GCMS

107, Ihyeon-ro 30beon-gil, Giheung-gu, Yongin-si, Gyeonggi-do, 16924, Korea

TEL : +82-31-270-1404 FAX : +82-31-260-9416

Letter of confirmation

Date: 8th Oct, 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, India and Peru.

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 and B.1.621.1) 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), lineage B.1.621(GISAID accession ID: EPI_ISL_1582981, Mu variant 1) and lineage B.1.621.1(GISAID accession ID: EPI_ISL_1820954, Mu variant 2) 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 Zeptometrix 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:	Whole sequence	99.72 %	Conformity

	EPI_ISL_1582981	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 %	

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

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

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

	(GH clade, B.1.351)	

1.5 In-vitro experimental results (Cultured virus)

Source	Variant division	Kit test result
NCCP	Reference material (Wild type)	Reactive (LoD: 5 X 10^4 PFU/mL)
NCCP	British variant (GRY clade, B.1.1.7)	Reactive (LoD: 5 X 10^3 PFU/mL)
NCCP	South African variant (GH clade, B.1.351)	Reactive (LoD: 5 X 10^3 PFU/mL)
NCCP	Brazil variant (GR clade , P.2)	Reactive (LoD: 5 X 10^3 PFU/mL)
NCCP	India variant (G clade , B.1.617.2)	Reactive (LoD: 5 X 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 and Mu(1 & 2) 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

Jin-Woo Jeon
Leader of Immuno-diagnostics team, R&D center

Green Cross Medical Science Corporation

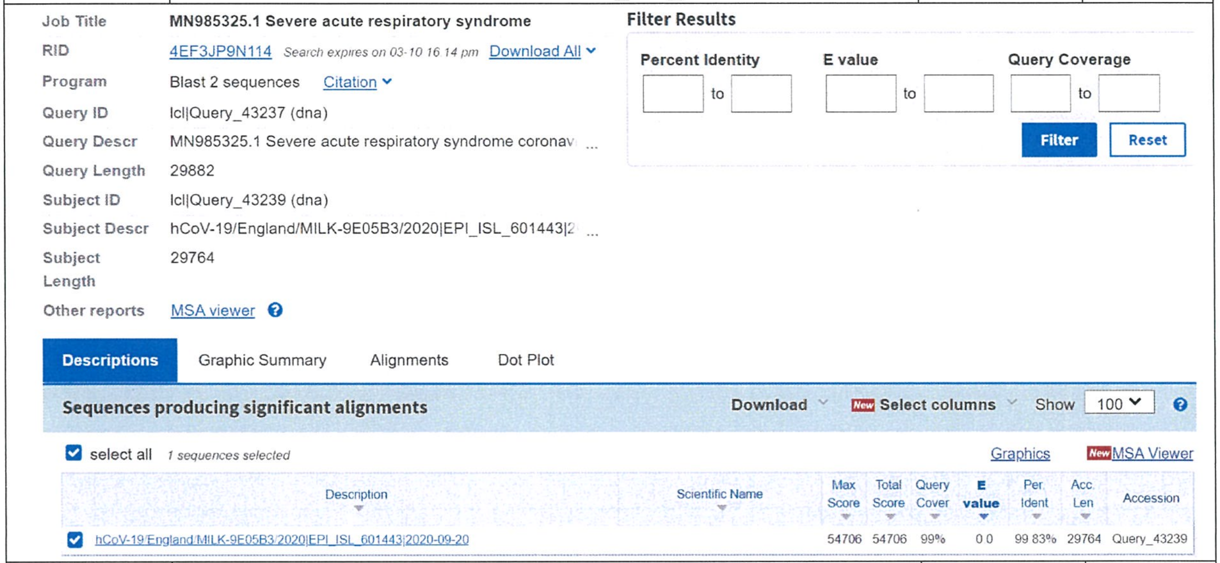
Reference.

[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 lcl|Query_43237 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 29882
Subject ID lcl|Query_43239 (dna)
Subject Descr hCoV-19/England/MILK-9E05B3/2020|EPI_ISL_601443|2 ...
Subject Length 29764
Other reports MSA viewer

Filter Results

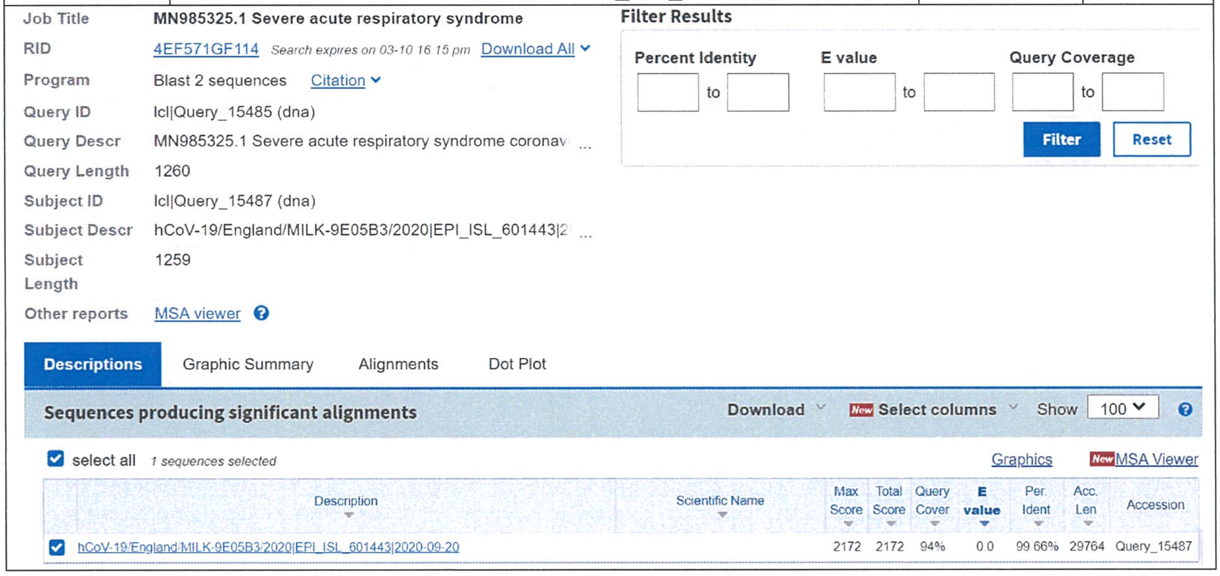
Percent Identity ☐ to ☐
E value ☐ to ☐
Query Coverage ☐ to ☐

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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 lcl|Query_15485 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 1260
Subject ID lcl|Query_15487 (dna)
Subject Descr hCoV-19/England/MILK-9E05B3/2020|EPI_ISL_601443|2 ...
Subject Length 1259
Other reports MSA viewer

Filter Results

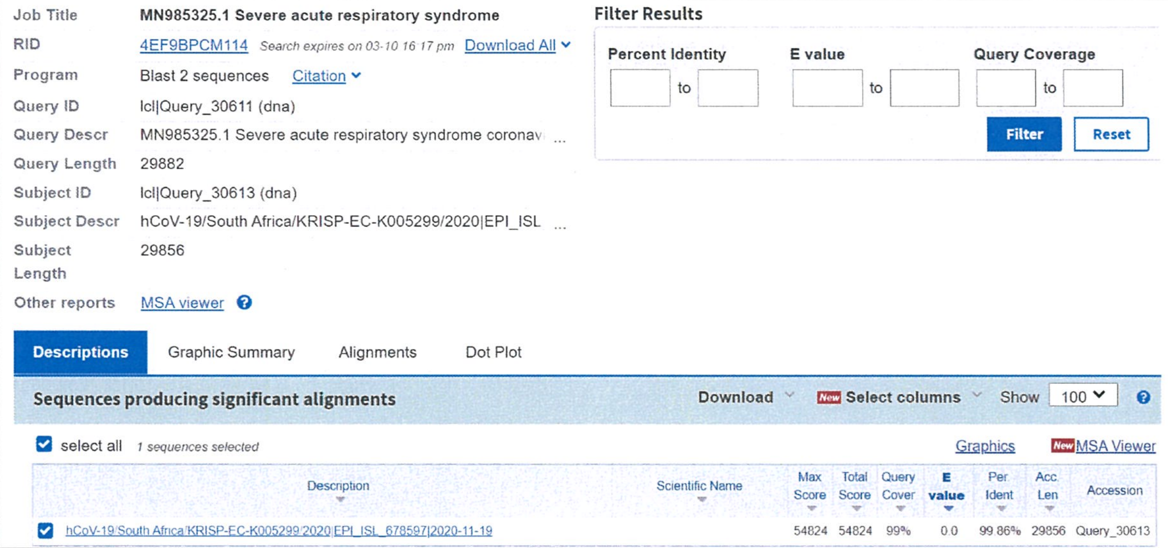
Percent Identity ☐ to ☐
E value ☐ to ☐
Query Coverage ☐ to ☐

