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Letter of confirmation

Date: 29th Nov, 2021

To whom it may concern

Recently SARS-CoV-2 variant with multiple spike protein mutations has been observed in the various countries. (United Kingdom, South Africa, Brazil, India, Peru and ETC.)

According to WHO, the new strain of SARS-CoV-2 was found to affect the performance of some diagnostic assays with an S gene target.

Using the gene sequence published through GISAID [1] and the strain sequence used in the development stage, GCMS R&D team internally analyzed the reactivity of the GENEDIA W COVID-19 and the new strains of SARS-CoV-2 (Lineage B.1.117, Lineage B.1.351, Lineage P.1, Lineage B.1.617, Lineage B.1.617.1, Lineage B.1.617.2, Lineage B.1.617.3, Lineage B.1.618, Lineage C.37, Lineage AY.1, B.1.621, B.1.621.1 and B.1.1.529) through in-silico analysis.

In addition, it was confirmed that the in-silico analysis and the in-vitro experimental results were consistent with the Green Cross Medical Science's kit by securing the recombinant protein, heat-inactivated virus and cultured SARS-CoV-2 viruses.

1.1 Methods

The antigen used in the development of this product is ATCC VR-1986HK(NCBI Accession No: MN985325.1) and sequence alignment was performed based on this sequence.

Four SARS-CoV-2 variants sequence are obtained via GISAID.

Sequence of lineage B.1.1.7(GISAID accession ID: EPI_ISL_601443, British variant), lineage B.1.351(GISAID accession ID: EPI_ISL_678597, South African variant), lineage P.1(GISAID accession ID: EPI_ISL_792680, Brazil variant), lineage B.1.617(GISAID accession ID: EPI_ISL_1595896, India variant), lineage B.1.617.1(GISAID accession ID: EPI_ISL_2533592, India variant), lineage B.1.617.2(GISAID accession ID: EPI_ISL_1419152, India variant), lineage B.1.617.3(GISAID accession ID: EPI_ISL_2508617, India variant), lineage B.1.617.4(GISAID accession ID: EPI_ISL_2503243, India variant), lineage C.37(GISAID accession ID: EPI_ISL_1111285, Lambda variant) and lineage AY.1(GISAID accession ID: EPI_ISL_2552218, Delta plus variant), lineage B.1.621(GISAID accession ID: EPI_ISL_1582981, Mu variant 1), lineage B.1.621.1(GISAID accession ID: EPI_ISL_1820954, Mu variant 2 and lineage B.1.1.529(GISAID accession ID: EPI_ISL_6825395, Omicron variant) are analyze with corresponding sequence(MN985325.1). The sequence analysis was performed in two ways, entire sequence alignment and nucleocapsid protein sequence alignment (28,274-29,533 bp).

The study was conducted in-silico analysis using the basic local alignment search tool (BLAST) function of NCBI webpage [2]. The BLAST is an algorithm and program for comparing primary biological sequence information. This program search enables a researcher to compare a subject sequence with an object sequence, and calculate similarity.

In addition, heat-inactivated virus and the cultured virus(Cultured) were obtained through

Zeptomatrix Corp.(USA) and National Culture Collection for Pathogens(KOREA) and recombinant antigen was purchased, and it was decided to add to the effectiveness of the in-silico analysis through in-vitro experiments using this specimen.

