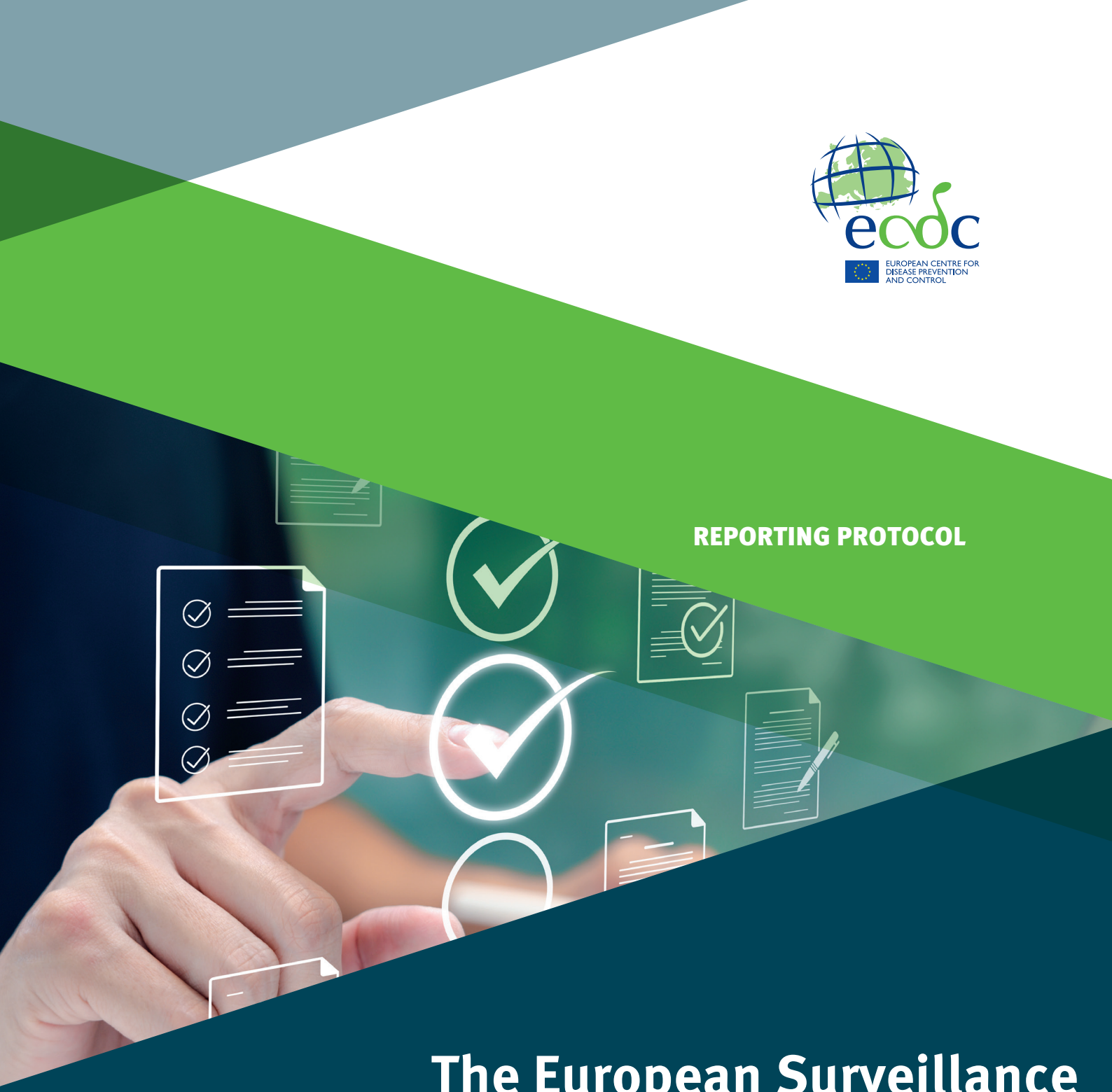


REPORTING PROTOCOL

The European Surveillance System (TESSy)

Integrated respiratory virus surveillance Reporting Protocol Version 1.8

February 2025

Contents

Summary of changes to current metadata

The following changes have been made to SARISURV:

- 08/03/2024: BrandLastCOVID19Dose coded value list has been updated.
- 07/12/2023: BrandLastCOVID19Dose coded value list has been updated.
- 27/11/2023: BA.2.86 added to the coded value list for VirusVariantCOVID
- Precondition (repeatable variable with coded value list) and Complications (repeatable variable with coded value list) have been added. The individual variables for preconditions and complications have been removed: ASTH, CANC, CARDIACDIS, DIAB, HYPERT, HIV, IMMUNEOTH, IMMUNO, KIDNEY, LIVER, LUNG, DEMENT, OBES, PREG, PREGTRIM, SMOKE, ARDS, BRONCH, COAG, ENCEPH, LONGCOVID, MYOCARD, PIMS, PNEU. Precondition Coded value list for Precondition now includes DOWNS (Down's Syndrome) and PREM (Prematurity).
- Variable OtherSymptoms changed to be repeatable, with coded value list added. The individual variables for symptoms other than cough and fever have been removed: ANOS, AGEUS, DIARR, HEAD, PAINMUSC, RUNOS, SBREATH, SORETHR, VOMIT, GENERALDETER.
- ResultSARSCoV2 was added which replaces the two previous variables ResultPCRSARSCoV2 and ResultRADTSARSCoV2 (which have been removed). Additionally, ResultCtValuePCRSARSCoV2, PreviousInfluenza, and WgsEnaId have been removed.
- RSVtype variable added.
- RSV vaccination variables added (RSVvaccinated, RSVvaccinatedMother, RSVvacDate, RSVVacProduct).
- NumberOfCovid19VaccDose, BrandLastCOVID19Dose, DateLastCOVID19VaccDose have been added. The following variables linked to vaccination status have been removed: NCoVVacFirstDose, NCoVVacFirstBrand, NCoVVacFirstDate, NCoVVacSecDose, NCoVVacSecBrand, NCoVVacSecDate, NCoVVacThirdDose, NCoVVacThirdBrand, NCoVVacThirdDate, NCoVVacFourthDose, NCoVVacFourthBrand, NCoVVacFourthDate, InfluenzaVaccinatedPrevSeason, InfluenzaVaccinatedSecLastSeason, YearLastPCV, YearLastPPV, LTCF and PlaceOfNotification have been removed.
- Coded value list for Outcome updated: DIEDOTH and DIEDUNK have been added, DISCHARGED renamed to ALIVE.
- DrugUsedProphylaxis and DrugUsedTreatment coded value lists have been updated.
- 29/07/2024: KP.3 added to the coded value list for VirusVariantCOVID

The following changes have been made to INFLSARIAGGR:

- Variables that have been added: unknown age cases (for SARI admissions, SARI admissions to ICU/HDU, SARI deaths, hospital admission denominators, catchment population denominators, specimens tested for influenza, specimens positive for influenza, specimens tested for SARS-CoV-2, specimens positive for SARS-CoV-2, specimens tested for RSV and specimens positive for RSV), NumSpecimensRSVTypeA, NumSpecimensRSVTypeB
- Variables that have been deleted: total cases (for SARI admissions, SARI admissions to ICU/HDU, SARI deaths, hospital admission denominators, catchment population denominators, specimens tested for influenza, specimens positive for influenza, specimens tested for SARS-CoV-2, specimens positive for SARS-CoV-2, specimens tested for RSV and specimens positive for RSV)

- Variables NumSpecimensSWOAH1DetectSARI and NumSpecimensSWOAH1N1DetectSARI were renamed to NumSpecimensAH1pdm09DetectSARI and NumSpecimensAH1N1pdm09DetectSARI. Number of SARI specimens positive for influenza A(H1) not N subtyped and Number of SARI specimens positive for influenza A(H1N1) other than pdm09 were removed from metadata.

The following changes have been made to SARISURVDENOM:

- Variables that have been added: unknown age cases (for SARI admissions, hospital admission denominators and catchment population denominators).
- Variables that have been deleted: total cases (for SARI admissions, hospital admission denominators and catchment population denominators).

