TESSy - The European Surveillance System

Integrated respiratory virus surveillance: RESPISEVERE/RESPISURV/RESPIAGGR Reporting Protocol Version 1.5, 14 August 2023

Contents

Summary of changes to current metadata

V1.5 (14 August 2023)

- Updated coded value list for the variable VirusVariant (for RESPISURV) for reporting of XBB.1.5-like+F456L (XBB.1.5-like lineages (spike mutations Q183E, F486P, F490S) with additional spike mutation F456L)
- Removal of the coded value for XBB (Pango lineage XBB and sub-lineages, excluding XBB.1.5 and its sub-lineages)

V1.4 (21 July 2023)

- Launch of RESPIAGGR
- Updated coded value list for the variable Indicator (for RESPISEVERE) for reporting of deaths (DEATH)

V1.3 (13 January 2023)

- Updated coded value list for the variable VirusVariantCOVID (for RESPISURV) for reporting of XBB.1.5 (Pango lineage XBB with additional mutation S486P. Mutational proxy: Spike: Q183E, F486P, F490S) and modification to the definition of XBB (Pango lineage XBB and sub-lineages, excluding XBB.1.5 and its sub-lineages)

V1.2 (13 December 2022)

- Updated coded value list for the variable VirusVariantCOVID (for RESPISURV) for reporting of XBB (Pango lineage XBB and sub-lineages).

V1.1 (October 2022)

- New influenza strains added to coded value lists in AntigenicGroup and GeneticClade.
- BQ.1 (Pango lineage BQ.1 and sub-lineages) added to coded value list VirusVariantNCOV [27 October 2022]

How to use this document

This Reporting Protocol provides information for reporting countries' data managers in three main sections:

- *Reporting to TESSy* – contains guidelines on how to prepare data for submission to TESSy, deadlines for data submission, subject-specific information (e.g. new changes to metadata), and links to further information.
- *Annex* – contains:
    - The metadata set for the subject(s) covered by this Reporting Protocol.

Finding further information

Paragraphs denoted by the information icon tell where you can find further information.

Updated links to all the schedules, documentation and training materials mentioned in this Reporting Protocol are included in the *TESSy Technical Guidelines & Tools* (see the menu 'Technical Guidelines and Tools' when logged in TESSy), including:

- Metadata sets and history.
- Tutorials for data transformation using respectively Excel and Access.
- TESSy user documentation.
- *CSV* and *XML* transport protocols.

Copyright

Introduction

This Reporting Protocol describes integrated data collection for influenza, SARS-CoV-2, and potentially other respiratory viruses (such as RSV or new viruses of public health concern) in the EU/EEA and wider WHO European Region. It includes two integrated record-types:

1. **RESPISURV** for reporting of **case-based data by pathogen** for cases meeting one or more of the following criteria:
    - Positive cases presenting to primary care sentinel surveillance systems (where data are available in case-based format)
    - Cases that have been sequenced or genotyped (SARS-CoV-2) or (sub)typed/lineage determined (influenza) irrespective of disease severity
    - Data on severe cases (hospitalised, requiring respiratory support, ICU admission or fatal) that are not covered by existing SARI surveillance systems (and therefore reported into SARISURV), irrespective of whether variant/type/lineage is available

    Data reported into RESPISURV should ideally link laboratory and case information including virus characterisation and antiviral resistance data. Unlinked data can be reported to INFLANTIVIR if not possible to report to RESPISURV for the season 2022/23, however double reporting should be minimized as much as possible.
2. **RESPISEVERE** for reporting of **age-disaggregated hospital and ICU indicators** (new admissions, numbers of current inpatients and deaths due to respiratory illness associated with the pathogen), aggregated by week, indicator, and pathogen.
3. **RESPIAGGR** for reporting of **age-disaggregated detections and tests from sentinel and non-sentinel surveillance system** by week and pathogen.

Please note that:

1. All data collected are shared with the World Health Organisation – Regional Office for Europe (WHO/Europe) on a daily basis to fulfil Member States reporting requirements to WHO. Duplicate reporting is therefore not required.
2. If data have not been uploaded in TESSy and approved on time it will not be possible to include the data in weekly reports. If you are unable to meet this deadline, please contact the ECDC Influenza and other respiratory viruses surveillance team (*ecdc.influenza@ecdc.europa.eu* , *covid.surveillance@ecdc.europa.eu*, and copy *tessy@ecdc.europa.eu*).
3. Case-based data on human infections with zoonotic influenza viruses should be reported to **INFLZOO** metadata set and aggregated to **INFLZOOAGGR**.
4. Aggregated and case-based data from SARI surveillance systems should be reported to **INFLSARIAGGR, SARISURV** and denominator data to **SARIDENOM**.
5. Case-based data from laboratory-based surveillance on influenza-confirmed patients in hospitals should continue to be reported to **INFLSARI**.

Definitions

Case definition: Cases should be reported according to the current *EU case definition*. Data on probable and possible cases are not collected.

Definition of a hospitalised case: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to a hospital or ICU/HDU facility. Patients admitted to hospital for isolation purposes and not because of clinical need should not be counted as hospitalised cases where it is possible to make a distinction.

Definition of a case admitted to an intensive care unit (ICU) or a high dependency unit (HDU)[1]: A patient who has tested positive for COVID-19 (within 14 days prior to admission or during

[1] *High dependency unit: a unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward*

the current admission) presenting with severe symptoms/complications from COVID-19 that require admission to an ICU/HDU facility.

For reporting the number of current hospital or ICU/HDU in-patients (to RESPISEVERE), COVID-19 cases in hospital or ICU/HDU should continue to be counted even after they test negative provided the current hospital or ICU/HDU stay is a consequence of the COVID-19 infection. Weekly counts are estimated based on the number in hospital or ICU/HDU as of Wednesday for the week of reporting.

Aim

To support the timely and complete reporting of key information for influenza, COVID-19, and potentially other respiratory virus infections (such as RSV or new viral diseases of public health concern).