1.2 In-silico analysis results

Division	Accession No	Region	Similarity	Conclusion
Lineage B.1.1.7 (British variant)	GISAID accession ID: EPI_ISL_601443	Whole sequence	99.83 %	Conformity
		Nucleocapsid protein	99.66 %	
Lineage B.1.351 (South African variant)	GISAID accession ID: EPI_ISL_678597	Whole sequence	99.86 %	Conformity
		Nucleocapsid protein	99.92 %	
Lineage P.1 (Brazil variant)	GISAID accession ID: EPI_ISL_792680	Whole sequence	99.84 %	Conformity
		Nucleocapsid protein	99.49 %	
Lineage B.1.617 (India variant)	EPI_ISL_1595896	Whole sequence	99.87 %	Conformity
		Nucleocapsid protein	99.75 %	
Lineage B.1.617.1 (India variant)	GISAID accession ID: EPI_ISL_2533592	Whole sequence	93.40 %	Conformity
		Nucleocapsid protein	98.39 %	
Lineage B.1.617.2 (India variant)	GISAID accession ID: EPI_ISL_1419152	Whole sequence	99.92 %	Conformity
		Nucleocapsid protein	99.66 %	
Lineage B.1.617.3 (India variant)	GISAID accession ID: EPI_ISL_2508617	Whole sequence	99.88 %	Conformity
		Nucleocapsid protein	99.75 %	
Lineage B.1.618 (India variant)	GISAID accession ID: EPI_ISL_2503243	Whole sequence	99.92 %	Conformity
		Nucleocapsid protein	96.92 %	
Lineage C.37 (Lambda variant)	GISAID accession ID: EPI_ISL_1111285	Whole sequence	99.89 %	Conformity
		Nucleocapsid protein	99.44 %	
Lineage AY.1 (Delta plus variant)	GISAID accession ID: EPI_ISL_2552218	Whole sequence	99.82 %	Conformity
		Nucleocapsid protein	99.58 %	

Lineage B.1.621 (Mu variant 1)	GISAID accession ID: EPI_ISL_1582981	Whole sequence	99.72 %	Conformity
		Nucleocapsid protein	99.83 %	
Lineage B.1.621.1 (Mu variant 2)	GISAID accession ID: EPI_ISL_1820954	Whole sequence	99.93 %	Conformity
		Nucleocapsid protein	99.92 %	
Lineage B.1.1.529 (Omicron variant)	GISAID accession ID: EPI_ISL_6825395	Whole sequence	99.66 %	Conformity
		Nucleocapsid protein	99.01 %	

1.3 In-vitro experimental results (Recombinant Ag)

Division	N protein mutation site	Kit test result
British variant (B.1.1.7)	D3L, R203K, G204R, S235F	Reactive
South African variant (B.1.351)	T205I	Reactive
Brazil variant (P.1)	P80R, R203K, G204R	Reactive
India variant (B.1.617)	R203K, D377Y	Reactive
India variant (B.1.617.1)	R203M, D377Y	Reactive
India variant (B.1.617.2)	D63G, D377Y, R203M	Reactive
India variant (B.1.617.3)	P67S, D377Y, R203M	Reactive
India variant (B.1.618)	G18S, A119S, A217S, M234I, E367Q	Reactive
Lineage C.37 (Lambda variant)	G204R, G214C, P13L, R203K, T366I	Not-Tested
Lineage AY.1 (Delta plus variant)	A252S, D63G, D377Y, G215C, R203M	Not-Tested
Lineage B.1.621 (Mu variant 1)	T205I	Not-Tested
Lineage B.1.621.1 (Mu variant 2)	T205I	Not-Tested
Lineage B.1.1.529 (Omicron variant)	N E31del, N G204R, N P13L, N R32del, N R203K, N S33del,	Not-Tested



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1.4 In-vitro experimental results (Heat-Inactivated virus)

Source	Variant division	Kit test result
Zeptomatrix	SARS-CoV-2 (Heat-inactivated) USA-WA1/2020 (Wild type)	Reactive
Zeptomatrix	British variant (GRY clade, B.1.1.7)	Reactive
Zeptomatrix	South African variant (GH clade, B.1.351)	Reactive

1.5 In-vitro experimental results (Cultured virus)

Source	Variant division	Kit test result
NCCP	Reference material (Wild type)	Reactive (LoD: 5×10^3 PFU/mL)
NCCP	British variant (GRY clade, B.1.1.7)	Reactive (LoD: 5×10^2 PFU/mL)
NCCP	South African variant (GH clade, B.1.351)	Reactive (LoD: 5×10^2 PFU/mL)
NCCP	Brazil variant (GR clade, P.2)	Reactive (LoD: 5×10^3 PFU/mL)
NCCP	India variant (G clade, B.1.617.2)	Reactive (LoD: 5×10^3 PFU/mL)

* NCCP: National Culture Collection for Pathogens(KOREA)

As a result of in-silico analysis using the above two tools, GENEDIA W COVID-19 Ag are expected to have almost the same nucleocapsid protein reactivity against British, South African, Brazil, India, Lambda Delta plus, Mu(1 & 2) and Omicron strains as the USA/WA/01 strain used as a standard material.

