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Letter of confirmation

Date: 24th June, 2021

To whom it may concern

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

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 and Lineage AY.1) 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) 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.

<https://blast.ncbi.nlm.nih.gov/>

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 Information of sequence

Source	Virus designation	Accession No	Division	WHO label
NCBI	SARS-CoV-2/human/USA/WA-CDC-WA1/2020	MN985325.1	Reference material	-
GISAIID	hCoV-19/England/MILK-9E05B3/2020	EPI_ISL_601443	British variant (B.1.1.7)	Alpha
GISAIID	hCoV-19/South Africa/KRISP-EC-K005299/2020	EPI_ISL_678597	South African variant (B.1.351)	Beta
GISAIID	hCoV-19/Japan/IC-0561/2021*	EPI_ISL_792680	Brazil variant (P.1)	Gamma
GISAIID	hCoV-19/India/KA-NIMH-SEQ-280/2021	EPI_ISL_1595896	India variant (B.1.617)	-
GISAIID	hCoV-19/Ireland/C-NVRL-e90IRL79644/2021	EPI_ISL_2533592	India variant (B.1.617.1)	Kappa
GISAIID	hCoV-19/India/WB-1931500912396/2021	EPI_ISL_1419152	India variant (B.1.617.2)	Delta
GISAIID	hCoV-19/Singapore/842/2021	EPI_ISL_2508617	India variant (B.1.617.3)	-
GISAIID	hCoV-19/India/WB-1931300254172/2021	EPI_ISL_2503243	India variant (B.1.618)	-
GISAIID	hCoV-19/Peru/LIM-INS-387/2021	EPI_ISL_1111285	Lambda variant (C.37)	Lambda
GISAIID	hCoV-19/England/MILK-1681BC1/2021	EPI_ISL_2552218	Delta plus variant (AY.1)	-

* Airport Quarantine Station in Japan. COVID-19 positive case who entered from Brazil.

1.3 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 %	

1.4 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

1.5 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

1.6 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: National Culture Collection for Pathogens(KOREA)



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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 and Delta plus 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 there was no significant difference between the in-silico analysis and the in-vitro experimental results.

However, the above prediction based on data analysis and recombinant antigen's reactivity (Brazil, India variants), therefore it cannot be assured of its applicability. So, the appropriate test for new strain of SARS-CoV-2 is necessary to conduct.

Sincerely,

A handwritten signature in black ink that reads 'Jin-woo Jeon'. The signature is written in a cursive style and is positioned above a solid blue horizontal line.

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																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 4EF3JP9N114 Search expires on 03-10 16 14 pm Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID lcl Query_43237 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 29882</p> <p>Subject ID lcl Query_43239 (dna)</p> <p>Subject Descr hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2 ...</p> <p>Subject Length 29764</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></p> <p>Filter Reset</p>																				
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 4EF571GF114 Search expires on 03-10 16 15 pm Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID lcl Query_15485 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 1260</p> <p>Subject ID lcl Query_15487 (dna)</p> <p>Subject Descr hCoV-19/England/MILK-9E05B3/2020 EPI_ISL_601443 2 ...</p> <p>Subject Length 1259</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></p> <p>Filter Reset</p>		Nucleocapsid protein																		
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Sequence	Lineage B.1.351 (South African variant) GISAIID accession ID: EPI_ISL_678597	Range	Whole sequence																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 4EF9BPCM114 Search expires on 03-10 16 17 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID Icl Query_30611 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 29882</p> <p>Subject ID Icl Query_30613 (dna)</p> <p>Subject Descr hCoV-19/South Africa/KRISP-EC-K005299/2020 EPI_ISL ...</p> <p>Subject 29856</p> <p>Length</p> <p>Other reports MSA viewer ⓘ</p>																					
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 4EF75C27114 Search expires on 03-10 16 16 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID Icl Query_20487 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 1260</p> <p>Subject ID Icl Query_20489 (dna)</p> <p>Subject Descr hCoV-19/South Africa/KRISP-EC-K005299/2020 EPI_ISL ...</p> <p>Subject 1259</p> <p>Length</p> <p>Other reports MSA viewer ⓘ</p>																					
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Sequence	Lineage P.1 (Brazil variant) GISAID accession ID: EPI_ISL_792680	Range	Whole sequence																		
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 5V430FXR114 Search expires on 03-27 15:42 pm Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Icl Query_45279 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 1260</p> <p>Subject ID Icl Query_45281 (dna)</p> <p>Subject Descr hCoV-19/Japan/IC-0561/2021 EPI_ISL_792680 2021-01-02</p> <p>Subject 1259</p> <p>Length</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>		Nucleocapsid protein																		
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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													

