

UShER: Ultrafast Sample placement on Existing tRee

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Fasta Sequence	Size (?)	#Ns (?)	#Mixed (?)	Bases aligned (?)	Inserted bases (?)	Deleted bases (?)	#SNVs used for placement (?)	#Masked SNVs (?)	Nextstrain clade (?)	Pango lineage (?)	Neighboring sample in tree (?)	Lineage of neighbor (?)	#Imputed values for mixed bases (?)	#Maximally parsimonious placements (?)	Parsimony score (?)	Subtree number (?)
Scotland/LSPA-3E62463/2022	29718 (?)	0 (?)	1 (?)	29718 (?)	0	59 (?)	68 (?)	2 (?)	22B (Omicron)	BA.5.2	Canada/ON-PHL-22-24473/2022 EPI_ISL_13504549 2022-06-13	BA.5.2	1 (?)	1	0	1 (view in Nextstrain)
Scotland/LSPA-3E3B700/2022	29724 (?)	0 (?)	0	29724 (?)	0	53 (?)	71 (?)	1 (?)	21M (Omicron)	BA.2.18	England/LSPA-3DF2C25/2022 OW854082.1 2022-05-02	BA.2.18	0	1	0	2 (view in Nextstrain)
Scotland/QEUEH-3DC59CA/2022	29724 (?)	0 (?)	0	29724 (?)	0	53 (?)	71 (?)	2 (?)	21M (Omicron)	BA.2.1	Scotland/QEUEH-3DAE314/2022 OW815214.1 2022-04-21	BA.2.1	0	1	1	3 (view in Nextstrain)
Scotland/QEUEH-3D90306/2022	29709 (?)	0 (?)	0	29709 (?)	0	68 (?)	73 (?)	1 (?)	22A (Omicron)	BA.4	Scotland/QEUEH-3D8F2D0/2022 OW687262.1 2022-04-19	BA.4	0	1	0	4 (view in Nextstrain)
Scotland/QEUEH-3D43C43/2022	29724 (?)	0 (?)	0	29724 (?)	0	53 (?)	71 (?)	1 (?)	22C (Omicron)	BA.2.12.1	USA/UT-UPHL-220812097234/2022 EPI_ISL_14581044 2022-05-29	BA.2.12.1	0	3	0	5 (view in Nextstrain)
Scotland/CVR14531/2022	29625 (?)	29 (?)	0	29587 (?)	9 (?)	39 (?)	58 (?)	0	21K (Omicron)	BA.1.1	OV728320.1 2022-01-13	BA.1.1	0	1	0	6 (view in Nextstrain)
Scotland/QEUEH-36897FC/2022	29721 (?)	0 (?)	0	29721 (?)	0	56 (?)	61 (?)	1 (?)	21M (Omicron)	XE	France/ARA-HMN-22052250274/2022 EPI_ISL_13462404 2022-05-16	XE	0	2	0	7 (view in Nextstrain)
Scotland/QEUEH-36491AF/2022	29715 (?)	0 (?)	1 (?)	29715 (?)	0	62 (?)	57 (?)	0	21M (Omicron)	BA.3	Poland/PZH-GUM-7182/2022 EPI_ISL_9266850 2022-01-04	BA.3	1 (?)	1	0	8 (view in Nextstrain)
Scotland/QEUEH-2D86BD1/2021	29764 (?)	0 (?)	2 (?)	29764 (?)	0	13 (?)	43 (?)	4 (?)	21J (Delta)	AY.43	Scotland/QEUEH-2E5CFF5/2021 OV318519.1 2021-12-12	AY.43	0	1	0	9 (view in Nextstrain)
Scotland/QEUEH-2D7F704/2021	29755 (?)	0 (?)	2 (?)	29755 (?)	0	22 (?)	38 (?)	4 (?)	21J (Delta)	AY.46.5	Scotland/QEUEH-2D417B0/2021 OV450177.1 2021-12-04	AY.46.5	0	1	0	10 (view in Nextstrain)
Scotland/QEUEH-1BA3933/2021	29775 (?)	0 (?)	0	29768 (?)	3 (?)	10 (?)	35 (?)	1 (?)	21H (Mu)	B.1.621	England/PHEC-R30ARCD2/2021 2021-08-09	B.1.621	0	1	0	11 (view in Nextstrain)
Scotland/QEUEH-1B0246E/2021	29777 (?)	0 (?)	0	29770 (?)	4 (?)	9 (?)	42 (?)	0	20J (Gamma,V3)	P.1	Scotland/QEUEH-1B0246E/2021 OU565182.1 2021-08-04	P.1	0	1	0	12 (view in Nextstrain)
Scotland/QEUEH-1725CCB/2021	29781 (?)	0 (?)	0	29774 (?)	3 (?)	4 (?)	38 (?)	1 (?)	21H (Mu)	B.1.621	USA/FL-BPHL-11620/2021 OL417224.1 2021-06-19	B.1.621	0	1	0	13 (view in Nextstrain)
Scotland/QEUEH-1585B0A/2021	29763 (?)	1437 (?)	0	28326 (?)	0	19 (?)	35 (?)	0	20I (Alpha,V1)	B.1.1.7	Scotland/QEUEH-1578997/2021 OU283041.1 2021-05-11	B.1.1.7	0	1	0	14 (view in Nextstrain)
Scotland/QEUEH-158D786/2021	29763 (?)	0 (?)	2 (?)	29763 (?)	0	19 (?)	39 (?)	0	20I (Alpha,V1)	B.1.1.7	Scotland/QEUEH-156AF3C/2021 OU279463.1 2021-05-08	B.1.1.7	2 (?)	1	0	15 (view in Nextstrain)
Scotland/CAMC-14DE972/2021	29772 (?)	0 (?)	0	29772 (?)	0	10 (?)	20 (?)	1 (?)	21F (Iota)	B.1.526	USA/PA-CDC-STM-000041666/2021 MW891419.1 2021-03-21	B.1.526	0	1	0	16 (view in Nextstrain)
Scotland/QEUEH-147E6F5/2021	29781 (?)	125 (?)	3 (?)	29656 (?)	0	1 (?)	33 (?)	1 (?)	21B (Kappa)	B.1.617.1	Scotland/QEUEH-14C89B7/2021 OU242784.1 2021-04-02	B.1.617.1	3 (?)	1	0	17 (view in Nextstrain)
Scotland/QEUEH-13ADEF6/2021	29709 (?)	542 (?)	0	29167 (?)	0	73 (?)	27 (?)	1 (?)	21D (Eta)	B.1.525	Scotland/QEUEH-13ADC1A/2021 OU060759.1 2021-03-08	B.1.525	0	1	1	18 (view in Nextstrain)