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/England/MILK-9E05B3/2020|EPI_ISL_601443|2020-09-20		2172	2172	94%	0.0	99.66%	29764	Query_15487

Sequence	Lineage B.1.351 (South African variant) GISAID accession ID: EPI_ISL_678597	**Range**	Whole sequence



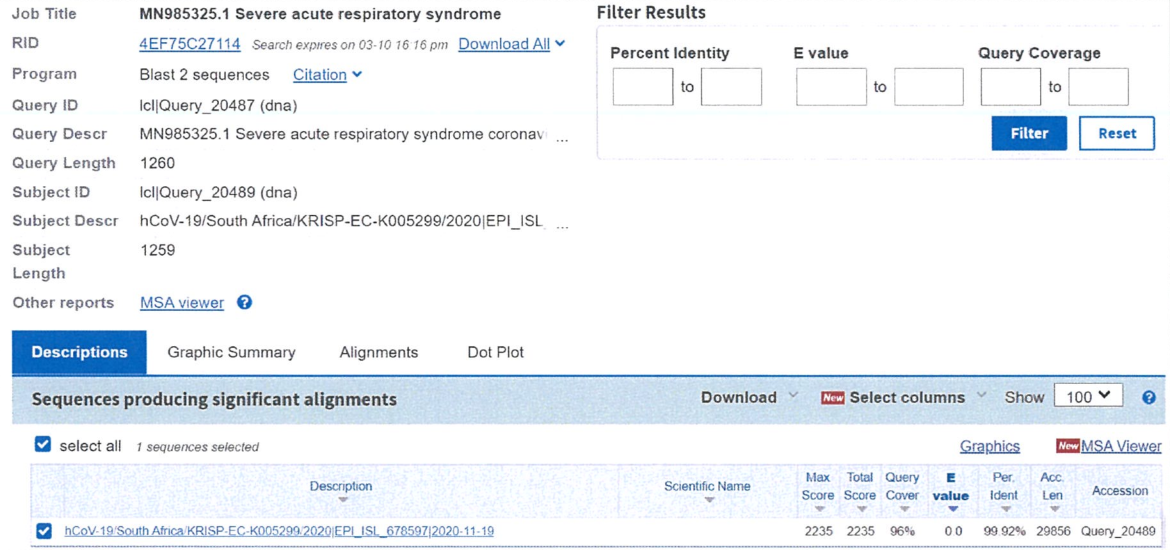
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	4EF9BPCM114 *Search expires on 03-10 16 17 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_30611 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_30613 (dna)
Subject Descr	hCoV-19/South Africa/KRISP-EC-K005299/2020|EPI_ISL ...
Subject Length	29856
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/South Africa/KRISP-EC-K005299/2020|EPI_ISL_678597|2020-11-19		54824	54824	99%	0.0	99.86%	29856	Query_30613

Sequence	Lineage B.1.351 (South African variant) GISAID accession ID: EPI_ISL_678597	**Range**	Nucleocapsid protein



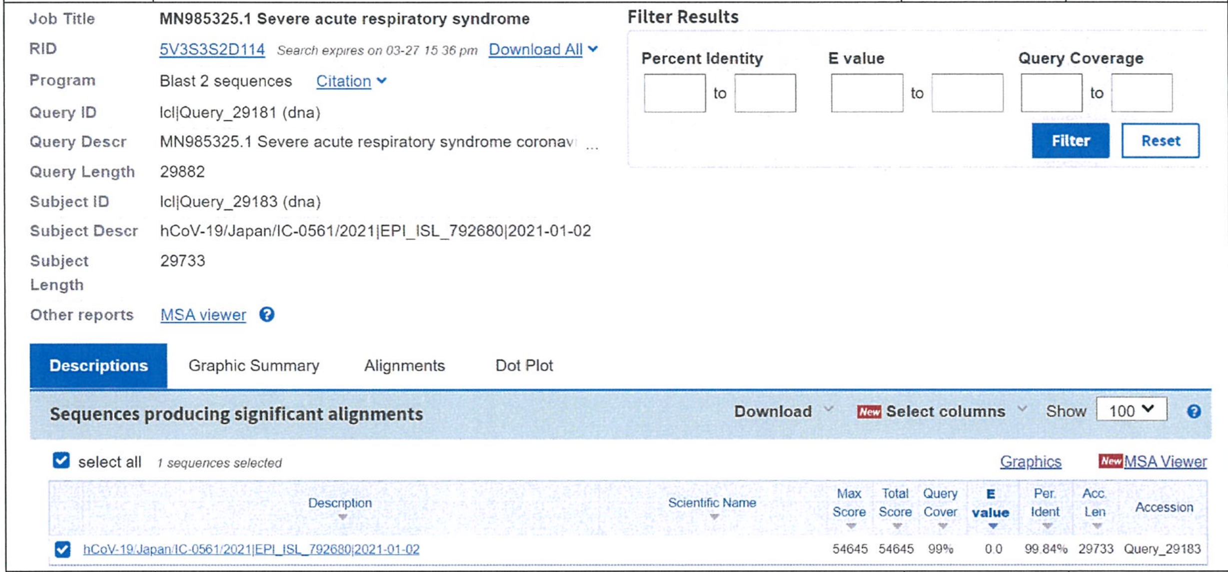
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	4EF75C27114 *Search expires on 03-10 16 16 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_20487 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_20489 (dna)
Subject Descr	hCoV-19/South Africa/KRISP-EC-K005299/2020|EPI_ISL ...
Subject Length	1259
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/South Africa/KRISP-EC-K005299/2020|EPI_ISL_678597|2020-11-19		2235	2235	96%	0.0	99.92%	29856	Query_20489

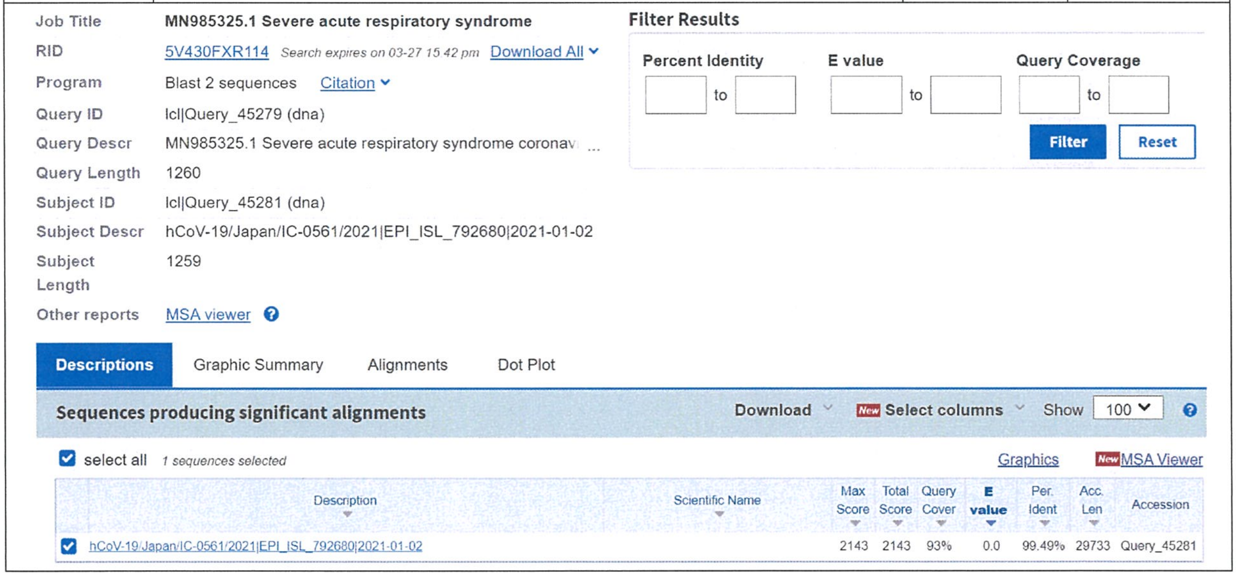
Sequence	Lineage P.1 (Brazil variant) GISAID accession ID: EPI_ISL_792680	**Range**	Whole sequence



Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	5V3S3S2D114 *Search expires on 03-27 15 36 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_29181 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_29183 (dna)
Subject Descr	hCoV-19/Japan/IC-0561/2021|EPI_ISL_792680|2021-01-02
Subject Length	29733
Other reports	MSA viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Japan/IC-0561/2021|EPI_ISL_792680|2021-01-02		54645	54645	99%	0.0	99.84%	29733	Query_29183

