	100.00%	MT291827.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/HZ-162/2020_complete genome	39316	39316	100%	0.0	100.00%	MT253699.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate nCoV-FIN-29-Jan-2020_complete genome	39316	39316	100%	0.0	100.00%	MT020781.2
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/TWN/COMH-CGU-01/2020_complete genome	39316	39316	100%	0.0	100.00%	MT192759.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/CHN/WH-09/2020_complete genome	39316	39316	100%	0.0	100.00%	MT093631.2
✓	Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CruiseA-2/2020_complete genome	39316	39316	100%	0.0	100.00%	MT159718.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CruiseA-9/2020_complete genome	39316	39316	100%	0.0	100.00%	MT159719.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CruiseA-12/2020_complete genome	39316	39316	100%	0.0	100.00%	MT159709.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV/USA-CAB/2020_complete genome	39316	39316	100%	0.0	100.00%	MT106053.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/NPI_81-TW/2020_complete genome	39316	39316	100%	0.0	100.00%	MT072688.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate HZ-1_complete genome	39316	39316	100%	0.0	100.00%	MT039873.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/PI/CAMS-WH-04/2019_complete genome	39316	39316	100%	0.0	100.00%	MT019532.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/PI/CAMS-WH-02/2019_complete genome	39316	39316	100%	0.0	100.00%	MT019530.1
✓	Wuhan seafood market pneumonia virus, genome assembly_chromosome_whole_genome	39316	39316	100%	0.0	100.00%	LR757995.1
✓	Severe acute respiratory syndrome coronavirus 2 isolate HCoV-229E_complete genome	39316	39316	100%	0.0	100.00%	MN095530.1

Fig. 2.2 BLAST analysis of ORF1ab polyprotein coding gene

266–21555 bp). The gene sequences of Surface Glycoprotein (S), Nucleocapsid Protein (N), ORF3a polyprotein, Membrane Glycoprotein (M), Envelope Protein (E), ORF6, ORF7a, ORF8 and ORF10 were the other sequences to be analyzed (Fig. 2.2).

Inference: From the above BLAST analysis of ORF1AB polyprotein gene sequence it can be inferred that all the organisms that belong to SARS Corona Virus 2 family share completely identical sequence for this gene. Thus ORF1AB is conserved evolutionarily and might not be the reason for the variations among the isolates.

A similar comparison was performed for the genes coding for **Surface Glycoprotein S, Nucleocapsid Protein N, ORF3a polyprotein, Membrane Glycoprotein M, Envelope Protein E, ORF6, ORF7a, ORF8 and ORF10**. It was revealed that all these sequences are completely conserved and do not have any variable regions within the SARS corona 2 family. The above analysis related to the conservation study of the SARS Corona virus 2 reveals that all these 10 important genes share 99 to 100% sequence identity to the other SARS Corona Virus 2 family isolates. Thus there are no regions which are variable and are not the reason for evolution of any novel strain.