Scotland/QEUH-138F944/2021	29777 (?)	567 (?)	0	29203 (?)	4 (?)	9 (?)	36 (?)	0	20J (Gamma,V3)	P.1	Scotland/QEUH-138F944/2021 OU061529.1 2021-03-03	P.1	0	1	0	19 (view in Nextstrain)
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Subtree 1: Unrelated sample

[view subtree 1 in Nextstrain](#)

Scotland/LSPA-3E62463/2022

Differences from the reference genome (NC_045512.2): C241T, T670G, C1627T, C2790T, C3037T, G4184A, C4321T, C9344T, A9424G, C9534T, C10029T, C10198T, G10447A, C10449A, G12160A, G12310A, C12880T, C14408T, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22882G, T22917G, G22992A, C22995A, A23013C, T23018G, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C23854A, G23948T, A24424T, T24469A, C25000T, C25584T, C26060T, C26270T, G26529A, C26577G, G26709A, T27543C, C27807T, C27889T, T27956G, A28271T, C28311T, A28330G, G28881A, G28882A, G28883C, A29510C

Base values imputed by parsimony:

- 19716: C

Mutations along the path from the root of the phylogenetic tree to Scotland/LSPA-3E62463/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > T9866C > T26858C > C27259A > C27382G > C27384T > T27383A > G23040A > T23018G > T22917G > G12160A > G22200T > G26529A > T22200G > C27889T > A28330G > C1627T > G12310A > T27956G > T27543C

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Canada/ON-PHL-22-24473/2022|EPI_ISL_13504549|2022-06-13: lineage [BA.5.2](#)

