



BARBARA FERRER, Ph.D., M.P.H., M.Ed.  
**Director**

MUNTU DAVIS, M.D., M.P.H.  
**County Health Officer**

MEGAN McCLAIRE, M.S.P.H.  
**Chief Deputy Director**

JEFFREY D. GUNZENHAUSER, M.D., M.P.H.  
**Director, Disease Control Bureau**

NICOLE M. GREEN, Ph.D., D(ABMM)  
**Director, Public Health Laboratories**  
 12750 Erickson Avenue  
 Downey, CA 90242  
 TEL (562) 658-1330 • FAX (562) 401-5999

[www.publichealth.lacounty.gov](http://www.publichealth.lacounty.gov)

BOARD OF SUPERVISORS

Hilda L. Solis  
**First District**  
 Holly J. Mitchell  
**Second District**  
 Sheila Kuehl  
**Third District**  
 Janice Hahn  
**Fourth District**  
 Kathryn Barger  
**Fifth District**

**February 20, 2021**

**SUBJECT: SARS-COV2 SEQUENCING RESULTS**

**Cumulative Summary of Sequencing Efforts:**

Samples successfully sequenced to date	XXX	
Samples in current run	XX/XX successful (XX samples failed)	
Variant analysis	Current Run	Cumulative Total
UK Variant 20I/501Y.V1, Lineage B.1.1.7	X	X
South African Variant 20H/501Y.V2 Lineage B.1.351	X	X
Japanese/Brazilian Variant 20J/501Y.V3 Lineage B.1.1.28/B.1.1.248/P.1	X	X
Rio de Janeiro/Brazilian Variant 20B Lineage B.1.1.28(E484K)/P.2	X	X
Information related to L452R variant	Cumulative Total	
Number of samples classified as clade 20C	X	
Number of samples with Spike L452R mutation	X	
Number of samples with 5-site mutations (Lineage B.1.429 - Spike L452R, Spike S13I, Spike W152C, ORF1a I4205V, and ORF1b D1183Y)	X	

\*See Appendix for details.

**Current Report:**

LACPHL successfully performed SARS-CoV-2 whole genome sequencing (WGS) on XX respiratory samples consisting of specimens submitted to LACPHL for COVID-19 testing, specimen referred from clinical laboratories for sequencing, and specimens collected as part of an outbreak investigation at XXX.

Details of each specimen are described in the table below.

**Table 1** Details on specimens included in this report

Sample ID	PHL Accession#	Collection Date (YYYY-MM-DD)	Submitter
1	XXXXX	YYYY-MM-DD	X
2	XXXXX	YYYY-MM-DD	X
3	XXXXX	YYYY-MM-DD	X
4	XXXXX	YYYY-MM-DD	X
5	XXXXX	YYYY-MM-DD	X
6	XXXXX	YYYY-MM-DD	X
7	XXXXX	YYYY-MM-DD	X
8	XXXXX	YYYY-MM-DD	X
9	XXXXX	YYYY-MM-DD	X
10	XXXXX	YYYY-MM-DD	X
11	XXXXX	YYYY-MM-DD	X
12	XXXXX	YYYY-MM-DD	X
13	XXXXX	YYYY-MM-DD	X
14	XXXXX	YYYY-MM-DD	X
15	XXXXX	YYYY-MM-DD	X
16	XXXXX	YYYY-MM-DD	X
17	XXXXX	YYYY-MM-DD	X
18	XXXXX	YYYY-MM-DD	X
19	XXXXX	YYYY-MM-DD	X
20	XXXXX	YYYY-MM-DD	X

**Whole-Genome Sequencing and Data Analysis:**

Total nucleic acid from each remnant specimen was used as a template for cDNA synthesis and tiling PCR using ARTIC primers version 3 (<https://artic.network/resources/ncov/ncov-amplicon-v3.pdf>). PCR products were used as input for sequencing library preparation using Illumina DNA Prep Kit and IDT for Illumina DNA/RNA UD Indexes Set A or B. Libraries were pooled and sequenced on Illumina MiSeq platform using MiSeq Sequencing Reagent V2 (2 x 250). A Human Specimen Control (prepared from cultured human cell line) was included as a negative control throughout the process. Raw data was processed using Monroe v1.0.0 pipeline ([https://staph-b.github.io/staphb\\_toolkit/workflow\\_docs/monroe/](https://staph-b.github.io/staphb_toolkit/workflow_docs/monroe/)). SARS-CoV-2 clade determination and mutation identification was determined using NextClade (<https://clades.nextstrain.org/>). Lineage analysis was performed using Pangolin v2.1.7 (<https://pangolin.cog-uk.io/>) with the most updated lineage database at the time of analysis (database dated 2/18/21).

