

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active. Contents lists available at ScienceDirect

# Virus Research



# Mutational cascade of SARS-CoV-2 leading to evolution and emergence of omicron variant

Kanika Bansal<sup>a,\*</sup>, Sanjeet Kumar<sup>b,\*</sup>

<sup>a</sup> CSIR-Institute of Microbial Technology, Chandigarh, India
 <sup>b</sup> Gangadhar Meher University, Sambalpur, Odisha, India

### ARTICLE INFO

#### Keywords:

SARS-CoV-2, COVID-19, genome-wide, evolution, variants, VOC, VOI, VUM, SNP, mutation, non-synonymous, silent mutation, spike, RNA dependent RNA polymerase, NSP, UTR: Abbreviations: VOC, variant of concern VOI, variant of interest VUM, variant of interest VUM, variant under monitoring NSP, non-structural protein UTR, untranslated region rdrp, RNA dependent RNA polymerase

### ABSTRACT

*Background:* Emergence of new variant of SARS-CoV-2, namely omicron, has posed a global concern because of its high rate of transmissibility and mutations in its genome. Researchers worldwide are trying to understand the evolution and emergence of such variants to understand the mutational cascade events.

*Methods*: We have considered all omicron genomes (n = 302 genomes) available till 2nd December 2021 in the public repository of GISAID along with representatives of variants of concern (VOC), i.e., alpha, beta, gamma, delta, and omicron; variant of interest (VOI) mu and lambda; and variant under monitoring (VUM). Whole genome-based phylogeny and mutational analysis were performed to understand the evolution of SARS CoV-2 leading to emergence of omicron variant.

*Results*: Whole genome-based phylogeny depicted two phylogroups (PG-I and PG-II) forming variant specific clades except for gamma and VUM GH. Mutational analysis detected 18,261 mutations in the omicron variant, majority of which were non-synonymous mutations in spike (A67, T547K, D614G, H655Y, N679K, P681H, D796Y, N856K, Q954H), followed by RNA dependent RNA polymerase (rdrp) (A1892T, I189V, P314L, K38R, T492I, V57V), ORF6 (M19M) and nucleocapsid protein (RG203KR).

*Conclusion:* Delta and omicron have evolutionary diverged into distinct phylogroups and do not share a common ancestry. While, omicron shares common ancestry with VOI lambda and its evolution is mainly derived by the non-synonymous mutations.

# 1. Introduction

Throughout the globe resurgence of COVID-19 cases has been linked to the emergence of new variants of concern (https://www.hopkinsmedicine.org/health/conditions-and-diseases/coronavirus/first-and-second-waves-of-coronavirus) (Thakur et al., 2021). Currently, the world is witnessing a new variant namely, omicron which was first reported in South Africa on 24th November 2021 from the specimen collected on 9th November 2021(https://www.who.int/publications/m/item/enhancing-readiness-for-omicron-(b.1.1.529)-technical-brief-and-priority-actions-for-member-states). On 26th November 2021, World Health Organisation (WHO) assigned omicron to the 'variant of concern' (VOC) category due to its ability to poses a higher risk of reinfection as compared to previously reported variants (https://www.who.int/news/item/26–11–2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern; https://www.who.int/news/item/28–11–2021-upd ate-on-omicron). According to the 1st December 2021 update, omicron is reported in at least 23 countries from five out of six WHO regions, with most cases in Africa and Europe (https://www.cnbc. com/2021/12/01/-

 $who-says-omicron-has-been-found-in-23-countries-across-the-world. \\ html).$ 

There is a lot of uncertainty surrounding the omicron variant. For its risk assessment, scientists and researchers are investigating the intensity of its spread, extent of its infection, effectiveness of detection methods, therapeutics, and vaccine efficacy (Knoll & Wonodi, 2021; Lipsitch & Dean, 2020; Pegu et al., 2021). The onset of omicron is reported with mild diseases suggests its low or mild severity than its previous counterparts like delta (Ewen Callaway, 2021; E. Callaway & Ledford, 2021).

\* Corresponding author.

https://doi.org/10.1016/j.virusres.2022.198765

Received 7 December 2021; Received in revised form 21 February 2022; Accepted 27 March 2022 Available online 31 March 2022 0168-1702/© 2022 Elsevier B.V. All rights reserved.





Abbreviations: VOC, Variant of concern; VOI, Variant of interest; VUM, Variant under monitoring; NSP, Non-structural protein; UTR, Untranslated region; rdrp, RNA dependent RNA polymerase.

E-mail addresses: kanikabansal@imtech.res.in (K. Bansal), ksanjeet.ibab@gmail.com (S. Kumar).

### K. Bansal and S. Kumar

It is known to have a very high mutation rate with more than 30 mutational changes in its spike protein (Ewen Callaway, 2021) (https://www.who.int/publications/m/item/enhancing-- read-

iness-for-omicron-(b.1.1.529)-technical-brief-and-priority-actions-for-member-states)

Globally, high risk of reinfection with omicron variant and its ability to evade vaccine-induced immunity resulting in the emergence of new variants of SARS-CoV-2 (Pulliam et al., 2021). Since COVID-19 inception, researchers have been trying to investigate its origin and evolution (Bansal, Kumar, & Patil, 2021; Singh & Soojin, 2021; Tang et al., 2020). We are currently witnessing a global molecular arms race between SARS-CoV-2 and its preventive therapeutics based on diverse regimes such as DNA, RNA, protein or inactivated whole-virion, etc. (Andreadakis et al., 2020; Corey, Mascola, Fauci, & Collins, 2020; Sharma, Sultan, Ding, & Triggle, 2020). This global crisis can be addressed by a very rapid immunization program worldwide. Moreover, the real-time monitoring of evolutionary cascade of SARS-CoV-2 leading to novel variants is utmost. Earlier investigation of several VOC and VOI suggests some of the crucial mutations for viral survival and high infectivity in humans (Boehm et al., 2021; Kumar & Bansal, 2021; Schmidt et al., 2021). However, mutations giving rise to omicron and intra-omicron genomic diversity are not yet analyzed at a population level.

In the present study, we aim to look for the mutational profile of under-monitoring variants reported till now to understand the emergence of a heavily mutated variant named omicron. Interestingly, whole genome-based phylogeny suggests two major phylogroups PG-I and PG-II. Further, mutational analysis depicted the key role of non-synonymous mutations in the evolution of novel variant. Such genome-wide mutational landscape is required for surveillance and vaccine development.



Fig. 1. Maximum likelihood whole genome-based phylogeny of SARS-CoV-2 VOCs, VOIs and VUMs. Here, phylogroups (PG-I and PG-II) and clades (alpha, beta, gamma, delta, omicron, mu etc.) are marked with respective colors as indicated. Bootstrap values are represented by the radius of circle at the nodes. Common ancestry of omicron and lambda is marked by black star.

Table 1

Metadata of the VOCs, VOIs and VUMs strains used in the present study.