Subtree 2: Unrelated sample

[view subtree 2 in Nextstrain](#)

Scotland/LSPA-3E3B700/2022

Differences from the reference genome (NC_045512.2): C241T, T670G, C2790T, C3037T, G4184A, C4321T, C6033T, G6476T, C9344T, A9424G, C9534T, C9866T, C10029T, C10198T, G10447A, C10449A, C12789T, C12880T, C14408T, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, A22812C, G22813T, T22882G, G22992A, C22995A, A23013C, A23040G, A23055G, A23063T, T23075C, C23248T, A23403G, C23525T, T23599G, C23604A, C23854A, G23948T, A24424T, T24469A, C25000T, C25584T, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, G27382C, A27383T, T27384C, C27641T, C27807T, A28271T, C28311T, G28881A, G28882A, G28883C, A29510C

Mutations along the path from the root of the phylogenetic tree to Scotland/LSPA-3E3B700/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > G22113A > C23248T > A12658G > A22812C > A22113G > G12658A > C27641T > C11653T > C6033T, G6476T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: England/LSPA-3DF2C25/2022|OW854082.1|2022-05-02: lineage [BA.2.18](#)

Subtree 3: Unrelated sample

[view subtree 3 in Nextstrain](#)

Scotland/QEUH-3DC59CA/2022

Differences from the reference genome (NC_045512.2): C222T, C241T, T670G, C2790T, C3037T, A3069G, G4184A, C4321T, A6790G, C9344T, A9424G, C9534T, C9866T, C10029T, C10198T, G10447A, C10449A, C12789T, C12880T, C14408T, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22882G, G22992A, C22995A, A23013C, A23040G, A23055G, A23063T, T23075C, A23403G, G23429A, C23525T, T23599G, C23604A, C23854A, G23948T, A24424T, T24469A, C25000T, C25584T, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, G27382C, A27383T, T27384C, C27807T, A28271T, C28311T, G28881A, G28882A, G28883C, A29510C, C29555T

Mutations along the path from the root of the phylogenetic tree to Scotland/QEUH-3DC59CA/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > C12789T > C29555T > A3069G, A6790G > G23429A > Scotland/QEUH-3DC59CA/2022: C222T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QEUH-3DAE314/2022|OW815214.1|2022-04-21: lineage [BA.2.1](#)

Subtree 4: Unrelated sample

[view subtree 4 in Nextstrain](#)

Scotland/QEUH-3D90306/2022

Differences from the reference genome (NC_045512.2): C241T, T670G, A895G, C913T, C2790T, C3037T, G4184A, C4321T, G7360T, C9344T, A9424G, C9534T, C10029T, C10198T, G10447A, C10449A, G12160A, C12880T, C14408T, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, C22851T, T22882G, T22917G, G22992A, C22995A, A23013C, T23018G, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C23854A, G23948T, A24424T, T24469A, C25000T, C25584T, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, G27382C, A27383T, T27384C, G27788T, C27807T, G28048T, A28271T, C28311T, C28724T, G28881A, G28882A, G28883C, A29510C

Mutations along the path from the root of the phylogenetic tree to Scotland/QEUH-3D90306/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > G23040A > T22917G > T23018G > T9866C > G27788T > C28724T > A895G > C913T > G7360T > C22851T > G28048T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QEUH-3D8F2D0/2022|OW687262.1|2022-04-19: lineage [BA.4](#)

Subtree 5: Unrelated sample

[view subtree 5 in Nextstrain](#)

Scotland/QEUH-3D43C43/2022

Differences from the reference genome (NC_045512.2): C241T, T670G, C2790T, C3037T, G4184A, C4321T, C9344T, A9424G, C9534T, C9866T, C10029T, G10447A, C10449A, C11674T, C12880T, C14408T, T15009C, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, C21721T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22882G, T22917A, G22992A, C22995A, A23013C, A23040G, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C23673T, C23854A, G23948T, A24424T, T24469A, C25000T, C25416T, C25584T, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, G27382C, A27383T, T27384C, C27807T, A28271T, C28311T > C28724T > A895G > C913T > G7360T > C22851T > G28048T

