

Virus detail	
Virus name:	hCoV-19/Wuhan/AP8/2020
Accession ID:	EPI_ISL_1655937
Type:	betacoronavirus
Clade	S
Pango Lineage	A (version: 2021-04-14)
AA Substitutions	NS3 Q116H, NS3 Q185H, NS8 L84S
Variant	
Passage details/history:	Original
Sample information	
Collection date:	2020-01-25
Location:	Asia / China / Wuhan
Host:	Human
Additional location information:	
Gender:	Male
Patient age:	32
Patient status:	Released
Specimen source:	Sputum
Additional host information:	
Sampling strategy:	
Outbreak:	
Last vaccinated:	
Treatment:	
Sequencing technology:	Illumina MiSeq
Assembly method:	Geneious 10.2.4
Coverage:	
Comment:	
Institute information	
Originating lab:	State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong
Address:	Laboratory Block LKS Faculty of Medicine 21 Sassoon Road Pokfulam Hong Kong SAR
Sample ID given by the originating laboratory:	
Submitting lab:	State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong
Address:	Laboratory Block LKS Faculty of Medicine 21 Sassoon Road Pokfulam Hong Kong SAR
Sample ID given by the submitting laboratory:	
Authors:	Jia Wang, Lifeng Li, Yiu Man Cheung, Huachen Zhu, Yi Guan
Submitter information	
Submitter:	Cheung, William
Submission Date:	2021-04-20
Address:	Laboratory Block LKS Faculty of Medicine 21 Sassoon Road Pokfulam Hong Kong SAR

Important note: In the GISAID EpiFlu™ Database Access Agreement, you have accepted certain terms and conditions for viewing and using data regarding influenza viruses. To the extent the Database contains data relating to non-influenza viruses, the viewing and use of these data is subject to the same terms and conditions, and by viewing or using such data you agree to be bound by the terms of the GISAID EpiFlu™ Database Access Agreement in respect of such data in the same manner as if they were data relating to influenza viruses.