Furthermore, After the reactivity test with actual virus and recombinant antigen, it was confirmed that the reactivity to SARS-CoV-2 variants (UK, South Africa, Brazil, India) was equal or higher than that of wild-type viruses.

Sincerely,

Jin-Woo Jeon

Leader of Immuno-diagnostics team, R&D center

Green Cross Medical Science Corporation

Reference.

- [1]. GISAID.org
 [2]. Blast.ncbi.nlm.nih.gov

Raw data

Sequence	Lineage B.1.1.7 (British variant) GISAID accession ID: EPI_ISL_601443	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID 4EF3JP9N114 Search expires on 03-10 16:14 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID Icl Query_43237 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronav ... Query Length 29882 Subject ID Icl Query_43239 (dna) Subject Descr hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2 ... Subject Length 29764 Other reports MSA viewer ⓘ	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
<div style="display: flex; justify-content: space-between;"> Descriptions Graphic Summary Alignments Dot Plot </div> <div style="border: 1px solid #ccc; padding: 5px;"> <p>Sequences producing significant alignments Download ▾ New Select columns ▾ Show 100 ▾ ⓘ</p> <p><input checked="" type="checkbox"/> select all 1 sequences selected Graphics New MSA Viewer</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th>Description</th> <th>Scientific Name</th> <th>Max Score</th> <th>Total Score</th> <th>Query Cover</th> <th>E value</th> <th>Per. Ident</th> <th>Acc. Len</th> <th>Accession</th> </tr> </thead> <tbody> <tr> <td><input checked="" type="checkbox"/> hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2020-09-20</td> <td></td> <td>54706</td> <td>54706</td> <td>99%</td> <td>0.0</td> <td>99.83%</td> <td>29764</td> <td>Query_43239</td> </tr> </tbody> </table> </div>				Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	<input checked="" type="checkbox"/> hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2020-09-20		54706	54706	99%	0.0	99.83%	29764	Query_43239
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<input checked="" type="checkbox"/> hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2020-09-20		54706	54706	99%	0.0	99.83%	29764	Query_43239													
Sequence	Lineage B.1.1.7 (British variant) GISAID accession ID: EPI_ISL_601443	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID 4EF571GF114 Search expires on 03-10 16:15 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID Icl Query_15485 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronav ... Query Length 1260 Subject ID Icl Query_15487 (dna) Subject Descr hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2 ... Subject Length 1259 Other reports MSA viewer ⓘ	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Sequence	Lineage B.1.351 (South African variant) GISAID accession ID: EPI_ISL_678597	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID 4EF9BPCM114 Search expires on 03-10 16:17 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID lcl Query_30611 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 29882 Subject ID lcl Query_30613 (dna) Subject Descr hCoV-19/South Africa/KRISP-EC-K005299/2020 EPI_ISL_ ... Subject Length 29856 Other reports MSA viewer ⓘ	Filter Results <table border="1"> <tr> <td>Percent Identity</td> <td>E value</td> <td>Query Coverage</td> </tr> <tr> <td><input type="text"/> to <input type="text"/></td> <td><input type="text"/> to <input type="text"/></td> <td><input type="text"/> to <input type="text"/></td> </tr> <tr> <td colspan="3" style="text-align: right;"> <input type="button" value="Filter"/> <input type="button" value="Reset"/> </td> </tr> </table>			Percent Identity	E value	Query Coverage	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="button" value="Filter"/> <input type="button" value="Reset"/>											
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Sequence	Lineage B.1.351 (South African variant) GISAID accession ID: EPI_ISL_678597	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID 4EF75C27114 Search expires on 03-10 16:16 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID lcl Query_20487 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 1260 Subject ID lcl Query_20489 (dna) Subject Descr hCoV-19/South Africa/KRISP-EC-K005299/2020 EPI_ISL_ ... Subject Length 1259 Other reports MSA viewer ⓘ	Filter Results <table border="1"> <tr> <td>Percent Identity</td> <td>E value</td> <td>Query Coverage</td> </tr> <tr> <td><input type="text"/> to <input type="text"/></td> <td><input type="text"/> to <input type="text"/></td> <td><input type="text"/> to <input type="text"/></td> </tr> <tr> <td colspan="3" style="text-align: right;"> <input type="button" value="Filter"/> <input type="button" value="Reset"/> </td> </tr> </table>			Percent Identity	E value	Query Coverage	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="button" value="Filter"/> <input type="button" value="Reset"/>											
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Sequence	Lineage P.1 (Brazil variant) GISAID accession ID: EPI_ISL_792680	Range	Whole sequence																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 5V3S3S2D114 <small>Search expires on 03-27 15:36 pm</small> Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Ic Query_29181 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ...</p> <p>Query Length 29882</p> <p>Subject ID Ic Query_29183 (dna)</p> <p>Subject Descr hCoV-19/Japan/IC-0561/2021 EPI_ISL_792680 2021-01-02</p> <p>Subject Length 29733</p> <p>Other reports MSA viewer ⓘ</p>	<p>Filter Results</p> <p>Percent Identity <input type="text"/> to <input type="text"/></p> <p>E value <input type="text"/> to <input type="text"/></p> <p>Query Coverage <input type="text"/> to <input type="text"/></p> <p>Filter Reset</p>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Japan/IC-0561/2021 EPI_ISL_792680 2021-01-02		2143	2143	93%	0.0	99.49%	29733	Query_45281													