Mutations along the path from the root of the phylogenetic tree to Scotland/QEUH-3D43C43/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > G23040A > T22917G > T23018G > T9866C > G27788T > C28724T > A895G > C913T > G7360T > C22851T > G28048T

T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > C25416T > C26737T > C11674T > T22917A > T15009C > C21721T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: USA/UT-UPHL-220812097234/2022|EPI_ISL_14581044|2022-05-29: lineage [BA.2.12.1](#)

Subtree 6: Unrelated sample

[view subtree 6 in Nextstrain](#)

Scotland/CVR14531/2022

Differences from the reference genome ([NC_045512.2](#)): C241T, C1973T, C2470T, A2832G, C3037T, G4127A, T5386G, G8393A, C10029T, C10449A, A11537G, T13195C, C14408T, C15240T, A18163G, C21762T, C21846T, G22578A, G22599A, T22673C, C22674T, T22679C, C22686T, G22813T, T22882G, G22898A, G22992A, C22995A, A23013C, A23040G, G23048A, A23055G, A23063T, T23075C, C23202A, A23403G, C23525T, T23599G, C23604A, C23854A, G23948T, C24130A, A24424T, T24469A, C24503T, C25000T, C25584T, C26270T, A26530G, C26577G, G26709A, A27259C, C27807T, A28271T, C28311T, G28881A, G28882A, G28883C

Mutations along the path from the root of the phylogenetic tree to Scotland/CVR14531/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > A26530G > A24130C > A11537G > G8393A, G26530A > G23048A > C23202A > G22898A, A26530G > C24130A > A2832G > T13195C > A23048G > C24503T > T5386G > G23048A > G22599A > C2470T > C1973T > G4127A

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: OV728320.1|2022-01-13: lineage [BA.1.1](#)

Subtree 7: Unrelated sample

[view subtree 7 in Nextstrain](#)

Scotland/QUEU-36897FC/2022

Differences from the reference genome ([NC_045512.2](#)): C241T, A2832G, C3037T, C3241T, T5386G, G5924A, G8393A, C10029T, C10449A, C12880T, C14408T, C14599T, C15714T, C17410T, A18163G, C19955T, A20055G, C21618T, T22200G, G22578A, C22674T, T22679C, C22686T, A22688G, G22775A, A22786C, G22813T, T22882G, G22992A, C22995A, A23013C, A23040G, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C23854A, G23948T, A24424T, T24469A, C25000T, C25584T, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, G27382C, A27383T, T27384C, C27807T, A28271T, C28311T, G28881A, G28882A, G28883C, A29510C

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEU-36897FC/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C17410T, C22673T > G27382C, A27383T, T27384C > C9344T, A9424G, C9866T > A22786C > A22688G > A29510C > C10198T > C2790T > C22792T > T4321C > G670T > A4184G > T2790C > A2832G > T5386G > G8393A > C25624T > T9344C, G9424A, T9534C > T9866C > T10198C > A10447G > T25624C > A11537G > G5924A > C3241T > G11537A, T22792C > C14599T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: France/ARA-HMN-22052250274/2022|EPI_ISL_13462404|2022-05-16: lineage [XE](#)

Subtree 8: Unrelated sample

[view subtree 8 in Nextstrain](#)

Scotland/QUEU-36491AF/2022

Differences from the reference genome ([NC_045512.2](#)): C241T, T670G, C832T, C1912T, C3037T, G4184A, C4321T, C9534T, C10029T, G10447A, C10449A, C11235T, A12422M, C12664T, C12880T, C14408T, C15714T, A18163G, C21762T, C21846T, G22578A, C22674T, T22679C, C22686T, G22775A, G22813T, T22882G, G22898A, G22992A, C22995A, A23013C, A23040G, A23055G, A23063T, T23075C, A23403G, C23525T, T23599G, C23604A, C23707T, C23854A, G23948T, A24424T, T24469A, C26060T, C26270T, C26577G, G26709A, C26858T, A27259C, C27807T, A28271T, C28311T, G28881A, G28882A, G28883C, C29311T, A29510C

Base values imputed by parsimony:

- 12422: A

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEU-36491AF/2022:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C21846T > C10029T > C15240T, C23854A, G23948T, C27807T > C21762T, C24130A, A28271T > C10449A, C23525T, T23599G, C23604A, C26270T, C28311T > C25000T > A23055G, A23063T, T23075C, A27259C > G22578A, C22674T, T22679C, C22686T, A24424T, C25584T > T22673C, A23040G, T24469A > G22992A, C22995A, A23013C > A18163G, C26577G > G26709A > T22882G > G22813T > C22673T > T21762C > T21846C > A24130C > T15240C > T22200G > G22775A > C19955T > G10447A, C15714T, C26060T > A20055G, T22673C > T670G, G4184A, C4321T, C26858T > C9534T > C12880T, C21618T > C10198T, T19955C > G22200T > T26060C > T9534C, C21762T, C21846T > G20055A, T21618C > T10198C, G22898A > C22673T, T25000C, T25584C > C832T, C9534T, C26060T > A29510C > C11235T > C29311T > C1912T, C23707T > C12664T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Poland/PZH-GUM-7182/2022|EPI_ISL_9266850|2022-01-04: lineage [BA.3](#)

Subtree 9: Unrelated sample

[view subtree 9 in Nextstrain](#)

Scotland/QUEU-2D86BD1/2021

Differences from the reference genome ([NC_045512.2](#)): G210T, C241T, C829T, C3037T, G4181T, T5449C, G6309A, C6402T, C7124T, C8986T, G9053T, C10029T, A11201G, A11332G, C13671A, C14408T, G15451A, C15952A, C16466T, C18744T, C19220T, C19512T, C21618G, T22917G, C22995A, A23403G, C23604G, C24130T, C25469T, T26767C, C26873T, C27513T, T27638C, C27689T, C27752T, C27874T, A28299T, A28461G, G28881T, G28916T, G29402T, C29708T, G29742T

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEU-2D86BD1/2021:

C14408T > C241T > C3037T > A23403G > G29742T > T22917G > T27638C > G28881T > C21618G > G210T > G29402T > C23604G > C25469T > C22995A > C27752T > A28461G > C16466T > T26767C > G15451A > C10029T > C19220T > G28916T > G4181T > C27874T > C6402T > C7124T > G9053T > C8986T > T6402C > T19220C > A11332G > C19220T > A11201G > C6402T > A28299T > A15952A > C18744T > C24130T > C829T > C27689T > G6309A > T5449C > C19512T > C13671A > C27513T > C29708T > C26873T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QUEU-2E5CFF5/2021|OV318519.1|2021-12-12: lineage [AY.43](#)

Subtree 10: Unrelated sample

[view subtree 10 in Nextstrain](#)

Scotland/QUEU-2D7F704/2021

Differences from the reference genome ([NC_045512.2](#)): G210T, C241T, C3037T, G4181T, C6402T, C6968T, C7124T, C8986T, G9053T, C10029T, C10977T, A11201G, A11332G, C14408T, G15451A, C15569T, T16242G, C16466T, C19220T, T21607C, C21618G, T22917G, C22995A, A23403G, C23604G, C25469T, G26526T, T26767C, C27596T, T27638C, C27643T, C27752T, C27874T, A28461G, G28881T, G28916T, G29402T, G29742T

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEU-2D7F704/2021:

C14408T > C241T > C3037T > A23403G > G29742T > T22917G > T27638C > G28881T > C21618G > G210T > G29402T > C23604G > C25469T > C22995A > C27752T > A28461G > C16466T > T26767C > G15451A > C10029T > C19220T > G28916T > G4181T > C27874T > C6402T > C7124T > G9053T > C8986T > T6402C > T19220C > A11332G > C19220T > A11201G > C6402T > A28299T > C10977T > C15569T > T16242G > C27643T > C27596T > C6968T > T21607C > G26526T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QUEU-2D417B0/2021|OV450177.1|2021-12-04: lineage [AY.46.5](#)

Subtree 11: Unrelated sample

[view subtree 11 in Nextstrain](#)

Scotland/QUEU-1BA3933/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, G1685T, C2433T, C3037T, A3428G, T4684C, C4878T, C6037T, C10029T, A11451G, T12748A, A13057T, C14408T, C16751A, C17491T, G18412T, C18877T, T19035C, C20148T, C21846T, G22599A, G22813T, G23012A, A23063T, A23403G, C23604A, G25563T, A26492T, C27925A, C28005T, C28093T, A28272T, G28378T, C28657T, C28887T

