

Virus detail

Virus name:	hCoV-19/Belgium/rega-47745/2023
Accession ID:	EPI_ISL_18492450
Type:	betacoronavirus
Clade:	GRA
Pango Lineage:	JN.1.1 (Pango v.4.3.1 consensus call), Omicron (BA.2-like) (Scorpio)
AA Substitutions:	Spike A27S, Spike A264D, Spike A570V, Spike D405N, Spike D614G, Spike D796Y, Spike E484K, Spike E554K, Spike F157S, Spike F486P, Spike G142D, Spike G339H, Spike G446S, Spike H69del, Spike H245N, Spike H655Y, Spike I332V, Spike ins16MPLF, Spike K356T, Spike K417N, Spike L24del, Spike L212I, Spike L216F, Spike L452W, Spike L455S, Spike N211del, Spike N440K, Spike N450D, Spike N460K, Spike N481K, Spike N501Y, Spike N679K, Spike N764K, Spike N969K, Spike P25del, Spike P26del, Spike P621S, Spike P681R, Spike P1143L, Spike Q498R, Spike Q954H, Spike R21T, Spike R158G, Spike R403K, Spike R408S, Spike S50L, Spike S371F, Spike S373P, Spike S375F, Spike S477N, Spike S939F, Spike T19I, Spike T376A, Spike T478K, Spike V70del, Spike V127F, Spike V213G, Spike V445H, Spike V483del, Spike Y144del, Spike Y505H, E T9I, M A63T, M A104V, M D3H, M Q19E, M T30A, N E31del, N G204R, N P13L, N Q229K, N R32del, N R203K, N S33del, N S413R, NS3 T223I, NS7a R25K, NS7b F19L, NSP1 S135R, NSP2 A31D, NSP2 F319L, NSP3 A1892T, NSP3 G489S, NSP3 K1155R, NSP3 N1708S, NSP3 T24I, NSP3 V238L, NSP4 L264F, NSP4 T327I, NSP4 T492I, NSP5 P132H, NSP6 F108del, NSP6 G107del, NSP6 R252K, NSP6 S106del, NSP6 V24F, NSP9 T35I, NSP12 P323L, NSP13 R392C, NSP14 I42V, NSP15 T112I
Variant:	VOI GRA (JN.1+JN.1.*) first detected in Luxembourg/Iceland
Passage details/history:	Original

Sample information

Collection date:	2023-11-04
Location:	Europe / Belgium / Lubbeek
Host:	Human
Additional location information:	Other: Postal Code:3210
Gender:	Female
Patient age:	87
Patient status:	unknown
Specimen source:	Oropharyngeal swab
Additional host information:	
Sampling strategy:	baseline surveillance
Outbreak:	
Last vaccinated:	
Treatment:	
Sequencing technology:	Nanopore MinION
Assembly method:	Artic Network methods
Coverage:	140x (average)x
Comment:	⬠ Insertion of 12 nucleotides when compared to the reference WIV04 sequence. Gap of 42 nucleotides when compared to the reference WIV04 sequence.

Institute information

Originating lab:	KU Leuven, Rega Institute, Clinical and Epidemiological Virology
Address:	Rega institute, Herestraat 49 box 1040, BE3000 Leuven, Belgium
Sample ID given by the originating laboratory:	
Submitting lab:	KU Leuven, Rega Institute, Clinical and Epidemiological Virology
Address:	Rega institute, Herestraat 49 box 1040, BE3000 Leuven, Belgium
Sample ID given by the submitting laboratory:	ZIDU53896
Authors:	Anne-Sophie Logist, Bram Van Holm, Bert Vanmechelen, Piet Maes

Submitter information

Submitter:	Maes, Piet
Submission Date:	2023-11-10
Address:	

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.