**Criteria for sequence passing QC:**

- Percent genome coverage > 90%
- Mean sequencing depth > 1000
- Mean base quality > 30
- Mean mapping quality > 30

Results are described in the following pages.

## 1. WGS Sequence Quality and Clade/Lineage Analysis

Table 2 Summary of SARS-CoV-2 WGS Sequence Quality and Clade/Lineage

Sample ID	PHL Accession#	Percent Coverage	Mean Seq Depth	Mean Base Quality	Mean Mapping Quality	Clade	Lineage	L452R Mutation	5-site Mutation*
<b>1</b>	<b>XXXXX</b>	<b>99.5084</b>	<b>4059.43</b>	<b>38.2</b>	<b>51.2</b>	<b>20I/501Y.V1</b>	<b>B.1.1.7</b>	<b>-</b>	<b>-</b>
2	XXXXX	99.5051	3083.51	38.2	51.1	20C	B.1	-	-
3	XXXXX	99.1673	3842.79	38.2	51.2	20C	B.1.429	+	+
4	XXXXX	99.5719	4369.95	38.2	52.2	20C	B.1.429	+	+
5	XXXXX	99.7994	1867.66	38.2	51.4	20C	B.1.429	+	+
6	XXXXX	99.5586	4286.85	38.2	51.4	20C	B.1.429	+	+
7	XXXXX	99.6054	3434.04	38.2	51.1	20C	B.1.429	+	+
8	XXXXX	99.5184	2599.83	38.2	51.4	20C	B.1.427	+	-
9	XXXXX	99.6321	3550.51	38.2	51.5	20C	B.1.427	+	-
10	XXXXX	99.7224	3610.66	38.2	51.2	20C	B.1.427	+	-
11	XXXXX	99.2609	1267.53	38.2	51.3	20C	B.1.429	+	+
12	XXXXX	99.8361	4598.37	38.3	56.1	20C	B.1.429	+	+
13	XXXXX	99.3178	1642.89	38.2	51.1	20C	B.1.429	+	+
14	XXXXX	99.3914	1710.45	38.2	51.6	20C	B.1.429	+	+
15	XXXXX	99.388	2146.21	38.2	51	20C	B.1.429	+	+
16	XXXXX	99.9431	2131.05	38.2	51.2	20C	B.1.427	+	-
17	XXXXX	99.6489	1653.49	38.2	51.9	20C	B.1.429	+	+
18	XXXXX	95.89	1555.11	38.2	51.4	20C	B.1.429	+	+
19	XXXXX	99.4181	3116.74	38.2	51.5	20C	B.1.429	+	+
20	XXXXX	98.7125	1683.19	38.2	51.1	20C	B.1.429	+	+

\* Spike L452R, Spike S13I, Spike W152C, ORF1a I4205V, and ORF1b D1183Y

Note: UK VOC-202012/01 Variant is of Clade 20I/501Y.V1 and Lineage B.1.1.7.

South African Variant is of Clade 20H/501Y.V2 and Lineage B.1.351

Japanese/Brazilian Variant is of Clade 20J/501Y.V3 and Lineage B.1.1.248 or P.1

Rio de Janeiro/Brazilian Variant is of Clade 20B Lineage B.1.1.28(E484K) or P.2

## 2. Mutational Analysis of Samples

Table 3 List of genetic alterations in each sequenced sample (comparison to Wuhan-Hu-1 strain GenBank: MN908947.3)