The following changes have been made to RESPISURV:

- 08/03/2024: BrandLastCOVID19Dose coded value list has been updated.
- 07/12/2023: BrandLastCOVID19Dose coded value list has been updated.
- 27/11/2023: BA.2.86 added to the coded value list for VirusVariantCOVID
- Previously requested case-based data from primary care sentinel surveillance and influenza virus characterisation data should no longer be reported to RESPISURV. The type of data that can be reported to RESPISURV is summarised in the Introduction section below. Data previously reported to INFLSARI should be reported to RESPISURV.
- Removed from RESPISURV: antigenic group, date of sample collection, ENA identifier, genetic clade, HA sequence aa resistance mutations, interpretation M2blocker resistance testing, interpretation oseltamivir resistance testing, interpretation PA blocker testing, interpretation zanamivir resistance testing, M2 sequence aa resistance mutations, NA sequence aa resistance mutations, PA sequence aa resistance mutations. Data should be reported to INFLANTIVIR instead.
- DIEDUNK has been added to the coded value list for Outcome.
- InfluenzaTypeSubtype coded value list has been updated.
- Drug Used for Prophylaxis and Drug Used for Treatment coded value list has been updated.
- Precondition coded value list has been updated: DOWNS and PREM.
- RSVtype variable and RSV vaccination variables added (RSVVaccinated, RSVVaccinatedMother, RSVVacDate, RSVVacProduct).
- 29/07/2024: KP.3 added to the coded value list for VirusVariantCOVID

The following changes have been made to INFLANTIVIR:

- 4/12/2024: Influenza AntigenicGroup and GeneticClade coded value lists have been updated.
- 27/11/2023: Influenza AntigenicGroup and GeneticClade coded value lists have been updated.
- Variables that have been added: SequenceID
- InfluenzaTypeSubtype coded value list has been updated.

The following changes have been made to RESPIAGGR:

- InfluenzaTypeSubtype coded value list has been updated.

The following changes have been made to NCOVVARIANT:

- 27/11/2023: BA.2.86 added to the coded value list for VirusVariant
- 29/07/2024: KP.3 added to the coded value list for VirusVariant

The following changes have been made to RESPISEVERE:

- InfluenzaTypeSubtype and RSVType have been added.

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 data collection for influenza, COVID-19, and other respiratory viruses (such as RSV or new viruses of public health concern) in the EU/EEA and wider WHO European Region. Data collection is integrated for most datasets in line with the *operational considerations* for respiratory virus surveillance in Europe.

Aim

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

Objectives

Weekly outputs focus mainly on Objectives 1,2 and 3 (outlined in Table 1). Objectives 4 and 5 can be addressed with detailed analysis using a combination of the reported record types.

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.

5. Assess vaccine effectiveness against influenza, COVID-19, and other respiratory virus infections where locally feasible.

Record types

All record types except INFLANTIVIR and NCOVVARIANT are integrated record types that are based on reporting of a syndrome (ILI, ARI or SARI) and/or the reporting of lab-confirmed infections by pathogen(s) specified by the relevant variable. Table 1 provides an overview of data collection of sentinel and non-sentinel data and indicates how these data map to the objectives outlined above. Reporting of sentinel data should be prioritised. Non-sentinel data should be reported as complementary data, particularly if sentinel data is missing, insufficient or not representative.

The following record types exist in TESSy. Included variables for each record type are outlined below in the annex.

1. **INFLCLINAGGR** for reporting of weekly age-disaggregated primary care syndromic data (ILI/ARI) and qualitative indicators.
2. **RESPIAGGR** for reporting of age-disaggregated counts of laboratory-confirmed detections and tests from sentinel and non-sentinel surveillance system by week and pathogen.
3. **RESPISEVERE** for reporting of age-disaggregated counts of hospital, ICU indicators (new admissions, current inpatients) and deaths due to respiratory illness associated with the pathogen aggregated by week, indicator, and pathogen.
4. **RESPISURV** for reporting of case-based data by pathogen for cases meeting one or more of the following criteria:
    - 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). This includes data from laboratory-based confirmed cases in hospital settings previously reported to INFLSARI.