Variant	strain	Strain_analysis	virus gisaid_epi date region	country division location region_	ex country_e division_e segment	length host age sea	pangolin_i GISAII	_cl originating submitting authors uni	date_submitted
Omicron	hCoV-19/HongKong/VM21044713-1/2021 hCoV-19/Botswana/R40859_8HP_3321001248/2021	VOC_Dmicron_hCoV-19/HongKong/VM21044713-172021 VOC_Dmicron_hCoV-19/Botswana/R40859_BHP_3321001248/2021	betacoron [PI_ISL_64 11/11/2021 Adva betacoron [PI_ISL_64 11/11/2021 Advica	Botswana South East Greater G: Africa	Botswana South East genome	29752 Human 36 Ma 29684 Human 57 Fer	ale 8.1.1.529 GR	Botswana Botswana Sikhulle h https://w	a 23/11/2021
Omicron	hCoV-19/8019W8N0/M0080_804_3121001247/2021 hCoV-19/8019W8N0/M00805_8049_3321001245/2021	VOC_Omicron_hCoV-19/Botswana/R40858_BHP_3321001247/2021 VOC_Omicron_hCoV-19/Botswana/R40858_BHP_3321001245/2021	betacoron [PI_ISL_64 11/11/2021 Africa	Botswana South East Greater Gr Africa	Botswana South East genome	29584 Human 33 Fer	ale 8.1.1.529 GR	Botswana Botswana Sikhulle h https://w	a 23/11/2021
Omicron	hCoV-19/SouthAfrics/NECD-N21600-0003569/2021 hCoV-19/SouthAfrics/NECD-N21602-00040380/2021	VOC_Dmicron_hCoV-19/SouthAfrica/NKD-N21600-D803569/2021 VOC_Dmicron_hCoV-19/SouthAfrica/NKD-N21602-D8040380/2021	betacoron [PI_ISL_64 14/11/2021 Africa betacoron [PI_ISL_64 15/11/2021 Africa	South Afric Gauteng Africa South Afric Gauteng Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29804 Human 27 Fer 29804 Human 28 Fer	ale 8.1.1.529 GR ale 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	n 23/11/2021 n 23/11/2021
Omicron	hCoV-19/SouthAfrics/NICD-N21603-0X64204/2021 hCoV-19/SouthAfrics/NICD-N21604-0X64219/2021	VOC_Omicron_hCoV-19/SouthAfrics/NKD-N21603-DX64204/2021 VOC_Omicron_hCoV-19/SouthAfrics/NKD-N21604-DX64219/2021	betacoron [PI_ISL_64 16/11/2021 Africa betacoron [PI_ISL_64 16/11/2021 Africa	South Afric Gauteng Africa South Afric Gauteng Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29804 Human 35 Ma 29804 Human 29 Ma	e 8.1.1.529 GR e 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	a 23/11/2021 a 23/11/2021
Omicron	hCoV-19/SouthAfrica/NICD-N21605-0X64490/2021 hCoV-19/SouthAfrica/NICD-N21606-0X64492/2021	VOC_Omicron_hCoV-19/SouthAfrica/NKD-N21605-0X64490/2021 VOC_Omicron_hCoV-19/SouthAfrica/NKD-N21606-0X64492/2021	betacoron [PI_ISL_64 15/11/2021 Africa betacoron [PI_ISL_64 15/11/2021 Africa	South Afric Gauteng Africa South Afric Gautene Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29804 Human 21 uni 29804 Human 35 uni	nown 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	a 23/11/2021 a 23/11/2021
Omicron	hCoV-19/SouthAfrica/NICD-N21607-0X64624/2021 hCoV-19/Between/H40861_BHP_3321001244/2021	VOC_Dmicron_hCoV-19/SouthAfrica/NICD-N21607-DX64624/2021 VOC_Dmicron_hCoV-19/Botxwana/940861_BHP_3321001244/2021	betacoron (PI ISL 64 16/11/2021 Africa betacoron (PI ISL 64 11/11/2021 Africa	South Afric Gauteng Africa Botswana South East Greater Gi Africa	South Afrii Gauteng genome Botswana South East errome	29804 Human 0 Fer 29714 Human 64 Ma	ale 8.1.1.529 GR e 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w Botswara Botswara Skhulle & https://w	n 23/11/2021 n 24/11/2021
Omicron	hCoV-19/HongKong/VM21045145/2021 hCoV-19/Koveb4frice/MICLN21601-0004008/2021	VGC_Dmkron_hCoV-19/HongKong/VM21045145/2021 VGC_Dmkron_hCoV-19/Kowthdefina/MKD-M21401_D004008/2021	betacoron [PLISL_64 18/11/2021 Asia batacoron [PLISL_64 15/11/2021 Asia	Hong Kong Asia South Mick Gautana Africa	Hong Kong genome South Afria Gautena genome	29752 Human 62 Ma 29804 Human 38 Eer	e 8.1.1.529 GR	HOME QU Hong Kong Alan KL. T https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032188/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-KO32188/2021	betacoron EPI ISL 66 17/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome	29852 Human 14 Fer	ule 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w	n 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032191/2021	VOC_Omicron_hCoV-19/SouthAfrica/CEI8-6815P-6032191/2021	betacoron EPI_ISL_64 17/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afria Gauteng genome	29871 Human 21 Ma	e 8.11.529 GR	National H CERJ, Cent Kathleen S https://w	a 25/11/2021
Omicron	hCoV-19/300HWHCa/CER-KRSP-K032192/2021 hCoV-19/SouthAfrica/CER-KRSP-K032195/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEB-KRISP-K032195/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEB-KRISP-K032195/2021	betacoron EPUSL_66 15/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome	29798 Human 29 Ma 29813 Human 46 Fer	ale 8.1.1.529 GR	National H CER, Cent Kathleen S https://w National H CER, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032197/2021 hCoV-19/SouthAfrica/CER-KRSP-K032198/2021	VGC_Dmicron_hCoV-19/SouthAfrica/CEB-K083P-K0831197/2021 VGC_Dmicron_hCoV-19/SouthAfrica/CEB-K083P-K0831198/2021	betacoron EPI_ISL_66 15/11/2021 Africa betacoron EPI_ISL_66 14/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29813 Human 46 Fer 29852 Human 0.4 Fer	ule 8.1.1.529 GR ule 8.1.1.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032199/2021 hCoV-19/SouthAfrica/CER-KRSP-K032201/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEI8-K013P-K032199/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEI8-K013P-K032201/2021	betacoron EPI_ISL_66 15/11/2021 Africa betacoron EPI_ISL_66 16/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29848 Human 27 Fer 29800 Human 52 Ma	ale 8.1.1.529 GR e 8.1.1.529 GR	National H CERJ, Centi Kathleen S https://w National H CERJ, Centi Kathleen S https://w	n 25/11/2021 n 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERi-KRSP-K032203/2021 hCoV-19/SouthAfrica/CERi-KRSP-K032204/2021	VOC_Omicron_hCoV-19/SouthAfrica/CEI8-KRISP-K032203/2021 VOC_Omicron_hCoV-19/SouthAfrica/CEI8-KRISP-K032204/2021	betacoron EPI_ISL_66 16/11/2021 Africa betacoron EPI_ISL_66 17/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29869 Human 53 Ma 29852 Human 22 Fer	e 8.1.1.529 GR ule 8.1.1.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERi-KRISP-K032205/2021 hCoV-19/SouthAfrica/CERi-KRISP-K032205/2021	VOC_Dmicron_hCaV-19/SouthAfrica/CEI8-KRISP-K033205/2021 VOC_Dmicron_hCaV-19/SouthAfrica/CEI8-KRISP-K033206/2021	betacoron EPI_ISL_66 18/11/2021 Africa betacoron EPI_ISL_66 18/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gautene City of Joh Africa	South Afris Gauteng genome South Afris Gautena eenome	29791 Human 34 Fer 29842 Human 21 Fer	ule 8.1.1.529 GR ule 8.1.1.529 GR	National H CERJ, Centi Kathleen S https://w National H CERJ, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERi-KRSP-R032207/2021 hCoV-19/SouthAfrica/CERi-KRSP-R032207/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEB-K032207/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEB-K032207/2021	betacoron EPUSL_66 18/11/2021 Africa batacoron EPUSL_66 18/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gautene Serkhares Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29852 Human 37 Fer 29550 Human 17 Fer	ule 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032211/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032211/2021	betacoron EPI_ISL_66 18/11/2021 Africa batacoron EPI_ISL_66 13/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome	29790 Human 55 Fer	ule 8.1.1.529 GR	National H CER, Cent Kathleen S https://w	n 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERi-KHSP-K032215/2021	VCC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032215/2021	betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afric Gauteng genome	29802 Human 24 Fer	ale 8.11529 GR	National H CERJ, Cent Kathleen S https://w	a 25/11/2021
Omicron	hCoV-19/SouthArray/CEN-KRSP-KR32216/2021 hCoV-19/SouthAfrica/CER-KRSP-KR32217/2021	VCC_Dmicron_hCoV-19/SouthAfrica/CEB-4015P-6031216/2021 VCC_Dmicron_hCoV-19/SouthAfrica/CEB-4015P-6031217/2021	betacoron EPI_ISL_66 17/11/2021 Africa betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29850 Human 36 Fer 29852 Human 31 un	ule 8.1.1.529 GR nown 8.1.1.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRSP-K032218/2021 hCoV-19/SouthAfrica/CER-KRSP-K032219/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEI8-KRISP-K032218/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEI8-KRISP-K032219/2021	betacoron EPI_ISL_66 19/11/2021 Africa betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29805 Human 28 Fer 29805 Human 49 Ma	ule 8.1.1.529 GR e 8.1.1.529 GR	National H CERJ, Centi Kathleen S https://w National H CERJ, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032221/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032223/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KBISP-K032221/2021 VOC_Omicron_hCoV-19/SouthAfrica/CER-KBISP-K032223/2021	betacoron EPI_ISL_66 19/11/2021 Africa betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29859 Human 31 uni 29808 Human 23 Fer	nown 8.11.529 GR ale 8.11.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032226/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032227/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032226/2021 VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032227/2021	betacoron EPI_ISL_66 19/11/2021 Africa betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29870 Human 53 Fer 29869 Human 23 Ma	ule 8.1.1.529 GR e 8.1.1.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032228/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032231/2021	VOC_Dmicron_hCaV-19/SouthAfrica/CEN-KRISP-K032228/2021 VOC_Dmicron_hCaV-19/SouthAfrica/CEN-KRISP-K032231/2021	betacoron EPI_ISL_66 19/11/2021 Africa betacoron EPI ISL 66 22/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gautene City of Joh Africa	South Afrii Gauteng genome South Afrii Gautena genome	29857 Human unknown Fer 29869 Human 39 Fer	ule 8.1.1.529 GR ule 8.1.1.529 GR	National H CERJ, Cent Kathleen S https://w National H CERJ, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERi-KRSP-R032232/2021 hCoV-19/SouthAfrica/CERi-KRSP-R032232/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEN-KRISP-K031232/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEN-KRISP-K032233/2021	betacoron EPUSL_66 22/11/2021 Africa batacoron EPUSL_66 22/11/2021 Africa	South Afric Gauteng City of Joh Africa South Mric Gautene City of Joh Africa	South Afris Gauteng genome South Afris Gauteng genome	29842 Human 27 Fer 29815 Human 22 Fer	ule 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032237/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032237/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032237/2021	betacoron EPI_ISL_66 21/11/2021 Africa batacoron EPI_ISL_66 23/11/2021 Africa	South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome	29788 Human 40 Fer	ale 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w	a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032239/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032230/2021	betacoron EPI_ISL_66 22/11/2021 Africa	South Afric Gauteing City of Joh Africa	South Afric Gauteng genome	29864 Human 27 Fer	ale 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w	a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERE-KRISP-K032242/2021 hCoV-19/SouthAfrica/CERE-KRISP-K032242/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CER-4815F-8032241/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CER-4815F-8032242/2021	betacoron EPI_ISL_66 20/11/2021 Africa betacoron EPI_ISL_66 20/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29816 Human 19 Ma 29852 Human 13 Ma	e 8.1.1.529 GR e 8.1.1.529 GR	National H CERI, Centi Kathleen S https://w National H CERI, Centi Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRSP-K032243/2021 hCoV-19/SouthAfrica/CERI-KRSP-K032244/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CERI-KRISP-K032243/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CERI-KRISP-K032244/2021	betacoron EPI_ISL_66 20/11/2021 Africa betacoron EPI_ISL_66 20/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29795 Human 45 Fer 29792 Human 29 Ma	whe 8.1.1.529 GR e 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032245/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032246/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032245/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032246/2021	betacoron EPI_ISL_66 20/11/2021 Africa betacoron EPI_ISL_66 19/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng Sediberg Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29796 Human 55 Fer 29869 Human 14 Ma	ule 8.1.1.529 GR e 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032248/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032250/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032248/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032250/2021	betacoron EPI_ISL_66 21/11/2021 Africa betacoron EPI_ISL_66 22/11/2021 Africa	South Afric Gauteng City of Joh Africa South Afric Gauteng City of Joh Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29867 Human 27 Fer 29867 Human 70 Fer	ule 8.1.1.529 GR ule 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032251/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032253/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032251/2021 VOC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032253/2021	betacoron EPI_ISI_66 22/11/2021 Africa betacoron EPI_ISI_66 22/11/2021 Africa	South Afric Gauteng City of Joh Africa South Miric Gautene City of Joh Mirica	South Afrii Gauteng genome South Afrii Gautenz earnome	29866 Human unknown Fer 29852 Human 38 Fer	ule 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032254/2021 hCoV-19/SouthAfrica/DBCD-M21665-02021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032254/2021 VOC_Omicron_hCoV-19/SouthAfrica/MCD-M31655/1011	betacoron EPI_ISL_66 22/11/2021 Africa battooron EPI_ISL_63 20/11/2021 Africa	South Afric Gauteng City of Joh Africa South Mile Goutene Miles	South Afrii Gauteng genome	29860 Human 52 Fer 19824 Human 37 Fer	ale 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w	a 25/11/2021
Omicron	hCoV-19/SouthAfrica/NICD-N21668/2021	VOC_Omicron_hCoV-19/SouthAfrica/NICD-N21668/2021 VOC_Omicron_hCoV-19/SouthAfrica/NICD-N21668/2021	betacoron EPI_ISL_67 20/11/2021 Africa	South Afric Gauteng Africa	South Afri Gauteng genome	29841 Human 21 Fer	ule 8.11.529 GR	LANCET LA National II Amoako D https://w	a 25/11/2021
Omicron	hCoV-19/SouthAfrica/NICD-N21672/2021 hCoV-19/SouthAfrica/NICD-N21672/2021	VOC_DMICron_NOV-19/SouthAfrica/NKD-N21671/2021 VOC_DMICron_NOV-19/SouthAfrica/NKD-N21672/2021	betacoron EPI_JSL_67 20/11/2021 Africa betacoron EPI_JSL_67 20/11/2021 Africa	South Africa Africa South Afric Gauteng Africa	South Afrii Gauteng genome	25841 numan 53 Ma 25808 Human 47 Ma	<ul> <li>6.1.1.529 GR</li> <li>8.1.1.529 GR</li> </ul>	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	a 25/11/2021
Omicron Omicron	hLov-19/SouthAfrica/NICD-N21673/2021 hCoV-19/SouthAfrica/NICD-N21674/2021	VOL_UMICTOR_NCoV-19/SouthAfrica/NKD-N21673/2021 VOC_Omicror_NCoV-19/SouthAfrica/NKD-N21674/2021	betacoron EPI_ISI_67 20/11/2021 Africa betacoron EPI_ISI_67 20/11/2021 Africa	South Mric Gauteng Mrica South Mric Gauteng Mrica	South Afrii Gauteng genome South Afrii Gauteng genome	29835 Human 38 Ma 29842 Human 12 Fer	e 8.1.1.529 GR wie 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	a 25/11/2021 a 25/11/2021
Omicron Omicron	hCoV-19/SouthAfrica/NICD-N21675/2021 hCoV-19/SouthAfrica/NICD-N21676/2021	VOC_Omicron_hCoV-19/SouthAfrica/NICD-N21675/2021 VOC_Omicron_hCoV-19/SouthAfrica/NICD-N21676/2021	betacoron EPI_ISI_67 20/11/2021 Africa betacoron EPI_ISI_67 20/11/2021 Africa	South Mrix Gauteng Mrica South Mrix Gauteng Mrica	South Afrii Gauteng genome South Afrii Gauteng genome	29816 Human 17 Fer 29827 Human 35 Ma	ale 8.1.1.529 GR e 8.1.1.529 GR	LANCET LA National Ir Amoako D https://w LANCET LA National Ir Amoako D https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/HongKong/VM21044713_WHP5047-55-iseq/2021 hCoV-19/Botswana/R4285_BHP_A4C25114/2021	V0C_0micron_hCoV-19/HongKong/VM21044713_WHP5047-S5-iseq/2021 V0C_0micron_hCoV-19/Botswana/R4285_BHP_AAC25114/2021	betacoron EPI_ISI_67 15/11/2021 Asia betacoron EPI_ISI_67 11/11/2021 Africa	Hong Kong Asia Botswana Lobatse Africa	Hong Kong genome Botswana Lobatse genome	29540 Human 36 Ma 29593 Human 43 Ma	e 8.1.1.529 GR e 8.1.1.529 GR	Hong Kong School of F Dominic N https://w Botswana Botswana Sikhulile h https://w	a 25/11/2021 a 25/11/2021
Omicron	hCoV-19/8otswana/842890_8HP_000842207/2021	V0C_Omicron_hCoV-19/Botswana/R42890_BHP_000842207/2021	betacoron EPI_ISL_67 21/11/2021 Africa	Botswana Gaborone Africa Botowana Gaborone Africa	Botswana Gaborone genome	29584 Human 58 Ma 19714 Human 28 Ma	e 8.1.1.529 GR	Botswana Botswana Sikhuille h https://w	a 25/11/2021
Omicron	hCoV 19/80tswana/R43815_BHP_000842375/2021	V0C_Omicron_hCoV-15/Botswana/R43815_BHP_000842375/2021	betacoron EPI_JSL_67 21/11/2021 Africa	Botswana Palapye Africa	Botswana Palapye genome	29714 Human 44 Ma	e 8.1.1.529 GR	Palapye Pr Botswana Sikhulie h https://w	a 26/11/2021
Omicron	hCoV-19/8015Walle/H43888_BHP_121142561/2021	V0C_0micron_hCoV-19/Botswana/R43834_BHP_AAC25685/2021 V0C_0micron_hCoV-19/Botswana/R43834_BHP_AAC25685/2021	betacoron EPI_ISL_67 22/11/2021 Africa	Botswana Gaborone Africa	Botswana Gaborone genome	29714 Human 32 Fer	ule 8.11.529 GR	Botswana Botswana Sikhulle h https://w	w 26/11/2021
Omicron	hCoV-19/805wana/R43871_8HP_121142518/2021 hCoV-19/8otswana/R43814_8HP_000842147/2021	VOC_DImicron_PCoV-19/8065wana/R43871_8HP_121142518/2021 VOC_DImicron_PCoV-19/8065wana/R43814_8HP_000842147/2021	betacoron EPI_ISL_67 21/11/2021 Africa betacoron EPI_ISL_67 21/11/2021 Africa	Botswana Gaborone Africa Botswana Palapye Africa	Botswana Gaborone genome Botswana Palapye genome	29714 Human 48 Ma 29714 Human 39 Ma	e 8.1.1.529 GR e 8.1.1.529 GR	Palapye Pr Botswana Sikhulile h https://w	a 26/11/2021 a 26/11/2021
Omicron	hCoV-19/8otswana/R43867_8HP_2021010142/2021 hCoV-19/8otswana/R43870_8HP_4021000195/2021	V0C_Dmicron_hCoV-19/8ocswana/R43867_8HP_2021010142/2021 V0C_Dmicron_hCoV-19/8ocswana/R43870_8HP_4021000195/2021	betacoron EPI_ISL_67 23/11/2021 Africa betacoron EPI_ISL_67 23/11/2021 Africa	Botswana Gaborone Africa Botswana Gaborone Africa	Botswana Gaborone genome Botswana Gaborone genome	29714 Human 47 Ma 29714 Human 38 Ma	e 8.11529 GR e 8.11529 GR	Botswana Botswana Sikhulile h https://w Botswana Botswana Sikhulile h https://w	a 26/11/2021 a 26/11/2021
Omicron	hCoV-19/Botswana/R43833_BHP_AAC25682/2021 hCoV-19/Botswana/R43865_BHP_2021010151/2021	V0C_Omicron_hCoV-19/Botswana/R43833_BHP_AAC25682/2021 V0C_Omicron_hCoV-19/Botswana/R43865_BHP_2021010151/2021	betacoron EPI_ISI_67 22/11/2021 Africa betacoron EPI_ISI_67 23/11/2021 Africa	Botswana Gaborone Mrica Botswana Gaborone Mrica	Botswana Gaborone genome Botswana Gaborone genome	29707 Human 5 Ma 29714 Human 52 Ma	e 8.11.529 GR e 8.11.529 GR	Botswana Botswana Sikhuille h https://w Botswana Botswana Sikhuille h https://w	n 26/11/2021 n 26/11/2021
Omicron	hCoV-19/8otswana/R43866_8HP_521004487/2021 hCoV-19/8otswana/R43816_8HP_000837253/2021	VOC_Omicron_hCoV-19/Botswana/R43866_BHP_521004487/2021 VOC_Omicron_hCoV-19/Botswana/R43816_BHP_000837253/2021	betacoron EPI_ISL_67 23/11/2021 Africa betacoron EPI_ISL_67 17/11/2021 Africa	Botswana Gaborone Africa Botswana Palapye Africa	Botswana Gaborone genome Botswana Palapye genome	29714 Human 47 Ma 29714 Human 45 Ma	e 8.1.1.529 GR e 8.1.1.529 GR	Botswana Botswana Sikhuille h https://w Palapye Pr Botswana Sikhuille h https://w	a 26/11/2021 a 26/11/2021
Omicron	hCoV-19/8otswana/843864_8HP_121142532/2021 hCoV-19/taW/LOM-Sacco Var T96348/2021	VOC_Omicron_hCoV-19/Botswana/R43864_BHP_121142532/2021 VOC_Omicron_hCoV-19/Italiv/LOM-Sacco_Var_T96348/2021	betacoron EPI_ISL_67 23/11/2021 Africa betacoron EPI ISL 67 22/11/2021 Europe	Botswana Gaborone Africa Italy Lombardia Europe	Botswana Gaborone genome Italy Lombardia genome	29714 Human 35 Ma 29799 Human 40-49 uni	e 8.1.1.529 GK nown 8.1.1.529 GR	Botswana Botswana Sikhulile h https://w Policlinico Laboratory Valeria Mi https://w	a 26/11/2021 a 26/11/2021
Omicron	hCoV-19/SouthAfrica/CER+KRISP-K032212/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032212/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032252/2021	betacoron EPI_ISI_67 18/11/2021 Africa batacoron EPI_ISI_67 23/11/2021 Africa	South Mrk Gauteng City of Joh Mrka South Mrk Gautene City of Joh Mrka	South Afril Gauteng genome	29850 Human 36 Ma 19849 Human 23 Fee	e 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w	a 26/11/2021 a 26/11/2021
Omicron	hCoV-19/8elgium/rega-20174/2021	VOC_Omicron_hCoV-19/Belgium/rega-20174/2021	betacoron EPI_ISL_67 24/11/2021 Europe	Belgium Sint-Pieters-Leeuw Europe	Belgium Sint-Pieter genome	29584 Human 32 Fer	ale 8.11529 GR	KU Leuven KU Leuven Torry Waw https://w	a 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K030836/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER+4815P-4030836/2021	betacoron EPI_ISL_67 12/11/2021 Africa	South Airk Gauteng Airka	South Afril Gauteng genome	29753 Human 35 Fer	ale 8.11.529 GR	National H CERI, Cent Kathleen S https://w	a 27/11/2021
Omicron	hCoV-19/500th4frica/CERi-KRISP-K030837/2021 hCoV-19/South4frica/CERi-KRISP-K030838/2021	VOC_Dmicron_hCoV-19/SouthAfrica/CEN+ARISP-K030837/2021 VOC_Dmicron_hCoV-19/SouthAfrica/CEN+KRISP-K030838/2021	betacoron EPI_ISL_67 11/11/2021 Africa betacoron EPI_ISL_67 11/11/2021 Africa	South Afric Gauteng Africa South Afric Gauteng Africa	South Afrii Gauteng genome South Afrii Gauteng genome	29852 Human 21 Fer	ale 8.1.1.529 GR ale 8.1.1.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	a 27/11/2021 a 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K030840/2021 hCoV-19/SouthAfrica/CERI-KRISP-K030842/2021	VOC_Omicron_hCoV-19/SouthAfrica/CER+KRISP-K030840/2021 VOC_Omicron_hCoV-19/SouthAfrica/CER+KRISP-K030842/2021	betacoron EPI_ISI_67 9/11/2021 Africa betacoron EPI_ISI_67 12/11/2021 Africa	South Mric Gauteng Mrica South Mric Gauteng Mrica	South Afrii Gauteng genome South Afrii Gauteng genome	29820 Human 34 Ma 29851 Human 21 Fer	e 8.11.529 GR mie 8.11.529 GR	National H CERI, Cent Kathleen S https://w National H CERI, Cent Kathleen S https://w	n 27/11/2021 n 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032258/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032271/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032258/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032271/2021	betacoron EPI_ISL_67 19/11/2021 Africa betacorox EPI_ISL_67 19/11/2021 Africa	South Mric KwaZulu-Natal Mrica South Mri KwaZulu-Natal Africa	South Afrii KwaZulu-N genome South Afrix KwaZulu-N genome	29782 Human 26 Fer 29783 Human 38 Fem	nle 8.1.1.529 GR Ne 8.1.1.529 GR	National H CERI, Cent Nokukhan https://w National H CERI, Cent Nokukhan https://ww	a 27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032283/2021 hCoV-19/Jsrael/SMC-2022800/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032283/2021 VDC_Omicron_hCoV-19/Jyan//SMC-7022800/2021	betacorors EPUISL_67 22/11/2021 Africa betacorors EPUISL_67 20/11/2021 Africa	South Afrik KwaZulu-Natal Africa Israel Asia	South Afric KwaZulu-A genome Israel genome	29490 Human 62 Fem 29787 Human 34 unkt	ile 8.1.1.529 GR	National H CERI, Cent Nokukhani https://ww Shamir Mr Shamir Mr Nir Bairw Chttps://ww	27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrica/CER-WRISP-W032284/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032284/2021 UDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032284/2021	betacorors EPI_ISL_63 23/11/2021 Africa betacorors EPI_ISL_63 17/11/2021 Africa	South Afrik KwaZulu-Natal Africa South Afrik Gauteon, Tehwana Africa	South Afrik KwaZulu-A genome South Afrik Gentees aroome	29873 Human 61 Fem 19383 Human 56 Fem	de 8.1.1.529 GR	National H CERI, Cent Nokukhani https://ww 7880/NWI CERI Cent Arms Strack https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032319/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032319/2021	betacorors EPI_ISL_67 17/11/2021 Africa	South Afri Gauteng Tshwane Africa	South Afric Gauteng genome	29742 Human 21 Fem	de 8.1.1.529 GR	ZARV/NHL CERL Cent Army Stryid https://ww 2481/1041 CERL Cent Army Stryid https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CER-MRSP-R032331/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-R032324/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-R032331/2021	betacoros EPI_ISL_63 16/11/2021 Africa	South Afra Gauteng Tshwane Africa South Afra Gauteng Tshwane Africa	South Afric Gauteng genome	29732 Human 43 Fem	8.1.1.529 GR	ZARV/NHL CERL Cent Arry Stryth https://ww ZARV/NHL CERL Cent Arry Stryth https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-RRISP-R002338/2021 hCoV-19/SouthAfrica/CERI-RRISP-R002341/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-RRISP-K032338/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-RRISP-K032341/2021	betacoron [P]_5L_63 16/11/2021 Africa betacoron [P]_5L_63 16/11/2021 Africa	South Afris Gauteng Tshwarie Africa South Afris Gauteng Tshwarie Africa	South Afric Gauteng genome South Afric Gauteng genome	29180 Human 39 Fem 29727 Human 23 Mai	8.1.1.529 GR 8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Stryd https://ww ZARV/NHL CERI, Cent Arry Stryd https://ww	27/13/2021 27/13/2021