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Sequence	Lineage B.1.617 (India variant) GISAID accession ID: EPI_ISL_1595896	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID ZTHCU7Y611N <small>Search expires on 04-20 07:49 am</small> Download All <input type="checkbox"/> Program Blast 2 sequences Citation <input type="checkbox"/> Query ID Icl Query_393529 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 29882 Subject ID Icl Query_393531 (dna) Subject Descr hCoV-19/India/KA-NIMH-SEQ-280/2021 EPI_ISL_159589 ... Subject 29865 Length Other reports MSA viewer <input type="checkbox"/>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/India/KA-NIMH-SEQ-280/2021 EPI_ISL_1595896 2021-03-19		54866	54866	99%	0.0	99.87%	29865	Query_393531													
Sequence	Lineage B.1.617 (India variant) GISAID accession ID: EPI_ISL_1595896	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID ZTHG2TXH11N <small>Search expires on 04-20 07:51 am</small> Download All <input type="checkbox"/> Program Blast 2 sequences Citation <input type="checkbox"/> Query ID Icl Query_408531 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 1260 Subject ID Icl Query_408533 (dna) Subject Descr hCoV-19/India/KA-NIMH-SEQ-280/2021 EPI_ISL_159589 ... Subject 1259 Length Other reports MSA viewer <input type="checkbox"/>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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<input checked="" type="checkbox"/> hCoV-19/India/KA-NIMH-SEQ-280/2021 EPI_ISL_1595896 2021-03-19		2241	2241	96%	0.0	99.75%	29865	Query_408533													