Sample ID	PHL Accession#	Genetic Alteration* (Gene Name:Alteration)		
		Substitutions	Deletions	Insertions
1	XXXXX	N:M1X, <b>N:D3L,N:R203K,N:G204R,N:S235F,ORF1a:T1001I,ORF1a:A1708D</b> ,ORF1a:K2143N,ORF1b:P314L,ORF1b:K1383R,ORF1b:E1871G,ORF3a:A99T, <b>ORF8:Q27*,ORF8:R52I,ORF8:Y73C,S:N501Y,S:A570D,S:D614G,S:P681H,S:T716I,S:S982A,S:D1118H</b>	<b>ORF1a:S3675-F3677-,S:H69-V70-,S:Y144-</b>	None
2	XXXXX	N:T205I,ORF1a:T265I,ORF1a:P885L,ORF1a:A1473V,ORF1a:L3951F,ORF1a:T4249I,ORF1b:H73Y,ORF1b:P314L,ORF1b:A1291S,ORF1b:R1737L,ORF1b:S2258N,ORF3a:Q57H,ORF3a:L85F,ORF8:S24L,ORF8:P70L,ORF8:Q72H, <b>S:D614G</b>	None	None
3	XXXXX	N:T205I, <b>N:M234I</b> ,ORF1a:T265I,ORF1a:T814I, <b>ORF1a:I4205V</b> ,ORF1a:D4218N,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:V100L, <b>S:S13I,S:V62F,S:W152C,S:L452R,S:D614G</b>	None	None
4	XXXXX	N:T205I,ORF1a:T265I,ORF1a:T2978I,ORF1a:M3780V, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
5	XXXXX	N:T205I, <b>N:M234I</b> ,ORF1a:T265I,ORF1a:L3210F,ORF1a:K3215R,ORF1a:N3243K, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:V100L, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
6	XXXXX	N:T205I,ORF1a:T265I,ORF1a:M2606I,ORF1a:A2994V, <b>ORF1a:I4205V</b> ,ORF1b:P314L,ORF1b:G1129C, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:E110*, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
7	XXXXX	N:T205I,ORF1a:T265I,ORF1a:S376L,ORF1a:K1280N, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF1b:Q1878R,ORF3a:Q57H, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	ORF1a:F1028-S1029-	None
8	XXXXX	N:T205I,ORF1a:T265I,ORF1a:P1472S,ORF1a:T2877I,ORF1a:S3158T,ORF1b:P314L,ORF1b:P976L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:A65V,ORF8:I74V, <b>S:S13I,S:W258L,S:L452R,S:D614G</b>	None	None
9	XXXXX	N:T205I,ORF1a:T265I,ORF1a:T2877I,ORF1a:S3158T,ORF1b:P314L,ORF1b:P976L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:A65V, <b>S:S13I,S:W152C,S:W258L,S:L452R,S:D614G</b>	None	None
10	XXXXX	N:T205I,ORF1a:T265I,ORF1a:T2877I,ORF1a:S3158T,ORF1b:P314L,ORF1b:P976L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:A65V, <b>S:S13I,S:W258L,S:L452R,S:D614G</b>	None	None
11	XXXXX	N:T205I,ORF1a:T265I,ORF1a:M2606I,ORF1a:A2994V, <b>ORF1a:I4205V</b> ,ORF1b:P314L,ORF1b:G1129C, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:E110*, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
12	XXXXX	N:T205I,ORF1a:T265I,ORF1a:M2606I,ORF1a:A2994V, <b>ORF1a:I4205V</b> ,ORF1b:P314L,ORF1b:G1129C, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:E110*, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
13	XXXXX	N:T205I,ORF1a:T265I,ORF1a:T3459M, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:D35Y, <b>S:S13I,S:W152C,S:L452R,S:S494P,S:D614G</b>	None	None
14	XXXXX	N:T205I, <b>N:M234I</b> ,ORF1a:T265I,ORF1a:T1474I, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:W45S,ORF8:V100L, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
15	XXXXX	N:T205I, <b>N:M234I</b> ,ORF1a:T265I,ORF1a:L3210F,ORF1a:K3215R,ORF1a:N3243K, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:V100L, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
16	XXXXX	N:T205I,ORF1a:T265I,ORF1a:S3158T,ORF1b:P314L,ORF1b:P976L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None
17	XXXXX	N:T205I,N:G238C,N:D348H,ORF1a:T265I,ORF1a:I1128V,ORF1a:T3459M, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:K21R,ORF3a:Q57H, <b>S:S13I,S:W152C,S:G181A,S:L452R,S:D614G</b>	None	None

18	W44929	N:T205I,ORF1a:T265I,ORF1a:A2279T, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H, <b>S:S13I,S:P26S,S:W152C,S:L452R,S:D614G</b>	None	None
19	W44930	N:T205I,N:S413I,ORF1a:T265I, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF9b:S50L, <b>S:S13I,S:P26S,S:W152C,S:L452R,S:D614G</b>	None	None
20	W44934	N:T205I, <b>N:M234I</b> ,ORF1a:T265I,ORF1a:Q362R,ORF1a:D2299N, <b>ORF1a:I4205V</b> ,ORF1b:P314L, <b>ORF1b:D1183Y</b> ,ORF3a:Q57H,ORF8:V100L, <b>S:S13I,S:W152C,S:L452R,S:D614G</b>	None	None

\*In comparison to Wuhan-Hu-1 strain (GenBank: MN908947.3)

EXAMPLE

### **Result Interpretation:**

1. We identified one additional sample containing the UK 20I/501Y.V1 Variant from XXXXX.
2. For all other samples in this run, we did not detect patterns of mutations indicative of the the South African 20H/501Y.V2 Variant, the Japanese/Brazilian 20J/501Y.V3/P.1 Variant, and the Rio de Janeiro/Brazilian 20B/B.1.1.28(E484K)/P.2 Variant.