Omicron	hCoV-19/SouthAfrics/CER-KRISP-K032343/2021 hCoV-19/SouthAfrics/CER-KRISP-K032344/2021	VDC_Omicron_hCoV-19/SouthAfrica/CEIU-8815P-8032343/2021 VDC_Omicron_hCoV-19/SouthAfrica/CEIU-8815P-8032344/2021	betacorors EPLISL_63 16/11/2021 Africa betacorors EPLISL_63 16/11/2021 Africa	South Afris Gauteng Tshwane Africa South Afris Gauteng Tshwane Africa	South Afric Gauteng genome South Afric Gauteng genome	29795 Human 47 Fem 29847 Human 37 Fem	ile 8.1.1.529 GR ile 8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Strydk https://ww ZARV/NHL CERI, Cent Arry Strydk https://ww	27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrics/CERI-KNISP-K032348/2021 hCoV-19/SouthAfrics/CERI-KNISP-K032359/2021	VDC_Omicron_hCoV-19/SouthAfrica/CEIU-6RISP-6032348/2021 VDC_Omicron_hCoV-19/SouthAfrica/CEIU-6RISP-6032359/2021	betacoron EPI_ISL_63 16/11/2021 Africa betacoron EPI_ISL_63 16/11/2021 Africa	South Afris Gauteng Tshware Africa South Afris Gauteng Tshware Africa	South Afric Gauteng genome South Afric Gauteng genome	29655 Human unknown Fem 29757 Human 12 Fem	ile 8.1.1.529 GR ile 8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Stryck https://ww ZARV/NHL CERI, Cent Arry Stryck https://ww	27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032365/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032366/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032365/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032366/2021	betacoron EPI_ISL_63 15/11/2021 Africa betacoron EPI_ISL_63 15/11/2021 Africa	South Afrie Gauteng Tshwane Africa South Afrie Gautene Tshwane Africa	South Afric Gauteng genome South Afric Gautene genome	29650 Human 21 Fem 29744 Human 27 Fem	ne 8.1.1.529 GR ne 8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Stryd https://ww ZARV/NHL CERI, Cent Arry Stryd https://ww	27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032367/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032367/2021	betacoron EPI_ISL_63 15/11/2021 Africa	South Afris Gauteng Tshwane Africa	South Afric Gauteng genome South Mix Goutene genome	29729 Human 54 Fem 19604 Human 21 Mail	ile 8.1.1.529 GR	ZARV/NHL CERI, Cent Army Stryde https://ww ZARV/NHL CERI, Cent Army Stryde https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032373/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-RRISP-0032373/2021	betacoron EPUSL_67 13/11/2021 Africa	South Afrie Gauteng Tshwane Africa	South Afric Gauteng genome	29800 Human 38 Mak	8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Stryth https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-IRISP-K032190/2021 hCoV-19/SouthAfrica/CERI-IRISP-K032202/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-K032190/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-K032202/2021	betacoron EPUSL_68 16/11/2021 Africa	South Africa Africa	South Afric Gauteng genome	29850 Human 32 Mak	8.1.1.529 GR	National H CERI, Cent Kathleen S https://ww	27/11/2021
Omicron	hCoV-19/SouthAfrica/CER-KRISP-R032225/2021 hCoV-19/SouthAfrica/CER-KRISP-R032235_2/2021	VOC_Omicron_hCoV-19/SouthAfrica/CEN-KRSP-R052225/2021 VOC_Omicron_hCoV-19/SouthAfrica/CEN-KRSP-R032235_2/2021	betacoron EPI_ISL_68 19/11/2021 Africa betacoron EPI_ISL_68 22/11/2021 Africa	South Afrie Gauteng Africa	South Afric Gauteng genome South Afric Gauteng genome	29788 Human 49 Hem 29847 Human 39 Fem	ne 8.1.1.529 GR ne 8.1.1.529 GR	National H CERI, Cent Kathleen S https://ww National H CERI, Cent Kathleen S https://ww	27/11/2021 27/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032249/2021 hCoV-19/Australia/NSW-RPAH-1933/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032249/2021 VDC_Omicron_hCoV-19/Australia/NSW-RPAH-1933/2021	betacorors EPU_SL_68 22/11/2021 Africa betacorors EPU_SL_68 27/11/2021 Oceania	South Afric Gauteng Africa Australia New South Sydney Oceania	South Afric Gauteng genome Australia New South genome	29870 Human unknown Mak 29693 Human unknown unkn	8.1.1.529 GR own 8.1.1.529 GR	National H CERI, Cent Kathleen S https://ww New South Microbiol: Foster, C.; https://ww	27/11/2021 28/11/2021
Omicron	hCoV-19/England/MILK-2867570/2021 hCoV-19/England/ALDP-284DF63/2021	VDC_Omicron_hCoV-19/England/MILK-2867570/2021 VDC_Omicron_hCoV-19/England/ALDP-284DF63/2021	betacorors EPUISL_6E 21/11/2021 Europe betacorors EPUISL_6E 20/11/2021 Europe	United Kin England Europe United Kin England Europe	United Kin England genome United Kin England genome	29747 Human unknown unkn 29747 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Lighthousi Welkome The Lighth https://ww Lighthousi Welkome Jacquelyn https://ww	28/11/2021 28/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032300/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032326/2021	VOC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-#032300/2021 VOC_Omicron_hCoV-19/SouthAfrica/CERI-#RISP-#032326/2021	betacoron EPI_ISL_68 17/11/2021 Africa betacoron EPI_ISL_68 17/11/2021 Africa	South Mri Gauteng Tshwane Africa South Mri Gauteng Tshwane Africa	South Mirk Gauteng genome South Mirk Gauteng genome	29730 Human 20 Fem 29732 Human 31 Mak	le 8.1.1.529 GR 8.1.1.529 GR	ZARV/NHL CERL Cent Army Stryd https://ww ZARV/NHL CERL Cent Army Stryd https://ww	28/11/2021 28/11/2021
Omicron	hCoV-19/SouthAfrica/CERI-KRISP-K032332/2021 hCoV-19/SouthAfrica/CERI-KRISP-K032340/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032332/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-KRISP-K032340/2021	betacorors EPI_ISL_68 16/11/2021 Africa betacorors EPI_ISL_68 16/11/2021 Africa	South Mri Gauteng Tshwane Africa South Mri Gauteng Tshwane Africa	South Mrk Gauteng genome South Mrk Gauteng genome	29767 Human 54 Mail 29730 Human 41 Fem	8.1.1.529 GR	ZARV/NHL CERL Cent Arry Stryd https://ww ZARV/NHL CERL Cent Arry Stryd https://ww	28/11/2021 28/11/2021
Omicron	hCoV-19/SouthAfrics/CERI-KRISP-K032342/2021 hCoV-19/SouthAfrics/CERI-KRISP-K032342/2021	VDC_Omicron_hCoV-19/SouthAfrica/CERI-RESP-0032342/2021 VDC_Omicron_hCoV-19/SouthAfrica/CERI-RESP-0032345/2021	betacoron EPI_EL_68 16/11/2021 Africa betacoron EPI_EL_68 16/11/2021 Africa	South Afris Gauteng Tshwane Africa South Afris Gauteng Tshwane Africa	South Afric Gauteng genome South Afric Gauteng genome	29769 Human 26 Mail 29798 Human 31 Mail	8.1.1.529 GR 8.1.1.529 GR	ZARV/NHL CERL Cent Army Stryth https://ww ZARV/NHL CERL Cent Army Stryth https://ww	28/11/2021 28/11/2021
Omicron	hCoV-19/SouthAfrica/CER-RRISP-R032355/2021	VDC_Omicron_hCoV-19/SouthAfrica/CIRI-RRISP-R032355/2021 UDC_Omicron_hCoV-19/SouthAfrica/CIRI-RRISP-R032355/2021	betacoros EPI_ISL_68 16/11/2021 Africa betacoros EPI_ISL_68 16/11/2021 Africa	South Afris Gauteng Tshwane Africa South Afris Gautena, Tshwane Africa	South Afric Gauteng genome South Afric Gauteng genome	29847 Human 33 Fem 29551 Human 20 Fem	le 8.1.1.529 GR	ZARV/NHL CERI, Cent Arry Stryd https://ww 7489/NHL CERI, Cent Arry Stryd https://ww	28/11/2021
Omicron	hCoV-19/SouthAfrics/CEIN-KRISP-K032360/2021 hCoV-19/SouthAfrics/CEIN-KRISP-K032360/2021	VDC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032360/2021 VDC_Omicron_hCoV-19/SouthAfrica/CER-KRISP-K032360/2021	betacoron EPI ISL 68 16/11/2021 Africa betacoron EPI ISL 68 14/11/2021 Africa	South Afris Gauteng Tshwane Africa South Afris Gautene Tshwane Africa	South Afric Gauteng genome South Afric Gauteng announ	29795 Human 18 Mail 29767 Human 6 from	8.1.1.529 GR	ZARV/NHL CERI, Cent Amy Stryth https://ww ZARV/NHL CERI, Cent Amy Stryth https://ww	28/11/2021 28/11/2021
Omicron	hCoV-19/Austria/MUV-0239/2021	VDC_Omicron_hCoV-19/Austria/MUV-0229/2021 VDC_Omicron_hCoV-19/Austria/MUV-0229/2021	betacoron EPI_ISL_68 28/11/2021 Europe betacoron EPI_ISL_68 28/11/2021 Europe	Austria Tyrol Schwaz Europe	Austria Tyrol genome	29693 Human unknown unkn	own 8.1.1.529 GR	Institute o Institute o David Bant https://ww Desarane National & Socia Main Int	28/11/2021 39/11/2021
Omicron	hCoV-19/Canada/ON-NML-249358/2021	VDC_Omicron_hCoV-19/Canada/ON-NML-249558/2021 VDC_Omicron_hCoV-19/Canada/ON-NML-249558/2021	betacoron EPI_5L_5E 23/11/2021 North A betacoron EPI_5L_5E 23/11/2021 North A	mi Canada Ontario North An Amtralia New Seath Sudow	n Canada Ontario genome	29693 Human 50-59 Mail	8.1.1.529 GR	Dynacare National N Anna Maje https://ww New South Microbiols Forter A Jac	29/11/2021 39/11/2021
Omicron	HC0V-19/Addrema(HC0V-9/AH-1935)/2021 HCoV-19/Addrema(HC0V-8/AH-1937/2021	VDC_Omicron_hCoV-19/Australia/NSW-8PAH-1935/2021 VDC_Omicron_hCoV-19/Australia/NSW-8PAH-1937/2021	betacoron EPUSL_68 28/11/2021 Oceania betacoron EPUSL_68 28/11/2021 Oceania	Australia New South Sydney Oceania Australia New South Sydney Oceania	Australia New South genome	29693 Human unknown unkn	own 8.1.1.529 GR	New South Microbiol: Foster, C.; https://ww New South Microbiol: Foster, C.; https://ww	29/11/2021
Omicron	hLov-19/HongKong/VM21045834/2021 hCoV-19/Germany/32703755/2021	VLKOMICTON_FCXV-19/HongKong/VM21045834/2021 VDC_Omicron_FCXV-19/Germany/32703755/2021	betacoron EPI_ISL_68 26/11/2021 Asia betacoron EPI_ISL_68 26/11/2021 Europe	rong Kong Asia Germany Hesse Europe	Germany Hesse genome	29747 Human 37 Mali 29708 Human 31 Fem	8.1.1.529 GR de 8.1.1.529 GR	nome Qua Hong Kong Alan K.L. T: https://ww Institute fc Institute fc Toptan T., https://ww	29/11/2021 29/11/2021
Omicron	ncov-19/bngland/MILK-28987AD/2021 hCoV-19/England/MILK-2895A89/2021	VGC_OMICTON_PCOV-15/England/MILK-2898740/2021 VOC_Omicron_PCoV-15/England/MILK-2895A89/2021	betacoron EPI_SL_6E 22/11/2021 Europe betacoron EPI_SL_6E 22/11/2021 Europe	United Kin England Europe United Kin England Europe	United Kin, England genome United Kin, England genome	29747 Human unknown unkn 29747 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	ughthousi Welkome The Lighth https://ww Lighthousi Welkome The Lighth https://ww	29/11/2021 29/11/2021
Omicron Omicron	hCoV-19/Netherlands/NH-RIVM-71071/2021 hCoV-19/Netherlands/NH-RIVM-71072/2021	VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71071/2021 VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71072/2021	betacoron EPUSL_68 26/11/2021 Europe betacoron EPUSL_68 26/11/2021 Europe	Netherlan Noord-Holland Europe Netherlan Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol genome	29752 Human unknown unkn 29752 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Dutch COI National ir Adam Meij https://ww Dutch COI National ir Adam Meij https://ww	29/11/2021 29/11/2021
Omicron Omicron	hCoV-19/Netherlands/NH-RIVM-71074/2021 hCoV-19/Netherlands/NH-RIVM-71075/2021	VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71074/2021 VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71075/2021	betacoron EPI_SL_68 26/11/2021 Europe betacoron EPI_SL_68 26/11/2021 Europe	Netherlan Noord-Holland Europe Netherlan Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol genome	29752 Human unknown unkn 29752 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Dutch COI National ir Adam Meij https://ww Dutch COI National ir Adam Meij https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/Netherlands/NH-RIVM-71076/2021 hCoV-19/Netherlands/NH-RIVM-71077/2021	VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71076/2021 VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71077/2021	betacoron EPI_ISL_68 26/11/2021 Europe betacoron EPI_ISL_68 26/11/2021 Europe	Netherlan Noord-Holland Europe Netherlan Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol genome	29464 Human unknown unkn 29749 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Dutch COV National in Adam Meij https://ww Dutch COV National in Adam Meij https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/Netherlands/NH-RIVM-71078/2021 hCoV-19/Netherlands/NH-RIVM-71079/2021	VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71078/2021 VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71079/2021	betacoron EPI_ISL_68 26/11/2021 Europe betacoron EPI_ISL_68 26/11/2021 Furnee	Netherian Noord-Holland Europe Netherian Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol genome	29752 Human unknown unkn 29752 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Dutch CO4 National Ir Adam Mei https://ww Dutch CO4 National Ir Adam Mei https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/Netherlands/NH-RIVM-71081/2021 hCoV-19/Netherlands/NH-RIVM-71087/2071	VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71081/2021 VDC_Omicron_hCoV-19/Netherlands/NH-RIVM-71081/2021	betacoron EPI_5L_68 26/11/2021 Europe betacoron EPI 5L_68 26/11/2021 Europe	Netherlan Noord-Holland Europe Netherlan Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol menome	29752 Human unknown unkn	own 8.1.1.529 GR	Dutch CO4 National in Adam Meij https://ww Dutch CO4 National in Adam Meij https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/Netherlands/NH-RIVM-71083/2021 hCoV-19/Netherlands/NH-RIVM-71083/2021	VDC_Omicron_hCoV-19/Netherlands/Net-RIVM-71083/2021 VDC_Omicron_hCoV-19/Netherlands/Net-RIVM-71083/2021	betacoron EPI_5L_68 26/11/2021 Europe betacoron EPI_5L_68 26/11/2021 Europe	Netherian Noord-Holland Europe Netherian Noord-Holland Europe	Netherian: Noord-Hol genome Netherian: Noord-Hol amore	29752 Human unknown unkn	own 8.1.1.529 GR	Dutch CO4 National in Adam Mei https://ww Dutch CO4 National in Adam Mei https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/HongKong/HKU-211129-001/2021	VOC_Omicron_hCoV-19/HongKong/HKU-211129-001/2021	betacoron IPI ISL 68 14/11/2021 Asia	Hong Kong Asia	Hong Kong genome	29752 Human unknown unkn	own 8.1.1.529 GR	Departme Departmer Kelvin K.W https://ww	29/11/2021
Ornicron	hCoV-19/SouthAfrica/Tygerberg_3060/2021	VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3060/2021	betacorors EPI_ISL_68 22/11/2021 Africa	South Afris Western C Cape Town Africa	South Afric Western C genome	29746 Human unknown unkn 29746 Human 44 Fem	ile 8.1.1.529 GR	PathCare, Division of Jean Marit https://ww	29/11/2021
Ornicron	hCoV-19/SouthAfrica/Tygerberg_3082/2021 hCoV-19/SouthAfrica/Tygerberg_3082/2021	VLK_umeron_hCoV-19/SouthAfrica/Tygerberg_3058/2021 VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3082/2021	betacoron EPI_BL_68 22/11/2021 Africa betacoron EPI_BL_68 21/11/2021 Africa	south Afra Western C Cape Town Africa South Afra Western C Cape Town Africa	south Afric Western C genome South Afric Western C genome	29745 Human 39 Mail 29745 Human 52 Mail	8.1.1.529 GR 8.1.1.529 GR	vamCare, Devision of Jean Marit https://ww Division of Division of Susan Engl https://ww	29/11/2021 29/11/2021
Ornicron	hCoV-19/SouthAfrica/Tygerberg_3072/2021 hCoV-19/SouthAfrica/Tygerberg_3059/2021	VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3072/1021 VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3059/2021	betacoron EPI_6L_68 25/11/2021 Africa betacoron EPI_6L_68 23/11/2021 Africa	South Afris Western C Cape Town Africa South Afris Western C Cape Town Africa	South Afric Western C genome South Afric Western C genome	29737 Human 26 Fem 29746 Human 62 Mak	m 8.1.1.529 GR 8.1.1.529 GR	PathCare, Division of Jean Marit https://ww PathCare, Division of Jean Marit https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/SouthAfrica/Tygerberg_3056/2021 hCoV-19/SouthAfrica/Tygerberg_3066/2021	VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3056/2021 VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3066/2021	betacoron EPI_ISL_68 24/11/2021 Africa betacoron EPI_ISL_68 19/11/2021 Africa	South Afrie Western C Cape Town Africa South Afrie Western C Cape Town Africa	South Afric Western C genome South Afric Western C genome	29746 Human 35 Mai 29746 Human 40 Mai	8.1.1.529 GR 8.1.1.529 GR	Division of Division of Susan Engl https://ww PathCare, Division of Jean Marit https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/SouthAfrica/Tygerberg_3058/2021 hCoV-19/SouthAfrica/Tygerberg_3054/2021	VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3068/2021 VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3054/2021	betacoron EPI_ISL_6E 19/11/2021 Africa betacoron EPI_ISL_6E 24/11/2021 Africa	South Afrie Western C Cape Town Africa South Afrie Western C Cape Town Africa	South Afric Western C genome South Afric Western C genome	29746 Human 47 Mail 29746 Human 35 Fem	8.1.1.529 GR ile 8.1.1.529 GR	PathCare, Division of Jean Marit https://ww Division of Division of Susan Ener https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/SouthAfrica/Tygerberg_3083/2021 hCoV-19/SouthAfrica/Tweetherg_3057/3021	VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3083/2021 VDC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3063/2021	betacoron EPI_ISL_6E 22/11/2021 Africa betacoron EPI_ISL_6E 22/11/2021 Africa	South Afrie Western C Cape Town Africa South Afrie Western C Caren Trees Africa	South Afric Western C genome South Afric Western C associate	29746 Human 26 Fem 29746 Human 56 F	ile 8.1.1.529 GR	Division of Division of Susan Engl https://ww PathCare, Division of Iran March Inter-	29/11/2021 29/11/2021
Omicron	hCoV-19/SouthAfrica/Tygerberg_3055/2021 hCol-19/SouthAfrica/Tygerberg_3055/2021	VOC_Omicron_hCoV-19/SouthAfrica/Tygerberg_3055/2021	betacoron EPI_SL_68 24/11/2021 Africa	South Afrik Western C Cape Town Africa	South Afric Western C genome	29746 Human 34 Mail	8.1.1.529 GR	Division of Division of Susan Englishtps://www. BathCare, Division of Susan Englishtps://www.	29/11/2021
Omicron	hCoV-19/SouthAfrica/Tygerberg_3069/2021 hCoV-19/SouthAfrica/Tygerberg_3069/2021	VGC_OMICTOR_RC0V-159/SouthAtrica/Tygerberg_3064/2021 VOC_Omicron_RC0V-159/SouthAfrica/Tygerberg_3069/2021	betacoron EPI_ISL_68 23/11/2021 Africa betacoron EPI_ISL_68 23/11/2021 Africa	South Afrik Western C Cape Town Africa South Afrik Western C Cape Town Africa	South Afric Western C genome South Afric Western C genome	29746 Human 51 Mail 29746 Human 27 Mail	8.1.1.529 GR 8.1.1.529 GR	PaulCare, Division of Jean Marit https://ww PathCare, Division of Jean Marit https://ww	29/11/2021 29/11/2021
Omicron Omicron	nLov-19/Spain/MD-HGUGM-5821169/2021 hCoV-19/Italy/CAM-COLLI-COTUGNO-A10117/2021	vux_umcron_hCoV-19/Spain/MD-HGUGM-5821169/2021 VDC_Omicron_hCoV-19/Italy/CAM-COLLI-COTUGNO-A10117/2021	betacoron EPI_SL_68 28/11/2021 Europe betacoron EPI_SL_68 28/11/2021 Europe	spain Madrid Europe Italy Campania Europe	sparn Madrid genome Italy Campania genome	29754 Human 51 Mai 29645 Human 77 Fem	8.1.1.529 GR le 8.1.1.529 GR	Hospital G Hospital G Sergio Bue https://ww Microbiok Microbiok Claudia Tik https://ww	29/11/2021 29/11/2021
Omicron Omicron	hCoV-19/htshy/CAM-COLL+COTUGNO-810118/2021 hCoV-19/htshy/CAM-COLL+COTUGNO-C10119/2021	VOC_Omicron_hCoV-19/httly/CAM-COLLI-COTUGNO-810118/2021 VOC_Omicron_hCoV-19/httly/CAM-COLLI-COTUGNO-C10119/2021	betacoron EPI_ISL_68 28/11/2021 Europe betacoron EPI_ISL_68 28/11/2021 Europe	Italy Campania Europe Italy Campania Europe	Italy Campania genome Italy Campania genome	29795 Human 8 Fem 29488 Human 81 Fem	ile 8.1.1.529 GR ile 8.1.1.529 GR	Microbiok Microbiok Claudia Tit https://ww Microbiok Microbiok Claudia Tit https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/CzechRepublic/XNL_2021-110119140/2021 hCoV-19/Reunion/PIMIT_Om1/2021	VDC_Omicron_hCoV-19/CzechRepublic/XNL_2021-110119140/2021 VDC_Omicron_hCoV-19/Reunion/PIMIT_Om1/2021	betacoron EPI_ISL_68 26/11/2021 Europe betacoron EPI_ISL_68 22/11/2021 Africa	Czech Rep Liberec Re Rynoltice Europe Reunion Africa	Czech Repi Liberec Reigenome Reunion genome	29770 Human 60 Fem 29747 Human 51 Mak	le 8.1.1.529 GR 8.1.1.529 GR	Regional E Regional H Tomas Zaji https://ww CERBALU/ UMR PIMF David A W https://ww	29/11/2021 29/11/2021
Omicron	hCoV-19/Scotland/QEUH-28A62F6/2021 hCoV-19/Scotland/QEUH-28A62F6/2021	VDC_Omicron_hCoV-19/Scotland/QEUH-28A62F6/2021 VDC_Omicron_hCoV-19/Scotland/QEUH-28A62F6/2021	betacoron EPI_5L_6E 23/11/2021 Europe betacoron EPI_5L_6E 23/11/2021 Europe	United Kin Scotland Europe United Kin Scotland Europe	United Kin, Scotland genome United Kin, Scotland	29747 Human unknown unkn 29747 Human unknown unkn	own 8.1.1.529 GR	Lighthousi Welkome Harper Vachttps://ww Lighthousi Welkome Harper Vachttps://ww	30/11/2021 30/11/2021
Omicron	hCoV-19/Scotland/QLUH-28A450C/2021	VDC_Omicron_hCoV-19/Scotland/QEUH-2BA650C/2021 UDC_Omicron_hCoV-19/Scotland/QEUH-2BA650C/2021	betacoron IPI_51_64 23/11/2021 Europe	United Kin Scotland Europe	United Kin Scotland genome	29747 Human unknown unkn	own 8.1.1.529 GR	Lighthousi Wellcome Harper Vachttps://ww	30/11/2021
Omicron	hCoV-19/Sweden/10190023/2021	VDC_Omicron_hCoV-19/3weeden/10190023/2021	betacoron 691,61,68 19/11/2021 Europe	Sweden Skane Europe	Sweden Skane genome	29644 Human unknown unkn	own 8.1.1.529 GR	Swedish n. The Public Maximiliar https://ww Maximiliar https://ww	30/11/2021
Omicron	hCoV-19/Germany/87-WVP-000009711/2021	VDC_Omicron_hCaV-19/Germany/87-MVP-00009711/2021 VDC_Omicron_hCaV-19/Germany/87-MVP-00009711/2021	betacoron EPI_51_68 27/11/2021 Europe betacoron EPI_51_68 27/11/2021 Europe	Germany warana neunich Europe Germany Bavaria Munich Europe	Germany Bavaria genome	29746 Human 65 Fem 29745 Human 66 Mai	8.1.1.529 GR	Max von P. Laboratory Max Maen https://ww Max von P. Laboratory Max Maen https://ww Max-won D. Laboratory Max Maen https://ww	30/11/2021 10/11/2021
Ornicron	https://www.uk/sermany/87-MWP-000009705/2021 https://www.uk/proves.com/article/prove	VLK_Umicron_hCoV-19/Germany/87-MVP-005009706/2021 VDC_Omicron_hCoV-19/Portugal/PT21722/2021	betacoron EPI_5L_68 26/11/2021 Europe betacoron EPI_5L_68 27/11/2021 Europe	Portugal Europe	Portugal genome	29747 Human 34 Mali 29777 Human unknown unkn	8.1.1.529 GR own 8.1.1.529 GR	neux von P. Laboratory Mix Muen https://ww Germano i Instituto N. Borges et i https://ww	30/11/2021 30/11/2021
Omicron Omicron	htov-19/Portuga(/PT21715/2021 htov-19/Portuga(/PT21716/2021	VDC_Dmicron_hCaV-19/Portugal/PT21715/2021 VDC_Omicron_hCaV-19/Portugal/PT21716/2021	betacoron EPI_6L_68 27/11/2021 Europe betacoron EPI_6L_68 27/11/2021 Europe	Portugal Europe Portugal Europe	Portugal genome Portugal genome	29795 Human unknown unkn 29795 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Germano i Instituto N Borges et i https://ww Germano i Instituto N Borges et i https://ww	30/11/2021 30/11/2021
Omicron Omicron	hCoV-19/Portugal/PT21727/2021 hCoV-19/Portugal/PT21717/2021	VDC_Omicron_hCoV-19/Portugal/PT21727/2021 VDC_Omicron_hCoV-19/Portugal/PT21717/2021	betacoron EPI_ISL_68 27/11/2021 Europe betacoron EPI_ISL_68 27/11/2021 Europe	Portugal Europe Portugal Europe	Portugal genome Portugal genome	29793 Human unknown unkn 29795 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Germano i Instituto N Borges et i https://ww Germano i Instituto N Borges et i https://ww	30/11/2021 30/11/2021
Omicron Omicron	hCoV-19/Portugal/PT21718/2021 hCoV-19/Portugal/PT21719/2021	VDC_Omicron_hCoV-19/Portugal/PT21718/2021 VDC_Omicron_hCoV-19/Portugal/PT21719/2021	betacoron EPI_SL_68 27/11/2021 Europe betacoron EPI_SL_68 27/11/2021 Europe	Portugal Europe Portugal Europe	Portugal genome Portugal genome	29783 Human unknown unkn 29794 Human unknown unkn	own 8.1.1.529 GR own 8.1.1.529 GR	Germano i Instituto N Borges et i https://ww Germano i Instituto N Borges et i https://ww	30/11/2021 30/11/2021