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Sequence	Lineage B.1.617.1 (India variant) GISAID accession ID: EPI_ISL_2533592	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGSWV1RD114 <small>Search expires on 06-16 16:23 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_7629 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 29882 Subject ID lcl Query_7631 (dna) Subject Descr hCoV-19/Ireland/C-NVRL-e90IRL79644/2021 EPI_ISL_25 ... Subject Length 29758 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Sequence	Lineage B.1.617.1 (India variant) GISAID accession ID: EPI_ISL_2533592	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGSNRJJS114 <small>Search expires on 06-16 16:20 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_22685 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 1260 Subject ID lcl Query_22687 (dna) Subject Descr hCoV-19/Ireland/C-NVRL-e90IRL79644/2021 EPI_ISL_25 ... Subject Length 1259 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
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Sequence	Lineage B.1.617.2 (India variant) GISAID accession ID: EPI_ISL_1419152	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGSZZDTR114 Search expires on 06-16 16:25 pm Download All <input type="checkbox"/> Program Blast 2 sequences Citation <input type="checkbox"/> Query ID lcl Query_19677 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronav ... Query Length 29882 Subject ID lcl Query_19679 (dna) Subject Descr hCoV-19/India/WB-1931500912396/2021 EPI_ISL_14191 ... Subject Length 29769 Other reports MSA viewer <input type="checkbox"/>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/India/WB-1931500912396/2021 EPI_ISL_1419152 2021-03-04		35427	52748	96%	0.0	99.92%	29769	Query_19679													
Sequence	Lineage B.1.617.2 (India variant) GISAID accession ID: EPI_ISL_1419152	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGSYNXWP114 Search expires on 06-16 16:24 pm Download All <input type="checkbox"/> Program Blast 2 sequences Citation <input type="checkbox"/> Query ID lcl Query_49311 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronav ... Query Length 1260 Subject ID lcl Query_49313 (dna) Subject Descr hCoV-19/India/WB-1931500912396/2021 EPI_ISL_14191 ... Subject Length 1259 Other reports MSA viewer <input type="checkbox"/>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Sequence	Lineage B.1.617.3 (India variant) GISAID accession ID: EPI_ISL_2508617	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGT39VEN114 <small>Search expires on 06-16 16:27 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_29497 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 29882 Subject ID lcl Query_29499 (dna) Subject Descr hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30 Subject Length 29838 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30		46797	54511	99%	0.0	99.88%	29838	Query_29499													
Sequence	Lineage B.1.617.3 (India variant) GISAID accession ID: EPI_ISL_2508617	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGT1BZDR114 <small>Search expires on 06-16 16:26 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_61177 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 1260 Subject ID lcl Query_61179 (dna) Subject Descr hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30 Subject Length 1259 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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<input checked="" type="checkbox"/> hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30		2213	2213	95%	0.0	99.75%	29838	Query_61179													



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Sequence	Lineage B.1.618 (India variant) GISAID accession ID: EPI_ISL_2503243	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGT635MK114 <small>Search expires on 06-16 16:28 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_25495 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 29882 Subject ID lcl Query_25497 (dna) Subject Descr hCoV-19/India/WB-1931300254172/2021 EPI_ISL_25032 ... Subject Length 29776 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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<input checked="" type="checkbox"/> hCoV-19/India/WB-1931300254172/2021 EPI_ISL_2503243 2021-03-31		13361	51116	93%	0.0	99.92%	29776	Query_25497													
Sequence	Lineage B.1.618 (India variant) GISAID accession ID: EPI_ISL_2503243	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID CGT4W2Y4114 <small>Search expires on 06-16 16:28 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID lcl Query_63443 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 1260 Subject ID lcl Query_63445 (dna) Subject Descr hCoV-19/India/WB-1931300254172/2021 EPI_ISL_25032 ... Subject Length 1259 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
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Sequence	Lineage C.37 (Lambda variant) GISAIID accession ID: EPI_ISL_1111285	Range	Whole sequence																		
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021-01-18		54999	54999	99%	0.0	99.89%	29901	Query_56241													
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<p>Sequences producing significant alignments Download ▼ New Select columns ▼ Show 100 ▼ ⓘ</p> <p><input checked="" type="checkbox"/> select all 1 sequences selected Graphics New MSA Viewer</p> <table border="1" style="width:100%; border-collapse: collapse;"> <thead> <tr> <th>Description</th> <th>Scientific Name</th> <th>Max Score</th> <th>Total Score</th> <th>Query Cover</th> <th>E value</th> <th>Per. Ident</th> <th>Acc. Len</th> <th>Accession</th> </tr> </thead> <tbody> <tr> <td><input checked="" type="checkbox"/> hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021-01-18</td> <td></td> <td>2285</td> <td>2285</td> <td>99%</td> <td>0.0</td> <td>99.44%</td> <td>29901</td> <td>Query_8799</td> </tr> </tbody> </table>				Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	<input checked="" type="checkbox"/> hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021-01-18		2285	2285	99%	0.0	99.44%	29901	Query_8799
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021-01-18		2285	2285	99%	0.0	99.44%	29901	Query_8799													