Objectives

1. Monitor the intensity, geographical spread and temporal patterns of influenza, COVID-19, and other respiratory virus infections to inform mitigation measures.

2. Monitor severity, risk factors for severe disease, and assess the impact on healthcare systems of influenza, COVID-19, and other respiratory virus infections to inform mitigation measures.

3. Monitor changes and characteristics of circulating and emerging respiratory viruses, particularly virological changes of influenza viruses, SARS-CoV-2, and other respiratory viruses to inform treatment, drug, and vaccine development.

4. Describe the burden of disease associated with influenza, COVID-19, and other respiratory virus infections.

Reporting to TESSy

When, what and how to report

Deadline for reporting:

Please note that prior to the 2023/2024 season reporting deadline will be aligned for all pathogens. Until then the current reporting deadline apply:

> **COVID-19:** Tuesday 23:59 for NCOVAGGR, NCOVVARIANT, NCOVTEST, RESPISEVERE, RESPIAGGR, and RESPISURV. Thursday 10:00 for all SARI recordtypes. Further detail on reporting of COVID-19 can be found on the *ECDC website*.
>
> **Influenza and RSV**: Thursday 10:00 for all recordtypes. Further detail on reporting of Influenza can be found on the on the *ECDC website.*

Preparing data

Data may be entered directly in TESSy for individual records ('Manually create a record'). For any batch reporting by file upload (CSV or XML format) please note that once the data has been exported from your national database it needs to be in a format that TESSy can accept (see 'checking metadata').

Checking metadata

The TESSy metadata define the fields and valid data formats for input to TESSy for a given subject.

To ensure data can be saved correctly in TESSy, please check the data are correctly formatted according to the most recent metadata set.

Changes to the metadata for the subject of this Reporting Protocol are described in:

- *Changes to current metadata* – changes since the last Reporting Protocol.
- *Annex Metadata change history* – all preceding changes.

It is especially important to focus on:

Field formats

> Many fields require that data are formatted in a specific way. For example, dates must be in the **YYYY-MM-DD** format; dates in the DD/MM/YYYY format will be rejected.

Coded values

> Some fields only permit the use of specific values (coded values). For example, **M**, **F**, **UNK**, or **Other** are the coded values for *Gender* and any other value in a *Gender* field will be rejected.

The metadata file contains all the definitions and rules you need to comply with to format your data correctly for every subject (usually a disease). The file can be downloaded as an Excel file from the TESSy documents website.

By filtering the fields in the file by subject, you can see the fields required for your subject and the rules applying to these fields.

The *Tessy User Guide* provides an overview of how you work with the metadata file, and the TESSy user documentation provides in-depth details on metadata.

Submitting your data

Data are submitted through the TESSy web interface (go to **Upload**). Previously reported data can be found through the review tab (see below).

The *Tessy User Guide* provides an overview of how you submit files to TESSy and in-depth descriptions of all the upload methods.

Finalising your submission

The compliance of your data with the validation rules in the metadata is checked automatically during the data upload process.

The result of your upload – i.e. rejected or validated – is displayed immediately after the check in the **Validation details** webpage has completed. Please review the result carefully:

- If your file has been rejected, there will be a message explaining each instance of non-compliance with the metadata that you need to correct.
- If your file has been validated, there might be warnings and remarks relating to possible data quality issues or to potential overwriting of existing records that you should consider.

When you file has been validated and you are satisfied that all corrections have been made, please ensure prompt approval – unapproved uploads can block the approval of other uploads.

- The TESSy user documentation provides information on reviewing validation results and adjusting reporting periods to avoid overwriting existing records.
- General training and guidance on reporting is available on the *TESSy website*. A training video on reporting COVID-19 data is available in the *ECDC virtual academy*.

TESSy HelpDesk

Email:	*TESSy@ecdc.europa.eu*
Telephone number:	**+46-(0)8-5860 1601**
Availability:	9:00 – 16:00 Stockholm time, Monday to Friday (except ECDC Holidays)

Annex – Integrated Respiratory viral disease metadata

Revisions of the integrated respiratory viral disease metadata sets

The most recent metadata set is available from the TESSy website under technical guidelines and tools tab (as shown below).

Metadata sets

Current record type versions

Table 1 shows the record type versions to be used when reporting integrated respiratory viral disease (Record type: RESPI) data to TESSy.

Table 1: RESPI record type versions

Record type	Type of data	Record type version
RESPIAGGR	Case-based[2]	1
RESPISURV	Case-based	1
RESPISEVERE	Case-based[2]	1

RESPIAGGR metadata record type version 1

The **RESPIAGGR** metadata, record type version 1 is used for reporting of **age-disaggregated sentinel and non-sentinel indicators** (tests and detections) for influenza, SARS-CoV-2 and RSV. Data reported to RESPIAGGR should have the surveillance type, pathogen, influenza type/subtype and RSV type specified.

Common TESSy variables

Record id (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national respiratory virus diseases surveillance system
- anonymous.

[2]RESPISEVERE and RESPIAGGR are "case-based" record types as they allow multiple rows for the same week. However, the number of hospital/ICU/HDU admissions or current inpatients (RESPISEVERE) and the number of tests/detections (RESPIAGGR) are reported in an aggregated way.

Record type (mandatory)

Field: RecordType

Coding: RESPIAGGR

The record type defines the structure and the format of the data reported (case based reporting or aggregate reporting). The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: Numeric

The version of the record type defines the current structure of the data reported. If no RecordTypeVersion is provided in the batch, it is set automatically with current version of the Record type.This variable is not mandatory as TESSy concludes the record type version from the metadata set indicated by default. However, RecordTypeVersion is required when no metadata set is provided at upload or when a RecordTypeVersion, other than the current one, needs to be used.

Subject (mandatory)

Field: Subject

Coding: RESPIAGGR

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource

Coded value list name: [Data sources]

Coding: Can be created/ modified by the National Coordinator

The data source specifies the source from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. If needed multiple data sources per country can be entered by different users to facilitate reporting.