(continued on next page)

Omicron hCoV-19/Portuga//PT21720/2021 Omicron hCoV-19/Portuga//PT21721/2021 Omicron hCoV-19/Portuga//PT21725/2021	VDC_Omicron_HCoV-19/Portugal/PT21720/2021 VDC_Omicron_HCoV-19/Portugal/PT21721/2021 VDC_Omicron_HCoV-19/Portugal/PT21725/2021	beiscron PE, S., 61 27/11/0211 Group Portugal Europa Portugal genome 39793 Human unitiveu univerum 11.1539 GR Genmanon Institute M Bo beiscron PE, S., 61 27/11/0211 Group Portugal Europa Portugal genome 3979 Human univeuw univeum 11.1539 GR Genmanon Unitabate M Bo beiscron PE 64 27/11/0211 Group Portugal Europa Portugal Genome 2978 Human univeuw univeum 11.1539 GR Genmanon Unitabate M Bo
Omicron hCoV-19/Portugal/PT21726/2021 Omicron hCoV-19/Portugal/PT21726/2021 Omicron hCoV-19/Portugal/PT21723/2021	VOC_Omicron_NCoV-19/Portugal/PT21726/2021 VOC_Omicron_NCoV-19/Portugal/PT21724/2021 VOC_Omicron_NCoV-19/Portugal/PT21723/2021	beaccore PU, SC, 64 27/11/2021 Europe Portugal Europe Portugal genome 29831 Human unknown utknown 8.1.1.529 GR Germano Isstitution Na     beaccores PU, SC, 64 27/11/2021 Europe Portugal Europe Portugal genome 29804 Human unknown 1.1.1.529 GR Germano Isstitution Na     beaccores PU, SC, 64 27/11/2021 Europe Portugal Europe Portugal genome 29904 Human unknown 1.1.1.529 GR Germano Isstitution Na     beaccores PU, SC, 64 27/11/2021 Europe Portugal Europe Portugal genome 29904 Human unknown 1.1.529 GR Germano Isstitution Na     beaccores PU, SC, 64 27/11/2021 Europe Portugal Europe Portugal genome 29904 Human unknown utknown 8.1.1.529 GR Germano Isstitution Na
Omicron hCoV-19/SouthAfrica/NICD-N21256/2021 Omicron hCoV-19/SouthAfrica/NICD-N21261/2021 hCoV-19/SouthAfrica/NICD-N21261/2021	VDC_Omicron_hCoV-19/SouthWrica/NICD-N21256/2021 VDC_Omicron_hCoV-19/SouthWrica/NICD-N21261/2021 VDC_Omicron_hCoV-19/SouthWrica/NICD-N21261/2021	betaccrone (FI_16_61 10/11/2021 Africa South Afrin Gauteng Africa South Afric Gauteng genome 29722 Human 25 Male B.1.1.529 GR HILIBUIC National in Am betaccrone (FI_16_61 10/11/2021 Africa South Afric Gauteng Africa South Afric Gauteng genome 29729 Human 23 Female B.1.1.529 GR HILIBUIC National In Am betaccrone (FI_16_61 62) 10/11/2021 Africa South Afric Gauteng Africa South Afric Gauteng genome 29719 Human 23 Female B.1.1.529 GR HILIBUIC National In Am betaccrone (FI_16_61 62) 10/11/2021 Africa South Afric Gauteng Africa South Afric Gauteng genome 2014 Human 23 Female B.1.1.529 GR HILIBUIC National In Am
Omicron hCoV-19/Brazi/SP-HAE-ID989/2021 Omicron hCoV-19/Brazi/SP-HAE-ID989/2021 Omicron hCoV-19/Brazi/SP-HAE-ID990/2021	VOC_Omicron_hCaV-19/binal/SP-HIAE-0989/2021 VOC_Omicron_hCaV-19/Binal/SP-HIAE-0989/2021 VOC_Omicron_hCaV-19/Binal/SP-HIAE-0999/2021	betaccen (P) (s, 0) 1/1/2021 contract foruit is software contract for the software contract for
Omicron HCoV-19/Austria/MUIV-0230/2021 Omicron HCoV-19/Austria/MUIV-0231/2021 Omicron HCoV-19/Spain/MD-HGUGM-5835945/2021	VDC_Omicron_HCW-19/Austria/MUN-0230/2021 VDC_Omicron_HCW-19/Austria/MUN-0231/2021 VDC_Omicron_HCW-19/Spain/MD-HGUGM-5835945/2021	betaceren PJ_8_67 3/11/x021 turope Autoria Tyrol Schwaz Europe Austria Tyrol generene 2969 Human untexone 15.1529 GM Indibutie bistikas dD betaceren PJ_8_67 3/11/x021 Europe Austria Tyrol Schwaz Europe Austria Tyrol generene 2969 Human untexone 15.1529 GM Indibutie bistikas dD betaceren PJ_8_67 3/11/x021 Europe Spain Madrid Europe Spain Madrid generene 29749 Human 6 Female 8.1.1529 GM Hospital G Hospital G Hospital G
Omicron hCoV-19/Brazil/SP-IAL-6479/2021 Omicron hCoV-19/Japan/IC-2278/2021 Omicron hCoV-19/SouthAfrica/NICD-N21437/2021	VDC_Omicron_hCoV-19/Brazil/SP-14L-6479/2021 VDC_Omicron_hCoV-19/Japan/IC-2278/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21437/2021	betacrone PFL8_66 127/11/022 South-AmetBeall Sto-Paulo Guaruhos South Ame Beal SooPaulo genome 2981 Human 129 Male 8.11.529 GR Grupo CR Instituto A CU betacrone PFL8_66 128/11/0221 Adia Jopan Adia Japan genome 29753 Human unitromu uninoum 8.11.529 GR SARS-GVP Pathogen Tx betacrone PFL8_66 19/11/0221 Adia South Afric Sauth Afric Sauth Afric Sauth Afric Sauth Afric Sauth Afric Sauth
Omicron hCoV-19/SouthAfrica/NICD-N21438/2021 Omicron hCoV-19/SouthAfrica/NICD-N21439/2021 Omicron hCoV-19/SouthAfrica/NICD-N21440/2021	VOC_Omicron_hCoV-19/SouthWrica/NICD-N21438/2021 VOC_Omicron_hCoV-19/SouthWrica/NICD-N21439/2021 VOC_Omicron_hCoV-19/SouthWrica/NICD-N21440/2021	betaccore PL_6L_61 ID/11/2021 Africa South Afric Guzeng Africa South Afric Guzeng genome 29751 Human unknown unknown B.11.529 GR Lancet Lat National ir Am betaccore PL_6L_61 ID/11/2021 Africa South Afric Guzeng Africa South Afric Guzeng genome 29751 Human unknown B.11.529 GR Lancet Lat National ir Am betaccore PL_6L_61 ID/11/2021 Africa South Afric Guzeng Africa South Afric Guzeng genome 29751 Human unknown B.11.529 GR Lancet Lat National ir Am betaccore PL_6L_61 ID/11/2021 Africa South Afric Guzeng Africa South Afric South Afric South Afric South Africa South Afric South Africa
Omicron hCoV-19/SouthAfrica/NICD-N21641/2021 Omicron hCoV-19/SouthAfrica/NICD-N21642/2021	VDC_Omicron_hCoV-19/SouthAfrica/NECD-N21441/2021 VDC_Omicron_hCoV-19/SouthAfrica/NECD-N21442/2021	bestreeren (F. 1996) and fall Statemer (F. 1997) and fall
Omicron hCoV-19/SouthAfrica/NICD-N23443/2021 Omicron hCoV-19/SouthAfrica/NICD-N23444/2021 Omicron hCoV-19/SouthAfrica/NICD-N23446/2021	VDC_Omicron_hCoV-19/SouthAfrica/NED-N21443/2021 VDC_Omicron_hCoV-19/SouthAfrica/NED-N21444/2021 VDC_Omicron_hCoV-19/SouthAfrica/NED-N21446/2021	betaceron (P), 85, 61 15/11/2021 Arica South Afric Gusterg Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown Unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas unbrown unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas Unbrown 14.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg genome 20751 Humas Unbrown Unbrown 8.11.529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown Humas Unbrown 15.1529 0R Lancet Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown 15.1529 District Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown 15.1529 District Lak National Ir Arica South Afric Gusterg Genome 20751 Humas Unbrown 15.1529 District Lak National Ir Arica South 15.1520 Humas Unbrown 15.1529 District Lak Nati
Omicron hCoV-19/SouthAfrica/NICD-N21447/2021 Omicron hCoV-19/SouthAfrica/NICD-N21448/2021 Omicron hCoV-19/SouthAfrica/NICD-N21448/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21447/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21448/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21449/2021	betacoron (PL)(S), 65 16/11/2021. Africa. South Afric Gusteng Africa. South Afric Gasteng genome. 20151. Human: unknown unknown 8.11.529 68. Lanset Lak National in Am betacoron (PL)(S), 65 16/11/2021. Africa. South Afric Gasteng Africa. South Afric Gasteng genome. 20151. Human: unknown M. 11.529. 68. Lanset Lak National in Am betacoron (PL) 66. 16 16/11/2021. Africa. South Afric Gasteng. Africa. South Afric Gasteng genome. 20151. Human: unknown M. 11.529. 68. Lanset Lak National in Am betacoron (PL) 66. 16 16/11/2021. Africa.
Omicron hCoV-19/SouthAfrica/NICD-N21450/2021 Omicron hCoV-19/SouthAfrica/NICD-N21451/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21450/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21451/2021	bestacron (PLIS), 61 16/11/2021 Mrka South Mrki Gauterg Mrka South Mrk Gauterg genome 29751 Human unknown unknown B.1.529 GR Lancet Lat National ir Am bestacron (PLIS), 61 16/11/2021 Mrka South Mrki Gauterg Mrka South Mrk Gauterg genome 29751 Human unknown B.1.529 GR Lancet Lat National ir Am
Omicron hCoV-19/SouthAnica/NICD-N21452/2021 Omicron hCoV-19/SouthAnica/NICD-N21453/2021 Omicron hCoV-19/SouthAnica/NICD-N21454/2021	VDC_Omicron_hCoV-19/SouthWhCa/NICD-N21453/2021 VDC_Omicron_hCoV-19/SouthWhCa/NICD-N21453/2021 VDC_Omicron_hCoV-19/SouthWhCa/NICD-N21454/2021	bettacons (P_1_b_m) = 16/11/2021 Minas Subth Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown withown 8.11.529 GR Lancett Lik Notional if Arr bettacons (P1_b_m) = 61/11/2021 Minas South Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown withown 8.11.529 GR Lancett Lik Notional if Arr bettacons (P1_b_m) = 11/11/2021 Minas South Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown unknown 8.11.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown unknown 8.11.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown unknown 8.11.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Guteng Arrica South Amini Gateng genome 29751 Human unknown unknown 8.11.529 GR Lancett Lik Notional if Arris South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas South Amini Gateng genome 29751 Human unknown unknown 1.51.529 GR Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas Arr Lancett Lik Notional if Arr Bettacons (P1_b_m) = 11/11/2021 Minas Arr Lancett Lik Notional if Arr La
Omicron hCoV-19/SouthAfrica/NICD-N21614/2021 Omicron hCoV-19/SouthAfrica/NICD-N21618/2021 Omicron hCoV-19/SouthAfrica/NICD-N21620/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21614/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21618/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21620/2021	betacoron (PL/BL_64 12/11/2021 Africa South Afrii Gusterg Africa South Afric Gusterg genome 29751 Human 56 Male 8.1.1.529 GR Ampeth Li National ir Am betacoron (PL/BL_64 12/11/2021 Africa South Afrii Gusterg Africa South Afric Gusterg genome 2013) Human 68 Female 8.1.1.529 GR Ampeth Li National ir Am betacoron (PL 64 13/11/2021 Africa Guster) Africa Gusterg Africa Combine Gusterg 2013) Human 68 Female 8.1.1.529 GR Ampeth Li National ir Am
Omicron HCoV-19/SouthAfrica/NICD-N21623/2021 Omicron HCoV-19/SouthAfrica/NICD-N21627/2021	VDC_Omicron_hCoV-19/SouthAfrica/NECD-N21623/2021 VDC_Omicron_hCoV-19/SouthAfrica/NECD-N21627/2021	betraceron (PL/S), 61 17/11/2021 Africa South Afrii Mparmilanga Africa South Afric Mparmilar genome 20751 Human 29 Female 8.11.529 00 Ampath La National Ir Am betraceron (PL/S), 61 18/11/2021 Africa South Afrii Gauteng Africa South Afric Gauteng genome 20687 Human 35 Female 8.11.529 08 Ampath Li National Ir Am
Omicron KCN-19/SouthAlrica/NICD-N21630/2021 Omicron KCN-19/SouthAfrica/NICD-N21631/2021 Omicron KCN-19/SouthAfrica/NICD-N21633/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21630/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21631/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21633/2021	betaceron DP_US_01 17/11/2021 Arria South Afrin Guareng Africa South Afric Guareng genome 2951 Human 19 manual 8.11.529 69 Ampletic Likeloval if Arr betaceron DP_US_61 13/11/2021 Africa South Afric Guareng Africa South Afric Guareng genome 2951 Human 20 Female 8.11.529 69 Ampletic Likeloval if Arr betaceron DP_US_61 17/11/2021 Africa South Afric Guareng Africa South Afric Guareng genome 2951 Human 47 Male 8.11.529 69 Ampletic Likeloval if Arr
Omicron hCoV-19/SouthAfrica/NICD-N21634/2021 Omicron hCoV-19/SouthAfrica/NICD-N21635/2021 Omicron hCoV-19/SouthAfrica/NICD-N21638/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21634/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21635/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21638/2021	betacoren EPLS_65 12/11/2021 Mrica South Afrin Gutzeng Africa South Afric Gutzeng genome 29511 Human 4 Female 8.11.529 GR Ampetita Discional if An betacoren EPLS_65 18/11/2021 Mrica South Afric Gutzeng Africa South Afric Gutzeng genome 29411 Human 30 Female 8.11.529 GR Ampetita Discional in An betacoren EPLS_65 15 /21/2022 Mrica South Mric Gutzeng Africa South Afric Gutzeng genome 29511 Human 32 Mile 8.11.529 GR Ampetita Discional in An betacoren EPLS_65 15 /21/2022 Mrica South Mric Gutzeng Africa South Afric Gutzeng genome 29511 Human 32 Mile 8.11.529 GR Ampetita Discional in An
Omicron hCoV-19/SouthAfrica/NICD-N21641/2021 Omicron hCoV-19/SouthAfrica/NICD-N21644/2021	VDC_Omicron_hCoV-19/SouthMrica/NICD-N21641/2021 VDC_Omicron_hCoV-19/SouthMrica/NICD-N21644/2021	bestacons (PL/SC, 66 16/11/2021 Africa South Afris Gauterg Africa South Afris Gauterg genome 29751 Human 19 Male 8.1.1529 GR Ampeth La National in Am bestacons (PL/SC, 66 16/11/2021 Africa South Afris Gauterg Africa South Afris Gauterg genome 29578 Human 21 Female 8.1.1529 GR Ampeth La National in Am
Omicron hCoV-19/SouthAfrica/NICD-N21648/2021 Omicron hCoV-19/SouthAfrica/NICD-N21648/2021	VDC_Omicron_hCoV-19/SouthAfrica/NED-N21648/2021 VDC_Omicron_hCoV-19/SouthAfrica/NED-N21648/2021	Betraction DPUSS, 61 1712/2023. Articla advantationsproge Printice advantation downlog genuine advantation of printice bulletace was engineering encoded and bulletace advantational advantational in America Statistical advantational advan
Omicron hCaV-19/SouthAfrica/NICD-N21650/2021 Omicron hCaV-19/SouthAfrica/NICD-N21651/2021 Omicron hCaV-19/SouthAfrica/NICD-N21655/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21650/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21651/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21655/2021	betzereren DPL/S, 64 17/11/2021 Africa South Afrin Gusterg Africa South Afric Gusterg genome 29511 Human 5 Mile 8.11.529 GR Ampath La National Ir Am betzereren DPL/S, 64 17/11/2021 Africa South Afrin Gusterg Africa South Afric Gusterg genome 29511 Human 18 Mule 8.11.529 GR Ampath La National Ir Am betzereren DPL/S, 64 17/11/2021 Africa South Afrin Gusterg Africa South Afric Gusterg genome 29511 Human 16 Mule 8.11.529 GR Ampath La National Ir Am
Omicron hCaV-19/SouthAfrica/NICD-N21656/2021 Omicron hCaV-19/SouthAfrica/NICD-N21657/2021	VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21656/2021 VDC_Omicron_hCoV-19/SouthAfrica/NICD-N21657/2021	betacoron (PE), <u>66</u> 17/11/2021 Mrka South Afrii Gauteng Africa South Afrii Gauteng genome 29751 Human 35 Male 8.1.1.529 GR Ampeth La Nacional ir Am betacoron (PL), <u>66</u> 13/11/2021 Mrka South Afrii Gauteng Africa South Afrii Gauteng genome 29751 Human 28 Male 8.1.1.529 GR Ampeth La Nacional ir Am
Omicron hCoV-19/SouthAfrica/NICD-N21660/2021 Omicron hCoV-19/SouthAfrica/NICD-N21660/2021 Omicron hCoV-19/SouthAfrica/NICD-N21661/2021	VOC_Omicron_hCoV-19/SouthWhice/NiCD-N21660/2021 VOC_Omicron_hCoV-19/SouthWhice/NiCD-N21660/2021 VOC_Omicron_hCoV-19/SouthWhice/NiCD-N21661/2021	bestraces (PL_96, eff. 1211/1221 Mrka South Mini Wettern C provide (Mini Wettern C provide 12951 Human 14 Final e Statistica (Mini Wettern C provide 12951 Human 15 Final e B.1.1529 GR Ampeth La National In Amber La Nati
umicron hCoV-19/Tapan/JC-2279/2021 Omicron hCoV-19/England/MUX-28E8E12/2021 Omicron hCoV-19/England/ALDP-28E8D0A0/2021	VUC_Omicron_hCoV-19/lapan/lC-2279/2021 VDC_Omicron_hCoV-19/England/MUX-29E8E12/2021 VDC_Omicron_hCoV-19/England/ALDP-28E8E0A0/2021	testscron ur Jus, 95 27/11/2021. Adu Japan Adu Japan genome 29/9/5 Human unknown Uulhown B.1.1.529 GR SyM5-Col- Pathgam Ty,     testscron IPJ, 66, 65 25/11/2021. Turope United III. Tegland Europe United XII. Tigland genome 29/9/7 Human unknown stuhown B.1.1.529 GR Uphthown. Welcome Has     testscron IPJ, 66, 65 25/11/2021. Turope United III. Tegland Europe United XII. Turope United XII
Omicron hCoV-19/England/MUX-28F501C/2021 Omicron hCoV-19/Scotland/QEUH-28EC476/2021 Division hCoV-19/Scotland/QEUH-28EC476/2021	VDC_Omicron_hCoV-19/England/MEX-20/501C/2021 VDC_Omicron_hCoV-19/Sociland/QEUH-20/501C/2021 VDC_Omicron_hCoV-19/Sociland/QEUH-20/502076/2021	betaccen (P) (8), 67 25/11/2021 turope United lin England Europe United Kin England Europe Unite
Dreicron HCoV-19/Scotland/OEUH-28D0184/2021 Dreicron HCoV-19/Scotland/OEUH-28D0213/2021	VDC_Omicron_hCaV-19/Scotland/QEUH-2800184/2021 VDC_Omicron_hCaV-19/Scotland/QEUH-2800184/2021 VDC_Omicron_hCaV-19/Scotland/QEUH-2800211/2021	betacore (PLS, 62, 21)/12021 Europa United tis Solution Europa United Kin Social genome 29/47 Intrina Uniteriore United Kin Social Utiphtboak Wilkome Ha betacore (PLS, 62, 21)/12021 Europa United Kin Social Europa United Kin Social genome 29/47 Huma Uniteriore United Kin Social Utiphtboak Wilkome Ha
Umicron nCoV-19/Scotland/QEUH-288E079/2021 Omicron hCoV-19/Belgium/ULG-22181/2021 Omicron hCoV-19/Ghana/TRA-2298/2021	VUX_Umicron_hCoV-19/Scotland/QEUH-288E079/2021 VDC_Omicron_hCoV-19/Belgium/ULG-22181/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2298/2021	textorem UFUS_E2 arX1120021 Europe United tin Scottand Europe United Kin Scottand genome 29474 Human unitrown unitrown List.293 GR Uphthodau Wellcome H beraceron EPUS_65 29/11/20021 Europe Belgium Sim-Agatha-Berchem Europe Belgium Sim-Agatha genome 29684 Human 28 Male 8.11.1529 GR Unitersity GIGA MAKE betraceron EPUS_65 25/11/20021 Marka Ghana Accra Mirca Ghana Accra genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Acca Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca Mirca Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mirana Detaceron EPUS_65 25/11/20021 Marka Ghana Acca genome 29684 Human 35 Male 8.11.529 GR National H Mational H Mationa
Omicron hCoV-19/Ghana/TRA-2303/2021 Omicron hCoV-19/Ghana/TRA-2314/2021 Omicron hCoV-19/Ghana/TRA-2314/2021	VOC_Omicron_hCoV-19/Ghana/TRA-2303/2021 VOC_Omicron_hCoV-19/Ghana/TRA-2314/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2342/2022	bestoron PFUSL_65 25/11/2021 Africa Ghuna Accca Mirica Ghuna Accca genome 26664 Human 38 Female 8.11.529 GR National in Nation
Omicron hCoV-19/Ghans/TRA-2292/2021 Omicron hCoV-19/Ghans/TRA-2294/2021	VDC_Omicron_hCoV-19/Ghana/TRA-2292/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2294/2021	bestcoron (P), (S., 65 24/1), 2202 Africa Ghana Accea Africa Ghana Accea genome 20464 human 14 Million (H. National I Malional I M. National I
umicron nCoV-19/Ghana/TRA-2288/2021 Omicron hCoV-19/Ghana/TRA-2310/2021 Omicron hCoV-19/Ghana/TRA-2311/2021	VLA_Umicron_hCoV-19/Ghuna/TRA-2288/2021 VDC_Omicron_hCoV-19/Ghuna/TRA-2310/2021 VDC_Omicron_hCoV-19/Ghuna/TRA-2311/2021	ensectore Ur. 0, 9, 4/v1,2022 Arica Chana Accea Arica Ghana Accea genome 2060H huma 47 Male 8.11.529 GR National National I National National National National National National National National National Nati
Dmicron hCaV-19/Ghana/TRA-2312/2021 Dmicron hCaV-19/Ghana/TRA-2317/2021 Dmicron hCaV-19/Ghana/TRA-2339/2021	VDC_Omicron_hCoV-19/0hana/TRA-2312/2021 VDC_Omicron_hCoV-19/0hana/TRA-2317/2021 VDC_Omicron_hCoV-19/0hana/TRA-2339/2021	betacoron (PL) 65, 65 25/11/2021. Africa Chana Accra Africa Chana Accra genome 20684 Human 42 Male 8.11.529 68 National in National in Marianal in Mariana in Marian Mariana in Mariana in Mari
Omicron hCoV-19/Ghana/TRA-2286/2021 Omicron hCoV-19/Ghana/TRA-2275/2021	VDC_Omicron_hCoV-19/Ghana/TRA-2286/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2275/2021	betractor (E. 192, 65 24/11/2021 Mrka Ghana Accra Mrka Ghana Accra genome 26684 Human 31 Female 8.11.529 GR National in Nation
Dmicron hCoV-19/Ghana/TRA-2299/2021 Dmicron hCoV-19/Ghana/TRA-2315/2021 Dmicron hCoV-19/Ghana/TRA-2289/2021	VDC_Omicron_hCoV-19/Ghana/TRA-2299/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2315/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2289/2021	betaccons PE_0_61 52/11/2021 Mrica Ghana Accra Mrica Ghana Accra genome 26684 Human 42 Mule 8.11.529 GR National in Normal in Reconsul in With the testacons PE_0_61 52/11/2021 Mrica Ghana Accra Mrica Ghana Accra genome 26684 Human 36 Female 8.11.529 GR National in Normal in Reconsul in With testacons PE_0.61 52 /11/2021 Mrica Ghana Accra Mrica Ghana Accra genome 26684 Human 31 Mule 8.11.529 GR National in Normal in Reconsul in With testacons PE_0.61 52 /11/2021 Mrica Ghana Accra genome 26684 Human 31 Mule 8.11.529 GR National in Normal International in Normal Networks PE_0.61 52 /11/2021 Mrica Ghana Accra Mrica Ghana Accra genome 26684 Human 31 Mule 8.11.529 GR National in Normal International Internatio
Omicron hCoV-19/Ghana/TRA-2309/2021 Omicron hCoV-19/Ghana/TRA-2380/2021 Omicron hCoV-19/Ghana/TRA-2380/2021	VDC_Omicron_hCoV-19/Ghana/TRA-2309/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2280/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2280/2021	betacoron (PL/BL_64 25/11)/2021 Mrko Ghana Accra Mrica Ghana Accra genome 29664 Human 31 Female 8.11.529 GR National in National in Waternal in Maternal in Matern
micron hCoV-19/Ghana/TRA-2306/2021 micron hCoV-19/Ghana/TRA-2296/2021	VDC_Omicron_hCoV-19/Uhana/TRA-2306/2021 VDC_Omicron_hCoV-19/Uhana/TRA-2306/2021	Detraction D. S., D. 2011 Adda Allan Al