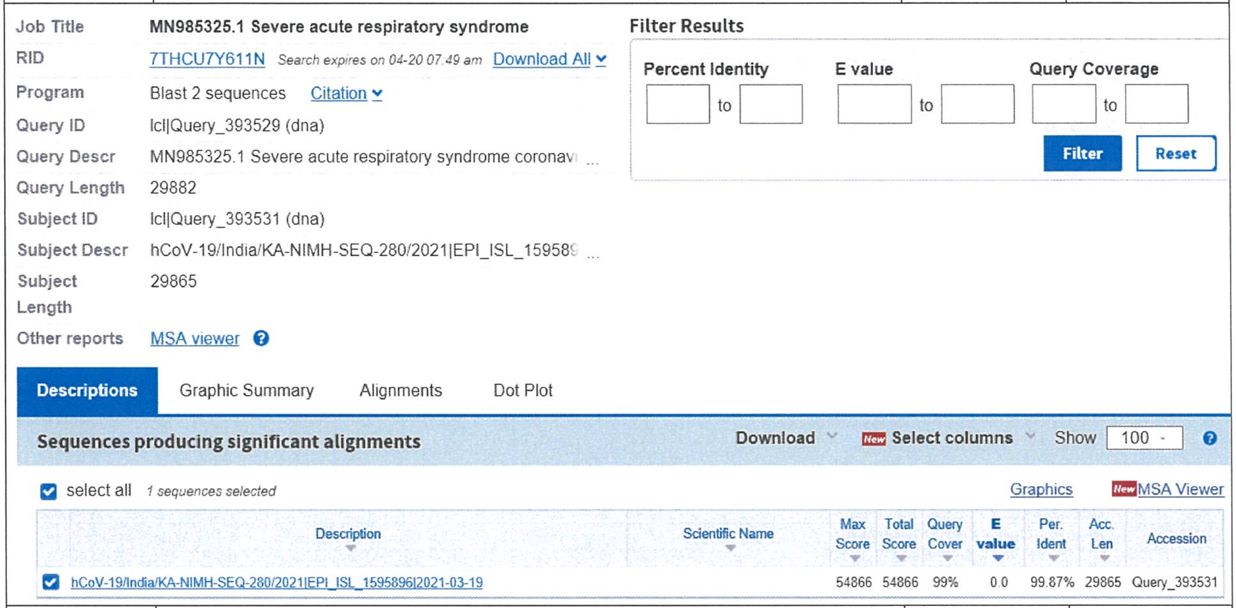
Sequence	Lineage P.1 (Brazil variant) GISAID accession ID: EPI_ISL_792680	**Range**	Nucleocapsid protein



Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	5V430FXR114 *Search expires on 03-27 15 42 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_45279 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_45281 (dna)
Subject Descr	hCoV-19/Japan/IC-0561/2021|EPI_ISL_792680|2021-01-02
Subject Length	1259
Other reports	MSA viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



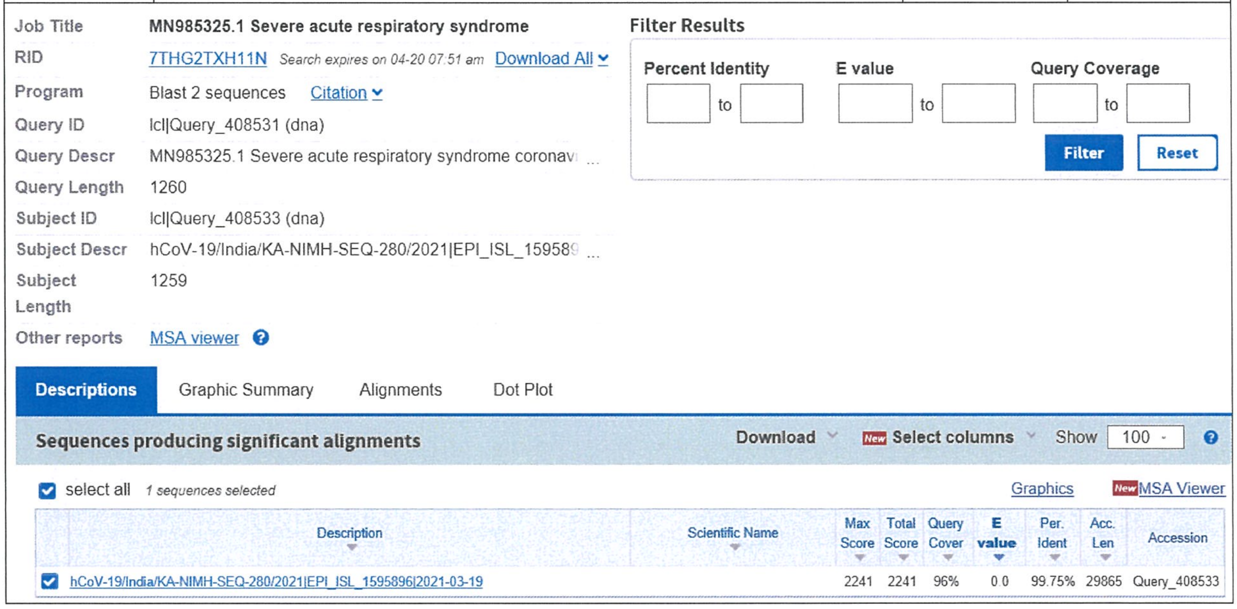
Job Title MN985325.1 Severe acute respiratory syndrome
RID 7THCU7Y611N *Search expires on 04-20 07:49 am* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_393529 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 29882
Subject ID lcl|Query_393531 (dna)
Subject Descr hCoV-19/India/KA-NIMH-SEQ-280/2021|EPI_ISL_15958 ...
Subject Length 29865
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



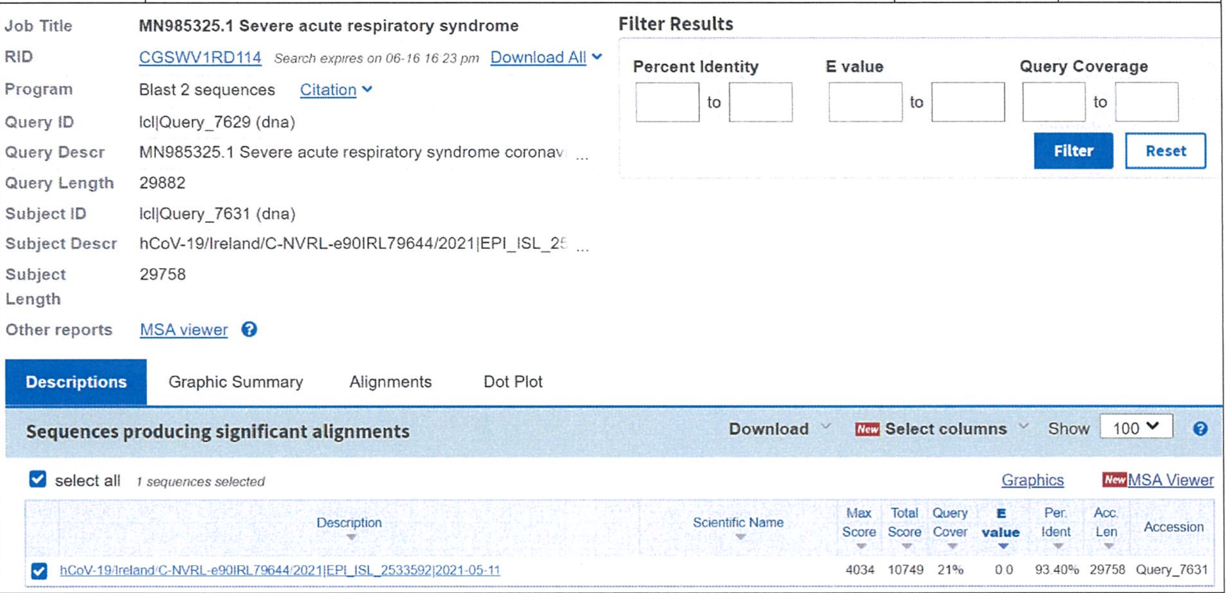
Job Title MN985325.1 Severe acute respiratory syndrome
RID 7THG2TXH11N *Search expires on 04-20 07:51 am* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_408531 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 1260
Subject ID lcl|Query_408533 (dna)
Subject Descr hCoV-19/India/KA-NIMH-SEQ-280/2021|EPI_ISL_15958 ...
Subject Length 1259
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/India/KA-NIMH-SEQ-280/2021|EPI_ISL_1595896|2021-03-19		2241	2241	96%	0.0	99.75%	29865	Query_408533

Sequence	Lineage B.1.617.1 (India variant) GISAID accession ID: EPI_ISL_2533592	**Range**	Whole sequence