Status (mandatory)

Field: Status

Coded value list name: [Statuses]

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Report a new or update a previously reported record (default).

The field 'Status' is used for updating data; the default is NEW/UPDATE. By choosing DELETE the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Reporting country (mandatory)

Field: ReportingCountry

Coded value list name: [Countries]

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week for which the reported data refers. This is the date used by the national surveillance institute/organisation in reports and official statistics. The date used for statistics can vary from country to country but is it is preferably the date the case was notified to the national health authorities (notification date). For RESPIAGGR, the date should ideally be based on the date of sample.

Epidemiological variables

Age 00-04

Field: Age00-04

Coding: Numeric

Number of patients for age group 0-4 years corresponding to the reported indicator, newly reported for week of reporting.

Age 05-14

Field: Age05-14

Coding: Numeric

Number of patients for age group 05-14 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-29

Field: Age15-29

Coding: Numeric

Number of patients for age group 15-29 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-64

Field: Age15-64

Coding: Numeric

Number of patients for age group 15-64 years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 15-29 and 30-64 separately.

Age 30-64

Field: Age30-64

Coding: Numeric

Number of patients for age group 30-64 years corresponding to the reported indicator, newly reported for week of reporting.

Age 65+

Field: Age65+

Coding: Numeric

Number of patients for age group 65+ years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 65-79 and 80+ separately.

Age 65-79

Field: Age65-79

Coding: Numeric

Number of patients for age group 65-79 years corresponding to the reported indicator, newly reported for week of reporting.

Age 80+

Field: Age80+

Coding: Numeric

Number of patients for age group 80+ years corresponding to the reported indicator, newly reported for week of reporting.

Age UNK

Field: AgeUnk

Coding: Numeric

Number of patients with unknown age, newly reported for week of reporting.

Indicator (mandatory)

Field: Indicator

Coded value list name: Indicator

Coding: Tests

Detection

Selected indicator to report either tests or detections.

Surveillance type (mandatory)

Field: SurvType
Coded value list name: SurvSystem
Coding: NONSTL = Non-sentinel
STL = Sentinel

Type of surveillance system through which the detections/ tests was notified.

Pathogen (mandatory)
Field: PathogenRESPI
Coded value list name: Pathogen
Coding: INFL = Influenza virus
MERS = MERS-CoV
RSV = Respiratory syncytial virus
SARSCOV2 = SARS-CoV-2
O = Other

Pathogen associated with tests or detections. If selecting Other, please specify which pathogen in Pathogen – Other.

Pathogen – Other
Field: PathogenOther
Coding: Text

Specified pathogen not captured in the coded values for Pathogen.

Influenza Type Subtype

Field- InfluenzaTypeSubtype
Coding: VirusTypeSARI:
A = A, not sub-typed
AH3 = A(H3), not N sub-typed
AH3N2 = A(H3N2)
B = B, lineage not determined
BVic = Influenza type B, Victoria lineage
BYam = Influenza type B, Yamagata lineage
PanAH1 = A(H1) pdm09
PanAH1N1 = A(H1N1) pdm09
UNK = Unknown
Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection.

RSV type
Field: RSVType
Coded value list name: RSVType
Coding: A
B
UNK

RSV type to be reported where RSV is reported for the variables Pathogen.

RESPISEVERE metadata record type version 1

Common TESSy variables

Record id (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national respiratory virus diseases surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: RESPISEVERE

The record type defines the structure and the format of the data reported (case based reporting or aggregate reporting). The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: Numeric

The version of the record type defines the current structure of the data reported. If no RecordTypeVersion is provided in the batch, it is set automatically with current version of the Record type. The current version of the RESPISEVERE record type is 1.

This variable is not mandatory as TESSy concludes the record type version from the metadata set indicated by default. However, RecordTypeVersion is required when no metadata set is provided at upload or when a RecordTypeVersion, other than the current one, needs to be used.

Subject (mandatory)

Field: Subject

Coding: RESPISEVERE

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource

Coding: Can be created/ modified by the National Coordinator

The data source specifies the source from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. If needed multiple data sources per country can be entered by different users to facilitate reporting.

Status (mandatory)

Field: Status

Coded value list name: [Statuses]

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Report a new or update a previously reported record (default).

The field 'Status' is used for updating data; the default is NEW/UPDATE. By choosing DELETE the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Reporting country (mandatory)

Field: ReportingCountry

Coded value list name: [Countries]

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week for which the reported data refers. This is the date used by the national surveillance institute/organisation in reports and official statistics. The date used for statistics can vary from country to country but is it is preferably the date the case was notified to the national health authorities (notification date). For RESPISEVERE, the date should ideally be based on the date of admission to hospital or ICU for the week in which the Wednesday fell that was used for estimation of the number of current inpatients in hospital or ICU/HDU (see Indicator variable).

Epidemiological variables

Age 00-04

Field: Age00-04

Coding: Numeric

Number of patients for age group 0-4 years corresponding to the reported indicator, newly reported for week of reporting.

Age 05-14

Field: Age05-14

Coding: Numeric

Number of patients for age group 05-14 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-29

Field: Age15-29

Coding: Numeric

Number of patients for age group 15-29 years corresponding to the reported indicator, newly reported for week of reporting.

Age 15-64

Field: Age15-64

Coding: Numeric

Number of patients for age group 15-64 years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 15-29 and 30-64 separately.

Age 30-64

Field: Age30-64

Coding: Numeric

Number of patients for age group 30-64 years corresponding to the reported indicator, newly reported for week of reporting.

Age 65+

Field: Age65+

Coding: Numeric

Number of patients for age group 65+ years corresponding to the reported indicator, newly reported for week of reporting. Please only use this reporting type if data are not report for 65-79 and 80+ separately.