Dmicron hCoV-19/Ghana/TRA-2271/2021 Dmicron hCoV-19/Ghana/TRA-2261/2021 Dmicron hCoV-19/Ghana/TRA-2265/2021	VDC_Omicron_hCoV-19/6hana/TRA-2271/2021 VDC_Omicron_hCoV-19/6hana/TRA-2261/2021 VDC_Omicron_hCoV-19/6hana/TRA-2265/2021	betaceron PL/S_61 24/11/2021 Africa Ghana Accra Africa Ghana Accra genome 2669 Human 39 Mile 8.11.529 60 Nutional in Nacional in Mica Ghana Accra genome 2669 Human 50 Mile 8.11.529 60 Nutional in Nacional in Mica Ghana Accra genome 2669 Human 50 Mile 8.11.529 60 Nutional in Nacional in Nacional in Mica Ghana Accra genome 2669 Human 51 Female 8.11.529 60 Nutional in Nacional in Naciona
Omicron hCoV-19/Ghana/TRA-2282/2021 Omicron hCoV-19/Ghana/TRA-2283/2021 Omicron hCoV-19/Ghana/TRA-2283/2021	VOC_Omicron_hCoV-19/Ghana/TRA-2282/2021 VOC_Omicron_hCoV-19/Ghana/TRA-2283/2021 VOC_Omicron_hCoV-19/Ghana/TRA-2283/2021	betacoron (PL)(S), 65 24/11/2021 Mrka Ghana Accra Mrka Ghana Accra genome 29693 Human 35 Male 8.11.529 GR National in Nationa
Dmicron hCoV-19/Ghana/TRA-2291/2021 Dmicron hCoV-19/Ghana/TRA-2308/2021	VOC_Omicron_hCoV-19/Ghana/TRA-2291/2021 VOC_Omicron_hCoV-19/Ghana/TRA-2308/2021	betraction (E.), 55 24/11/2021 Mrka Ghana Accra Mrka Ghana Accra genome 29693 Human 38 Female 8.1.1.529 GR National in Nationa
Dmicron hCoV-19/Ghana/TRA-2249/2021 Dmicron hCoV-19/Ghana/TRA-2300/2021 Dmicron hCoV-19/Ghana/TRA-2290/2021	VDC_Omicron_hCoV-19/Ghana/TRA-2249/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2300/2021 VDC_Omicron_hCoV-19/Ghana/TRA-2290/2021	betacrone 0FUS_64 22/11/2021 Mrica Ghana Accra Mrica Ghana Accra genome 29699 Hinnan 26 Female 8.1.1529 GR National in Nati
Dmicron hCoV-19/Ireland/MH-NVRL-521/RL00506672/2021 Dmicron hCoV-19/USA/CA-UCSF-CDL0R-SFDPH-C0001/2021	VDC_Omicron_hCoV-19/Ireland/MH-NVRI-52318L00506672/2021 VDC_Omicron_hCoV-19/USA/CA-UCSF-COLOR-SFDPH-CO201/2021 VDC_Omicron_hCoV-19/USA/CA-UCSF-COLOR-SFDPH-CO201/2021	betacoron 09/06_64 25/11/2021 Lurope Ireland Mosth Europe Ireland Meeth genome 29997 Humas 21-10 Female 8.1.1.529 GR National V National V Sational V Sati
Pricron hCoV-19/Australia/NSW-ICPMR-14639/2021 Pricron hCoV-19/Australia/NSW-RPAH-CoV2050/2021	VDC_Omicron_hCoV-19/Australia/NSW-ICPMR-14639/2021 VDC_Omicron_hCoV-19/Australia/NSW-RPAH-CoV2050/2021	Betracted D (26,5) = 911/2022 Oceania Australia New South Systemy Oceania Australia New South genome 20078 Human unknown unknown exhibition (15:20) 601 Human (15:20) 601 H
2micron hCoV-19/Germany/HE-FFM-30318738/2021 2micron hCoV-19/Germany/HE-FFM-30318739/2021 2micron hCoV-19/Germany/HE-FFM-30318740/2021	VDC_Omicron_NCaV-19/Germany/HE-FFM-30318738/2021 VDC_Omicron_NCaV-19/Germany/HE-FFM-30318739/2021 VDC_Omicron_NCaV-19/Germany/HE-FFM-30318740/2021	betacoron DFUS_04 22/11/2021 turope Germany Hisse Europe Germany Hesse genome 2014/ Human 32 Mile 8.11.529 GR institute first betacoron DFUS_64 23/11/2021 turope Germany Hisse Europe Germany Hesse genome 2014/ Human 35 Female 8.11.529 GR institute firstitute first betacoron DFUS_64 23/11/2021 turope Germany Hisse Europe Germany Hesse genome 2014/ Human 72 Female 8.11.529 GR
Dmicron hCoV-19/Germany/HE-FFM-30286807/2021 Dmicron hCoV-19/Germany/HE-FFM-30318741/2021 Dmicron hCoV-19/Germany/HE-FFM-30286808/2021	V0C_Omicron_hCoV-19/Germany/HE-FFM-30286807/2021 V0C_Omicron_hCoV-19/Germany/HE-FFM-30318741/2021 V0C_Omicron_hCoV-19/Germany/HE-FFM-30286808/2021	betacoron 6PLIS_65 22/11/2021 Europe Germany Hose Europe Germany Hose genome 29/47 Hinnan 41 Female 8.1.1.529 GA institute fractionate fra- betacoron 6PLIS_65 22/11/2021 Europe Germany Hose Europe Germany Hose genome 29/38 Hinnan 40 Male 8.1.1.529 GA institute fractionate frac- betacoron 6PLIS_65 22/11/2021 Europe Germany Hose Europe Germany Hose genome 29/34 Hinnan 38 Male 8.1.1.529 GA institute fractionate fractional fracti
micron hCoV-19/SouthKores/K0CA18124/2021 micron hCoV-19/SouthKores/K0CA18125/2021	VOC_Omicron_hCoV-19/SouthKores/KDCA18124/2021 VOC_Omicron_hCoV-19/SouthKores/KDCA18125/2021	betacoron GP_06_65 24/11/2021 Ada South Korea Ada South Korea genome 28972 Human 56 Female 8.1.1.529 GR Division of Division of A betacoron GP_06_65 22/11/2021 Ada South Korea Ada South Korea genome 29969 Human 46 Female 8.1.1.529 GR Division of Division of A betacoron GP_06_65 22/11/2021 Ada South Korea Ada South Korea 2006 Human 46 Female 8.1.1.529 GR Division of Division of A betacoron GP_06_65 22/11/2021 Ada South Korea Ada South Korea 2006 Human 46 Female 8.1.1.529 GR Division of Division of A betacoron GP_06_65 22/11/2021 Ada South Korea Ada South Korea 2006 Human 46 Female 8.1.1.529 GR Division of Division of A betacoron GP_06_65 22/11/2021 Ada South Korea Ada South Korea 2006 Human 46 Female 8.1.1.529 GR Division of Divi
ipha hCoV-19/England/PORT-2596F2/2020 ipha hCoV-19/England/PORT-2596F2/2020	VDC_Alpha_hCoV-19/England/PORT-2E90F2/2020 VDC_Alpha_hCoV-19/England/PORT-2E904D/2020	entraction of the grant of the second
Ipha hCoV-19/England/PORT-2E9C70/2020 Ipha hCoV-19/England/CAMB-18C9F8/2020 Ipha hCoV-19/England/CAMB-18CA22/2020	VDC_Alpha_hCoV-19/England/PORT-2E9C70/2020 VDC_Alpha_hCoV-19/England/CAMB-18C978/2020 VDC_Alpha_hCoV-19/England/CAMB-18CA22/2020	bitacron PU_S_X 2020 Europa United Sin England Europa United Sin England genome 29953 Human unitnewn utshonen 8.1.1.7 GHY Canter GP C0VD-19 An betacron PU_S_X 2020 Europa United Sin England Europa United Sin England genome 29953 Human unitnewn utshonen 8.1.1.7 GHY Departme C0VD-19 An betacron PU_S_X 2020 Europa United Sin England Europa United Sin England genome 29953 Human unitnewn utshonen 8.1.1.7 GHY Departme C0VD-19 An
Ipha hCoV-19/England/PORT-2E9891/2020 Ipha hCoV-19/England/205041766/2020 Ipha hCoV-19/England/205041766/2020	VDC_Alpha_hCoV-19/England/PORT-259891/2020 VDC_Alpha_hCoV-19/England/205041766/2020 VDC_Alpha_hCoV-19/England/PORT-259242/2020	betacoron 6PL(SL,7X 2000 Europe United Kin England Europe United Kin England genome 29/63 Human uninnew uninnew Extra COVID-19 An betacoron 6PL(SL,71 2000 Europe United Kin England Europe United Kin England genome 29/63 Human uninnew Human Kin 17 GW Registrate COVID-19 Hu betacoron 6PL Kin 72 2000 Europe United Kin England Europe United Kin England genome 29/63 Human uninnew Human Kin 17 GW Registrate COVID-19 Hu betacoron 6PL Kin 72 2000 Europe United Kin England Europe United Kin England genome 29/63 Human uninnew Human Kin 17 GW Centrefor (2010)-19 Hu betacoron 6PL Kin 72 2000 Europe United Kin England Europe United Kin England genome 29/63 Human uninnew Human Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe United Kin England Europe United Kin England genome 29/63 Human United Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe United Kin England Europe United Kin England genome 29/63 Human United Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe United Kin England Europe United Kin England genome 29/63 Human United Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe United Kin England genome 29/63 Human United Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe United Kin England genome 29/63 Human United Kin 17 GW Centrefor (2010)-19 Hu Benome United Kin 17 2000 Europe Eu
pha hCoV-19/England/PORT-2E9751/2020 pha hCoV-19/England/PORT-2E9750/2020	VOC_Alpha_hCoV-19/England/PORT-2E9751/2020 VOC_Alpha_hCoV-19/England/PORT-2E9750/2020	betraction (E.g., 77) 2000 Europe United in England Europe United Kin England genome 19763 Human Unitanum Unitanum LLLZ GRY Centre for COVID-19 An betraction (E.g., 77) 2000 Europe United Kin England Europe United Kin England genome 19763 Human Unitanum Unitanum BLLZ GRY Centre for COVID-19 An
pha hCoV-19/England/PORT-2E9/88/2020 pha hCoV-19/England/PORT-2E99E2/2020 pha hCoV-19/England/PORT-2E9A3A/2020	VDC_Alpha_hCoV-19/ingland/PORT-2199162/2020 VDC_Alpha_hCoV-19/ingland/PORT-219912/2020 VDC_Alpha_hCoV-19/ingland/PORT-219930/2020	bestcores DP_06_7.2 2020 Europe United In England Europe United Kin England genome 299/61 Human unknown Unitnown 16.11.7 GRV Centre for COVID-19 An bestcores DP_06_72 2020 Europe United Kin England Europe United Kin England genome 299/61 Human unknown 16.11.7 GRV Centre for COVID-19 An bestcores DP_06_72 2020 Europe United In England Europe United Kin England genome 299/61 Human unknown 16.11.7 GRV Centre for COVID-19 An
lpha hCoV-19/England/PORT-2E9A58/2020 lpha hCoV-19/England/CAMB-18D6B4/2020 lpha hCoV-19/England/CAMB-A97BE5/2020	VDC_Alpha_hCoV-19/England/PORT-259A58/2020 VDC_Alpha_hCoV-19/England/CAMB-18D684/2020 VDC_Alpha_hCoV-19/England/CAMB-4978E5/2020	betaccon DI EX 7. 2020 Europe United En England Europe United Kin England genome 20163 Human unitoxen unitoxen 18.1.27 GRY Centerfor COVD-19 An betaccon DI EX 7. 2020 Europe United En England Europe United Kin England genome 20163 Human unitoxen unitoxen 18.1.27 GRY Departme COVD-19 An betaccon DI EX 74. 2020 Europe United En England Europe United Kin England genome 20163 Human unitoxen unitoxen ELL7 GRY Departme COVD-19 An
ipha hCoV-19/England/PCRT-204F24/2020 ipha hCoV-19/England/PCRT-204F33/2020 ipha hCoV-19/England/PCRT-204F33/2020	VDC_Alpha_hCoV-19/England/PORT-204F24/2020 VDC_Alpha_hCoV-19/England/PORT-204F33/2020 VDC_Alpha_hCoV-19/England/PORT-204F33/2020	betacoren BH, SK, 24 2000 Europa United Ein England Europa United Kin
Ipha hCoV-19/England/PORT-204F8E/2020 Ipha hCoV-19/England/PORT-204FAC/2020	VOC_Alpha_hCoV-19/England/PORT-2D4F8E/2020 VOC_Alpha_hCoV-19/England/PORT-2D4FAC/2020	betacoron EP1, BC, 74 2000 Europe United fin England Europe United Kin England genome 29760 Human unitown unitown B.1.1.2 GRV Centre for COVID-19 An betacoron EP1, BC, 74 2000 Europe United Kin England Europe United Kin England genome 29760 Human unitown unitown B.1.1.2 GRV Centre for COVID-19 An
Incov-19/England/PORT-205002/2020 Ipha hCoV-19/England/PORT-205002/2020 Ipha hCoV-19/England/PORT-205020/2020	VOC_Alpha_hCoV-15/England/PORT-205022/2020 VOC_Alpha_hCoV-19/England/PORT-205022/2020 VOC_Alpha_hCoV-19/England/PORT-205020/2020	winnersen under eine eine eine eine eine eine eine ei
pha hCoV-19/England/PORT-20505D/2020 ta hCoV-19/England/205260233/2020 ta hCoV-19/England/205261884/2020	VDC_Alphs_hCoV-19/England/PORT-20505D/2020 VDC_Bets_hCoV-19/England/205260233/2020 VDC_Bets_hCoV-19/England/205261884/2020	betscrons (FULS), 74 2000 Europe United lin England Europe United Kin England genome 259/Ki Human unknown uknown 6.1.1.2 GR Centre for COVID-19 An betscrons (FULS), 72 2000 Europe United Kin England Europe United Kin England genome 288/Ki Human 29 Male 8.1.331 GH Registratic COVID-19 M betscrons (FULS), 72 2000 Europe United Kin England Europe United Kin England genome 288/Ki Human 37 Male 8.1.331 GH Registratic COVID-19 M betscrons (FULS), 72 2000 Europe United Kin England Europe United Kin England genome 288/Ki Human 17 Male 8.1.331 GH Registratic COVID-19 M
rta hCoV-19/Austria/CeMM1952/2020 rta hCoV-19/Zimbabwe/2W-29001/2020	VOC_Beta_HCoV-19/Austria/CeMM1952/2020 VOC_Beta_HCoV-19/Zimbabwe/ZW-29001/2020	britacoren (PI, IS, 35 2000 Europa Austria Europa Austria genoren 2017) Human unitzene usinoan 11.131 GM Austria/A Europa Austria/Europa/Pierra 2017) Human Unitzene usinoan 11.131 GM Austria/A Europa/Pierra 2017) Human 10 Male 11.1351 GM Austria/A Europa/Pierra 2017) Human 10 Male 11.1
na hCoV-19/Qatar/QA-QU_19-1-82/2020 na hCoV-19/Qatar/QA-QU_19-1-82/2020	VDC_Beta_hCoV-19/Qatar/QA-QU_19-1-82/2020 VDC_Beta_hCoV-19/Qatar/QA-QU_19-1-82/2020	Detraction (PL) (SL, 12020) C Markan Markan Sector Series Company Resemble 2017 Institute Internet Instrument Instrument Institute (SL) (SL) (SL) (SL) (SL) (SL) (SL) (SL)
tta hCoV-19/SouthAfrica/VIDA-KRISP-K012424/2020 tta hCoV-19/USA/SC-DHEC-1826/2020 tta hCoV-19/SouthAfrica/NICD-N00240/2020	VUC_Beta_hCoV-19/SouthAfrica/VIDA-KRISP-K012424/2020 VOC_Beta_hCoV-19/USA/SC DHEC-1826/2020 VOC_Beta_hCoV-19/SouthAfrica/NICD-N00240/2020	testscron trybu,2: 31,807000 Mrka Subh Alm Free State Africa South Alm Free State genome 29804 Human 21 Male 81,851 G Vacanesa XBSP, K20 Bal      testscron EP1,62,13 75/2000 Worth Amit USA South Carl genome 29800 Human Infraom Fenale 81,251 GH Mitrobiok Mitrobi
ta hCoV-19/South/frica/NICD-N00440/2020 ta hCoV-19/South/frica/NICD-R21068/2020	VOC_Beta_hCoV-19/SouthWrica/NICD-N00440/2020 VOC_Beta_hCoV-19/SouthWrica/NICD-R21058/2020 VOC_Beta_hCoV-19/SouthWrica/NICD-R21058/2020	betacores EPI, SL, 24 2020 Mina South Mina Mina Mina South Mina genome 28480 Human unknown uknown B.1.331. GH National I Am betacores EPI, SL, 24 2020 Mina South Mina Mina Mina Mina genome 28487 Human unknown uknown B.1.331. GH National I Mana Mina Mina Mina Mina Mina Mina Mina
ta hCoV-19/20mbabawe/CIR+R01076/2020 ta hCoV-19/20mbabawe/CIR+R015P-R011662/2020 ta hCoV-19/20mbabawe/CIR+R015P-R011643/2020	VDC_Beta_hCoV-19/2imbabwe/CBR-4015P-4011662/2020 VDC_Beta_hCoV-19/2imbabwe/CBR-4015P-4011662/2020 VDC_Beta_hCoV-19/2imbabwe/CBR-4015P-4011648/2020	ware and a series and a seri
Ia hCoV-19/SouthAfrica/VIDA-KRISP-K012818/2020 Ia hCoV-19/SouthAfrica/VIDA-KRISP-K012825/2020 Ia hCoV-19/SouthAfrica/VIDA-KRISP-K012823/2020	VDC_Beta_hCnV-19/SouthAfrica/VIDA-888P-8012818/2020 VDC_Beta_hCnV-19/SouthAfrica/VIDA-888P-8012825/2020 VDC_Beta_hCnV-19/SouthAfrica/VIDA-888P-8012823/2020	betracron IPU, S., 24 4/9/2020 Africa South Afric Gusteng Africa South Afric Gusteng persone 20037 Human unknown 61.3531 GPI Vaciones 20059 (2018) betracron IPU, S., 24 8/9/2020 Africa South Afri free State Africa South Afric Fes State genome 2007 Human Introven unknown 61.3531 GPI Vaciones 30059 (2018) betracron IPU, S., 24 9/9/2020 Africa South Afri Gusteng Africa South Afric South Afric South Afric South Afric South Africa Sout
ta hCoV-19/SouthAfrica/VIDA-KRISP-K012822/2020 hCoV-19/SouthAfrica/VIDA-KRISP-K012825/2020	VOC_Beta_hCoV-19/SouthAfrica/VIDA-KRISP-K012822/2020 VOC_Beta_hCoV-19/SouthAfrica/VIDA-KRISP-K012826/2020	betacoron PH_SL_24 9/9/2020 Africa South Afrin Gauteng Africa South Afrin Gauteng growme 29878 Human unitrown
a n.ov-19/5000047K3/VIDA-KRISP-0012913/2020 a hCoV-19/500004frka/VIDA-KRISP-0012912/2020 a hCoV-19/Rwanda/CV2217/2020	vox_ee6a_rx.on/15/200104/rxa/VID4-8859-8012913/2020 VOC_8eta_hCoV-15/South4/rka/VID4-8859-8012912/2020 VOC_8eta_hCoV-15/Rwanda/CV2217/2020	exerutors or cps_c+ i upty/xxiz Alma South Alm Listerg Arrica South Almi Casterg grome 29832 Hirman Introven urbinoven 8.1.351 GH Vaccines 2085/ Hirman Introven Introven Introven Introven Urbinoven 8.1.351 GH Vaccines 2085/ Hirman Introven I
a hCoV-19/UnitedArabEmirates/BTC-5011/2020 a hCoV-19/SouthAfrica/NICD-N19828/2020 hCoV-19/States/NICD-N19828/2020	VOC_Beta_NCoV-19/United/irabEmirates/BTC-5011/2020 VOC_Beta_NCoV-19/SouthWrica/NICD-N19828/2020 hCoV-19/Fance/PAC_PULARA1_ULd_2nze	betacoron EPU, SG, 51 20/02/2020 Adia United Ara Abu Dhabi Adia United Ara Abu Chabi genome 298/85 Human 73 Male B.1.351 GH BTC, Inhail H3 betacoron EPU, SG, 41 24/02/2020 Adria South Ahii MORTH WIZT Africa South Ahii MORTH WIZ South Care 2017/0 Human 78 Female B.1.351 GH TSHURDON National Ir Am betacoron EPU (BL 24 23/12/2020) Targer Frazer Stream Compress Texas Devices and the compress Association and the compression of the c
mma hCoV-19/USA/R-RED-FUL-39828238/2020 mma hCoV-19/USA/N-6DHQ409/2020	VDC_Gamma_hCeV-19/USA/IL-RED-FUL-39828238/2020 VDC_Gamma_hCeV-19/USA/IL-RED-FUL-39828238/2020	betraction (F), 62, 27 (V/2000 Korth Ans USA Indiana North Ans USA Indiana Renorma 2018) Human 193 Male P.1 Git SCH Quantities Proceedings 20180 Human 193 Male P.1 Git SCH Quantities Proceedings 20180 Human 193 Male P.1 Git SCH Quantities Proceedings 20180 Human 193 Male P.1 Git SCH Quantities Proceedings Proceedi
hCaV-19/USA/TX-HMH-MCaV-40896/2020 hCaV-19/USA/TX-HMH-MCaV-40905/2020 hCaV-19/USA/TX-HMH-MCaV-41509/2020	HCaV-19/USA/TX-HMH-MCaV-40896/2020 HCaV-19/USA/TX-HMH-MCaV-40905/2020 HCaV-19/USA/TX-HMH-MCaV-41509/2020	betacron IPU,S, 21 22/7/2020 North Ans USA Texas Houston North Ann USA Texas genome 260/31 Human unknown visihown P.1.1 Git Houston A Houston A Houston N Ho
arrma hCoV-19/Brazil/SP-I8_112782/2020 hCoV-19/USA/TX-HMH-MCoV-35197/2020	VDC_Gamma_hCoV-19/Brazil/SP-I8_112782/2020 hCoV-19/USA/TX-HMH-MCoV-35197/2020	bettacoren PF_06_54 76(2000 South Ammiliaria) Salo Paulo South Ammiliaria Salo Paulo S
+KLOV-19/USA/1X-HMH-MCoV-34830/2020 hCoV-19/Brazil/MS-HRMS_1490/2020 hCoV-19/Spain/GA-CHUVI-19025283/2020	ncuv-s9/USA/1X-HMH-MC0Y-34830/2020 VDC_Gamma_hCoV-19/Brazil/MS-HHM5_1490/2020 hCoV-19/Spain/GA-CHUV-19025283/2020	ueuruona cr.us., cz. z jęzdziada Korth Amir Kola. I elas i nostatin i North Amir Usa. Tetas grotomie 29811 Himman militowa u Michael II-11. G Houdenok Houstan fi A betracoro PE/US_L 61 24/8/2020 South Amir Baaul Matoo Grono Campo Gris South Amir Brazil. Mattoo Grono genome 29903 Himman 38 Male P.1.1. GR infectious Infectious Microbioli Microbioli A betracoro PE/US_L 61 6/9/2020 Istrope Spain Galica: Vigo Europe Spain Galica genome 2985 Himman 38 Male P.1.1.2. GV Microbioli Microbioli A
hCoV-19/Brazil/PE-FIOCRUZ-IAM3285/2020 amma hCoV-19/Brazil/PB-8A1200-250009713/2020 amma hCoV-19/Brazil/PB-L119-CD7789/2020	hCoV-19/Brazil/PE-FIOCRUZ-IAM3285/2020 VOC_Gamma_hCoV-19/Brazil/P8-BA1200-250009713/2020 VOC_Gamma_hCoV-19/Brazil/P8-L119-C077880/3010	betacross EPU, SL, 31 22/8/2000 South Ame Braal Pernambu Petrolina South Ame Braal Pernambu gerosme 29443 Human 27 Male P.1.12 G UACEN/PE Wallaulub Ma betacross EPU, SL 21 20/1/2020 South Ame Braal Paralsa Lingta South Ame Braal Paralsa gerosme 28423 Human ultrawa ultrawa 15 GA Laboretad Coordinacy Ma betacross EPU, SL 22 20/1/2020 South Ame Braal Paralsa Lingta South Ame Braal Paralsa gerosme 2017 Human ultrawa ultrawa 15 GA Laboretad Coordinacy Ma Betacross EPU, SL 22 20/1/2020 South Ame Braal Paralsa Coordinacy Ma Braan Paral
Samma hCoV-19/Brazil/GO-2732R1/2020 Samma hCoV-19/Brazil/SP-2389/2020	VDC_Gamma_hCeV-19/Brael/GO-273281/2020 VDC_Gamma_hCeV-19/Brael/SP-2389/2020	betraceon (P) (S, 21 24)/12/2020 South-Ametikaral Golds Galaxie South-Ametikaral Golds genome 20007 Human 91 Female P.1.14 GR Hospital destinato A Ci- betraceon (P) (S, 21 24)/12/202 South-Ametikaral Golds South-Ametikara (South-Ametikara) (South
among bend 10 Bendi the County Amage	In the set Reset OF FUNKER 310105 230 (2010)	Service of the service of the service of the service servic
Jamma HCoV-19/Brazil/RI-FUNED-330105720/2020 Jamma HCoV-19/Brazil/RI-FUNED-330107714/2020 Jamma HCoV-19/Brazil/RS-UMM38991/2020	VDC_Gamma_hCn/-19/Brazil/RJ-FUNED-330107714/2020 VDC_Gamma_hCn/-19/Brazil/RJ-FUNED-330107714/2020	beacered PU_SL_21 14/11/2003 South-HII Bitall Rio daruat fram fut south Amil Brail Rio Grand Campo Bo
Jamma         hCoV-19/Brazil/RJ-FUNED-390105720/2020           Jamma         hCoV-19/Brazil/RJ-FUNED-390105714/2020           Jamma         hCoV-19/Brazil/RJ-FUNED-39010714/2020           Samma         hCoV-19/Brazil/RJ-FUNED-39010714/2020           Samma         hCoV-19/Brazil/RJ-FUNED-39010714/2020           Samma         hCoV-19/USA/AL-A0PH-4665937/2020           hCoV-19/USA/AL-A0PH-4665937/2020         hCoV-19/USA/AL-A0PH-4665937/2020           Jamma         hCoV-19/USA/AL-A0PH-4665937/2020	VDC_atmm_LCu+1y1/sat/0+1y4/bit/0+210021742/0200 VDC_Gamm_LCu+1y1/sat/0+1y1/bit/03000774/2010 VDC_Gamm_LCu+1y1/sat/0514M8991/2020 VDC_Gamm_LCu+1y1/sat/041AADPH-4665937/2020 hCu+1y1/sat/05147_L088E55572020 VDC_Gamm_LCu+1y1/sat/05146_L088E55572020	Beatrance PT, R., 11         2011/COS South meant         Social and Canada Cana
Gamma         hciv1-39/Braul/PA1-UNED-33018724/20200           Gamma         hciv1-39/Braul/PA1-UNED-33018774/20200           Gamma         hciv1-39/Braul/PA1-MIRE-33018774/20200           Gamma         hciv1-39/Braul/PA1-MIRE-33018774/20200           Gamma         hciv1-39/Braul/PA1-440-3801774/20200           Gamma         hciv1-39/Braul/PA1-474_1A842559/2020           Gamma         hciv1-39/Braul/PA1-474_1A842559/2020           Gamma         hciv1-39/DA1-274_1A8455572020           Gamma         hciv1-39/DA1-274_1A547_20200           Gamma         hciv1-39/DA1-1546/2020	VCC_GrammLock119[bas](A-DURE)300391744(A020 VCC_GrammLock119[bas](A-DURE)3003917(A2020 VCC_GrammLock119[bas](A-DURE)4663937(2020 holv139[bas](R5:147_JA4K552(202) VCC_GrammLock119[bas](A-DURE)4663937(202) VCC_GrammLock119[bas](R5:146,L44R551/2020 VCC_GrammLock119[bas](R5:146,L44R551/2020 VCC_GrammLock119[bas](R5:146,VTM:1547(2020)	Matteriors DT-S., 1 Million Standard, Balling Kang, Sandard Kang, San