### **Cumulative Summary:**

For this sequencing run, we identified one additional sample containing the UK 20I/501Y.V1 Variant. We have not identified samples containing the South African 20H/501Y.V2 Variant, the Japanese/Brazilian 20J/501Y.V3 Variant, or the Rio de Janeiro/Brazilian 20B/B.1.1.28(E484K)/P.2 Variant.

### **Disclaimer:**

Interpretations are provided as heuristic guidelines only, based on review of literature, SNP, and phylogenetic analysis. Relationships among strains should be determined in conjunction with clinical, microbiologic, and epidemiologic information. This report may be used for investigational purposes and outbreak investigations only, where an outbreak has been determined by ACD program epidemiologists and is to be distinguished from a surveillance report. This analysis may not be used as a replacement for a thorough epidemiological investigation. This report may not be used for individual patient diagnostic purposes.

Testing performed by: **XXX XXXXXXXXXXX, PHM**  
**XXX XXXXXXXXXXX, CLS**

Report prepared by: **Peera Hemarajata, MD, PhD, D(ABMM)**

Report reviewed by: **Nicole M. Green, PhD, D(ABMM)**

## Appendix

Variant-defining mutations for the UK 20I/501Y.V1 Variant, South African 20H/501Y.V2 Variant, and Japanese/Brazilian B.1.1.248/P.1 Variant

Gene	Nucleotide	Amino acid	UK 20I/501Y.V1	SA 20H/501Y.V2	JP/BZ P.1	BZ P.2
ORF1ab	C1059T	T265I		+		
	C3267T	T1001I	+			
	C3828T	S1188L			+	
	G28048T	K1655N		+		
	5230T	A1708D	+			
	A5648C	K1795Q			+	
	T6954C	I2230T	+			
	A10323G	K3353R		+		
	T10667G	L3468V				+
	11288-11296 del	SGF 3675-3677 del	+			
	C12053T	L3930F				+
Spike	C21614T	L18F			+	
	C21621A	T20N			+	
	C21638T	P26S			+	
	21765-21770 del	HV 69-70 del	+			
	A21801C	D80A		+		
	G21974T	D138Y				
	21991-21993 del	Y144 del	+			
	G22132T	R190S			+	
	A22812C	K417T			+	
	G22813T	K417N		+		
	G23012A	E484K		+	+	+
	A23063T	N501Y	+	+	+	
	C23271A	A570D	+			
	A23403G	D614G	+	+	+	+
	C23525T	H655Y			+	
	C23604A	P681H	+			
	C23664T	A701V		+		
	C23709T	T716I	+			
	T24506G	S982A	+			
	C24642T	T1027I			+	
G24914C	D1118H	+				
G25088T	V1176F				+	
Orf8	C27972T	Q27stop	+			
	G28048T	R52I	+			
	A28111G	Y73C	+			
G28167A	E92K			+		
ORF3a	G25563T	Q57H		+		
	C25904T	S171L		+		
E	C26456T	P71L		+		
N	28280 GAT->CTA	D3L	+			
	C26456T	P71L		+		
	C28512G	P80R			+	
	G28628T	A119S				+
	G28882A	R203K				+
	G28883C	G204R				+
	G28975T	M234I				+
	C28977T	S235F	+			

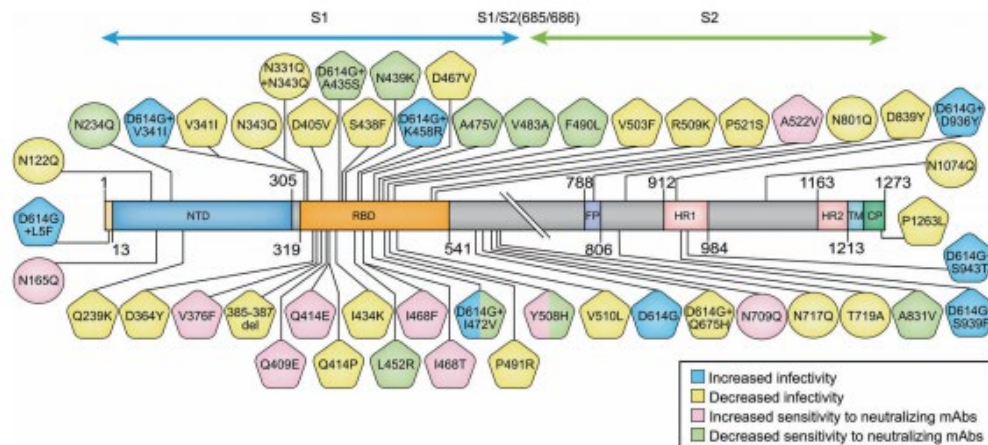
Table of mutations associated with phenotype – From Li et al. 2020. Cell. 182:1284–1294.