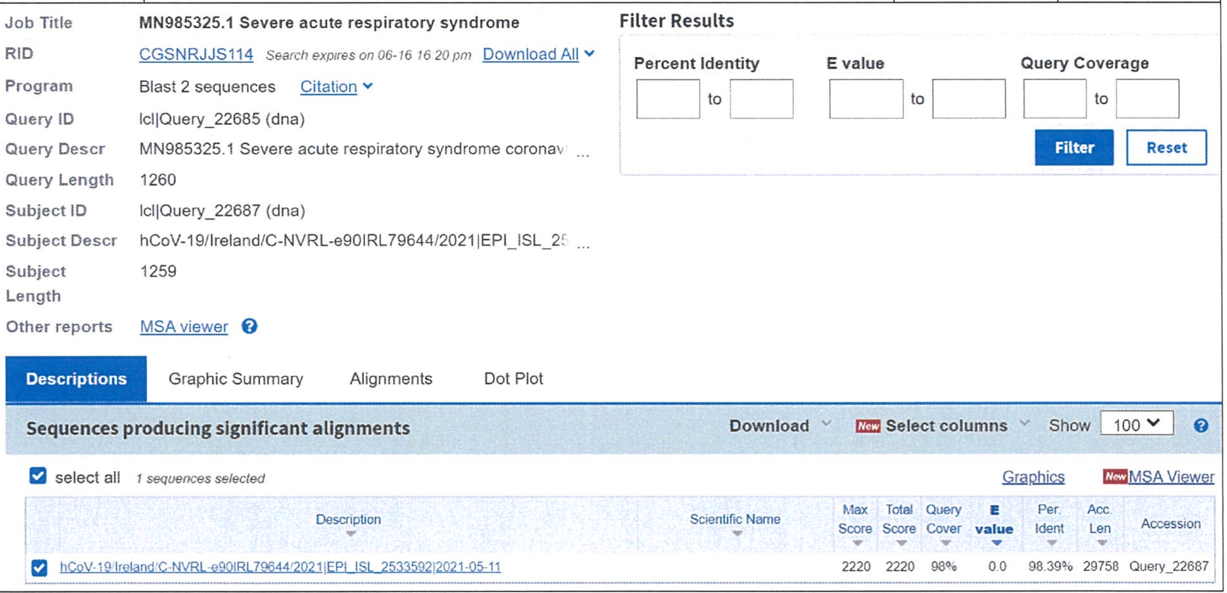
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGSWV1RD114 *Search expires on 06-16 16 23 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_7629 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_7631 (dna)
Subject Descr	hCoV-19/Ireland/C-NVRL-e90IRL79644/2021|EPI_ISL_25 ...
Subject Length	29758
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Ireland/C-NVRL-e90IRL79644/2021|EPI_ISL_2533592|2021-05-11		4034	10749	21%	0.0	93.40%	29758	Query_7631

Sequence	Lineage B.1.617.1 (India variant) GISAID accession ID: EPI_ISL_2533592	**Range**	Nucleocapsid protein



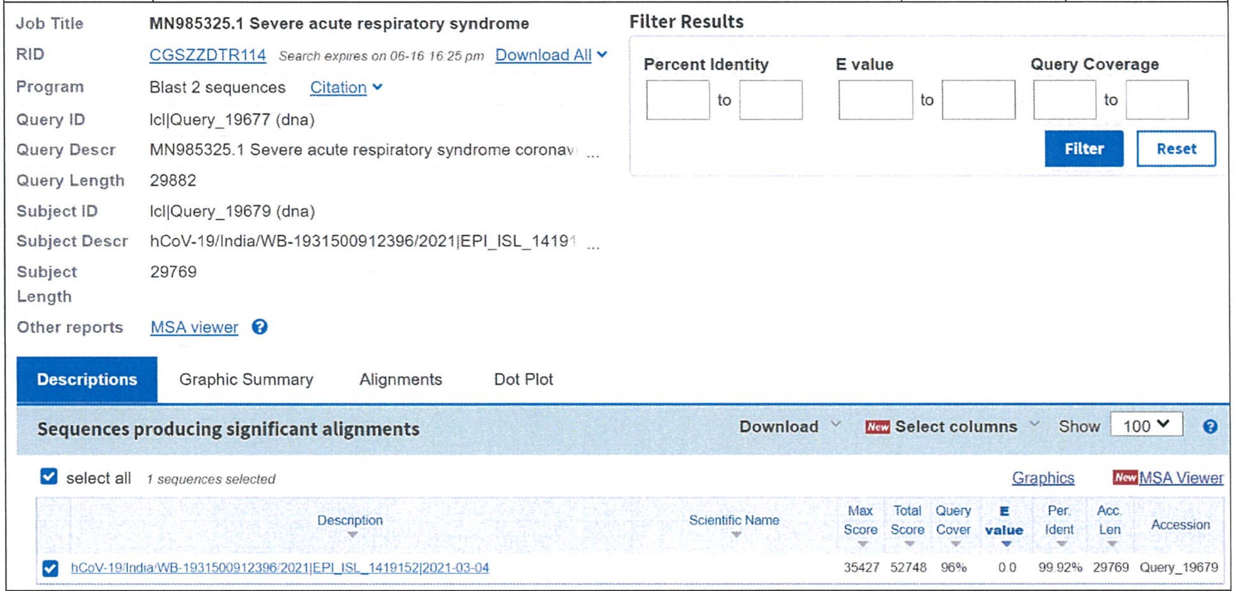
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGSNRJJS114 *Search expires on 06-16 16 20 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_22685 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_22687 (dna)
Subject Descr	hCoV-19/Ireland/C-NVRL-e90IRL79644/2021|EPI_ISL_25 ...
Subject Length	1259
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Ireland/C-NVRL-e90IRL79644/2021|EPI_ISL_2533592|2021-05-11		2220	2220	98%	0.0	98.39%	29758	Query_22687

Sequence	Lineage B.1.617.2 (India variant) GISAID accession ID: EPI_ISL_1419152	**Range**	Whole sequence



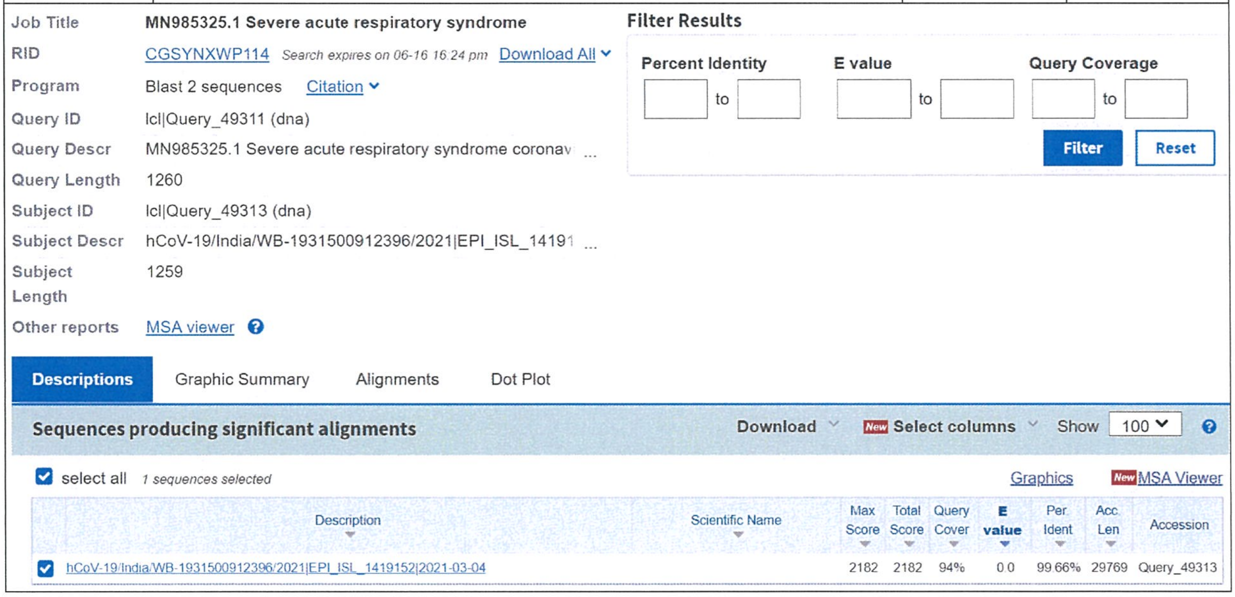
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGSZZDTR114 *Search expires on 06-16 16 25 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_19677 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_19679 (dna)
Subject Descr	hCoV-19/India/WB-1931500912396/2021|EPI_ISL_1419 ...
Subject Length	29769
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