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Sequence	Lineage AY.1 (Delta plus variant) GISAID accession ID: EPI_ISL_2552218	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID D8AATVFT114 <small>Search expires on 06-25 14:42 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID Icl Query_39095 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 29882 Subject ID Icl Query_39097 (dna) Subject Descr hCoV-19/England/MILK-1681BC1/2021 EPI_ISL_2552218 2021-06-09 Subject Length 29769 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/England/MILK-1681BC1/2021 EPI_ISL_2552218 2021-06-09		54691	54691	99%	0.0	99.82%	29769	Query_39097													
Job Title MN985325.1 Severe acute respiratory syndrome RID D8A2PUR3114 <small>Search expires on 06-25 14:38 pm</small> Download All <small>▼</small> Program Blast 2 sequences Citation <small>▼</small> Query ID Icl Query_58543 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 1260 Subject ID Icl Query_58545 (dna) Subject Descr hCoV-19/England/MILK-1681BC1/2021 EPI_ISL_2552218 2021-06-09 Subject Length 1259 Other reports MSA viewer <small>?</small>	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/England/MILK-1681BC1/2021 EPI_ISL_2552218 2021-06-09		2176	2176	94%	0.0	99.58%	29769	Query_58545													



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Sequence	Lineage B.1.621 (Mu variant 1) GISAID accession ID: EPI_ISL_1582981	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID K3D1BHRN11N Search expires on 09-04 13:35 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID lcl Query_274223 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 29882 Subject ID lcl Query_274225 (dna) Subject Descr hCoV-19/Colombia/NSA-INS-VG-1687/2021 EPI_ISL_158 ... Subject Length 29781 Other reports MSA viewer ⓘ	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Colombia/NSA-INS-VG-1687/2021 EPI_ISL_1582981 2021-03-10		9923	48717	88%	0.0	99.72%	29781	Query_274225													
Sequence	Lineage B.1.621 (Mu variant 1) GISAID accession ID: EPI_ISL_1582981	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID K3CZZH8011N Search expires on 09-04 13:34 pm Download All ▾ Program Blast 2 sequences Citation ▾ Query ID lcl Query_268885 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ... Query Length 1260 Subject ID lcl Query_268887 (dna) Subject Descr hCoV-19/Colombia/NSA-INS-VG-1687/2021 EPI_ISL_158 ... Subject Length 1259 Other reports MSA viewer ⓘ	Filter Results Percent Identity <input type="text"/> to <input type="text"/> E value <input type="text"/> to <input type="text"/> Query Coverage <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Colombia/NSA-INS-VG-1687/2021 EPI_ISL_1582981 2021-03-10		2215	2215	95%	0.0	99.83%	29781	Query_268887													



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Sequence	Lineage B.1.621.1 (Mu variant 2) GISAID accession ID: EPI_ISL_1820954	Range	Whole sequence																		
Job Title MN985325.1 Severe acute respiratory syndrome RID K3D4V4W3114 Search expires on 09-04 13:37 pm Download All ▼ Program Blast 2 sequences Citation ▼ Query ID lcl Query_65533 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 29882 Subject ID lcl Query_65535 (dna) Subject Descr hCoV-19/Colombia/BOL-INS-VG-2002/2021 EPI_ISL_182 ... Subject 29778 Length Other reports MSA viewer ?	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Colombia/BOL-INS-VG-2002/2021 EPI_ISL_1820954 2021-03-30		7579	44728	81%	0.0	99.93%	29778	Query_65535													
Sequence	Lineage B.1.621.1 (Mu variant 2) GISAID accession ID: EPI_ISL_1820954	Range	Nucleocapsid protein																		
Job Title MN985325.1 Severe acute respiratory syndrome RID K3DDUMMU114 Search expires on 09-04 13:42 pm Download All ▼ Program Blast 2 sequences Citation ▼ Query ID lcl Query_15883 (dna) Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ... Query Length 1260 Subject ID lcl Query_15885 (dna) Subject Descr hCoV-19/Colombia/BOL-INS-VG-2002/2021 EPI_ISL_182 ... Subject 1259 Length Other reports MSA viewer ?	Filter Results Percent Identity: <input type="text"/> to <input type="text"/> E value: <input type="text"/> to <input type="text"/> Query Coverage: <input type="text"/> to <input type="text"/> <input type="button" value="Filter"/> <input type="button" value="Reset"/>																				
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
<input checked="" type="checkbox"/> hCoV-19/Colombia/BOL-INS-VG-2002/2021 EPI_ISL_1820954 2021-03-30		2215	2215	95%	0.0	99.92%	29778	Query_15885													