# K. Bansal and S. Kumar Table 1 (continued)

(continued on next page)

#### Table 1 (continued)

Delta	hCoV-19/USA/TX-HMH-MCoV-49501/2020	VOC_Delta_hCoV-19/USA/TX-HMH-MCoV-49501/2020	betacoron EPI_ISL_52	13/7/2020 North Ame USA	Texas Houston	North Ame USA Texas genome	29783 Human	unknown unknown AY.122 GK	Houston N Houston N Randall J. ( https://ww	20/10/2021
Delta	hCoV-19/USA/TX-HMH-MCoV-48794/2020	VOC_Delta_hCoV-19/USA/TX-HMH-MCoV-48794/2020	betacoron EPI_ISL_55	15/7/2020 North Ame USA	Texas Houston	North Ami USA Texas genome	29783 Human	unknown unknown AY.100 GK	Houston & Houston & Randall J. Chttps://wv	20/10/2021
Delta	hCoV-19/USA/WV-WVU-WV121217/2020	VDC_Delta_hCoV-19/USA/WV-WVU-WV121217/2020	betacoron EPI_ISL_46	21/7/2020 North Ame USA	West Virginia	North Amc USA West Virgi genome	29818 Human	67 Male AY.25 GK	United Ho WVU and I James Den https://wv	1/10/2021
Delta	hCoV-19/Indonesia/IA-GS-EUK-RSRM-0168/2020	VOC_Delta_hCoV-19/indonesia/JA-GS-EUK-RSRM-0168/2020	betacoron EPI_ISL_52	29/7/2020 Asia Indone	sia Jambi Jambi	Asia Indonesia Jambi genome	29775 Human	50 Male AY.23 GK	Raden Mar Eijkman ReSukma Okt https://ww	21/10/2021
Delta	hCoV-19/Indonesia/IA-GS-EUK-RSRM-0169/2020	VOC Delta hCoV-19/indonesia/JA-GS-EUK-RSRM-0169/2020	betacoron EPI ISL 52	29/7/2020 Asia Indone	sia Jambi Jambi	Asia Indonesia Jambi genome	29769 Human	7 Male AY.23 GK	Raden Ma: Eilkman ReLydia V Pachttps://ww	21/10/2021
Delta	hCoV-19/Indonesia/JA-GS-EUK-RSRM-0170/2020	VOC Delta hCoV-19/Indonesia/JA-GS-EUK-RSRM-0170/2020	betacoron EPI ISL 53	29/7/2020 Asia Indone	ia Jambi Jambi	Asia Indonesia Jambi eenome	29769 Human	39 Male AY 24 GK	Raden Mar Eilkman Re Willy Agus https://ww	21/10/2021
Dalta	hColl 19/indoneria/IA-GS-EUK-RSPM-0177/2010	VDC Delta hColi 18/indoneria (IA-65-EUK-PSPM-0173 (2020	hetacoron ERI ISI SI	39/7/3030 Aria Jodone	ria Ismbi Ismbi	Aria Indonesia Jambi genorme	19769 Human	de Eemale AV 13 GK	Radao Ma Elikman Rejerrica RS https://ww	21/10/2021
Dalta	hCold 10/mdomenia (1A CC FUIX REDA 0200 (2010	VOC Delta (COV 10) Induces in U.S. CV COV IDAM OT A PLOTO	between EN_EL_EL	20/7/2020 Pain Indene	na Jambi Jambi	Asia Indonesia Jambi genome	20760 Human	33 Female AV33 CK	Reden Mar Eileman Re Eilema Old https://ww	21 (10/2022
Denta	nCov-19/Indonesia/1A-GS-EUK-RSKM-0200/2020	VOC_Derta_nc.ov+19/indonesia/IA+G5+EUK+K5KM+0200/2020	Detacoron EH_ISL_S2	29/7/2020 Asia Indone	sa Jamoi Jamoi	Asia Indonesia Jambi genome	29769 Human	32 Female AY 23 GK	Raden war Elikman Resukma Oktinttps://ww	21/10/2021
Delta	hCoV-19/England/PHEP-YYBYU1J/2020	VDC_Delta_hCoV-19/England/PHEP-YYBYUTI/2020	betacoron EPI_SL_52	3/8/2020 Europe United	Kin, England	Europe United Kin England genome	29769 Human	unknown unknown AY.4 GK	Respirator COVID-19 PHE Covid https://ww	18/10/2021
Delta	hCoV-19/USA/CA-LACPHL-AF03229/2020	VDC_Delta_hCoV-19/USA/CA-LACPHL-AF03229/2020	betacoron EPI_ISL_SC	12/8/2020 North Ame USA	California Los Ange	ale North Amc USA California genome	29598 Human	unknown unknown AY.3 GK	Torrance F Los Angele P. Hemara https://wv	12/10/2021
Delta	hCoV-19/USA/VI-Yale-10210/2020	VOC_Delta_hCoV-19/USA/VI-Yale=10210/2020	betacoron EPI_ISL_45	21/8/2020 North Ame USA	US Virgin I St. Croix	North Ame USA US Virgin I genome	29775 Human	unknown unknown B.1.617.2 GK	VIDOH (V) Grubaugh Joseph Fau https://ww	29/9/2021
Delta	hCoV-19/USA/VI-Yale-10211/2020	VOC Delta hCoV-19/USA/VI-Yale-10211/2020	betacoron EPI ISL 45	21/8/2020 North Ame USA	US Virgin I St. Croix	North Ame USA US Virgin Lgenome	29775 Human	unknown unknown AY.35 GK	VIDOH (V) Grubaugh Joseph Fas https://ww	29/9/2021
Delta	hCnlv_19/Eiii/Ei493/2020	VOC Delta hColl-19/Fiii/Fi493/2020	betacoron EPL ISL 45	25/8/2020 Oceania Eiii		Oreania Fili eenome	29835 Human	unknown unknown AY 82 G	Fili Centre Microbiol/ Sabukhan, https://ww	4/10/2021
Dalta	how 100/101/00 FEADOU 100/200 (2010	NOC Dates how an incarca scange is a second source (and	hatasana Dit di Di	31/0/2020 Nexts Arrel U.S.	California, Can Dian	North Ann 1874 Collinsia annua	20004 11	uning an	For Direct Anderson (CEADCH &) https://www.	10(10/2022
Dena	IIC0V-15/054/CA-364A/CH-105756/2020	VOC_DENA_IIC0V119/054/CA13E4ACH1109796/2020	Detaction EPI_BL_31	31/8/2020 North Alle 034	camorna sanoreg	o North Ank OSA Cantornia genome	2360+ Human	UNDIDWIT UNDIDWIT B.1.617.2 GK	samplego widersen i sewich winktps://wv	13/10/2021
Delta	hCoV-19/USA/WY-WYPHL-21070660/2020	VOC_Delta_hCoV-19/USA/WY-WYPHL-21070660/2020	betacoron EPI_ISL_45	2/9/2020 North Ame USA	Wyoming	North Ame USA Wyoming genome	29818 Human	10 Male AY.3 GK	Wyoming Wyoming I Jim Milder https://ww	28/9/2021
Delta	hCoV-19/India/MP-NCDC-2509230/2020	VOC_Delta_hCoV-19/India/MP-NCDC-2509230/2020	betacoron EPI_ISL_24	7/9/2020 Asia India	Madhya Pradesh	Asia India Madhya Pi genome	29778 Human	63 Male AY.122 GK	National C NCDC Delh Radhakrish https://ww	9/6/2021
Delta	hCoV-19/USA/ND-NDDH-4397/2020	VOC_Delta_hCoV-19/USA/ND-NDDH-4397/2020	betacoron EPI_ISL_48	9/9/2020 North Ame USA	North Dakota	North Ame USA North Dak genome	29775 Human	unknown unknown AY.44 GK	North Dak: North Dak: Lisa Winge https://ww	4/10/2021
Delta	bCoV-19/8wanda/CV2197/2020	VDC Delta hCoV-19/Rwanda/CV2197/2020	betacoron EPI ISI 43	10/9/2020 Africa Rwand	Nvarugenge	Africa Rwanda Nvarupeni penome	29804 Human	34 Male 81617.2 GK	Bwanda N. Africa Cerr Enatha Muhttos://ww	4/10/2021
Dalta	hColl-19/BurkinaEaso/CV1920/2020	VOC Delta hCol/-19/8-skinafaso/CV1920/2020	betacoron ERLIST 41	16/9/2020 Africa Burkins	En Ouaraciourou	Africa Burkina Ea Quanadou panoma	29842 Human	unknown unknown AY 36 GK	Centra Ho. Africa Cert Oleverne, Litters //ww	17/9/2021
Delta	hcov-19/60 kinaraso CV1920/2020	VOC_0413_0C0V-19/04/04/940/04/02020	betacoron en_oc_42	10/9/2020 Million Burking	Fra Ouagasougou	Africa Buikina Pa Obagadou genome	20000 10000	unknown unknown All.30 GK	Centre Ho Milita Cen Olawoye, Hittps //w/	17/9/2021
Dena	HC0V-19/B0H0HaF430/CV1921/2020	VOC_Dena_hcdv-19/bdronarasd/cv1921/2020	Detacoron EP1_ISL_42	16/9/2020 Ainta Borkina	i ra Coagadougou	Africa Buriona na Odagadou genome	29605 Human	UNKIDWIT UNKIDWIT AT.36 GK	Centre Hol Winta Cen Glawoye, Entips://wv	17/9/2021
Delta	hCoV-19/Mexico/AGU-InDRE_FB18599_54467/2020	VOC_Delta_hCoV-19/Mexico/AGU-inDRE_FB18599_S4467/2020	betacoron EPI_ISL_25	22/9/2020 North Ame Mexico	Aguascalientes	North Ame Mexico Aguascalie genome	29814 Human	22 Female AV.100 GK	LESP Agua Instituto di Claudia Wi https://ww	14/7/2021
Delta	hCoV-19/india/MH-ICMR-MCL_5716_5772/2020	VOC_Delta_hCoV-19/india/MH-ICMR-MCL_5716_5772/2020	betacoron EPI_ISL_34 2	020-10 Asia India	Maharashtra	Asia India Maharash genome	29873 Human	12 Male AY.50 GK	Indian Cou Indian Cou Pragya Yac https://ww	18/8/2021
Delta	hCoV-19/India/MH-KCMR-MCL 5715 5771/2020	VOC Delta hCoV-19/india/MH-ICMR-MCI, 5715 5771/2020	betacoron EPI ISL 34 2	020-10 Asia India	Maharashtra	Asia India Maharash genome	29886 Human	17 Female B.1.617.2 GK	Indian Cos Indian Cou Pragya Yac https://ww	18/8/2021
Delta	hCnV-19/France/PACJHU-38688-NovaE/2020	VOC Delta hCoV-19/France/PAC-HLL-38688-NovaE/2020	hetacoron EPL ISL 63	020-10 Europe Erappe	Provence., Marseille	e Furone France Provence econome	29689 Human	unknown unknown AY 43 GK	MEPHI Air MEPHI Air Anthony II https://ww	16/11/2021
	head to complex dates and the data (and	VIDLAN: NOW AD Colorado AND MC VID ADD (2001)	hata same CRU R1 A1	11/3/3033 Cauth Area Calamb	in Alexadelens	fauth Inc. Colombia Mandalan annana	20404 100000	universe formale R.1 (2)	Universide Institute M Kethening I https://www.	11/1/1011
in a		Volume incovers) countrally have the engagement been	beaution on on or	2022 2021 2020 2020	e la la	South Park Colonia in Magaalen genome	20002 11	Cholowin remote billori on	on the state of th	21) 572022
MU	HC8V-19/05A/CA-HC4-51W-000080848/2021	V01_M0_N0V-19/05//CA-HDA-STM-000080848/2021	betacoron EPI_ISL_20	2021 North Ame USA	California	North Ame USA California genome	29902 Human	unknown unknown B.1.621 GH	Helix Helix Celina And https://ww	21/0/2021
Mu	hCoV-19/England/PHEC-51028C/2021	VUI_Mu_hCoV-19/England/PHEC-31028C/2021	betacoron EPI_BL_2)	2021 Europe United	Kin England	Europe United Kin England genome	29819 Human	unknown unknown B.1.621 GH	Respirator COVID-19 PHE Covid https://ww	30/6/2021
Mu	hCoV-19/England/PHEC-313887/2021	VOI_Mu_hCoV-19/England/PHEC-313887/2021	betacoron EPI_ISL_23	2021 Europe United	Kin England	Europe United Kin England genome	29818 Human	unknown unknown B.1.621.1 GH	Respirator COVID-19 PHE Covid https://ww	30/6/2021
Mu	hCoV-19/England/PHEC-L306LE1C/2021	VOI Mu hCoV-19/England/PHEC-L306LE1C/2021	betacoron EPI ISL 23	2021 Europe United	Kin England	Europe United Kin England genome	29835 Human	unknown unknown B.1.621.1 GH	Respirator COVID-19 PHE Covid https://ww	30/6/2021
Mu	hCoV-19/England/PHEC-L306LE3A/2021	VOL Mu hCoV-19/England/PHEC-L306LE3A/2021	betacoron EPI ISL 23	2021 Europe United	Kin England	Europe United Kin England eenome	29834 Human	unknown unknown 8.1.621.1 GH	Respirator COVID-19 PHE Covid https://ww	30/6/2021
P.C.	hCol/ 19/Northereiroland/045C (307) 599 (2021	VIOL Mu, hCol/ 18/Northernization//9HEC (202) EP9/3021	hetacoron ERI ISI 31	3021 Europe Heitod	Kin Northern Ireland	Europe United Kin Northern Leanance	20920 Human	unknown unknown B16211 GH	Reminator COMD 19- BHE Could http://www	20/6/2021
in a	incov-representation in contract of the second second second	vor neg neg van het	bicacción chi_cic_ri	1011 Corope Onneo	NIT NOT CHARTEN IN	Carope Oniced Kin Northern Fightanie	23030 1101101		magnator covid-13-File covid inters)/wr	30) 0/ 2022
Mu	ncov-19/USA/FL/Shands-VTM-1545/2020	VUI_MU_NL0V-19/USA/FL-Shands-V1M-1545/2020	Decacoron EPI_DL_25 A	020-12 North Ame USA	FIORIDA	North Ame USA Horida genome	29747 Human	unknown unknown 8.1.621.1 GH	OF Health, Salemi Lab Magalis BF https://ww	19/7/2021
Mu	hCoV-19/USA/GA-GPHL-0609/2021	VOI_Mu_hCoV-19/USA/GA-GPHL-0609/2021	betacoron EPI_ISL_31	2021 North Ame USA	Georgia	North Ame USA Georgia genome	29835 Human	unknown unknown B.1.621 GH	GA Depart GA Depart Stacy Reev https://ww	27/7/2021
Mu	hCoV-19/USA/GA-GPHL-0611/2021	VOI_Mu_hCoV-19/USA/GA-GPHL-0611/2021	betacoron EPI_ISL_31	2021 North Ame USA	Georgia	North Ame USA Georgia genome	29835 Human	unknown unknown B.1.621 GH	GA Depart GA Depart Stacy Reev https://ww	27/7/2021
Mu	hCoV-19/Venezuela/Fal1944/2021	VDI Mu hCoV-19/Venezuela/Fal1944/2021	betacoron EPI ISL 35	21/1/2021 South Ame Venezu	ela Falcon	South Ame Venezuela Falcon penome	29831 Human	unknown unknown B.1.621 GH	Instituto V Laboratori Rossana C https://ww	19/8/2021
140	hColl-19/Erapse/IDE-CERRANC-0267669/3021	VIDL Mr. hColl-19/France/DE-CEREAUC-0767669/3021	betacoroo ERI ISI 35	2021 Europe Erapce	Ile-de-France	Europa Franca Ila-da-Erar papoma	29922 Human	28 Eemale B 1621 GH	10M Porte CERRA Net Bénédicte, https://www.	20/8/2021
1110	Le la Antine de contra antine la contra la contra la contra la contra de con	Volume 1 Contraction Contraction Contraction	becacoron chi_be_st	2022 Corope Trance	A straight	Europe france ne de trai genome	20012 110101	45 Small 04 Chr. Cl	LONG OF CONDUCTOR DETENDED IN THE PROPERTY OF	20/072022
MU	hcdv-19/Prance/OCC-CERBARC-0737599/2021	VOI_MU_RC8V-19/France/OCC-CERBARC-0737599/2021	becacoron EM_ISL_3:	2021 Europe France	Occitanie	Europe France Occitanie genome	29817 Human	15 Female 8.1.621 GH	Low Cerbi CERBA Hei benedicte Intips(/)w/	20/8/2021
Mu	hCoV-19/England/PHEC-545EbC/2021	VUI_Mu_hCoV-19/England/PHEL-345EbC/2021	Detacoron EPI_DL_35	2021 Europe United	Kin England	Europe United Kin England genome	29525 Human	unknown unknown 8.1.621 GH	Respirator COVID-19+ PHE Covid https://ww	23/8/2021
Mu	hCoV-19/France/IDF-CER8AHC-0786809/2021	VOI_Mu_hCoV-19/France/IDF-CERBAHC-0786809/2021	betacoron EPI_ISL_33	2021 Europe France	Ile-de-France	Europe France Ile-de-Frar genome	29843 Human	23 Female B.1.621 GH	EYLAU - UI CERBA Hei Bénédicte https://wv	26/8/2021
Mu	hCoV-19/France/CVL-CERBAHC-08428324/2021	VOI_Mu_hCoV-19/France/CVL-CER8AHC-08428324/2021	betacoron EPI_ISL_38	2021 Europe France	Centre-Val de Loire	Europe France Centre-Valgenome	29817 Human	6 Female 8.1.621 GH	Laboratoir CERBA He: Bénédicte https://wv	2/9/2021
Mu	hCoV-19/France/NAO-CERBAHC-09538751/2021	VOI Mu hCoV-19/France/NAQ-CERBAHC-09538751/2021	betacoron EPI ISL 41	2021 Europe France	Nouvelle-Aquitaine	Europe France Nouvelle-/ eenome	29827 Human	28 Female 8.1.621.1 GH	Cerballian CERBA Hei Bénédicte https://w/	15/9/2021
Ma	hColl 19/Colombia/MAC UTB.//G-024 (2021	VIDL Mu hCol/ 18/Colombio/VAC LITE VIS 024/3021	betacoron ERI ISI SE	3021 South Ams Colomb	in Malle del Caura	South Arry Colombia, 1/alle del C. esseren	19791 Human	unknown Mole B 1 621 GH	SVNI AB & Laboratori Fradu & Tribitor //www	27/10/2021
in a	hear-is/colonizar/me-on-volar/zari		biological biological	TOTT SOUTHING COUNTR		South Park Colonidar Valle del Cigendine	13701 1101101	CHOIDENT MARE D.1.021 ON	STREAD AT CADO AND THE AY A. THICK STAT	11/10/1011
MU	ncov-19/colomola/vwc-01P-vG-026/2021	V01_M0_RC0V-19/C00mbia/VAC-01P-VG-026/2021	Detacoron EM_DL_St	2021 South Ame Colome	valie del Cauca	south Ame colombia Valle dei cigenome	29781 Human	unknown Female 8.1.621 GH	SYNLAB AT Laboraton Fredy A. 12 https://wv	27/10/2021
Mu	hCoV-19/Colombia/VAC-UTP-VG-027/2021	VOI_Mu_hCoV-19/Colombia/VAC-UTP-VG-027/2021	betacoron EPI_ISL_St	2021 South Ame Colomk	na Valle del Cauca	South Ame Colombia Valle del C genome	29781 Human	unknown Female 8.1.621 GH	SYNLAB AT Laboratori Fredy A. Tr https://ww	27/10/2021
Mu	hCoV-19/Colombia/VAC-UTP-VG-029/2021	VOI_Mu_hCoV-19/Colombia/VAC-UTP-VG-029/2021	betacoron EPI_ISL_SE	2021 South Ame Colomb	sia Valle del Cauca	South Ame Colombia Valle del C genome	29775 Human	unknown Female B.1.621 GH	SYNLAB ÁI Laboratori Fredy A. Ti https://ww	27/10/2021
Mu	hCoV-19/Colombia/VAC-UTP-VG-025/2021	VOI_Mu_hCoV-19/Colombia/VAC-UTP-VG-025/2021	betacoron EPI_ISL_SE	2021 South Ame Colomb	via Valle del Cauca	South Ame Colombia Valle del C genome	29778 Human	unknown Male B.1.621 GH	SYNLAB AT Laboratori Fredy A. Ta https://ww	27/10/2021
Mu	bCoV-19/Colombia/VAC-UTP-VG-228/2021	VOL Mu hCoV-19/Colombia/VAC-UTP-VG-228/2021	betaroron EPI JSL SF	2021 South Ame Colomb	sia - Valle del Cauca	South Amy Colombia Valle del C penome	29781 Human	unknown Female 8.1.621 GH	SYNLAB ALLaboratori Fredy A. Tr https://ww	27/10/2021
Mu	h0x0419/0154/0N-LH000111869/2021	V01 Mit ECv/v19/US4/INJ H000111869/2021	hetacoron ERLIST ST	2021 North Ame USA	Indiana	North Ami ISA Indiana eenome	29299 Human	38 Female B 1621 GH	PPHC-Pure Animal Dis Robercoa Ebttos-//ww	29/10/2021
May No.	heavy to compare the contract of the contract	VOLMU_RCHVAD/CHURCHURCHURCHURCHURCHURCHURCHURCHURCHUR	betacoron cri_oc_or	14UO/2020 Cauth Arm Calamb	indiana	- Couth Ame Colembia Antionala genome	20703 Human	00 Male 0.1.021 Cil	COLUCE Laborated Idebab On https://ww	20/10/2022
Mu	hCov-19/Colombia/AN1-LDSP461/2020	VUI_Mu_hcoV-19/Colombia/ANI-LUSP461/2020	Detacoron EM_DL_65	14/10/2020 South Ame Colome	ila Antioquia Apartack	o south Ame Colombia Antioquia genome	29781 Human	89 Mare 8.1.621 GH	SUMER Laboraton Idabely Be https://ww	19/11/2021
	hCoV-19/Indonesia/JA-EUK-RSRM-175/2021	hCoV-19/Indonesia/JA-EUK-RSRM-175/2021	betacoron EPI_ISL_31	18/5/2021 Asia Indone	sia Jambi Jambi	Asia Indonesia Jambi genome	29782 Human	18 Female B.1.640 GH	RSUD Radi Elikman In: Sukma Okt https://ww	1/8/2021
GH	hCoV-19/Congo/FCRM-100-A32.28.09.21/2021	VUM_GH_hCoV-19/Congo/FCRM-100-A32.28.09.21/2021	betacoron EPI_ISL_55	28/9/2021 Africa Republ	ic o Brazzaville	Africa Republic o Brazzaville genome	29683 Human	39 Female 8.1.640 GH	Fondation Fondation Mfoutou Nhttps://ww	27/10/2021
GH	hCoV-19/Canada/OC-L00397423001/2021	VUM GH hCoV-19/Canada/QC-L00397423001/2021	betacoron EPI ISL 64	2/10/2021 North Ame Canada	Quebec	North Ams Canada Quebec eenome	29734 Human	34 unknown B.1.640 GH	Laboratoir Laboratoir Sandrine Nhttps://ww	18/11/2021
GH	hCoV-19/Switzerland/VD-FTH2-34362364/2021	VUM_GH_bCoV-19/Switzerland/VD-FTHZ-34362364/2021	hetacoron EPI ISI 55	6/10/2021 Europe Switzer	fan Vaud	Furone Switzerlan Vaud penome	29788 Human	unknown unknown 81640 GH	Viollier AF: Departmen Christian P https://ww	26/10/2021
CH	head 10/feelend (BUEC 3MONEMED (2021)	VIDA CH ECHI 10/Centered/DUCC 35404/54/00/2021	hataman DR. R. L.	11 (10/2021 Evenes United	Via Feeland	Furners United Kin Fanland annum	20220 Muman	uning an	Remission COMP 10, BUT Could bitmy/Aug	35 (10/3033
GH	ICOV-19/Eligalio/FREC-SM04EMF0/2021	VOW_GH_RCOV-15/Crighting) PHEC-SIMO4CMP0/2021	Detacoron EPI_DL_34	11/10/2021 Europe Onited	NIT ENgland	Europe onicea kin Englana Benome	23775 Homan	GINIOWIT GINIOWIT B.1.040 GH	Respirator COVID-13 PHE COVID TRUES J/W/	23/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727075/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727075/2021	betacoron EPI_SL_St	12/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29799 Human	9 Female B.1.640 GH	Laboratoir CHU Ponte GRULHIER https://ww	28/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727092/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727092/2021	betacoron EPI_ISL_SE	12/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29795 Human	9 Male B.1.640 GH	Laboratoir CHU Pontc GROLHIER https://ww	28/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727095/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727095/2021	betacoron EPI_ISL_56	12/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29821 Human	10 Male B.1.640 GH	Laboratoir CHU Pontc GROLHIER https://ww	28/10/2021
GH	hCoV-19/France/PAC-HCL021184595901/2021	VUM GH hCoV-19/France/PAC-HCL021184595901/2021	betacoron EPI ISL 55	12/10/2021 Europe France	Provence-+ Alpes-Ma	ar Europe France Provence- genome	29728 Human	36 Male 8.1.640 GH	LABORATE CNR Virus Antonin Be https://ww	4/11/2021
GH	hCnV-19/Erance/BBE-CHURENNES-8500727084/2021	VUM_GH_bCoV.19/Erance/BRE_CHURENNES.8500727084/2021	betacoron EPL ISL 5F	14/10/2021 Europe France	Bretarne Bannaler	c Furone France Bratagne ganome	29770 Human	10 Male 8 1 640 GH	Laboratoir CHILPontr GROLHIER https://ww	28/10/2021
GH	hColl 19/6rappe//DE-CE99AHC-10167435 (2021	VIIM GH hColl 19/Errors/IDE-CERRAHC-10162435/2011	betacoron ERI ISI SS	16/10/3021 Europe Erappe	Ile de France	Europe France lie-de-Francesone	19922 Human	26 Eemple B 1 640 G	19M Porte CEPPA Her Bénédiste https://www.	27/10/2021
- Child	te o and at the second and and and	ton_or_restants in the second restances	bracoron chi_dc_s.	rejacta corope mance	increased in the second	corope france ne-de-frangenome	LOULL HUMAN	30 1011010 011040 0	control construction of the state	27/20/20/20
GH	nCov-19/Scotland/GEOH-2706EB1/2021	VUM_GH_hCov-19/3cotiand/GEUH-27D6EB1/2021	Decadoron ENTRPTO	18/10/2021 Europe United	win scotland	Europe United kin Scotiand genome	29434 Human	unknown unknown 8.1.640 GH	Ughthousi Welicome Harper val https://wv	27/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727081/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727081/2021	betacoron EPI_ISL_56	18/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29770 Human	10 Male B.1.640 GH	Laboratoir CHU Ponte GROLHIER https://ww	28/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727095/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727096/2021	betacoron EPI_ISL_SE	18/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29829 Human	10 Male B.1.640 GH	Laboratoir CHU Pontc GROLHIER https://ww	28/10/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727078/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727078/2021	betacoron EPI_ISL_56	18/10/2021 Europe France	Bretagne Bannaleo	c Europe France Bretagne genome	29733 Human	5 Female B.1.640 GH	Laboratoir CHU Pontc GROLHIER https://ww	28/10/2021
GH	bCnV-19/Conro/FCRM-115-12574/2021	VUM_GH_bCoV-19/Contro/FCRM-115-12574/2021	betacoron EPI ISL 60	19/10/2021 Africa Republ	c o Brazzaville	Africa Republic o Brazzaville penome	29714 Human	32 Female 8.1.640 GH	Fondation Fondation Mfoutou Nhttps://wa	9/11/2021
GH	hCoV-19/France/BRE-CHURENNES-8600727100/2021	VUM_GH_hCoV-19/France/BRE-CHURENNES-8600727100/2021	betacoron EPI ISI 54	20/10/2021 Europe France	Bretagne Bannaler	c Europe France Bretagne eenome	29770 Human	12 Female 8.1.640 GH	Laboratoir CHU Ponte GROLHIER https://ww	28/10/2021
CU	hCriti 10/Crears (CCRIA 122 A22 20 10 21/2021	NUMA CU, hCall 10/Carra (FCDA4 422 422 20 10 21/2021	hatarara DE SI CC	20(10/2021 Males Deschi	a complete administer	Africa Description Descentific generation	20040 100000	A Female B 1 640 CII	Fondation Fondation Alfontan & https://www.	0(11/2022
CH	head to frame (the internal sector)	VIDA CH SCALING CONTRACTOR AND	katagana Di at 1	31 (10/3033 Funda -	Restance Ma	Former Present Bestame	20042 10000	16 Female B1647 CT	Lake Arel, National B Marine Br. Mt.	39 4 47 2021
on	Incoving/Praimeyone-Prozodd/2021	VOW_OR_ROOM SYN AND SHOT PERSON STATES	Decacoron EM_DL_64	21/10/2021 Europe France	erecagne vannes	curupe mance Bretagne genome	25755 Human	to remore B.1.640 GH	cabo Anary reduction in Marion Ballintips://ww	16/11/2021
GH	ncov-19/France/IDF-HMN-21112080204/2021	vow_on_ncov-19/France/IDF-HMN-21112080204/2021	Decacoron EPI_ISL_62	22/10/2021 Europe France	ille-de-France	Europe France lie-de-Frangenome	29741 Human	76 Male 8.1.640 GH	riopital Lo. Departmer Christophe https://wv	12/11/2021
GH	nLov-19/Italy/LAZ-IFD-10233054/2021	VUM_GH_RLoV-19/Italy/LAZ-IFO-10233054/2021	Detacoron EPI_ISL_S3	23/10/2021 Europe Italy	Lazio Rome	Europe Italy Lazio genome	29774 Human	unknown Male B.1.640 GH	INULS San IRCCS Regi Frauke Gov https://ww	31/10/2021
GH	hCoV-19/Congo/FCRM-118-A1/2021	VUM_GH_hCoV-19/Congo/FCRM-118-A1/2021	betacoron EPI_ISL_60	23/10/2021 Africa Republ	ic o Brazzaville	Africa Republic o Brazzaville genome	29714 Human	43 Female B.1.640 GH	Fondation Fondation Mfoutou N https://wv	9/11/2021
GH	hCoV-19/France/IDF-CER8AHC-10287496/2021	VUM_GH_hCoV-19/France/IDF-CERBAHC-10287496/2021	betacoron EPI_ISL 55	25/10/2021 Europe France	Ile-de-France	Europe France Ile-de-Frangenome	29814 Human	61 Male B.1.640 GH	LBM Bois ( CERBA He: Bénédicte https://wv	4/11/2021
GH	hCoV-19/Coneo/FCRM-120-A2/2021	VUM GH hCoV-19/Conro/FCRM-120-A2/2021	betacoron EPI ISI 67	25/10/2021 Africa Rendel	ic o Brazzaville	Africa Republic o Brazzaville eenome	29683 Human	35 Male 8.1.640 GH	Fondation Fondation Miloutou Nittee-//ww	9/11/2021
GH	hColl 19/6roppe0/DE-I9921976/3031	VIIM GH bColl 19/Errors/IDE-I9921976/3021	hetacoron ERI ISI 63	15/10/3021 Europa Erapsa	Ile de Frar Lisser	Europa Eranza lla da Erar annoma	19745 Human	61 Mile 81640 GH	Labo Apply National B. Marian Ro. https://ww	16/11/2021
on	ncov-soynankey/br-irr51670/2021	vow_or_ncov-x2/matkey/um-im/316/0/2021	sectoron pri_bl_b:	AU AU ZUZI EUROPE France	and departure cases	caropa mance ne-de-mar genome	23745 Human	at male B.1.640 GH	case wall records in marion by https://wi	10/11/2021
Lamoda	nCov-19/E008dof/UEES-12976/2021	V01_Lamoda_ncov-19/Ecuador/OEES-12976/2021	Decacoron EN_DI_IE	2021 South Ame Ecuado	r Guayas	South Ame Ecuador Guayas genome	29783 Human	unknown unknown C.37 GK	Umics Scie Umics Scie Deny Andr https://ww	19/4/2021
Lambda	hCoV-19/Peru/LIM-INS-8425/2020	VOI_Lambda_hCoV-19/Peru/LIM-INS-8425/2020	betacoron EPI_ISL_55	21/7/2020 South Ame Peru	Uma	South Ame Peru Lima genome	29769 Human	38 Male C.37 GR	Laboratori Laboratori Carlos Pad https://wv	5/11/2021
Lambda	hCoV-19/Argentina/INEI096534/2020	VOI_Lambda_hCoV-19/Argentina/INEI096534/2020	betacoron EPI_ISL_21	8/11/2020 South Ame Argenti	na Gudad Autonoma d	le South Ame Argentina Ciudad Au genome	29792 Human	27 Female C.37 GR	Servicio Vi Instituto N Baumeiste https://wv	19/5/2021
Lambda	hCoV-19/Peru/LIM-INS-895/2020	VOI_Lambda_hCoV-19/Peru/LIM-INS-895/2020	betacoron EPI_ISL 15	22/12/2020 South Amt Peru	Lima	South Ame Peru Lima genome	29495 Human	34 Female C.37 GR	Laboratori Laboratori Carlos Pad https://wv	11/4/2021
Lambda	hCoV-19/Peru/UM-UPCH-0372/2021	VOI Lambda hCoV-19/Peru/LIM-UPCH-0372/2021	betacoron EPI ISI 1/	1/1/2021 South Ame Penu	Uma	South Ame Peru Lima penome	29744 Human	unknown unknown C.37 GR	Instituto d Laboratori Lenin Mati https://ww	18/4/2021
Lambe	hColl,19/Pen//SAM,INS,2426/2021	VOL Lambda, hCrW-19/Denu/SAMJINS-2426/2021	hetacoron EPL IS1 22	8/1/2021 South Amr Pro-	San Martin	South Jens Paru San Martin comore	19791 Human	22 Male C 37 CP	Laboratori Laboratori Carlos Pad httm://www	14/8(2021
Londa .	1000 1000	VOL Landed ACAL TO Day CARE BIC 2421 (2021	between the state	old (2021 Could Am 7	Con Martin	South Las Day Contract genome	20704 Hoffield	22 mme C.37 DR	Laborated Laborated Codes Ped by	1-0-072021
camoda	1004-107-107-100-2421/2021	vor_termode_rcdv+10/P#0/3409-005/2421/2021	sectoron pri_bL_34	57 57 2021 SOUCH AME PERU	Sen Meron	soomens reru sammarul genome	23760 Human	20 Male 0.57 GK	casor and in caboratory carlos had https://wv	14/0/2021
Lambda	nuov-19/Peru/SAM-INS-2419/2021	vul_Lamoda_nLoV-19/Peru/SAM-INS-2419/2021	betacoron EPI_ISL_34	11/1/2021 South Ame Peru	San Martin	south Ame Peru San Martin genome	29783 Human	40 Female C.37 GR	Laboratori Laboratori Carlos Pad https://wv	14/8/2021
Lambda	hCoV-19/Peru/LIM-INS-731/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-731/2021	betacoron EPI_ISL_11	12/1/2021 South Ame Peru	Lima	South Ame Peru Lima genome	29495 Human	47 Female C.37 GR	Laboratori Laboratori Carlos Pad https://wv	4/3/2021
Lambda	hCoV-19/Peru/LIM-INS-734/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-734/2021	betacoron EPI_ISL_11	12/1/2021 South Ame Peru	Lima	South Ame Peru Lima genome	29495 Human	38 Female C.37 GR	Laboratori Laboratori Carlos Pad https://wv	4/3/2021
Lambda	hCoV-19/Peru/LIM-INS-737/2021	VOI Lambda hCoV-19/Peru/LIM-INS-737/2021	betacoron EPI ISI 11	12/1/2021 South Amr Peni	Uma	South Ame Peru Lima ennome	29495 Human	74 Female C.37 GR	Laboratori Laboratori Carlos Pad httns://wv	4/3/2021
Lambd-	hColl-19/Repu/CAL-INS-620/2021	VOL Lambda, hCoV-19/Renu/CALUNS-670/2021	betacoron ERI IC: 11	17/1/2021 South Am: "	Callan	South Ame Party Callan	19901 Mu	unknown unknown C 17 CP	Laboratori Laboratori Ronnia Gar https://ww	1/1/2022
Londa	heart 10/heart 114 INS 418/0011	101 Lambda Mart 10/000/011010/07/02021	betacoron Eff. Nº 11	12/1/2021 South Ame Peru	Limo	South Ame Date Lines	23301 Human	unknown unknown C.27 CP	Laboratori Laboratori Romine Garintps://ww	1/0/2021
Lamodá	mov-1977erd/UM-IND-416/2021	vor_camada_rcdx-19/P@u/LIM-IND-918/2021	vestoron cri_ol_11	x77 x7 2021 South Ame Peru	uma	Joourneite Peru Lima genome	29690 numan	GR GR GR	cassiant caboraton nonnie Gar https://ww	1/3/2021
Lambda	nLov-19/Peru/LIM-INS-419/2021	VUI_Lamoda_ncoV-19/Peru/LIM-INS-419/2021	Detacoron EPI_ISL_11	17/1/2021 South Ame Peru	uma	south Ame Peru Lima genome	29901 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Ga' https://wv	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-420/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-420/2021	betacoron EPI_ISL_11	17/1/2021 South Ame Peru	Uma	South Ame Peru Lima genome	29898 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Ga https://wv	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-421/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-421/2021	betacoron EPI_ISL 11	17/1/2021 South Ame Peru	Lima	South Ame Peru Lima genome	29895 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Gar https://wv	1/3/2021
Lambria	hCoV-19/Peru/LIM-INS-423/2021	VOI Lambda hCoV-19/Peru/LIM-INS-423/2021	betacoron EPI ISI 11	17/1/2021 South Ami Peni	Lima	South Ame Peru Lima eenome	29899 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Gar https://ww	1/3/2021
Lambda	hCoV-19/Penu/HM-INS-424/2021	VDL Lambda, bCoV-19/Peru/LIM-INS-424/2021	betacoron EPI (SI 11	17/1/2021 South Amr Perce	Lima	South Ame Peru Lima oscore	29863 Human	unknown unknown C 37 GP	Laboratori Laboratori Roppie Gar https://www	1/3/2021
Londo 1	head to man a list international	Vite Londole Actual Information Actual and A	katagana EN EL 11	12/1/2022 Fault Am 7	Lime	Fronth Jana Dance Linna genome	20005 100000	understand understand C.37 GK	Laborateri Laborateri Barela Carlet	1/2/2021
Lamoda	mov-rayeerd/UM-INS-450/2021	vor_camaga_rcc0v-19/P6f0/LIM-INS-430/2021	vevacoron EH_IGE_11	17/1/2021 South Ame Peru	uma	sousivente Peru Lima genome	29895 Human	unwnown unknown C.37 GR	cauviaion caboraton konnie Gai nttps://ww	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-433/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-433/2021	betacoron EPI_ISL_11	17/1/2021 South Ame Peru	Uma	South Ame Peru Lima genome	29901 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Gar https://ww	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-434/2021	VDI_Lambda_hCoV-19/Peru/LIM-INS-434/2021	betacoron EPI_ISL_11	17/1/2021 South Ame Peru	Lima	South Ame Peru Lima genome	29887 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Gar https://wv	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-436/2021	VDI_Lambda_hCoV-19/Peru/LIM-INS-436/2021	betacoron EPI_ISL_11	17/1/2021 South Ams Peru	Lima	South Ame Peru Lima genome	29901 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Ga https://wv	1/3/2021
Lambda	hCoV-19/Peru/LIM-INS-437/2021	VOI_Lambda_hCoV-19/Peru/LIM-INS-437/2021	betacoron EP1_ISL 11	17/1/2021 South Ame Peru	Uma	South Ame Peru Lima penome	29874 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Gar https://wv	1/3/2021
Lambd*	bCoV-19/Peru/LIM-INS-443/2021	VOI Lambda hCoV-19/Peru/LIM-INS-443/2021	betacoron EPI ISI 11	17/1/2021 South Amy Perm	Lima	South Ame Peru Lima nanome	29901 Human	unknown unknown C.37 GR	Laboratori Laboratori Ronnie Garhttm://www	1/3/2021
Londo -	bCold 10/Donu/CALINE 669/0071	WOLLSmithly MCNV 10/Deco//CALINE 659 (2021	hatarona Ell IS 11	18/1/2021 South Am. 2	Callan	South Amy Dates Callage	10000 Human	unknown unknown C37 CC	Informationi Informationi Romaio Gar https://www	1/2 (2024
ranner an	ment and and manufacture and a second second		error on the SF 11	any sy down about mind Peru		search the cause follows	arous mattan		construction and a construction of the constru	17-17-2022