Age 65-79

Field: Age65-79

Coding: Numeric

Number of patients for age group 65-79 years corresponding to the reported indicator, newly reported for week of reporting.

Age 80+

Field: Age80+

Coding: Numeric

Number of patients for age group 80+ years corresponding to the reported indicator, newly reported for week of reporting.

Age UNK

Field: AgeUnk

Coding: Numeric

Number of patients with unknown age, newly reported for week of reporting.

Indicator (mandatory)

Field: Indicator

Coded value list name: Indicator

Coding: HOSAD = Weekly hospital admissions due to respiratory illness associated with the pathogen

HOSINPAT = Current inpatients in hospital due to respiratory illness associated with the pathogen as of Wednesday for the week of reporting

ICUAD = Weekly ICU admissions due to respiratory illness associated with the pathogen

ICUINPAT = Current inpatients in ICU/HDU due to respiratory illness associated with the pathogen as of Wednesday for the week of reporting

DEATH = Weekly deaths due to respiratory illness associated with the pathogen

Selected indicator due to respiratory illness associated with the pathogen

Pathogen (mandatory)

Field: Pathogen

Coded value list name: PathogenRESPI

Coding: INFL = Influenza virus

MERS = MERS-CoV

RSV = Respiratory syncytial virus

SARSCOV2 = SARS-CoV-2

O = Other

Pathogen associated with severity indicator. If selecting Other, please specify which pathogen in Pathogen – Other.

Pathogen – Other

Field: PathogenOther

Coding: Text

Specified pathogen not captured in the coded values for Pathogen.

RESPISURV metadata

The RESPISURV metadata, **recordtype version 1** is used for case-based data by pathogen for cases meeting one or more of the following criteria: (1) Positive cases presenting to primary care sentinel surveillance systems (where data are available in case-based format); (2) Cases that have been sequenced or genotyped (SARS-CoV-2) or (sub)typed/lineage determined (influenza) irrespective of disease severity; (3) Data on severe cases (hospitalised, requiring respiratory support, ICU admission or fatal) that are not covered by existing SARI surveillance systems (and therefore reported into SARISURV), irrespective of whether variant/type/lineage is available.

Data reported into RESPISURV should ideally link laboratory and case information including virus characterisation and antiviral resistance data. Unlinked data can be reported, however double reporting should be minimized as much as possible. If not possible to report influenza virus characterisation data to RESPISURV, it is possible to continue reporting strain-based data to INFLANTIVIR for the season 2022/23.

Irrespective of case-based data reporting to RESPISURV, all countries should report aggregated data by week for COVID-19 and Influenza.

Common TESSy variables

Record id (mandatory)

Field: RecordId

Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It must be:

- unique within the national respiratory virus diseases surveillance system
- anonymous.

Record type (mandatory)

Field: RecordType

Coding: RESPISURV = Respiratory virus surveillance

The record type defines the structure and the format of the data reported (case based reporting or aggregate reporting). The record types are defined by ECDC and are related to the subject. Only valid combinations of subject, record type and data source are accepted.

Record type version

Field: RecordTypeVersion

Coding: Numeric

The version of the record type defines the current structure of the data reported. If no RecordTypeVersion is provided in the batch, it is set automatically with current version of the Record type. The current version of the RESPISEVERE record type is 1.

This variable is not mandatory as TESSy concludes the record type version from the metadata set indicated by default. However, RecordTypeVersion is required when no metadata set is provided at upload or when a RecordTypeVersion, other than the current one, needs to be used.

Subject (mandatory)

Field: Subject

Coding: RESPISURV = Respiratory virus surveillance

The subject describes the data to be reported.

Data source (mandatory)

Field: DataSource

Coding: Can be created/ modified by the National Coordinator

The data source specifies the source from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. If needed multiple data sources per country can be entered by different users to facilitate reporting.

Status (mandatory)

Field: Status

Coded value list name: [Statuses]

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Report a new or update a previously reported record (default).

The field 'Status' is used for updating data; the default is NEW/UPDATE. By choosing DELETE the selected record (or batch of data) will remain in TESSy but be marked as inactive; this data can be used to reconstruct data for a given date in the past.

Reporting country (mandatory)

Field: ReportingCountry

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

This variable identifies the country reporting the case.

Date used for statistics (mandatory)

Field: DateUsedForStatistics

Coding: yyyy-mm-dd (preferred)
yyyy-Www

This is the date used by the national surveillance institute/organisation in reports and official statistics. The date used for statistics can vary from country to country but is it is preferably the date the case was notified to the national health authorities (notification date). If date of notification is not available, then date of onset or date of sample collection can be used instead. Where date of onset and/or date of sample collection are available then please also report these fields separately as these are most useful for epidemiological analysis.

Epidemiological variables

Age

Field: Age

Coding: Numerical (0-120)
UNK = Unknown

Age of patient in years as reported in the national system at the time of disease onset.

Age in months

Field: AgeMonth

Coding: Numerical (0-23)
NA = Not applicable
UNK = Unknown

Age of patient in months as reported in the national system for cases <2 years of age at the time of disease onset.

Brand of last received COVID-19 vaccination dose

Field: BrandLastCOVID19Dose

Coded value list name: VaccineCOVID

Coding:

AZ = Vaxzevria – AstraZeneca
BECNBG = Inactivated – Beijing CNBG
BHACOV = Covaxin – Bharat
CAN = CanSino -Convidecia
CHU = Chumakov - Covi-Vac
COM = Comirnaty – Pfizer/BioNTech