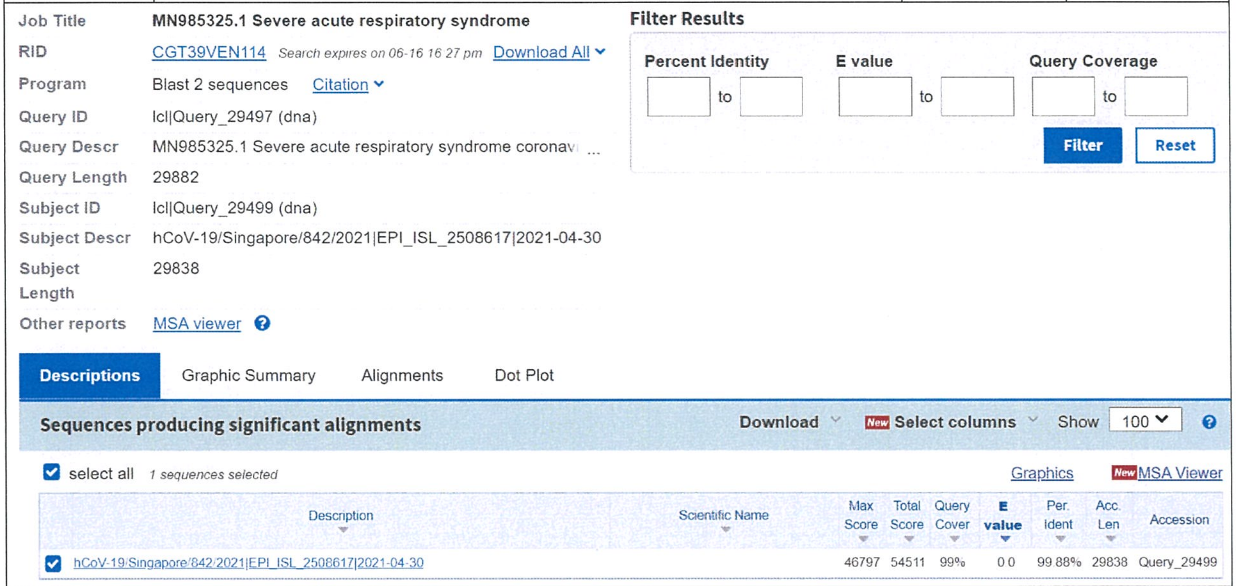
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGSYNXWP114 *Search expires on 06-16 16.24 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_49311 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_49313 (dna)
Subject Descr	hCoV-19/India/WB-1931500912396/2021|EPI_ISL_1419 ...
Subject Length	1259
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/India/WB-1931500912396/2021|EPI_ISL_1419152|2021-03-04		2182	2182	94%	0.0	99.66%	29769	Query_49313

Sequence	Lineage B.1.617.3 (India variant) GISAID accession ID: EPI_ISL_2508617	**Range**	Whole sequence



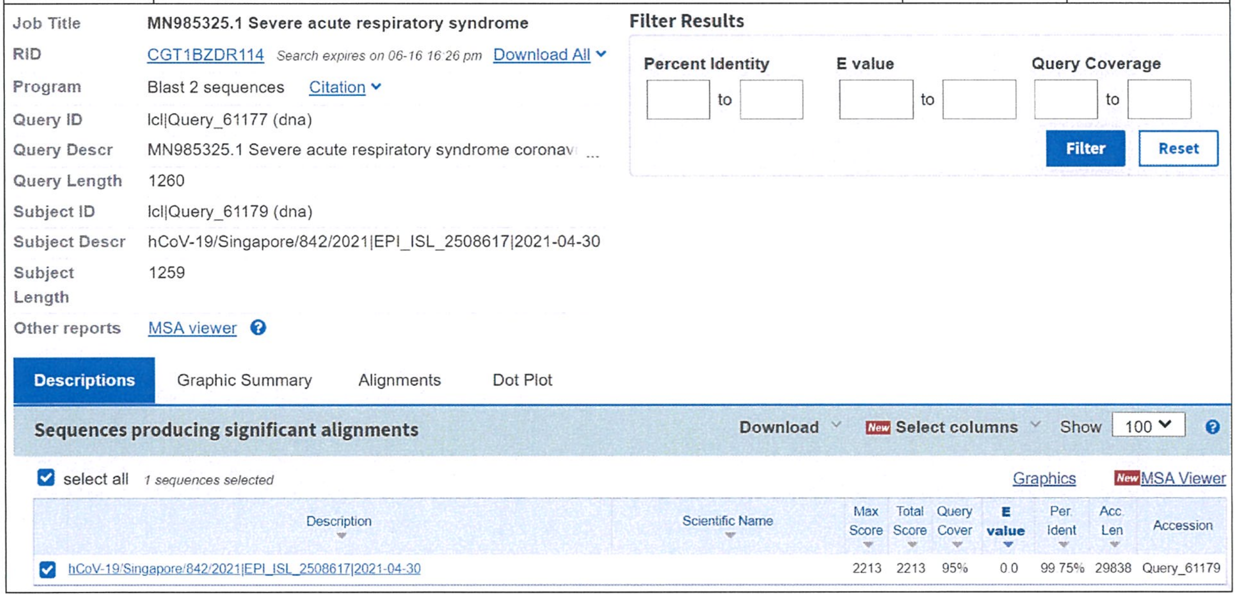
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGT39VEN114 *Search expires on 06-16 16 27 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_29497 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_29499 (dna)
Subject Descr	hCoV-19/Singapore/842/2021|EPI_ISL_2508617|2021-04-30
Subject Length	29838
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



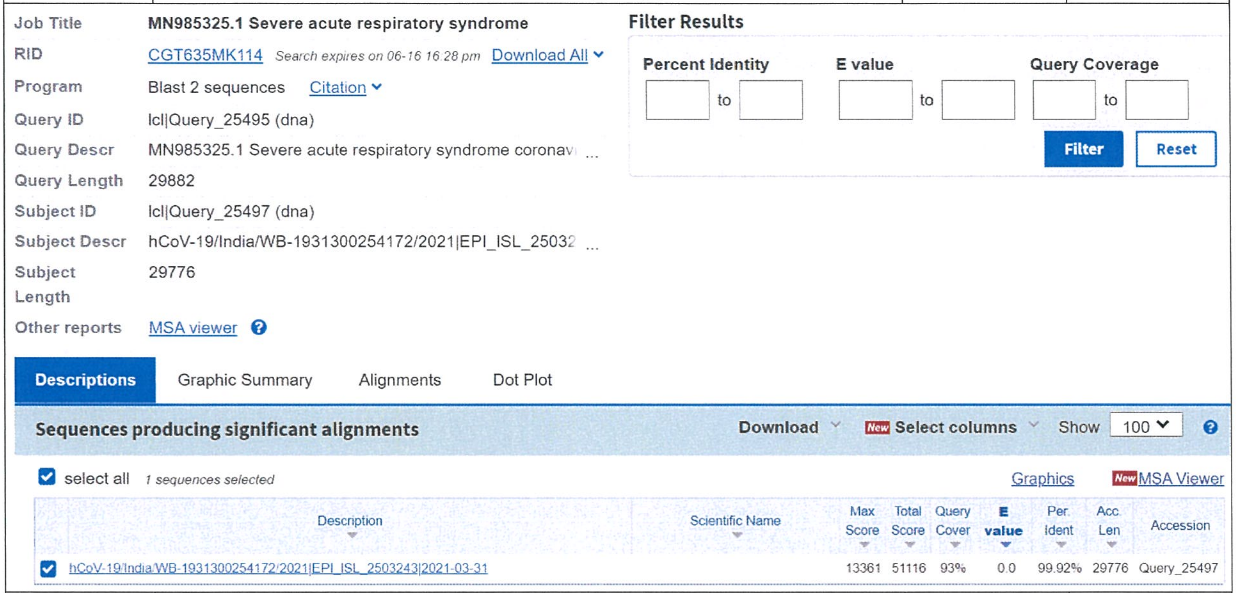
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CGT1BZDR114 *Search expires on 06-16 16 26 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_61177 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_61179 (dna)
Subject Descr	hCoV-19/Singapore/842/2021|EPI_ISL_2508617|2021-04-30
Subject Length	1259
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Singapore/842/2021|EPI_ISL_2508617|2021-04-30		2213	2213	95%	0.0	99.75%	29838	Query_61179

Sequence	Lineage B.1.618 (India variant) GISAID accession ID: EPI_ISL_2503243	**Range**	Whole sequence