### 2. Results

# 2.1. Phylogenomics suggests common ancestry of omicron and lambda variants

Whole genome-based phylogeny (n = 478 genomes) representing VOC (alpha, beta, gamma, delta, and omicron), VOI (mu and lambda) and VUM depicts two major phylogroups PG-I and PG-II (Fig. 1 and Table 1). Here, the reference strain of SARS-CoV-2 (Wuhan-Hu-1, NC\_045512.2) is taken as an outgroup. PG-I has VOC: gamma, beta, and delta; VOI: mu and VUM: GH. Whereas, PG-II includes VOC: alpha, omicron and VOI: lambda. Interestingly, two VOCs, delta and omicron, belong to different phylogroups. Phylogeny depicted that omicron shares a common ancestry with VOI lambda represented by a black asterisk in Fig. 1. Interestingly, three isolates from Italy (EPI\_ISL\_6854346, EPI\_ISL\_6854347, and EPI\_ISL\_6854348) form a diversified sub-lineage among the omicron population. Additionally, EPI\_ISL\_6886594 from Germany is a diversified omicron strain.

### 2.2. Very high non-synonymous mutations give rise to omicron

Mutation is driving the evolution and emergence of new variants of COVID-19 worldwide (Islam et al., 2021; Kumar & Bansal, 2021; Thakur et al., 2021). Availability of genomic resources have enabled the research community in tracking mutational events and linking them to new variants (Mercatelli & Giorgi, 2020; Rambaut et al., 2020). Analysis and routine surveillance from South Africa suggested omicron ability to evade immunity from prior infection as compared to other VOCs (Pulliam et al., 2021). In the present study, we intend to understand the evolution and emergence of omicron by its mutational landscape at population level.

We have performed a mutational analysis with respect to the reference genome of SARS-CoV-2 (NC\_045512.2) (Fig. 2). Total mutations detected in the dataset were 24,189, and omicron genomes constituted 18,261 mutations (supplementary table 1). For all the strains under study, we have calculated the total number of mutations detected (supplementary table 2). Average mutations per genome for the omicron variant were detected to be 60.5. For the limited genomes of VOCs, VOIs

K. Bansal and S. Kumar

Virus Research 315 (2022) 198765



Fig. 2. Mutational analysis of omicron. Six panel image displays the most mutated samples, overall mutations per samples, most frequent events per class of mutation category, changes of nucleotide per type, nucleotide wise most frequent events and protein level most frequent events for the genomes used in the study.

and VUMs, average mutations for GH, delta, mu, gamma, alpha, lambda and beta were 48, 39, 38.5, 37.8, 30.7, 27.4 and 24.2 respectively. This clearly depicts high number of mutations in the omicron variant as compared to other variants of SARS-CoV-2. Except for omicron, average mutations for other variants were calculated on the basis of limited genomes, which might not represent the true mutational events for them. Since, omicron is the recently emerged variant, aim of present study was to understand its mutational landscape at population level.

Interestingly, >97% (n = 17,703 mutations) of the mutations in omicron were in the coding region, and remaining 558 were detected in the extragenic region of the genome. Amongst the coding gene mutations, 2965 were indels while 14,738 were SNPs constituting nonsynonymous (n = 11,995 mutations) and synonymous mutations (n = 2743 mutations). Single nucleotide transitions are shown to be major mutational types amongst the SARS-CoV-2 genomes (Kumar & Bansal, 2021; Mercatelli & Giorgi, 2020).

Interestingly, mutational events are highly skewed towards the spike protein, which constitutes ~60% (n = 10,658) of the total mutations in the coding genomic region (n = 17,703) (Fig. 3). The majority of spike protein mutations encompass A67, T547K, D614G, H655Y, N679K, P681H, D796Y, N856K, Q954H, which are reported in all the omicron genomes analysed (Table 3). Count of mutations in the spike was followed by RNA dependent RNA polymerase (rdrp) (n = 4142) constituting A1892T, I189V, P314L, K38R, T492I, V57V in all omicron genomes analyzed (Fig. 3 and Table 3). Remaining 2903 mutations were detected in rest of the coding genomic region (Table 2, 3, and supplementary table 1), where M19M in ORF6, and RG203KR in nucleocapsid

protein are amongst the most prevalent mutations in omicron (Fig. 3).

### 2.3. Low intra-sequence diversity amongst omicron variant

Intra-strain diversity among the omicron variant strains reported worldwide will be crucial in understanding the genome dynamics and rapid evolution of SARS-CoV-2. We performed the mutational analysis on the current dataset using omicron (OL677199) isolated from Canada on 23rd November 2021 as the reference genome (supplementary table 3). Most of the strains (n = 298), irrespective of their geographic origin, had less than ten mutations depicting low intra-strain diversity among omicron strains. We found omicron variants had >55 mutations when compared with other VOCs and VOIs. However, four of the isolates two from Europe (Italy) (EPI\_ISL\_6854347 (n = 23 mutations) and EPI\_ISL\_6854346 (n = 14 mutations) and two from South Africa (EPI\_ISL\_6699742 (n = 12 mutations) and EPI\_ISL\_6774091 (n = 11 mutations) were most diversified among the omicron genomes.

### 3. Methods

# 3.1. Identification and procurement of SARS-CoV-2 genome from the public repository

We have considered all the available genomes of omicron variant available in public domain until 6 pm Indian Standard Time (IST) on 2nd December 2021 from GISAID (n = 302 genomes). A total of 25 strains from each variant of concern, namely alpha (B.1.1.7), beta (B.1.351),



**Fig. 3.** Mutational analysis of omicron (A) Number of mutations in the coding region is in the centre of the pie-chart representing indels (black), synonymous (yellow) and non-synonymous (red) SNPs. Type and number of mutations in the extergenic region is represented by pie charts blue, light blue and white as represented in the color legends. (B) Bar graph representing number of mutations in the genomic region of SARS-CoV-2. (C) Some of the top mutations (pl. refer Table 3 for all top mutations in omicron) among the omicron variant are represented by stars of black: indels, yellow: synonymous and red: non-synonymous mutations.

### Table 2

Genomic region wise mutational count of the omicron isolates by taking NC\_045512.2 as a reference.

Genomic region	Mutational count	Annotation
5'UTR	309	5' Untranslated region
NSP1	5	RNA dependent RNA polymerase
NSP2	31	
NSP3	1572	
NSP4	325	
NSP5	317	
NSP6	595	
NSP7	0	
NSP8	2	
NSP9	9	
NSP10	301	
NSP11	0	
NSP12a	0	
NSP12b	632	
NSP13	14	
NSP14	319	
NSP15	6	
NSP16	14	
S	10,658	Spike
ORF3a	313	ORF3a protein
E	296	Envelope
M	850	Membrane
ORF6	303	ORF6 protein
ORF7a	2	ORF7a protein
ORF7b	311	ORF7b protein
ORF8	4	ORF8 protein
N	823	Nucleocapsid protein
ORF10	1	ORF10 protein
3'UTR	249	3' Untranslated region

gamma (P.1) and delta (B.1.617.2) and variant of interest, namely lambda (C.37) and mu (B.1.621). We have also considered 25 strains from variant under monitoring, namely GH (B.1.640). These all strains are from their respective earlier reports in the public domain. Pangolin COVID-19 lineage assigner webserver (https://pangolin.cog-uk.io/) was used to truly demarcate the strains of across variants. The investigation suggested that 9 out of 25 strains does not belong to gamma (P.1) and 1 out of 25 strains doesn't belong to VUM GH (B.1.640) and were wrongly classified earlier. A detailed list of all the strains used in the study is provided in Table 1.

### 3.2. Phylogenetic analysis

A total of 477 high-quality genomes, including the major variants spread across the globe were taken into consideration. Multiple sequence alignment was performed for all the genomes using MAFFT v7.467 (Nakamura, Yamada, Tomii, & Katoh, 2018) followed by phylogenetic tree construction using fasttree v2.1.8 with double precision (Price, Dehal, & Arkin, 2010) with gamma time reversal method. Visualization of the obtained phylogenetic tree was performed using iTol v6 (Letunic & Bork, 2019). Different variants were marked in accordance with different colors as mentioned in the legends.

### 3.3. Mutational analysis

Mutational analysis of all the strains (n=477) in the study was performed with two different reference genomes. First with NC\_045512.2 (Wuhan-Hu-1) strain (reference SARS CoV-2 strain) and another with first reported strain of omicron variant (OL677199.1) (https://www. ncbi.nlm.nih.gov/nuccore/OL677199) using nucmer v3.1 (Delcher, Phillippy, Carlton, & Salzberg, 2002). We have used a well-documented R script described earlier (Mercatelli & Giorgi, 2020). Here, we have used gff3 annotation and reference genome file to extract genomic coordinate of SARS-CoV-2 proteins. R library package seqinr (https://cran. r-project.org/web/packages/seqinr/index.html) and biostring package (https://bioconductor.org/packages/release/bioc/html/Biostrings.ht ml) of bioconductor was implemented to obtain the list of all the mutational events. Mutational events were calculated with respect to two different references (Reference SARS CoV-2 strain: NC 045512.2) (https://www.ncbi.nlm.nih.gov/nuccore/NC\_045512.2) and omicron (https://www.ncbi.nlm.nih.gov/nuccore/OL677199) (OL677199.1) separately. Further, the average mutations for a variant were calculated by adding up the mutations in each variant and dividing them by the total number of genomes of the variant used in the present study.

## K. Bansal and S. Kumar

### Table 3

Top mutations (>185 in count) in omicron variant as compared to the reference sequence NC\_045512.2.