COMBA.1 = Comirnaty – Pfizer/BioNTech Original/Omicron BA.1
COMBA.4-5 = Comirnaty – Pfizer/BioNTech Original/Omicron BA.4-5
CVAC = Curevac - CVnCOV
HAYATVAC = Hayat VAC
JANSS = Ad26.COV 2.5 – Janssen
MOD = mRNA-1273 – Moderna
MODBA.1 = Spikevax Moderna bivalent Original/Omicron BA.1
MODBA.4-5 = Spikevax Moderna bivalent Original/Omicron BA.4-5
NVX = Novavax – Covovax
NVXD = Novavax – Nuvaxovid
QAZVAQ = QazCovid-In
SGSK = Sanofi GSK - Subunit
SIICOV = Covishield – SII
SIN = Coronavac – Sinovac
SPU = Sputnik V – Gamaleya
SPUL = Gamaleya - Sputnik-Light
SRCVB = EpiVacCorona – SRCVB
UNK = Unknown
VLA = COVID-19 Vaccine (inactivated, adjuvanted) Valneva – Valneva
WUCNBG = Inactivated – Wuhan CNBG
ZFUZ = Sino-Uzbek - ZF-UZ-VAC
ZIF = Anhui ZL – Zifivax

Brand/Type of last received COVID-19 vaccination dose

Coinfection
Field: Coinfection
Coded value list name: PathogenRESPI
Coding: INFL = Influenza virus
MERS = MERS-CoV
O = Other
RSV = Respiratory syncytial virus
SARSCOV2 = SARS-CoV-2

Viral pathogen detected at the same time point (i.e., in the same specimen or within a 14-day timeframe). For SARS-CoV-2 and influenza co-infections, the variables Pathogen and Coinfection should be used to indicate these two pathogens, with VirusVariantCOVID and InfluenzaTypeSubtype used to specify the SARS-CoV-2 variant and influenza (sub)type/lineage.

Coinfection – Other
Field: CoinfectionOther
Coding: Text
UNK = Unknown

Specified pathogen not captured in the coded values for Coinfection.

Complications
Field: Complications
Coded value list name: ComplicationsNCOV
Coding: AKI = Acute renal injury
ARDS = Acute respiratory distress syndrome
BRONCH = Bronchiolitis
ENCEPH = Encephalitis
HEARTFAIL = Heartfailure

MIS-C = Multisystem Inflammatory Syndrome in Children
MULTIFAIL = Multi-organ failure
MYOCARD = Myocarditis
NONE = None
O = Other (please specify separately)
OTHBAC = Other secondary bacterial infection
PNEU = Bacterial pneumonia (secondary)
SEPSIS = Sepsis
STILLBIRTH = Still birth as pregnancy outcome in a case
UNK = Unknown

Complication associated with illness. This variable can be repeated in the event of multiple complications.

Date last received COVID-19 vaccination dose

Field: DateLastVaccDose
Coding: yyyy-mm-dd
UNK= Unknown

Date last received COVID-19 vaccination dose.

Date of admission to hospital

Field: DateOfHospitalisation
Coding: yyyy-mm-dd
UNK = Unknown

Date of admission to hospital (exact date). If not applicable, please use 'UNK'.

Date of admission to Intensive Care Unit/High Dependency Unit

Field: DateOfICUHDU
Coding: yyyy-mm-dd
UNK = Unknown

Date of admission to intensive care unit or high dependency unit (exact date). If not applicable, please use 'UNK'.

Date of death

Field: DateOfDeath
Coding: yyyy-mm-dd
UNK = Unknown

Date of death (exact date). If not applicable, please use 'UNK'.

Date of hospital discharge

Field: DateOfDischarge
Coding: yyyy-mm-dd
UNK = Unknown

Date of discharge from hospital (exact date). If not applicable, please use 'UNK'.

Date of onset of disease

Field: DateOfOnset

Coding: yyyy-mm-dd
UNK = Unknown

Date of onset of symptoms (exact date). If not applicable, please use 'UNK'.

Drug Used for Prophylaxis

Field: DrugUsedProphylaxis

Coded value list name: DrugUsedRESPISURV

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
O = Other
UNK = Unknown

Antivirals used as prophylaxis in the 14 days before onset of illness. This variable can be repeated in the event of multiple drugs used.

Drug Used for Treatment

Field: DrugUsedTreatment

Coded value list name: DrugUsedRESPISURV

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
O = Other
UNK = Unknown

Antivirals used for treatment of the case during illness phase. This variable can be repeated in the event of multiple drugs used.

Gender

Field: Gender

Coded value list name: Gender

Coding: F = Female
M = Male
O = Other
UNK = Unknown

Gender of the reported case.

Health care worker
Field: HealthCareWorker
Coded value list name: YesNoUnk
Coding: N = No
UNK = Unknown
Y = Yes

Information on whether the case is a healthcare worker or not.

Hospitalisation
Field: Hospitalisation
Coded value list name: YesNoUnk
Coding: N = No
UNK = Unknown
Y = Yes

Admission to hospital.

Influenza type and subtype
Field: InfluenzaTypeSubtype
Coded value list: VirusTypeSARI
Coding: A = Influenza A, not sub-typed
PanAH1N1 = A(H1N1)pdm09
PanAH1 = A(H1)pdm09, not N-typed
AH3N2 = A(H3N2)
AH3 = A(H3), not N-typed
B = Influenza B no lineage
BVic = Influenza type B, Victoria lineage
BYam = Influenza type B, Yamagata lineage
UNK = Unknown or not applicable (where Pathogen is not Influenza)

Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection

Influenza vaccinated current season
Field: InfluenzaVaccinated
Coded value list name: YesNoUnk
Coding: N = No
UNK = Unknown
Y = Yes

Received influenza vaccination in the most recent influenza season.

Intensive care
Field: IntensiveCare
Coded value list name: YesNoUnk
Coding: N = No

UNK = Unknown
Y = Yes

Case required care in an intensive care unit or high dependency unit (unit with capabilities for more intensive observation, treatment and nursing care than can be provided on a regular ward).

Number of COVID-19 vaccination dose received

Field: NumberOfCovid19VaccDose
Coding: Numeric

Number of COVID-19 vaccination doses received.