**Table 1. Characteristics of Variants and Mutants**

	Group A	Group B	Group C
Number of variants or mutants	29	51	26
Increased infectivity	D614G, D614G+L5F, D614G+D936Y, D614G+S939F, D614G+S943T	D614G+V341I, D614G+K458R, D614G+I472V <sup>a</sup>	none
Decreased infectivity	Q239K, D839Y, P1263L, D614G+Q675H	V341I, D364Y, 385-387del, D405V, Q414P, I434K, S438F, D467V, P491R, V503F, R509K, V510L, P521S	N122Q, N343Q, N717Q, T719A, N801Q, N1074Q, N331Q+N343Q
Increased sensitivity to neutralizing mAbs	none	V367F, Q409E, Q414E, I468F, I468T, Y508H, A522V	N165Q, N709Q
Decreased sensitivity to neutralizing mAbs	A831V	N439K, L452R, A475V, V483A, F490L, Y508H, D614G+A435S, D614G+I472V <sup>a</sup>	N234Q
Increased sensitivity to convalescent sera	V615L	F338L, V367F, I468F, I468T	N149H, N149Q, N165Q, N331Q, N354D, N709Q, N1173Q
Decreased sensitivity to convalescent sera	Y145del, A831V, D614G+A831V, D614G+A879S, D614G+M1237I	Q414E, N439K, G446V, K458N, I472V, A475V, T478I, V483I, F490L, H519P, D614G+Q321L, D614G+I472V <sup>a</sup>	none

<sup>a</sup>D614G+I472V is the only variant with increased infectivity and decreased sensitivity to neutralizing mAb and convalescent sera. It is of note only one sequence is recorded in GISAID.

Diagram of mutations associated with phenotype – From Wang et al. 2020. Signal Transduction and Targeted Therapy. 5:185.





**Summary of Variants of Concern (VOCs) In Specimens Collected from LAC Residents**

#	Date Reported or Confirmed by DPH	Identified By	Patient Name	DOB	Notes	Clade	Lineage	Acc# or GISAID ID	Collection Date
1	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
2	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
3	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
4	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
5	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
6	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
7	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY
8	MM/DD/YY	XXXXX	XXXXX	MM/DD/YY	XXXXX	20I/501Y.V1	B.1.1.7	XXXXX	MM/DD/YY

EXAMPLE

## References

1. "Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations". Available at: <https://virological.org/t/preliminary-genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-the-uk-defined-by-a-novel-set-of-spike-mutations/563>
2. "Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa" Available at: <https://www.medrxiv.org/content/10.1101/2020.12.21.20248640v1.full>
3. "New mutant strain of new coronavirus detected in returnees from Brazil" Available at: <https://www.niid.go.jp/niid/ja/diseases/ka/corona-virus/2019-ncov/10107-covid19-33.html>
4. "Genetic Characteristics and Phylogeny of 969-bp S Gene Sequence of SARS-CoV-2 from Hawaii Reveals the Worldwide Emerging P681H Mutation" Available at: <https://www.biorxiv.org/content/10.1101/2021.01.06.425497v1>
5. "The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity" Available at: <https://www.cell.com/cell/pdf/S0092-8674%2820%2930877-1.pdf>
6. "Profiling and characterization of SARS-CoV2 mutants' infectivity and antigenicity" Available at: [https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7471320/pdf/41392\\_2020\\_Article\\_302.pdf](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7471320/pdf/41392_2020_Article_302.pdf)
7. "Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil" Available at: <https://www.medrxiv.org/content/10.1101/2020.12.23.20248598v1.full>
8. "Genomic Evidence of a Sars-Cov-2 Reinfection Case With E484K Spike Mutation in Brazil" Available at: <https://www.preprints.org/manuscript/202101.0132/v1>
9. Emerging SARS-COV2 Variants. CDC. Available at: <https://www.cdc.gov/coronavirus/2019-ncov/more/science-and-research/scientific-brief-emerging-variants.html>
10. "Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence". Available at: [https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(21\)00183-5/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)00183-5/fulltext)
11. "Global variation in the SARS-CoV-2 proteome reveals the mutational hotspots in the drug and vaccine candidates". Available at: <https://www.biorxiv.org/content/10.1101/2020.07.31.230987v3>