Spike         S         A67         deletion_frameshift         575         21,762         C         .         21,483         29,33           Predicted phosphoesterase, papain-like proteinase         NSP3         A1892T         SNP         302         8393         G         A         8124         29,33           Transmembrane protein         NSP6         I189V         SNP         302         11,537         A         G         11,259         29,33           Spike         S         T547K         SNP         302         23,202         C         A         22,915         29,33           Spike         S         D614G         SNP         302         23,202         C         A         22,915         29,33           Spike         S         D614G         SNP         302         23,225         C         T         23,238         29,33           Spike         S         H655Y         SNP         301         2832         A         G         256,672         29,33           Spike         S         N679K         SNP         301         28,329         A         G         256,662         29,33           Spike         S         N679K         S
Predicted phosphoesterase, papain-like proteinaseNSP3Als92TSNP302B1372GFB12029,3Transmembrane proteinNSP6II89VSNP30211,537AG11,25929,3RNA-dependent RNA polymerase, post-ribosomal frameshiftNSP12bP314LSNP30211,408CT14,10329,3SpikeST547KSNP30223,403AG23,11629,3SpikeSD614GSNP30223,403AG23,11629,3SpikeSD614GSNP30223,525CT23,23829,3SpikeSH655YSNP30123529AC26,97229,33SpikeSN679KSNP30123,599TG23,31229,33SpikeSN679KSNP30123,599TG23,31229,33SpikeSN679KSNP30123,599TG23,31229,33SpikeSN679KSNP30123,599TC12,91729,33SpikeSN679KSNP30123,604CA23,31729,33SpikeSP681HSNP30023,604CA23,31729,33SpikeSD796YSNP30023,604CA23,31729,33SpikeSO954
Transmembrane protein       NSP6       I189V       SNP       302       I1,537       A       G       I1,259       29,33         RNA-dependent RNA polymerase, post-ribosomal frameshift       NSP12b       P314L       SNP       302       14,408       C       T       14,130       29,33         Spike       S       T547K       SNP       302       23,202       C       A       22,915       29,33         Spike       S       D614G       SNP       302       23,403       A       G       23,238       29,34         Spike       S       D614G       SNP       302       23,525       C       T       23,238       29,33         Spike       S       H655Y       SNP       301       2832       A       G       2566       29,33         Predicted phosphoesterase, papain-like proteinase       S       N679K       SNP       301       28,599       T       G       23,312       29,33         Transmembrane protein       NSP4       T492I       SNP       301       10,029       C       T       9760       29,33         Spike       S       P681H       SNP       300       13,195       T       C       12,917
RNA-dependent RNA polymerase, post-ribosomal frameshift       NSP12b       P314L       SNP       302       14,408       C       T       14,130       29,33         Spike       S       D547K       SNP       302       23,202       C       A       22,915       29,33         Spike       S       D614G       SNP       302       23,403       A       G       23,116       29,33         Spike       S       H655Y       SNP       302       23,525       C       T       23,238       29,33         ORF6 protein       ORF6       M19M       SNP_silent       302       27,259       A       C       26,072       29,33         Spike       S       N679K       SNP       301       2832       A       G       2566       29,33         Spike       S       N679K       SNP       301       10,029       C       T       9760       29,33         Transmembrane protein       NSP4       T492I       SNP       301       10,029       C       T       29,366       29,67         Growth-factor-like protein       NSP10       V57V       SNP_silent       300       13,195       T       C       12,917       29,33
SpikeST547KSNP $302$ $23,202$ CA $22,915$ $29,35$ SpikeSD614GSNP $302$ $23,403$ AG $23,116$ $29,35$ SpikeSH655YSNP $302$ $23,525$ CT $23,232$ $29,35$ ORF6 proteinORF6M19MSNP_silent $302$ $27,259$ AC $26,567$ $29,35$ Predicted phosphoesterase, papain-like proteinaseNSP3K38RSNP $301$ $2832$ AG $2566$ $29,35$ SpikeSN679KSNP $301$ $23,599$ TG $23,312$ $29,33$ Transmembrane proteinNSP4T4921SNP $301$ $20,599$ TG $23,312$ $29,33$ Incaceapsid proteinNRG2038*SNP $301$ $23,599$ TC12,917 $29,33$ SpikeSN679KSNP $301$ $10,029$ CT $24,317$ $29,33$ SpikeSP681HSNP $300$ $23,604$ CA $23,317$ $29,33$ SpikeSN856KSNP $300$ $23,604$ CA $23,317$ $29,33$ SpikeSN951NSNP $300$ $24,130$ CA $23,317$ $29,33$ SpikeSN951NSNP $300$ $24,424$ AT $24,137$ $29,33$ SpikeSN951NSNP silent $297$ $3037$ </td
SpikeSD614GSNP30223,403AG23,11629,33SpikeSH655YSNP30223,525CT23,23829,33ORF6 proteinORF6M19MSNP_silent30227,259AC26,97229,33Predicted phosphoesterase, papain-like proteinaseNSP3K38RSNP30123,599TG26,97229,33SpikeSN679KSNP30123,599TG23,31229,33Transmembrane proteinNSP4T492ISNP30110,029CT976029,33Nucleocapsid proteinNSP4T492ISNP30110,029CT28,80629,63Growth-factor-like proteinNSP10V57VSNP_silent30023,604CA23,31729,33SpikeSD796YSNP30023,604CA23,31729,33SpikeSN856KSNP30024,130CA23,31729,33SpikeSN856KSNP30024,130CA23,31729,33Nucleocapsid proteinNNF2NSP1/Silent30024,424AT24,13729,33SpikeSN951/NSNP_silent29815,240CT14,6229,33SpikeST951/NSNP_silent29815,240CT14,62
SpikeSH655YSNP30223,525CT23,23829,33ORF6 proteinORF6M19MSNP_silent30227,259AC26,97229,33Predicted phosphoesterase, papain-like proteinaseNSP3K38RSNP3012832AG256,61229,33SpikeSN679KSNP30123,599TG23,51229,33Transmembrane proteinNSP4T4921SNP30110,029CT976029,33Nucleocapsid proteinNRG203K*SNP30128,881GGGAAT28,80629,63Growth-factor-like proteinNSP10V57VSNP_silent30023,604CA23,31729,33SpikeSD796YSNP30023,644CA23,65129,33SpikeSN856KSNP30024,130CA23,65129,33SpikeSQ954HSNP30024,424AT24,13329,33SpikeSQ954HSNP30024,424AT24,13329,33SpikeST951SNP30024,424AT24,13729,33SpikeST951SNP30024,846CT14,96229,33SpikeST951SNP29821,846CT21,56229,33Spike <td< td=""></td<>
ORF6 proteinORF6M19MSNP_silent30227,259AC26,97229,33Predicted phosphoesterase, papain-like proteinaseNSP3K38RSNP3012832AG256629,33SpikeSN679KSNP30123,599TG23,31229,33Transmembrane proteinNSP4T492ISNP30110,029CT976029,33Nucleocapsid proteinNRG203K*SNP30113,195TC12,91729,33SpikeNSP10V57VSNP_silent30023,604CA23,31729,33SpikeSP681HSNP30023,604CA23,84329,33SpikeSN856KSNP30024,130CA24,31729,33SpikeSN856KSNP30024,424A24,31729,33SpikeSN954HSNP30024,424A24,31729,33SpikeNRG203KRSNP30024,424A24,31729,33SpikeSN951NSNP_silent29815,240CT14,96229,33SpikeST951SNP29821,846CT21,56229,33SpikeST951SNP29723,37CT21,56229,33SpikeST951SNP2972
Predicted phosphoesterase, papain-like proteinase       NSP3       K38R       SNP       301       2832       A       G       2566       29,33         Spike       S       N679K       SNP       301       23,599       T       G       23,312       29,33         Transmembrane protein       NSP4       T492I       SNP       301       10,029       C       T       9,760       29,33         Nucleocapsid protein       N       RG203K*       SNP       301       10,029       C       T       28,861       GGG       A4       28,860       29,64         Growth-factor-like protein       NSP10       V57V       SNP silent       300       13,195       T       C       12,917       29,33         Spike       S       P681H       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       24,130       C       A       23,843       29,33         Spike       S       Q954H       SNP       300       24,424       A       T       24,843       29,33         RNA-dependent RNA polymerase, post-ribosomal frameshift       NSP12b       NSP14       SNP
Spike       S       N679K       SNP       301       23,599       T       G       23,312       29,33         Transmembrane protein       NSP4       T4921       SNP       301       10,029       C       T       9700       29,33         Nucleocapsid protein       N       RG203K*       SNP       301       28,881       GGG       AAT       28,806       29,60         Growth-factor-like protein       NSP10       V57V       SNP silent       300       13,195       T       C       12,917       29,33         Spike       S       P681H       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       23,948       G       T       23,661       29,343       29,33         Spike       S       D796Y       SNP       300       24,130       C       A       23,843       29,33         Spike       S       Q954H       SNP       300       24,424       A       T       24,843       29,33         Nucleocapsid protein       N       RG203KR       SNP       300       24,881       GGG       T       14,962       29,33
Transmembrane proteinNSP4T4921SNP $301$ $10,029$ CT $9760$ $29,33$ Nucleocapsid proteinNRG203K*SNP $301$ $28,881$ GGGAAT $28,806$ $29,67$ Growth-factor-like proteinNSP10 $V57V$ SNP_silent $300$ $13,195$ TC $12,917$ $29,33$ SpikeSP681HSNP $300$ $23,604$ CA $23,317$ $29,33$ SpikeSD796YSNP $300$ $23,644$ CA $23,843$ $29,33$ SpikeSN856KSNP $300$ $24,424$ AT $24,137$ $29,33$ SpikeSQ954HSNP $300$ $24,424$ AT $24,137$ $29,33$ Nucleocapsid proteinNRG203KRSNP $300$ $24,424$ AT $24,137$ $29,33$ Nucleocapsid proteinNRG203KRSNP $300$ $24,881$ GGGAAC $28,594$ $29,33$ RNA-dependent RNA polymerase, post-ribosomal frameshiftNSP12bN591NSNP_silent $298$ $15,240$ CT $14,962$ $29,33$ SpikeST951SNP $298$ $21,846$ CT $21,562$ $29,33$ SpikeSG339DSNP $297$ $3037$ CT $21,562$ $29,33$ SpikeSG339DSNP $297$ $25,78$ GA $22,291$ $29,33$ Spi
Nucleocapsid protein         N         RG203K*         SNP         301         28,881         GGG         AAT         28,806         29,60           Growth-factor-like protein         NSP10         V57V         SNP_silent         300         13,195         T         C         12,917         29,33           Spike         S         P681H         SNP         300         23,604         C         A         23,317         29,33           Spike         S         D796Y         SNP         300         23,604         C         A         23,843         29,33           Spike         S         D796Y         SNP         300         23,448         G         T         24,613         29,33           Spike         S         N856K         SNP         300         24,130         C         A         23,843         29,33           Spike         S         Q954H         SNP         300         24,424         A         T         24,137         29,33           Nucleocapsid protein         N         RG203KR         SNP         300         28,881         GGG         AAC         28,594         29,33           Spike         S         T951         SNP
Growth-factor-like protein       NSP10       V57V       SNP_silent       300       13,195       T       C       12,917       29,33         Spike       S       P681H       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       23,648       G       T       23,661       29,33         Spike       S       D796Y       SNP       300       24,130       C       A       23,843       29,33         Spike       S       Q954H       SNP       300       24,424       A       T       24,137       29,33         Nucleocapsid protein       N       RG203KR       SNP       300       24,881       GGG       AAC       28,594       29,33         Spike       S       T951       SNP       SNP       300       28,881       GGG       AAC       28,594       29,33         Spike       S       T951       SNP       SNP       298       21,846       C       T       21,562       29,33 <tr< td=""></tr<>
Spike       S       P681H       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       23,604       C       A       23,317       29,33         Spike       S       D796Y       SNP       300       23,948       G       T       23,661       29,33         Spike       S       N856K       SNP       300       24,130       C       A       23,843       29,33         Spike       S       Q954H       SNP       300       24,424       A       T       24,137       29,33         Nucleocapsid protein       N       RG203KR       SNP       300       24,881       GGG       AAC       28,594       29,33         Spike       S       T951       SNP       SNP       300       28,881       GGG       AAC       28,594       29,33         Spike       S       T951       SNP       SNP       298       21,846       C       T       14,962       29,33         Spike       S       G339D       SNP       297       3037       C       T       21,562       29,33         Spike
Spike     S     D/96Y     SNP     300     23,948     G     I     23,661     29,33       Spike     S     N856K     SNP     300     24,130     C     A     23,843     29,33       Spike     S     Q954H     SNP     300     24,130     C     A     23,843     29,33       Spike     S     Q954H     SNP     300     24,424     A     T     24,137     29,33       Nucleocapsid protein     N     RG203KR     SNP     300     28,881     GGG     AAC     28,594     29,33       RNA-dependent RNA polymerase, post-ribosomal frameshift     NSP12b     N591N     SNP_silent     298     15,240     C     T     14,962     29,33       Spike     S     T951     SNP     298     21,846     C     T     21,562     29,34       Spike     S     G339D     SNP     297     3037     C     T     21,562     29,34       Spike     S     G339D     SNP     297     22,578     G     A     22,291     29,33       Spike     S     G339D     SNP     297     25,584     C     T     25,297     29,33       ORF3a protein     ORF3a
Spike     S     N856K     SNP     300     24,130     C     A     23,843     29,33       Spike     S     Q954H     SNP     300     24,424     A     T     24,137     29,33       Nucleocapsid protein     N     RG203KR     SNP     300     24,424     A     T     24,137     29,33       RNA-dependent RNA polymerase, post-ribosomal frameshift     NSP12b     N591N     SNP_silent     298     15,240     C     T     14,962     29,33       Spike     S     T951     SNP     298     21,846     C     T     21,562     29,33       Predicted phosphoesterase, papain-like proteinase     NSP3     F106F     SNP_silent     297     3037     C     T     2771     29,33       Spike     S     G339D     SNP     297     22,578     G     A     22,291     29,33       ORF3a protein     ORF3a     T64T     SNP_silent     297     25,584     C     T     25,597     29,33       NA     5/UTR     241     extragenic     297     241     C     T     187     29,33
Spike     S     Q53 H     SNP     S00     24,74     A     I     27,15     27,55       Nucleocapsid protein     N     RG203KR     SNP     300     28,881     GGG     AC     28,594     29,33       RNA-dependent RNA polymerase, post-ribosomal frameshift     NSP12b     N591N     SNP_silent     298     21,846     C     T     14,962     29,33       Spike     S     T95I     SNP     298     21,846     C     T     21,562     29,33       Spike     S     T95I     SNP     297     3037     C     T     27,71     29,33       Spike     S     G339D     SNP     297     22,578     G     A     22,291     29,33       ORF3a protein     ORF3a     T64T     SNP_silent     297     25,584     C     T     25,597     29,33       NA     5'UTR     241     extragenic     297     241     C     T     187     29,36
RNA-dependent RNA polymerase, post-ribosomal frameshift     NSP12b     NS91N     SNP     500     25,661     GGG     FAC     26,574     27,574       Spike     298     15,240     C     T     14,662     29,334       Predicted phosphoesterase, papain-like proteinase     NSP3     F106F     SNP_silent     297     23,578     G     A     22,291     29,334       Spike     S     G339D     SNP     297     22,578     G     A     22,291     29,334       ORF3a protein     ORF3a     T64T     SNP_silent     297     25,584     C     T     25,297     29,344       NA     5'UTR     241     extragenic     297     241     C     T     187     29,664
Spike       S       T95I       SNP       298       21,846       C       T       21,562       29,33         Predicted phosphoesterase, papain-like proteinase       NSP3       F106F       SNP_silent       297       3037       C       T       27,71       29,33         Spike       S       G339D       SNP       297       22,578       G       A       22,291       29,33         ORF3a protein       ORF3a       T64T       SNP_silent       297       25,584       C       T       25,597       29,33         NA       5'UTR       241       extragenic       297       25,584       C       T       25,597       29,33
Predicted phosphoesterase, papain-like proteinase         NSP3         F106F         SNP_silent         297         3037         C         T         2771         29,33           Spike         S         G339D         SNP         297         22,578         G         A         22,291         29,33           ORF3a protein         ORF3a         T64T         SNP_silent         297         25,584         C         T         25,297         29,33           NA         5'UTR         241         extragenic         297         241         C         T         187         29,66
Spike         S         G339D         SNP         297         22,578         G         A         22,91         29,33           ORF3a protein         ORF3a         T64T         SNP_silent         297         25,584         C         T         25,972         29,33           NA         5'UTR         241         extragenic         297         241         C         T         187         29,66
ORF3a protein         ORF3a         T64T         SNP_silent         297         25,584         C         T         25,97         29,33           NA         5'UTR         241         extragenic         297         241         C         T         187         29,66
NA 5/UTR 241 extragenic 297 241 C T 187 29.6
3C-like proteinase NSP5 P132H SNP 296 10,449 C A 10,180 29,39
3'-to-5' exonuclease NSP14 142V SNP 296 18,163 A G 17,885 29,33
Envelope E T9I SNP 296 26,270 C T 25,983 29,39
ORF7b protein         ORF7b L17L         SNP_silent         296         27,807         C         T         27,520         29,33
Spike S N969K SNP 294 24,469 T A 24,182 29,33
Predicted phosphoesterase, papain-like proteinase NSP3 A889A SNP_silent 293 5386 T G 5120 29,30
Spike         S         L981F         SNP         292         24,503         C         T         24,216         29,33
Spike S D1146D SNP_silent 292 25,000 C T 24,713 29,34
Membrane M A63T SNP 289 26,709 G A 26,422 29,30
Predicted phosphoesterase, papain-like proteinase NSP3 \$1265 deletion 288 6513 GTT . 6246 29,33
Transmembrane protein NSP6 L105 deletion 287 11,286 TGTCTGGTT . 11,016 29,33
Spike S 168 deletion_tramesnitt 287 21,767 CATG . 21,486 29,33
Spirke         5         E404A         SWP         264         23,013         A         C         22,720         29,003           Sealing         C         C         C         C         A         D2,700         D2,700
opine 5 547/14 54r 265 22,572 G A 22,70 25,00
opine 5 1476k ovr 265 22,953 C A 22,70 25,00
Snike S Cl498R SNP 281 23,055 A G 22,765 29.37
Snike S N501Y SNP 281 23.063 A T 22.776 29.3
Spike S G496S SNP 280 23,048 G A 22,761 29,33
Spike S Y505H SNP 277 23,075 T C 22,788 29,3
Membrane M D3G SNP 275 26,530 A G 26,243 29,33
Membrane M Q19E SNP 272 26,577 C G 26,290 29,39
Spike         S         \$371L         SNP         270         22,673         TC         CT         22,386         29,39
Spike         S         S373P         SNP         270         22,679         T         C         22,392         29,34
Spike         S         G142         deletion         260         21,987         GTGTTTATT         .         21,702         29,39
Spike         S         S375F         SNP         260         22,686         C         T         22,399         29,39
ORF7b         E3*         SNP_stop         253         27,762         G         T         27,687         29,75
Spike         S         I210         insertion_frameshift         243         22,193         T         21,901         29,33
Spike S R214 insertion_frameshift 243 22,203 . A 21,916 29,33
Spike         S         R214R         SNP silent         243         22,204         T         A         21,917         29,33           Nucleonarid entries         Nucleonarid entries         Nucleonarid entries         0.10 <t< td=""></t<>
Nucleocapsid protein N E31 deletion 243 28,352 GAGACGCA . 28,0/4 29,3
Spirke         S         L212"         SNP stop         243         Z2,197         I         G         22,118         29,77           Solida         S         N011K         SNP         942         29,105         T         G         20,106         20,202         20,2
סטוגד ס איז
$\sigma_{\rm proc}$ $\sigma_{\rm L212c}$ $\sigma_{\rm VP}$ $242$ $22,127$ $r_{\rm A}$ $GC$ $21,902$ $22,50$
opmo o 2217 IIIseriuui 242 22,001 . AUC 21,910 229,00 Snika S V913 incartion framachift 242 29.909 A 91.014 20.9
$\gamma_{PAC}$ 0 $\tau_{PAT}$ instruction $2\tau_2$ $22_{5}02$ . A 21,914 22,50 NA 3'ITTR 28.271 extraornic 242 28.271 A T 27.084 20.2°
Nucleocansid protein N P131, SNP 241 28 311 C T 28.092 29.37
Spike S N764K SNP 234 23.854 C A 23.567 29.30
Spike S G446S SNP 203 22.898 G A 22.611 29.3
Spike S N440K SNP 199 22,882 T G 22,595 29,33
Spike S K417N SNP 183 22,813 G T 22,526 29,34

### **Funding Information**

Nil

### Author contribution statement

Both the authors' KB and SK have contributed equally to the data curation, analysis, and writing of the manuscript.

### CRediT authorship contribution statement

Kanika Bansal: Data curation, Formal analysis, Writing – original draft. Sanjeet Kumar: Data curation, Formal analysis, Writing – original draft.

### **Declaration of Competing Interest**

The author declares no competing interest.

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

### Acknowledgment

Authors acknowledge the support and motivation from Dr. Prabhu B. Patil – CSIR-Institute of Microbial Technology, Chandigarh. We are also thankful to Dr. Santosh Kumar Sethi for his kind support during the process of study. We also acknowledge GISAID initiative for extensive curation and availability of genomic resource in public domain.

### Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.virusres.2022.198765.

#### References

Andreadakis, Z., Kumar, A., Román, R.G., Tollefsen, S., Saville, M., Mayhew, S., 2020. The COVID-19 vaccine development landscape. Nat. Rev. Drug Discov. 19 (5), 305–306.

Bansal, K., Kumar, S., Patil, P.B., 2021. Codon usage pattern reveals SARS-CoV-2 as a monomorphic pathogen of hybrid origin with role of silent mutations in rapid Virus Research 315 (2022) 198765

evolutionary success. bioRxiv. https://doi.org/10.1101/2020.10.12.335521, 2020.2010.2012.335521.

Boehm, E., Kronig, I., Neher, R.A., Eckerle, I., Vetter, P., Kaiser, L., 2021. Novel SARS-CoV-2 variants: the pandemics within the pandemic. Clin. Microbiol. Infect.

Callaway, E., 2021. Heavily mutated coronavirus variant puts scientists on alert. Nature 25. https://doi.org/10.1038/d41586-021-03552-w.

- Callaway, E., Ledford, H., 2021. How bad is Omicron? What scientists know so far. Nature. https://doi.org/10.1038/d41586-021-03614-z.
- Corey, L., Mascola, J.R., Fauci, A.S., Collins, F.S., 2020. A strategic approach to COVID-19 vaccine R&D. Science 368 (6494), 948–950.

Delcher, A.L., Phillippy, A., Carlton, J., Salzberg, S.L., 2002. Fast algorithms for largescale genome alignment and comparison. Nucleic Acids Res. 30 (11), 2478–2483. Islam, O.K., Al-Emran, H.M., Hasan, M.S., Anwar, A., Jahid, M.I.K., Hossain, M.A., 2021.

Emergence of European and North American mutanty virtuals of SARS-CoV-2 in South-East Asia. Transboundary Emerg. Dis. 68 (2), 824–832.

Knoll, M.D., Wonodi, C., 2021. Oxford–AstraZeneca COVID-19 vaccine efficacy. Lancet North Am. Ed. 397 (10269), 72–74.

- Kumar, S., Bansal, K., 2021. Cross-sectional genomic perspective of epidemic waves of SARS-CoV-2: a pan India study. Virus research, 198642.
- Letunic, I., Bork, P., 2019. Interactive Tree Of Life (iTOL) v4: recent updates and new developments. Nucleic Acids Res. 47 (W1), W256–W259.
- Lipsitch, M., Dean, N.E., 2020. Understanding COVID-19 vaccine efficacy. Science 370 (6518), 763–765.
- Mercatelli, D., Giorgi, F.M., 2020. Geographic and genomic distribution of SARS-CoV-2 mutations. Front. Microbiol. 11, 1800.

Nakamura, T., Yamada, K.D., Tomii, K., Katoh, K., 2018. Parallelization of MAFFT for large-scale multiple sequence alignments. Bioinformatics 34 (14), 2490–2492.

Pegu, A., O'Connell, S.E., Schmidt, S.D., O'Dell, S., Talana, C.A., Lai, L., Corbett, K.S., 2021. Durability of mRNA-1273 vaccine–induced antibodies against SARS-CoV-2 variants. Science 373 (6561), 1372–1377.

Price, M.N., Dehal, P.S., Arkin, A.P., 2010. FastTree 2–approximately maximumlikelihood trees for large alignments. PLoS One 5 (3), e9490. https://doi.org/ 10.1371/journal.pone.0009490.

Pulliam, J.R.C., van Schalkwyk, C., Govender, N., von Gottberg, A., Cohen, C., Groome, M.J., Moultrie, H., 2021. Increased risk of SARS-CoV-2 reinfection associated with emergence of the Omicron variant in South Africa. medRxiv. https:// doi.org/10.1101/2021.11.11.21266068, 2021.2011.2011.21266068.

Rambaut, A., Loman, N., Pybus, O., Barclay, W., Barrett, J., Carabelli, A., Volz, E., 2020. Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations. Virological.

Schmidt, M., Arshad, M., Bernhart, S.H., Hakobyan, S., Arakelyan, A., Loeffler-Wirth, H., Binder, H., 2021. The evolving faces of the SARS-CoV-2 genome. Viruses 13 (9), 1764.

Sharma, O., Sultan, A.A., Ding, H., Triggle, C.R., 2020. A Review of the Progress and Challenges of Developing a Vaccine for COVID-19. Front. Immunol. 11, 2413.

Singh, D., Soojin, V.Y., 2021. On the origin and evolution of SARS-CoV-2. Exp. Mol. Med. 53 (4), 537–547.

- Tang, X., Wu, C., Li, X., Song, Y., Yao, X., Wu, X., Qian, Z., 2020. On the origin and continuing evolution of SARS-CoV-2. Natl. Sci. Rev. 7 (6), 1012–1023.
- Thakur, V., Bhola, S., Thakur, P., Patel, S.K.S., Kulshrestha, S., Ratho, R.K., Kumar, P., 2021. Waves and variants of SARS-CoV-2: understanding the causes and effect of the COVID-19 catastrophe. Infection, pp. 1–16.