

Virus detail	
<b>Virus name:</b>	hCoV-19/USA/MI-UM-10052670540/2023
<b>Accession ID:</b>	EPI_ISL_18110065
<b>Type:</b>	betacoronavirus
<b>Clade:</b>	GRA
<b>Pango Lineage:</b>	BA.2.86 (marker override)
<b>AA Substitutions:</b>	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 I670V, Spike ins16MPLF, Spike K356T, Spike K417N, Spike L24del, Spike L212I, Spike L216F, Spike L452W, 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 G243S, N P13L, N Q229K, N R32del, N R203K, N S33del, N S413R, NS3 T223I, NS8 T87I, NSP1 S135R, NSP2 A31D, NSP3 A1892T, NSP3 G489S, NSP3 N1708S, NSP3 T24I, NSP3 V238L, NSP4 L264F, NSP4 T327I, NSP4 T492I, NSP5 P132H, NSP6 F108del, NSP6 G107del, NSP6 S106del, NSP6 V24F, NSP9 T35I, NSP12 P323L, NSP13 R392C, NSP14 I42V, NSP15 T112I
<b>Variant:</b>	VUM GRA (BA.2.86) first detected in Denmark/Israel/USA
<b>Passage details/history:</b>	Original
Sample information	
<b>Collection date:</b>	2023-08-03
<b>Location:</b>	North America / USA / Michigan
<b>Host:</b>	Human
<b>Additional location information:</b>	
<b>Gender:</b>	unknown
<b>Patient age:</b>	unknown
<b>Patient status:</b>	unknown
<b>Specimen source:</b>	
<b>Additional host information:</b>	
<b>Sampling strategy:</b>	Baseline surveillance
<b>Outbreak:</b>	
<b>Last vaccinated:</b>	
<b>Treatment:</b>	
<b>Sequencing technology:</b>	Oxford Nanopore Midnight
<b>Assembly method:</b>	ARTIC Network pipeline Midnight
<b>Coverage:</b>	
<b>Comment:</b>	Stretches of NNNs (3.04% of overall sequence). Insertion of 12 nucleotides when compared to the reference WIV04 sequence. Gap of 42 nucleotides when compared to the reference WIV04 sequence. NSP16 without BLAST coverage.
Institute information	
<b>Originating lab:</b>	University of Michigan Clinical Microbiology Laboratory
<b>Address:</b>	2800 Plymouth Rd, Ann Arbor, MI, USA
<b>Sample ID given by the originating laboratory:</b>	
<b>Submitting lab:</b>	Lauring Lab, University of Michigan, Department of Microbiology and Immunology
<b>Address:</b>	1137 Catherine Street, Ann Arbor, MI, USA
<b>Sample ID given by the submitting laboratory:</b>	
<b>Authors:</b>	Baker
Submitter information	
<b>Submitter:</b>	Baker, Leigh
<b>Submission Date:</b>	2023-08-17
<b>Address:</b>	1137 Catherine Street 48109 Ann Arbor United States

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