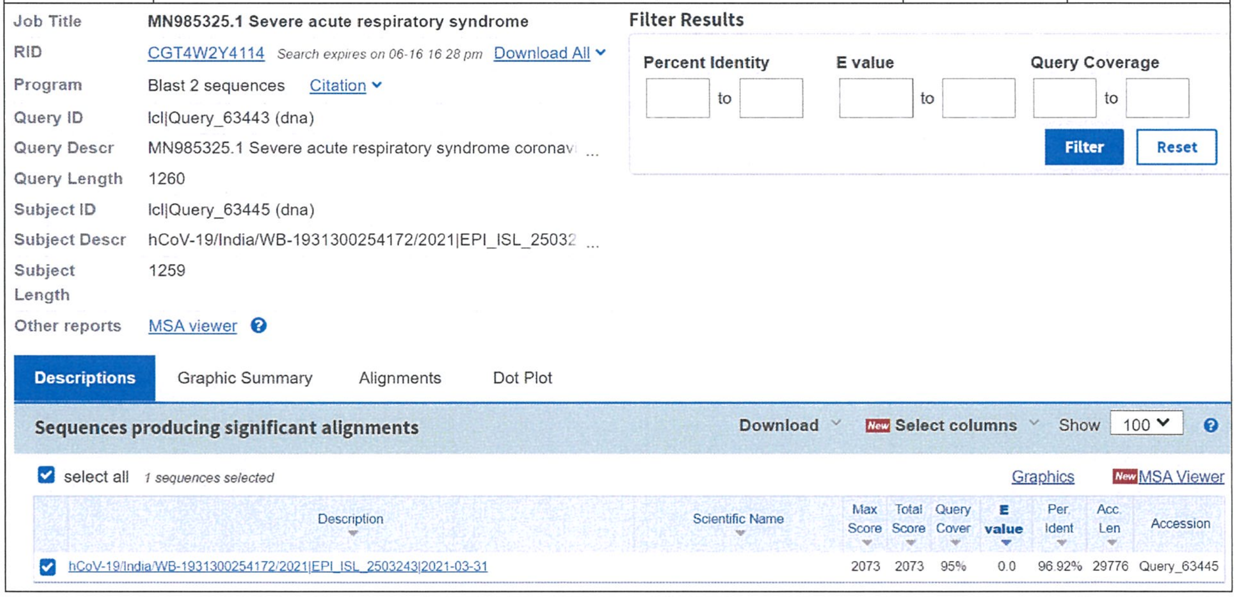
Job Title MN985325.1 Severe acute respiratory syndrome
RID CGT635MK114 *Search expires on 06-16 16 28 pm* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_25495 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 29882
Subject ID lcl|Query_25497 (dna)
Subject Descr hCoV-19/India/WB-1931300254172/2021|EPI_ISL_25032 ...
Subject Length 29776
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



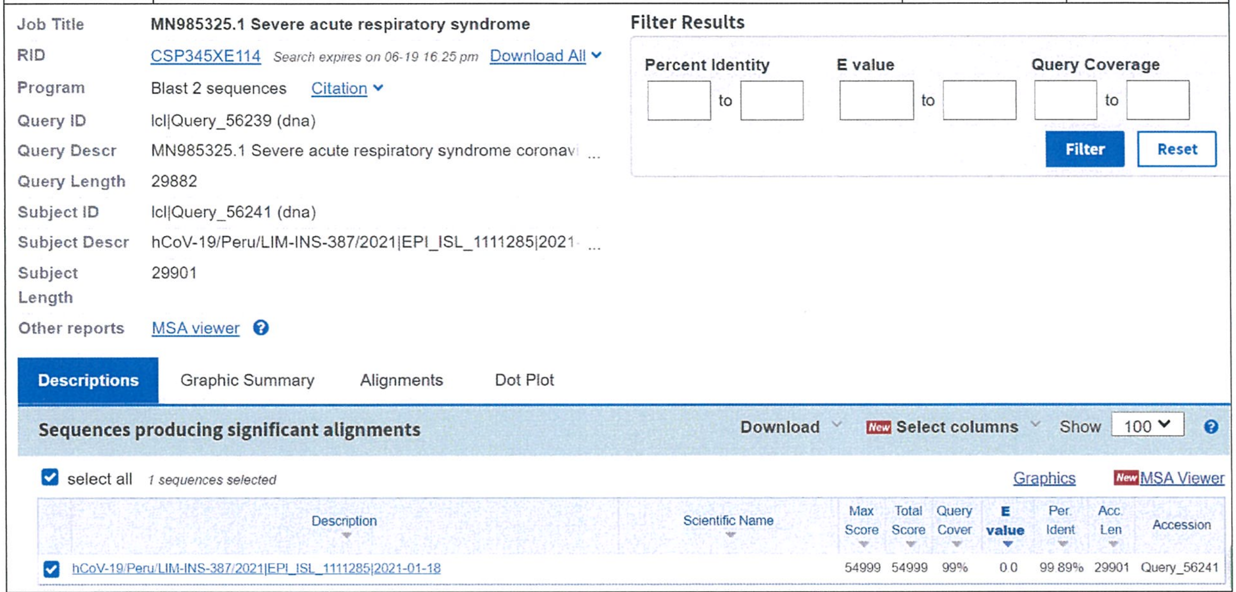
Job Title MN985325.1 Severe acute respiratory syndrome
RID CGT4W2Y4114 *Search expires on 06-16 16 28 pm* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_63443 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 1260
Subject ID lcl|Query_63445 (dna)
Subject Descr hCoV-19/India/WB-1931300254172/2021|EPI_ISL_25032 ...
Subject Length 1259
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/India/WB-1931300254172/2021|EPI_ISL_2503243|2021-03-31		2073	2073	95%	0.0	96.92%	29776	Query_63445

Sequence	Lineage C.37 (Lambda variant) GISAID accession ID: EPI_ISL_1111285	**Range**	Whole sequence



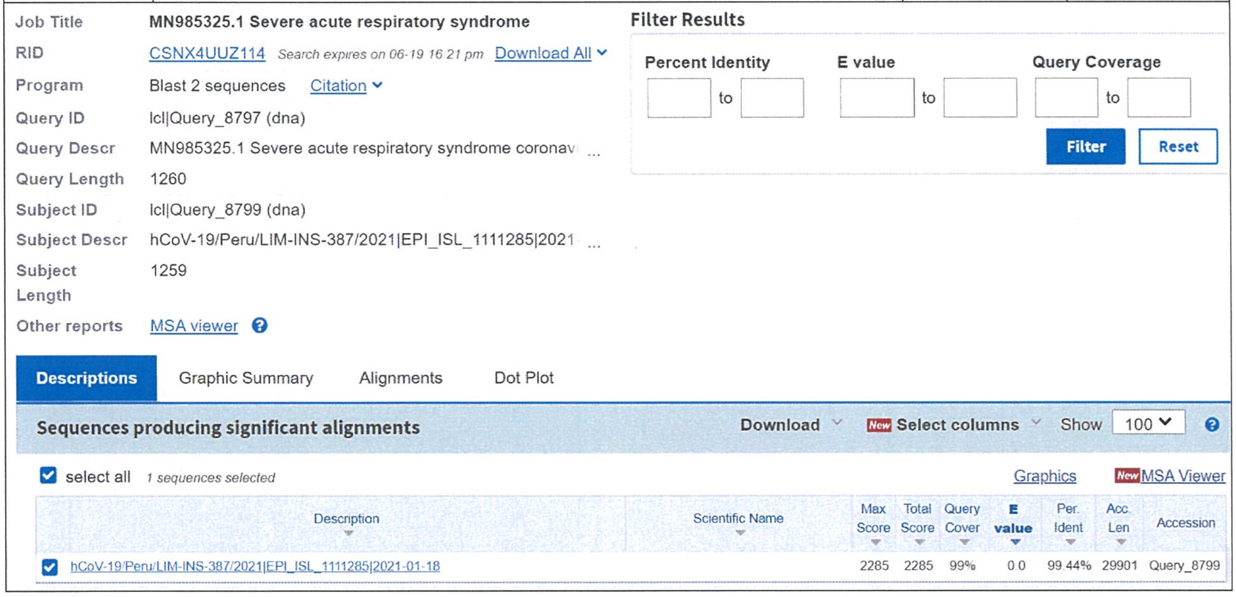
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CSP345XE114 *Search expires on 06-19 16 25 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_56239 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	29882
Subject ID	lcl|Query_56241 (dna)
Subject Descr	hCoV-19/Peru/LIM-INS-387/2021|EPI_ISL_1111285|2021- ...
Subject Length	29901
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