Sequence	Lineage B.1.617 (India variant) GISAID accession ID: EPI_ISL_1595896	Range	Whole sequence																		
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession													
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID 7THG2TXH11N Search expires on 04-20 07:51 am Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Icl Query_408531 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 1260</p> <p>Subject ID Icl Query_408533 (dna)</p> <p>Subject Descr hCoV-19/India/KA-NIMH-SEQ-280/2021 EPI_ISL_1595896 ...</p> <p>Subject Length 1259</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>		Nucleocapsid protein																		
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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																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGSWV1RD114 Search expires on 06-16 16:23 pm Download All</p> <p>Program Blast 2 sequences Citation</p> <p>Query ID lcl Query_7629 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 29882</p> <p>Subject ID lcl Query_7631 (dna)</p> <p>Subject Descr hCoV-19/Ireland/C-NVRL-e90IRL79644/2021 EPI_ISL_25 ...</p> <p>Subject Length 29758</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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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGSNRJJS114 Search expires on 06-16 16:20 pm Download All</p> <p>Program Blast 2 sequences Citation</p> <p>Query ID lcl Query_22685 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 1260</p> <p>Subject ID lcl Query_22687 (dna)</p> <p>Subject Descr hCoV-19/Ireland/C-NVRL-e90IRL79644/2021 EPI_ISL_25 ...</p> <p>Subject Length 1259</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>		Nucleocapsid protein																		
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Sequence	Lineage B.1.617.2 (India variant) GISAID accession ID: EPI_ISL_1419152	Range	Whole sequence																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGSZDTR114 Search expires on 06-16 16:25 pm Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Icl Query_19677 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 29882</p> <p>Subject ID Icl Query_19679 (dna)</p> <p>Subject Descr hCoV-19/India/WB-1931500912396/2021 EPI_ISL_14191 ...</p> <p>Subject 29769</p> <p>Length</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/India/WB-1931500912396/2021 EPI_ISL_1419152 2021-03-04		35427	52748	96%	0.0	99.92%	29769	Query_19679													
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGSYNXWP114 Search expires on 06-16 16:24 pm Download All ▼</p> <p>Program Blast 2 sequences Citation ▼</p> <p>Query ID Icl Query_49311 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...</p> <p>Query Length 1260</p> <p>Subject ID Icl Query_49313 (dna)</p> <p>Subject Descr hCoV-19/India/WB-1931500912396/2021 EPI_ISL_14191 ...</p> <p>Subject 1259</p> <p>Length</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>		Nucleocapsid protein																		
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Sequence	Lineage B.1.617.3 (India variant) GISAID accession ID: EPI_ISL_2508617	Range	Whole sequence																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGT39VEN114 Search expires on 06-16 16 27 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID lcl Query_29497 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 29882</p> <p>Subject ID lcl Query_29499 (dna)</p> <p>Subject Descr hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30</p> <p>Subject Length 29838</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></p> <p>Filter Reset</p>																				
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<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGT1BZDR114 Search expires on 06-16 16 26 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID lcl Query_61177 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 1260</p> <p>Subject ID lcl Query_61179 (dna)</p> <p>Subject Descr hCoV-19/Singapore/842/2021 EPI_ISL_2508617 2021-04-30</p> <p>Subject Length 1259</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></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/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																		
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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													
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CGT4W2Y4114 Search expires on 06-16 16 28 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID lcl Query_63443 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 1260</p> <p>Subject ID lcl Query_63445 (dna)</p> <p>Subject Descr hCoV-19/India/WB-1931300254172/2021 EPI_ISL_25032 ...</p> <p>Subject 1259</p> <p>Length</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></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													
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Sequence	Lineage C.37 (Lambda variant) GISAID accession ID: EPI_ISL_1111285	Range	Whole sequence																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CSP345XE114 Search expires on 06-19 16:25 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID lcl Query_56239 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 29882</p> <p>Subject ID lcl Query_56241 (dna)</p> <p>Subject Descr hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021- ...</p> <p>Subject 29901</p> <p>Length</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></p> <p style="text-align:right;">Filter Reset</p>																				
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<p>Sequences producing significant alignments Download ▾ New Select columns ▾ Show <input type="text" value="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; font-size: small;"> <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>54999</td> <td>54999</td> <td>99%</td> <td>0.0</td> <td>99.89%</td> <td>29901</td> <td>Query_56241</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		54999	54999	99%	0.0	99.89%	29901	Query_56241
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<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													
Sequence	Lineage C.37 (Lambda variant) GISAID accession ID: EPI_ISL_1111285	Range	Nucleocapsid protein																		
<p>Job Title MN985325.1 Severe acute respiratory syndrome</p> <p>RID CSNX4UUZ114 Search expires on 06-19 16:21 pm Download All ▾</p> <p>Program Blast 2 sequences Citation ▾</p> <p>Query ID lcl Query_8797 (dna)</p> <p>Query Descr MN985325.1 Severe acute respiratory syndrome coronavir ...</p> <p>Query Length 1260</p> <p>Subject ID lcl Query_8799 (dna)</p> <p>Subject Descr hCoV-19/Peru/LIM-INS-387/2021 EPI_ISL_1111285 2021- ...</p> <p>Subject 1259</p> <p>Length</p> <p>Other reports MSA viewer ?</p>	<p>Filter Results</p> <p>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"/></p> <p style="text-align:right;">Filter Reset</p>																				
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Sequence	Lineage AY.1 (Delta plus variant) GISAID accession ID: EPI_ISL_2552218	Range	Whole sequence																		
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Sequence	Lineage AY.1 (Delta plus variant) GISAID accession ID: EPI_ISL_2552218	Range	Nucleocapsid protein																		
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