Outcome

Field: Outcome
Coded value list name: OutcomeRESPI
Coding: ALIVE = Alive, recovered, cured, discharged from hospital
DIED = Died, as a result of viral respiratory infection
DIEDOTH = Died, other
STILLTREATMENT = Still on medical treatment related to viral respiratory infection (not recovered)
UNK = Unknown outcome

Outcome refers to the patient's vital status resulting from viral respiratory infection (indicated pathogen). If death occurred due to another disease or reason, 'DIEDOTHER' should be reported. If the patient is still ill at the time of reporting, code the outcome as 'STILLTREATMENT'. The outcome should be updated when the patient's final outcome is known.

Pathogen (mandatory)

Field: Pathogen
Coded value list name: PathogenRESPI
Coding: INFL = Influenza virus
MERS = MERS-CoV
O = Other
RSV = Respiratory syncytial virus
SARSCOV2 = SARS-CoV-2

This variable identifies the primary pathogen identified. If multiple pathogens were identified, please use the variable Coinfection to specify the second pathogen. For SARS-CoV-2 and influenza co-infections, the variables Pathogen and Coinfection should be used to indicate these two pathogens, with VirusVariantCOVID and InfluenzaTypeSubtype used to specify the SARS-CoV-2 variant and influenza (sub)type/lineage.

Pathogen - Other

Field: PathogenOther
Coding: Text
UNK = Unknown

Specified pathogen not captured in the coded values for Pathogen

Place of infection
Field: PlaceOfInfection
Coding: NUTS_GAUL

The probable place of infection should be provided at the NUTS 3 level. If the place of infection is not an EU/EEA country, then use GAUL nomenclature.

Place of residence
Field: PlaceOfResidence
Coding: NUTS_GAUL

Place of residence of patient at the time of disease onset. Select the most detailed NUTS for EU/EEA countries. If the residence of the case is not an EU/EEA country, then use GAUL nomenclature.

Precondition
Field: Precondition
Coded value list: Preconditions
Coding: ASPL = Asplenia
ASTH = Asthma
CANC = Cancer, malignancy
CARDIACDIS = Cardiac disorder, excluding hypertension
DIAB = Diabetes
HIV = HIV
HYPERT = Hypertension
IMMUNO = Immune deficiency
KIDNEY = Kidney-related condition, renal disease
LIVER = Liver-related condition, liver disease
LUNG = Chronic lung disease, excluding asthma
NEUROMUS = Neuromuscular disorder, chronic neurological
NONE = None
O = Other precondition
OBES = Obesity
PREG = Pregnancy, trimester is unknown
PREG1 = Pregnancy, 1st trim, the 1st trim is from week 1 to the end of week 12
PREG2 = Pregnancy, 2nd trim, the 2nd trim is from week 13 to the end of week 26
PREG3 = Pregnancy, 3rd trim, the 3rd trim is from week 27 to the end of the pregnancy
PREGPOST = Post-partum (<6 weeks)
SMOKE = Smoke
TB = Tuberculosis
UNK = Unknown precondition

Patient's underlying condition(s). This variable can be repeated in the event of multiple preconditions.

Primary care case definition
Field: CaseDefinitionPC
Coded value list: CaseDefinitionPCRESPISURV:
Coding: ARI = Acute respiratory infection
ILI = Influenza-like illness
OTH= Other
UNK = Unknown

Case definition used for cases detected through primary care sentinel surveillance.

Primary care case definition - Other

Field: CaseDefinitionPCOther

Coding: Text

UNK = Unknown

Specified case definition not captured in the coded values for Primary Care Case Definition.

Respiratory support

Field: RespSupport

Coded value list: RespSupportNCOV

Coding: ECMO = Extracorporeal membrane oxygenation

N = No

O = Other

OXYGEN = Oxygen therapy

UNK = Unknown

VENT = Ventilator including non-invasive pos pressure vent

Level of respiratory support given to patient

SARS-CoV-2 variant type

Field: VirusVariantCOVID

Coded value list: VirusVariantNCOV

Coding:

P.1 = P.1 variants (L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F)

S_GENE_DELETION = Variant virus with deletion in S-gene (defined by mutation: del 69-70 or by negative S-gene RT-PCR)

VARIANT_OTHER = Variants not included in the coded value list, please specify

B.1.525 = B.1.525 (mutations: E484K, D614G, Q677H)

B.1.427/B.1.429 = B.1.427/B.1.429 (mutations: L452R, D614G)

B.1.617.2 = B.1.617.2 (mutations: L452R, T478K, D614G, P681R); B.1.617.2 and all of its sublineages including AY sublineages

B.1.621 = B.1.621 (mutations: R346K, E484K, N501Y, D614G, P681H)

B.1.351 = B.1.351 (defined by mutations: D80A, D215G, E484K, N501Y, A701V)

B.1.1.7 = B.1.1.7 (mutations: del69-70, del144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H)

C.37= C.37 (mutations L452Q, F490S, D614G)

BA.1 = BA.1 or B.1.1.529 with mutations del69-70, ins214EPE, S371L, G496S, T547K

BA.2 = BA.2 or B.1.1.529 with mutations V213G, T376A, R408S

BA.2.75 = BA.2 sub-lineage with mutations D339H, G446S, N460K, and R493Q in the RBD, and mutations K147E, W152R, F157L, I210V, and G257S in the N-terminal domain of the Spike protein

BA.2+L452X = BA.2 and any of its sub-lineages with mutations at position 452 of the Spike protein

BA.3 = BA.3 or B.1.1.529 with mutations del69-70, ORF1a:A3657V, ORF3a:T22V

BA.4 = BA.4 or B.1.1.529 with mutations L452R, F486V, del69-70, NSP7b: L11F, N:P151S, ORF1a: Δ141-143

BA.5 = BA.5 or B.1.1.529 with mutations L452R, F486V, del69-70

BQ.1 = Pango lineage BQ.1 and sub-lineages

XBB.1.5 = Pango lineage XBB with additional mutation F486P. Mutational proxy: Spike: Q183E, F486P, F490S