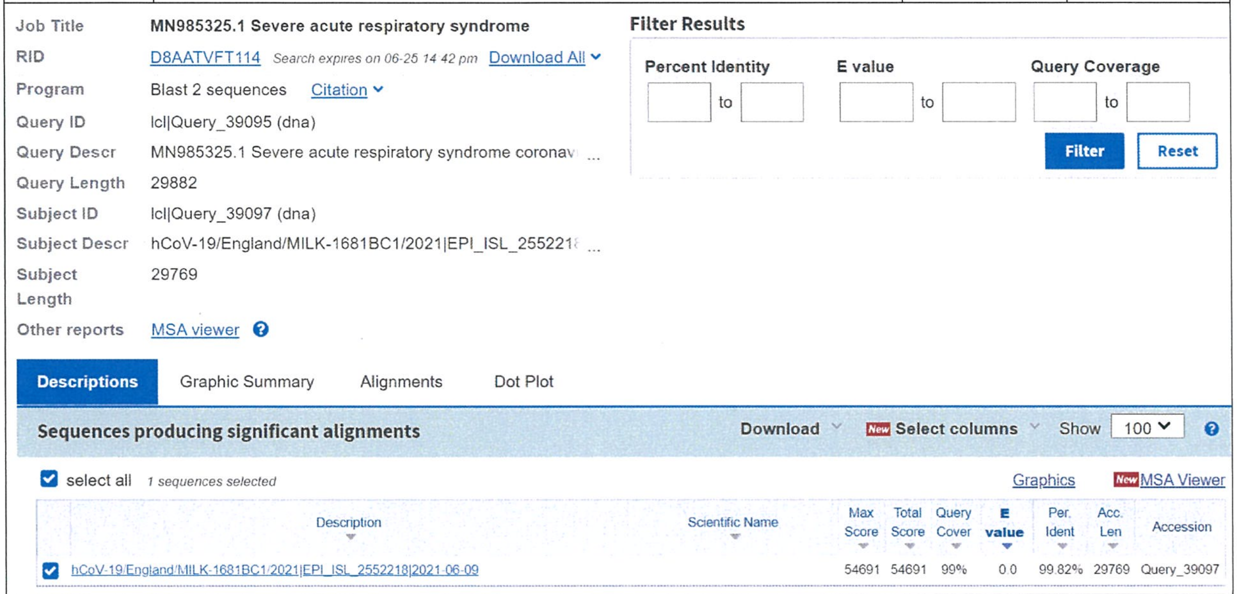
Job Title	**MN985325.1 Severe acute respiratory syndrome**
RID	CSNX4UUZ114 *Search expires on 06-19 16 21 pm* Download All
Program	Blast 2 sequences Citation
Query ID	lcl|Query_8797 (dna)
Query Descr	MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length	1260
Subject ID	lcl|Query_8799 (dna)
Subject Descr	hCoV-19/Peru/LIM-INS-387/2021|EPI_ISL_1111285|2021- ...
Subject Length	1259
Other reports	MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Peru/LIM-INS-387/2021|EPI_ISL_1111285|2021-01-18		2285	2285	99%	0.0	99.44%	29901	Query_8799

Sequence	Lineage AY.1 (Delta plus variant) GISAID accession ID: EPI_ISL_2552218	**Range**	Whole sequence



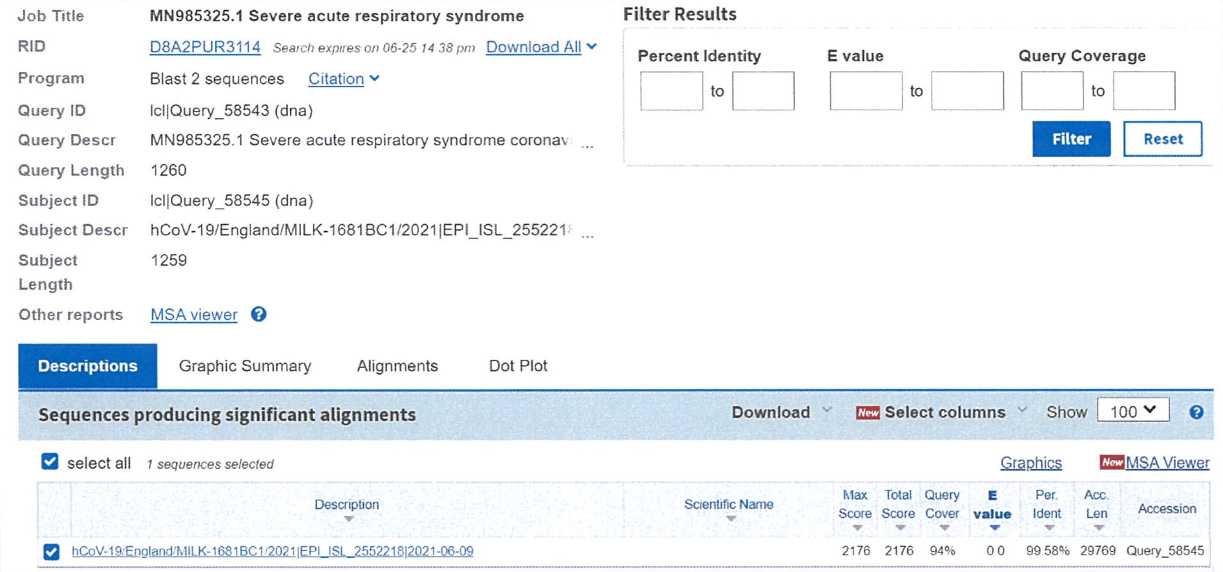
Job Title: **MN985325.1 Severe acute respiratory syndrome**
RID: D8AATVFT114 *Search expires on 06-25 14 42 pm* Download All
Program: Blast 2 sequences Citation
Query ID: lcl|Query_39095 (dna)
Query Descr: MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length: 29882
Subject ID: lcl|Query_39097 (dna)
Subject Descr: hCoV-19/England/MILK-1681BC1/2021|EPI_ISL_255221 ...
Subject Length: 29769
Other reports: MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/England/MILK-1681BC1/2021|EPI_ISL_2552218|2021-06-09		54691	54691	99%	0.0	99.82%	29769	Query_39097

Sequence	Lineage AY.1 (Delta plus variant) GISAID accession ID: EPI_ISL_2552218	**Range**	Nucleocapsid protein



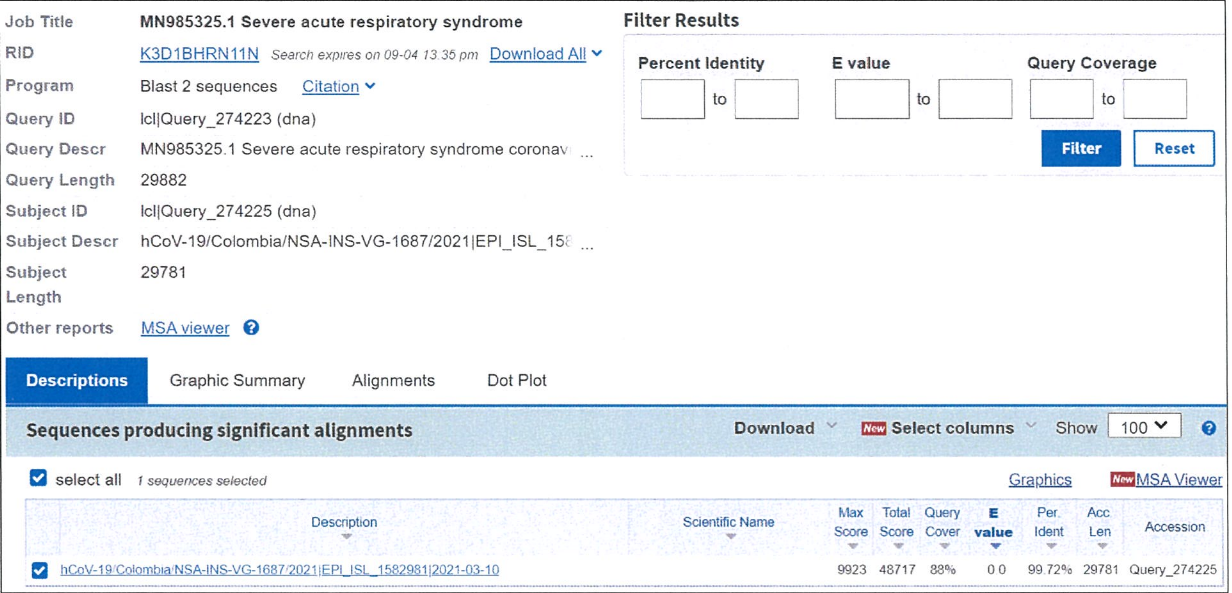
Job Title: **MN985325.1 Severe acute respiratory syndrome**
RID: D8A2PUR3114 *Search expires on 06-25 14 38 pm* Download All
Program: Blast 2 sequences Citation
Query ID: lcl|Query_58543 (dna)
Query Descr: MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length: 1260
Subject ID: lcl|Query_58545 (dna)
Subject Descr: hCoV-19/England/MILK-1681BC1/2021|EPI_ISL_255221 ...
Subject Length: 1259
Other reports: MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/England/MILK-1681BC1/2021|EPI_ISL_2552218|2021-06-09		2176	2176	94%	0.0	99.58%	29769	Query_58545

Sequence	Lineage B.1.621 (Mu variant 1) GISAID accession ID: EPI_ISL_1582981	**Range**	Whole sequence