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Sequence	Lineage B.1.1.529 (Omicron variant) GISAID accession ID: EPI_ISL_6825395	Range	Whole sequence
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID U8EWP5N11N <small>Search expires on 11-30 09:31 am</small> Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Ic Query_150399 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ...</p> <p>Query Length 29882</p> <p>Subject ID Ic Query_150401 (dna)</p> <p>Subject Descr hCoV-19/South Africa/CERI-KRISP-K032355/2021 EPI_IS ...</p> <p>Subject 29847</p> <p>Length</p> <p>Other reports MSA viewer ⓘ</p>	<p>Filter Results</p> <table style="width: 100%;"> <tr> <td style="text-align: center;">Percent Identity</td> <td style="text-align: center;">E value</td> <td style="text-align: center;">Query Coverage</td> </tr> <tr> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> </tr> <tr> <td colspan="3" style="text-align: right;"> <input type="button" value="Filter"/> <input type="button" value="Reset"/> </td> </tr> </table>	Percent Identity	E value	Query Coverage	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="button" value="Filter"/> <input type="button" value="Reset"/>		
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Descriptions	Graphic Summary Alignments Dot Plot
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Sequences producing significant alignments		Download ▼	New Select columns ▼	Show 100 ▼ ⓘ				
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Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<input checked="" type="checkbox"/> hCoV-19/South Africa/CERI-KRISP-K032355/2021 EPI_ISL_6825395 2021-11-16		54549	54549	99%	0.0	99.66%	29847	Query_150401

Sequence	Lineage B.1.1.529 (Omicron variant) GISAID accession ID: EPI_ISL_6825395	Range	Nucleocapsid protein
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID U8EY3TMG11N <small>Search expires on 11-30 09:32 am</small> Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Ic Query_207639 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavi ...</p> <p>Query Length 1260</p> <p>Subject ID Ic Query_207641 (dna)</p> <p>Subject Descr hCoV-19/South Africa/CERI-KRISP-K032355/2021 EPI_IS ...</p> <p>Subject 1259</p> <p>Length</p> <p>Other reports MSA viewer ⓘ</p>	<p>Filter Results</p> <table style="width: 100%;"> <tr> <td style="text-align: center;">Percent Identity</td> <td style="text-align: center;">E value</td> <td style="text-align: center;">Query Coverage</td> </tr> <tr> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> <td style="text-align: center;"> <input type="text"/> to <input type="text"/> </td> </tr> <tr> <td colspan="3" style="text-align: right;"> <input type="button" value="Filter"/> <input type="button" value="Reset"/> </td> </tr> </table>	Percent Identity	E value	Query Coverage	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="button" value="Filter"/> <input type="button" value="Reset"/>		
Percent Identity	E value	Query Coverage								
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<input type="button" value="Filter"/> <input type="button" value="Reset"/>										

Descriptions	Graphic Summary Alignments Dot Plot
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Sequences producing significant alignments		Download ▼	New Select columns ▼	Show 100 ▼ ⓘ				
<input checked="" type="checkbox"/> select all 1 sequences selected		Graphics New MSA Viewer						
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<input checked="" type="checkbox"/> hCoV-19/South Africa/CERI-KRISP-K032355/2021 EPI_ISL_6825395 2021-11-16		2172	2172	96%	0.0	99.01%	29847	Query_207641