XBB.1.5-like+F456L= XBB.1.5-like lineages (spike mutations Q183E, F486P, F490S) with additional spike mutation F456L

UNK = Sequence information unknown or not available

COVID-19 case with a variant virus of SARS-CoV-2 according to a mutation pattern of specific concern identified by sequence analysis or by a specific RT-PCR pattern. Each virus should only be reported once, using the most specific variant available, to avoid double reporting. If several apply, choose the most specific variant (highest number of matching mutations). The mapping of sublineages published at *https://www.ecdc.europa.eu/sites/default/files/documents/PathogenVariant_public_mappings.csv* should be used to determine how to assign specific sublineages to items in the coded value list above. Additional information about which specific sublineages have been mapped may optionally be provided in addition in VirusVariantCOVIDOther. Variants not included in the coded value list and/or which cannot be mapped to variants in the coded value list should be reported using VARIANT_OTHER with more details provided in VirusVariantCOVIDOther. If typing results are inconclusive, report UNK.

SARS-CoV-2 variant type - Other

Field: VirusVariantCOVIDOther

Coding: Text

UNK = Unknown

Specified variant type not captured in the coded values for VirusVariantCOVID variable as indicated in VARIANT_OTHER response for VirusVariantCOVID variable.

Sequencing category

Field: SequencingCategory

Coded value list: SequencingCategoryRESPISURV

Coding: REPSENTINEL = Representative, based on specimens from sentinel (primary care or SARI) surveillance

REPNONSENTINEL = Representative, based on a carefully selected subset of non-sentinel specimens

TARGETED = Targeted

UNK = Unknown

Sequencing category should be completed for samples where variant/subtype/type is known. Representative can be reported where the intention is to estimate the distribution of circulating variant/subtype/type in the population, based on samples taken in sentinel sites (REPSENTINEL) and/or from a carefully selected (representative) subset of non-sentinel specimens (REPNONSENTINEL), where this is needed to increase the volume of representative sequencing or genotyping to the desired detection threshold. Targeted sequencing can be reported for unusual events or clinical presentations, travel, outbreaks, etc.

Refer to *https://www.ecdc.europa.eu/en/publications-data/operational-considerations-respiratory-virus-surveillance-europe* for more details.

Surveillance system

Field: SurvSystem

Coded value list: SurvSystem

Coding: NONSTL = Non-sentinel

REG = Registry

STL = Sentinel

UNK = Unknown

Type of surveillance system through which the case was notified.

Laboratory variables

Antigenic group

Field: AntigenicGroup

Coded value list: AntigenicGroupINFL

Coding:

agAH1/Guangdong-Maonan/SWL1536/2019 = A(H1) A/Guangdong-Maonan/SWL1536/2019 (H1N1)-like

agAH1/Norway/25089/2022 = A(H1) A/Norway/25089/2022 (H1N1)-like

agAH1/Sydney/5/2021 = A(H1) A/Sydney/5/2021 (H1N1)-like

agAH1/Victoria/2570/2019 = A(H1) A/Victoria/2570/2019 (H1N1)-like

agAH1NOCAT = A(H1)pdm09 not attributed to category

agAH3/Cambodia/e0826360/2020 = A(H3) A/Cambodia/e0826360/2020-like

agAH3/Darwin/9/2021 = A(H3) A/Darwin/9/2021-like

agAH3/Denmark/3264/2019 = A(H3) A/Denmark/3264/2019 (H3N2)-like

agAH3/Kansas/14/2017 = A(H3) A/Kansas/14/2017 (H3N2)-like

agAH3NOCAT = A(H3) not attributed to category

agBVicB/Austria/1359417/2021 = B/Austria/1359417/2021-like (BVictoria/2/87 (V1A.3a.2)-lineage)

agBVicB/Brisbane/60/2008 = B/Brisbane/60/2008-like (B/Victoria/2/87 lineage)

agBVicB/Cote d'Ivoire/948/2020 = B/Cote d'Ivoire/948/2020-like (BVictoria/2/87 (V1A.3a.1)-lineage)

agBVicB/Netherlands/11267/2022 = B/Netherlands/11267/2022 (BVictoria/2/87 (V1A.3)-lineage)

agBVicB/Washington/02/2019 = B/Washington/02/2019-like (BVictoria/2/87 (V1A.3)-lineage)

agBVicNOCAT = B(Vic) lineage not attributed to category

agBYamB/Phuket/3073/2013 = B/Phuket/3073/2013-like (B/Yamagata/16/88 (Y3)-lineage)

agBYamNOCAT = B(Yam) lineage not attributed to category

Coded list of reference strains for influenza virus Antigenic group.

Date of sample collection

Field: DateOfSampleCollection

Coding: yyyy-mm-dd

UNK = Unknown

Date of collection of sample used for laboratory confirmation of the pathogen (exact date). If not available date of testing can be used (exact date). If not applicable, please use 'UNK'.

ENA identifier

Field: EnaId

Coding: Text

UNK = Unknown

European Nucleotide Archive (ENA) run identifier, based on which the sequence read data can be retrieved. Starts with ERR or SRR, i.e., not the sample or experiment which ERS/ERX or SRS/SRX.