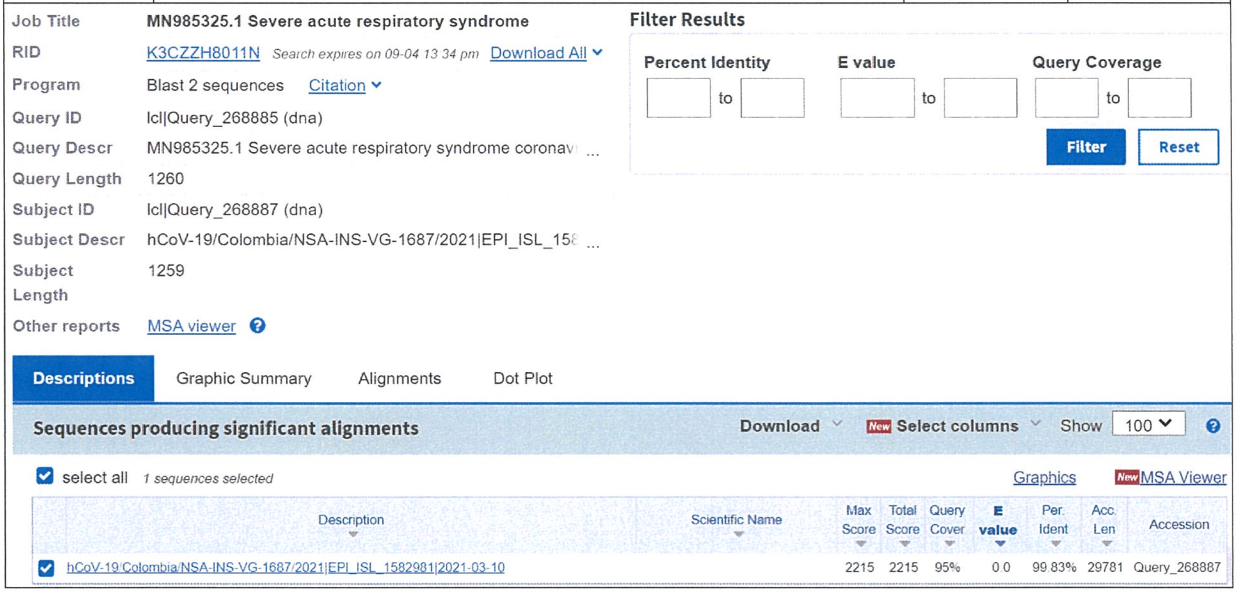
Job Title MN985325.1 Severe acute respiratory syndrome
RID K3D1BHRN11N *Search expires on 09-04 13:35 pm* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_274223 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 29882
Subject ID lcl|Query_274225 (dna)
Subject Descr hCoV-19/Colombia/NSA-INS-VG-1687/2021|EPI_ISL_15 ...
Subject Length 29781
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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



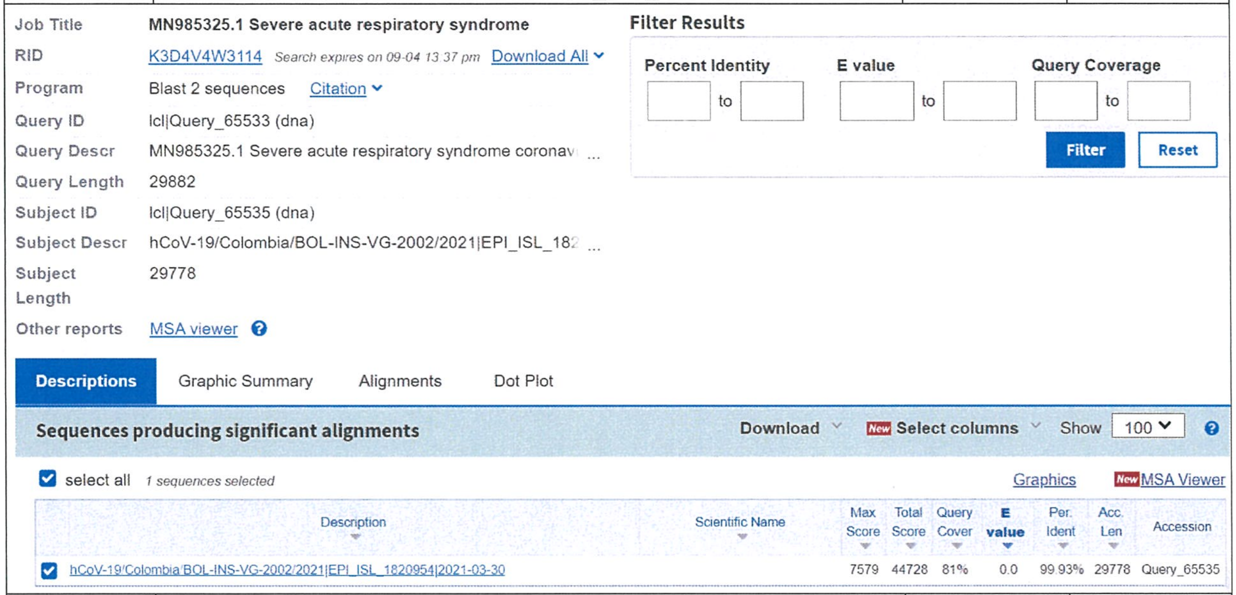
Job Title MN985325.1 Severe acute respiratory syndrome
RID K3CZZH8011N *Search expires on 09-04 13:34 pm* Download All
Program Blast 2 sequences Citation
Query ID lcl|Query_268885 (dna)
Query Descr MN985325.1 Severe acute respiratory syndrome coronav ...
Query Length 1260
Subject ID lcl|Query_268887 (dna)
Subject Descr hCoV-19/Colombia/NSA-INS-VG-1687/2021|EPI_ISL_15 ...
Subject Length 1259
Other reports MSA viewer

Sequences producing significant alignments

☑ select all *1 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Colombia/NSA-INS-VG-1687/2021|EPI_ISL_1582981|2021-03-10		2215	2215	95%	0.0	99.83%	29781	Query_268887

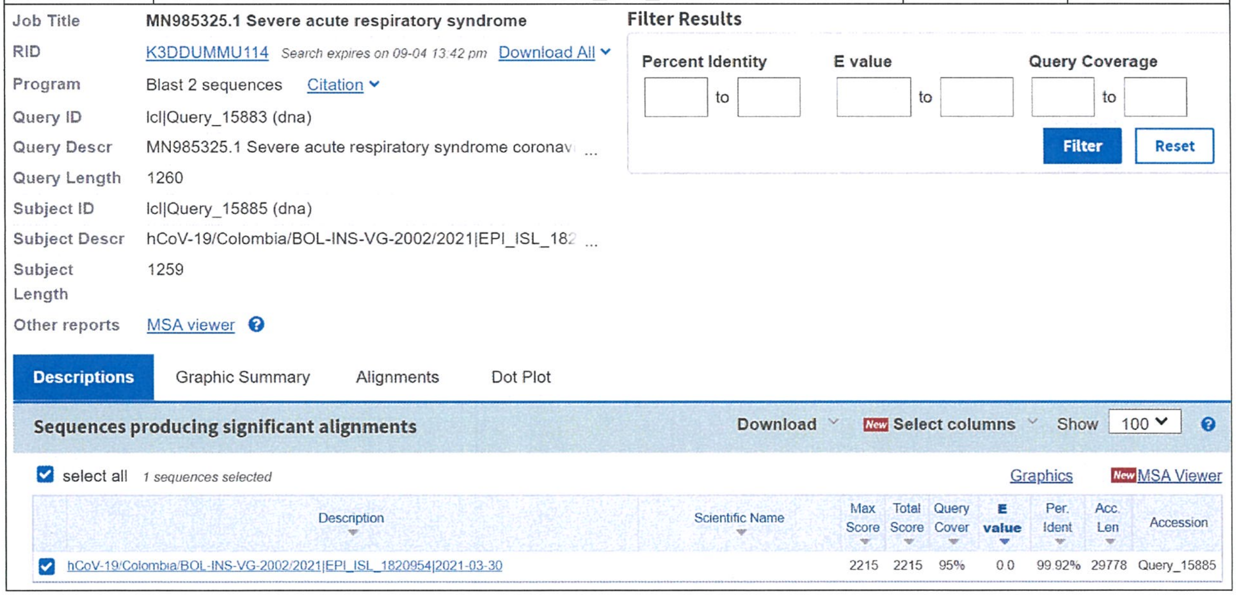
Sequence	Lineage B.1.621.1 (Mu variant 2) GISAID accession ID: EPI_ISL_1820954	**Range**	Whole sequence



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 coronav ...
Query Length	29882
Subject ID	lcl|Query_65535 (dna)
Subject Descr	hCoV-19/Colombia/BOL-INS-VG-2002/2021|EPI_ISL_182 ...
Subject Length	29778
Other reports	MSA viewer

☑	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	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 coronav ...
Query Length	1260
Subject ID	lcl|Query_15885 (dna)
Subject Descr	hCoV-19/Colombia/BOL-INS-VG-2002/2021|EPI_ISL_182 ...
Subject Length	1259
Other reports	MSA viewer

☑	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	hCoV-19/Colombia/BOL-INS-VG-2002/2021|EPI_ISL_1820954|2021-03-30		2215	2215	95%	0.0	99.92%	29778	Query_15885