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEU-1BA3933/2021:

C14408T > C241T > C3037T > A23403G > G25563T > C26735T > C18877T > T26735C > C28005T, C28093T > A21993C, C27925A > T19035C > A23063T, C23604A > C10029T, C21993A, C28887T > C19035T > G23012A > C6037T, A11451G, C17491T, C20148T, C21846T > C4878T > A13057T, A21993C, T21995A > G22599A > T19035C > A26492T > A3428G, A28272T > G28378T > C16751A > G18412T > G1685T, G22813T > T4684C > C2433T > T12748A > C28657T

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: England/PHEC-R30ARCD2/2021|2021-08-09: lineage [B.1.621](#)

Subtree 12: Unrelated sample

[view subtree 12 in Nextstrain](#)

Scotland/QUEUH-1B0246E/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, T733C, C1091T, C2749T, C3037T, C3828T, T5248C, A5648C, A6319G, A6613G, A10983G, C12049T, C12778T, C13860T, C14408T, C15960T, G17259T, C21614T, C21621A, C21638T, G21974T, G22132T, A22812C, C22858T, C22945T, G23012A, A23063T, A23403G, C23481T, C23525T, C24642T, G25008T, T25159C, C25413T, T26149C, G28167A, C28512G, A28877T, G28878C, G28881A, G28882A, G28883C

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEUH-1B0246E/2021:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C23525T > G23012A > G25088T > A6613G > T26149C > A22812C, A23063T > G21974T, A28877T, G28878C > C28512G > C13860T, G17259T > C12778T > A5648C > G28167A > C3828T > C24642T > T733C > A6319G > C2749T > C22812A > G22132T > C21614T > C21621A > C21638T > A22812C > A10983G > C22945T > C25413T > C15960T > T25159C > C1091T > T5248C > C22858T > C23481T > C12049T

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: Scotland/QUEUH-1B0246E/2021|OU565182.1|2021-08-04: lineage [P.1](#)

Subtree 13: Unrelated sample

[view subtree 13 in Nextstrain](#)

Scotland/QUEUH-1725CCB/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, G2945A, C3037T, C3173A, A3428G, C4878T, C6037T, C7764T, C10029T, T10654C, A11451G, A13057T, C14408T, C16101T, C17491T, C18329T, C18877T, T19035C, G19481T, C20148T, C20574T, C21846T, G22599A, G23012A, A23063T, A23403G, C23604A, G25563T, C25708T, A26096G, A26492T, C27925A, C28005T, C28093T, A28272T, T28618A, C28887T, T29661G

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEUH-1725CCB/2021:

C14408T > C241T > C3037T > A23403G > G25563T > C26735T > C18877T > T26735C > C28005T, C28093T > A21993C, C27925A > T19035C > A23063T, C23604A > C10029T, C21993A, C28887T > C19035T > G23012A > C6037T, A11451G, C17491T, C20148T, C21846T > C4878T > A13057T, A21993C, T21995A > G22599A > T19035C > A26492T > A3428G, A28272T > C25708T > T28618A > G19481T > C3173A > G2945A > C7764T > A26096G > C18329T, C20574T > T10654C > C16101T > T29661G

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: USA/FL-BPHL-11620/2021|OL417224.1|2021-06-19: lineage [B.1.621](#)

Subtree 14: Unrelated sample

[view subtree 14 in Nextstrain](#)

Scotland/QUEUH-1585B0A/2021

Differences from the reference genome ([NC_045512.2](#)): G204T, C241T, C913T, C2453T, C3037T, C3267T, C5986T, A6319G, T6954C, G8179A, C13329T, C14676T, C15279T, T16176C, A20379G, C22388T, A23063T, C23271A, A23403G, C23604A, C23709T, T24506G, G24914C, C25162T, T26551C, C27972T, G28048T, A28111G, G28280C, A28281T, T28282A, G28881A, G28882A, G28883C, C28977T

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEUH-1585B0A/2021:

C14408T > C241T > C3037T > A23403G > G25563T > C26735T > C18877T > T26735C > C28005T, C28093T > A21993C, C27925A > T19035C > A23063T, C23604A > C10029T, C21993A, C28887T > C19035T > G23012A > C6037T, A11451G, C17491T, C20148T, C21846T > C4878T > A13057T, A21993C, T21995A > G22599A > T19035C > A26492T > A3428G, A28272T > C25708T > T28618A > G19481T > C3173A > G2945A > C7764T > A26096G > C18329T, C20574T > T10654C > C16101T > T29661G

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: Scotland/QUEUH-1578997/2021|OU283041.1|2021-05-11: lineage [B.1.1.7](#)

Subtree 15: Unrelated sample

[view subtree 15 in Nextstrain](#)

Scotland/QUEUH-158D786/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, T400C, T786A, C913T, C2704T, C3037T, C3267T, C4543T, G5023R, C5388A, C5986T, T6954C, T7232Y, G8084A, C11497T, C14408T, C14676T, C15279T, T16176C, A17615G, A23063T, C23271A, A23403G, C23604A, C23709T, T24506G, G24914C, C27881T, C27972T, G28048T, A28111G, G28280C, A28281T, T28282A, C28708A, G28881A, G28882A, G28883C, C28977T, A29526G, T29789A

Base values imputed by parsimony:

- 5023: G
- 7232: T

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEUH-158D786/2021:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C884T > T28282A > T884C, G28280C, A28281T > A23063T > C15279T > C28977T > A28111G > T23063A > C913T > C5986T > C23709T > T6954C, A23063T > C23604A > C23271A > G24914C > T24506G > T16176C > C27972T > C14676T > C3267T > C5388A > G28048T > C2453T > T26551C > C22388T > C16293T > C13329T > A6319G > G204T, G8179A, C25162T > A20379G

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: Scotland/QUEUH-156AF3C/2021|OU279463.1|2021-05-08: lineage [B.1.1.7](#)

Subtree 16: Unrelated sample

[view subtree 16 in Nextstrain](#)

Scotland/CAMC-14DE972/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, C1059T, C3037T, A3069G, C9207T, T9867C, C14408T, A16500C, A20262G, C21846T, A22320G, G23012A, A23403G, C23664T, G25489T, C25517T, G25563T, C27925T, C28869T, G28975A

Mutations along the path from the root of the phylogenetic tree to Scotland/CAMC-14DE972/2021:

C14408T > C241T > C3037T > A23403G > G25563T > C1059T > A10323G > C28869T > G10323A > C23664T > G28975A > C25517T > T9867C, A20262G > A22320G > C21846T > A16500C > G23012A > C27925T > C9207T > G25489T > A3069G

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: USA/PA-CDC-STM-000041666/2021|MW891419.1|2021-03-21: lineage [B.1.526](#)

Subtree 17: Unrelated sample

[view subtree 17 in Nextstrain](#)

Scotland/QUEUH-147E6F5/2021

Differences from the reference genome ([NC_045512.2](#)): G210T, C241T, C835T, C2704Y, C3037T, C3457T, C4965T, A11201G, C14408T, G16591C, G16852T, G17523T, A20396G, T20401G, T21570G, C21846T, T21895C, G22022A, A22259R, T22917G, G23012C, C23277T, A23403G, C23604G, A24775T, C25469T, G25644T, C26681T, T26767G, T27638C, G28166A, C28638Y, G28881T, G29395C, G29402T, G29742T

Base values imputed by parsimony:

- 2704: C
- 22259: A
- 28638: C

Mutations along the path from the root of the phylogenetic tree to Scotland/QUEUH-147E6F5/2021:

C14408T > C241T > C3037T > A23403G > G29742T > T22917G > T27638C > G28881T > C21618G > G210T > G29402T > C23604G > G21618C > C25469T > G23012C > T21895C > C4965T > A24775T > G17523T > C26681T, T26767G > C3457T, A11201G > A20396G > G22022A > G16852T > T20401G > C21846T > A28271T > C835T > T28271A > T21570G > G28166A > C23277T > G16591C > G25644T > G29395C

Nearest neighboring GISAIID and/or public sequence already in phylogenetic tree: Scotland/QUEUH-14C89B7/2021|OU242784.1|2021-04-02: lineage [B.1.617.1](#)