Genetic clade

Field: GeneticClade

Coded value list: GeneticCladeINFL

Coding:

genAH1/Guangdong-Maonan/SWL1536/2019 = A(H1)pdm09 group 6B.1A.5a.1 representative A/Guangdong-Maonan/SWL1536/2019

genAH1/India/Pun-NIV312851/2021 = A(H1)pdm09 group 6B.1A.5a.2 representative A/India/Pun-NIV312851/2021

genAH1/Norway/25089/2022 = A(H1)pdm09 group 6B.1A.5a.2 representative A/Norway/25089/2022

genAH1/Slovenia/1489/2019 = A(H1)pdm09 group 6B.1A.7 repr, A/ Slovenia/1489/2019

genAH1/Sydney/5/2021 = A(H1)pdm09 group 6B.1A.5a.2 representative A/Sydney/5/2021

genAH1/Victoria/2570/2019 = A(H1)pdm09 group 6B.1A.5a.2 representative A/Victoria/2570/2019

genAH1NOClade = A(H1)pdm09 not attributed to clade

genAH1SubgroupNotListed = A(H1)pdm09 attributed to recognised group in the guidance but not listed here

genAH3/Bangladesh/4005/2020 = A(H3) group 3C.2a1b.2a.2 repr, A/Bangladesh/4005/2020

genAH3/Cambodia/e0826360/2020 = A(H3) group 3C.2a1b.2a.1 repr, A/Cambodia/e0826360/2020

genAH3/Darwin/9/2021 = A(H3) group 3C.2a1b.2a.2 representative A/Darwin/9/2021

genAH3/Denmark/3264/2019 = A(H3) group 3C.2a1b.1a representative A/Denmark/3264/2019

genAH3/Hong Kong/2671/2019 = A(H3) group 3C.2a1b.1b representative A/ Hong Kong/2671/2019

genAH3/Kansas/14/2017 = A(H3) group 3C.3a1 repr, A/ Kansas/14/2017

genAH3/Slovenia/8720/2022 = A(H3) group 3C.2a1b.2a.2 representative A/Slovenia/8720/2022

genAH3NOClade = A(H3) not attributed to clade

genAH3SubgroupNotListed = A(H3) attributed to recognised group in current guidance but not listed here

genBVicB/Austria/1359417/2021 = B(Vic)-lineage clade V1A.3a.2 repr, B/Austria/1359417/2021

genBVicB/Cote d'Ivoire/948/2020 = B(Vic)-lineage clade V1A.3a.1 repr, B/Cote d'Ivoire/948/2020

genBVicB/Netherlands/11267/2022 = B(Vic)-lineage clade V1A.3 representative B/Netherlands/11267/2022

genBVicB/Washington/02/2019 = B(Vic)-lineage clade V1A.3 repr, B/Washington/02/2019

genBVicCladeB/Brisbane/60/2008 = B(Vic)-lineage clade V1A representative B/Brisbane/60/2008

genBVicNOClade = B(Vic) lineage not attributed to clade

genBVicSubgroupNotListed = B(Vic) attributed to recognised group in current guidance but not listed here

genBYamB/Phuket/3073/2013 = B(Yam)-lineage clade Y3 representative B/Phuket/3073/2013

genBYamNOClade = B(Yam) lineage not attributed to clade

genBYamSubgroupNotListed = B(Yam) attributed to recognised group in current guidance but not listed here

Coded list of reference strains for Genetic clade for influenza viruses.

HA sequence aa resistance mutations

Field: HAAAMutations
Coding: Text

Listing of amino acid substitution in HA, separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. E190D for influenza viruses.

InterpretationM2BlockerResistanceTesting

Field: InterpretationM2BlockerResistanceTesting
Coded value list: InterpretationResistanceTest
Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
AAINP = Genotypic interpretation not possible
AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of M2BlockerResistanceTesting for influenza viruses.

InterpretationOseltamivirResistanceTesting

Field: InterpretationOseltamivirResistanceTesting
Coded value list: InterpretationResistanceTest
Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
AAINP = Genotypic interpretation not possible
AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of OseltamivirResistanceTesting for influenza viruses.

InterpretationPABlockerResistanceTesting

Field: InterpretationPABlockerResistanceTesting
Coded value list: InterpPABlockerResistanceTest
Coding: AAINP = Amino Acid substitution Interpretation not possible
AANS = No amino acid substitution in PA previously associated with reduced suscept
AARS = Amino acid substitution in PA previously associated with reduced susceptibility
NA = Not applicable

Interpretation of PABlockerResistanceTesting for influenza viruses.

InterpretationZanamivirResistanceTesting

Field: InterpretationZanamivirResistanceTesting

Coded value list: InterpretationResistanceTest

Coding: AAHRI = Amino acid substitution previously associated with highly reduced inhibition
AAINP = Genotypic interpretation not possible
AANI = No amino acid substitution prev assoc. with (highly)reduced inhibition
AARI = Amino acid substitution previously associated with reduced inhibition
HRI = Highly reduced inhibition
NA = Not applicable
NI = Normal inhibition
RI = Reduced inhibition

Interpretation of ZanamivirResistanceTesting for influenza viruses.

M2 sequence aa resistance mutations

Field: M2AAMutations

Coding: Text
UNK = Unknown

Listing of amino acid substitution in M2 separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. S31N for influenza viruses.

NA sequence aa resistance mutations

Field: NAAAMutations

Coding: Text
UNK = Unknown

Listing of amino acid substitution in NA separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. H275Y for influenza viruses.

PA sequence aa resistance mutations

Field: PAAAMutations

Coding: Text
UNK = Unknown

Listing of amino acid substitution in PA separated by semi colon. Format for reporting composition ALL relevant amino acid positions: e.g. I38T or I38M or I38 for influenza viruses.

Strain id

Field: StrainID

Coding: Text
UNK = Unknown

The name of the virus - For influenza: [A|B]/[country|region|city]/[number]/[year] (e.g. A/California/7/2009). For SARS-CoV-2: hCoV-19/[country|region|city]/[number]/[year] (e.g. hCoV-19/Sweden/23/2022). For RSV HRSV/[A|B][X]/[state/province/city.country name]/[number]/[year] (e.g. HRSV/A/Copenhagen.Denmark/54/2022).

NOTE: Please add StrainID if you have reported the variables AntigenicGroup, GeneticClade or VirusVariantCOVID to be able to link epi and lab data, especially if you are reporting those from two separate data sources.

Sequence identifier
Field: SequenceId
Coding: Text

UNK = Unknown

Sequence identifier for whole genome or whole or partial gene sequence, based on which the sequence read data can be retrieved from external database such as GISAID, GenBank or other db (except ENA). GISAID isolate sequence accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in EnaId variable.