Subtree 18: Unrelated sample

[view subtree 18 in Nextstrain](#)

Scotland/QUEUH-13ADEF6/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, C1498T, A1807G, G2659A, C3037T, C6285T, T8593C, C9565T, A12814G, C14407T, C14408T, C17172T, C18171T, A20724G, A21717G, C21762T, G23012A, A23403G, G23593C, T24224C, C24748T, C26305T, T26767C, C28308G, A28699G, C28887T, G29543T

Mutations along the path from the root of the phylogenetic tree to Scotland/QEUH-13ADEF6/2021:

C14408T > C241T > C3037T > A23403G > C28887T > T26767C > G23593C > C28308G, A28699G > A21717G > C26305T > T24224C > C24748T > G23012A > C1498T, C18171T, G29543T > C9565T > A1807G, T8593C > G2659A > C6285T, T9565C > C14407T > A20724G > C9565T > T11296G > C17172T > A12814G > Scotland/QEUH-13ADEF6/2021: C21762T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QEUH-13ADC1A/2021|OU060759.1|2021-03-08: lineage [B.1.525](#)

Subtree 19: Unrelated sample

[view subtree 19 in Nextstrain](#)

Scotland/QEUH-138F944/2021

Differences from the reference genome ([NC_045512.2](#)): C241T, T733C, C2749T, C3037T, C3828T, C4999T, A5648C, A6319G, A6613G, C11195T, C12778T, C13860T, C14408T, G17259T, C21614T, C21621A, C21638T, G21974T, G22132T, C22636T, A22812C, G23012A, A23063T, A23403G, C23525T, C24642T, G25088T, T26149C, C26455T, G28167A, C28512G, A28877T, G28878C, G28881A, G28882A, G28883C

Mutations along the path from the root of the phylogenetic tree to Scotland/QEUH-138F944/2021:

C14408T > C241T > C3037T > A23403G > G28881A > G28883C > G28882A > C23525T > G23012A > G25088T > A6613G > T26149C > A22812C, A23063T > G21974T, A28877T, G28878C > C28512G > C13860T, G17259T > C12778T > A5648C > G28167A > C3828T > C24642T > T733C > A6319G > C2749T > C22812A > G22132T > C21614T > C21621A > C21638T > A22812C > C26455T > C11195T > C4999T > C22636T

Nearest neighboring GISAID and/or public sequence already in phylogenetic tree: Scotland/QEUH-138F944/2021|OU061529.1|2021-03-03: lineage [P.1](#)

Downloads

- [SARS-CoV-2 phylogenetic tree with your samples \(Newick file\)](#)
- [TSV summary of sequences and placements](#)
- [TSV summary of S \(Spike\) gene changes](#)
- [ZIP archive of subtree Newick and JSON files](#)
- [Subtree with Scotland/LSPA-3E62463/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/LSPA-3E62463/2022 \(JSON file\)](#)
- [Subtree with Scotland/LSPA-3E3B700/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/LSPA-3E3B700/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-3DC59CA/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-3DC59CA/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-3D90306/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-3D90306/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-3D43C43/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-3D43C43/2022 \(JSON file\)](#)
- [Subtree with Scotland/CVR14531/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/CVR14531/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-36897FC/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-36897FC/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-36491AF/2022 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-36491AF/2022 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-2D86BD1/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-2D86BD1/2021 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-2D7F704/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-2D7F704/2021 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-1BA3933/2021 \(Newick file\)](#)
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- [Subtree with Scotland/QEUH-1725CCB/2021 \(Newick file\)](#)
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- [Subtree with Scotland/QEUH-1585B0A/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-1585B0A/2021 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-158D786/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-158D786/2021 \(JSON file\)](#)
- [Subtree with Scotland/CAMC-14DE972/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/CAMC-14DE972/2021 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-147E6F5/2021 \(Newick file\)](#)
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- [Subtree with Scotland/QEUH-13ADEF6/2021 \(Newick file\)](#)
- [Auspice JSON for subtree with Scotland/QEUH-13ADEF6/2021 \(JSON file\)](#)
- [Subtree with Scotland/QEUH-138F944/2021 \(Newick file\)](#)
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Added custom track of uploaded samples.

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