- COVID-19 cases that have been sequenced or genotyped and for which additional epidemiological information are available to facilitate variant severity assessment, including whether the cases experienced a severe outcome and the case's vaccination information. If this information is not available, then reporting via GISAID (or optionally NCOVVARIANT – see below) is sufficient.

5. **INFLSARIAGGR** for reporting of age-disaggregated data from SARI surveillance, including weekly counts of hospital admissions, hospital catchment population, SARI deaths, pathogen-specific tests and detections.
6. **SARISURV** for case-based reporting of SARI cases.
7. **SARISURVDENOM** for reporting of weekly denominators for the record type SARISURV (hospital catchment population and admissions, by age group).
8. **INFLANTIVIR** for reporting of strain-based influenza virus characterisation and antiviral susceptibility data.
9. **NCOVVARIANT (optional if GISAID data is reported)** for weekly aggregated reporting of SARS-CoV-2 variants of interest and of concern.

Case definitions

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

Please note that:

1. All data collected are shared with the World Health Organisation – Regional Office for Europe (WHO/Europe) on a weekly basis to fulfil Member States reporting requirements to WHO. Duplicate reporting to WHO HQ 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 Respiratory Viruses surveillance team (*ecdc.influenza@ecdc.europa.eu* with *tessy@ecdc.europa.eu* in copy).
3. Case-based data on human infections with zoonotic influenza viruses should be reported to **INFLZOO** metadata set and aggregated to **INFLZOOAGGR**. A separate reporting protocol is available.

Table 1: Surveillance objectives mapping to record type and type of data (sentinel vs. non-sentinel data) for weekly monitoring. Both case/strain-based and aggregate data is shown.

Objectives	**Sentinel data** (priority)	**Non-sentinel data** (complementary)
1. Monitor the intensity, geographical spread and temporal patterns of influenza, COVID-19, and other respiratory virus infections to inform mitigation measures.	**INFLCLINAGGR** age-disaggregated syndromic data (ILI/ARI) and qualitative indicators. **AND** **RESPIAGGR** age-disaggregated detections and tests from sentinel surveillance systems	**RESPIAGGR** age-disaggregated lab-confirmed detections and tests from non-sentinel surveillance systems
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.	**INFLSARIAGGR** age-disaggregated SARI data including denominator data (e.g., hospital catchment population) **OR** **SARISURV** case-based reporting of SARI cases **AND** **SARISURVDENOM** weekly denominators for the record type SARISURV	**RESPISEVERE** age-disaggregated hospital, ICU indicators and deaths **AND/OR** **RESPISURV** Case-based data by pathogen for severe cases that are not covered by existing SARI surveillance systems
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.	**SARS-CoV-2:** **GISAID** **OR** **TESSy** [1]	**SARS-CoV-2:** **GISAID** **OR** **TESSy**[1]
	Influenza: **INFLANTIVIR** strain-based influenza virus characterisation data **AND** **GISAID** [2]	**Influenza:** **INFLANTIVIR** strain-based influenza virus characterisation data **AND** **GISAID**[2]

[1] NCOVVARIANT (optional - for countries that prefer reporting of aggregate variant data to TESSy than GISAID) or RESPISURV (for countries able to report case-based variant data to TESSy)

[2] Raw sequencing data to be reported to the European Nucleotide Archive (ENA) if available.

Reporting to TESSy

When, what and how to report

Deadline for reporting:

Wednesday 23:59 CET for all record types. If you are unable to meet this deadline, please contact the ECDC Respiratory Viruses surveillance team (*ecdc.influenza@ecdc.europa.eu* and copy *tessy@ecdc.europa.eu*).

Preparing data

Data may be entered directly in EpiPulse Cases (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 EpiPulse Cases (TESSy) metadata define the fields and valid data formats for input for a given subject.

To ensure data can be saved correctly in EpiPulse Cases (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 EpiPulse Cases (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

The TESSy / Upload page is accessible from the EpiPulse > **Report** > **Cases menu**. Data are submitted through the EpiPulse Cases web interface (go to **Upload**). Previously reported data can be found through the review tab. The TESSy / Review page is accessible from the EpiPulse > **Manage** > **Edit case / Case validation** menu.

The *EpiPulse Cases (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.

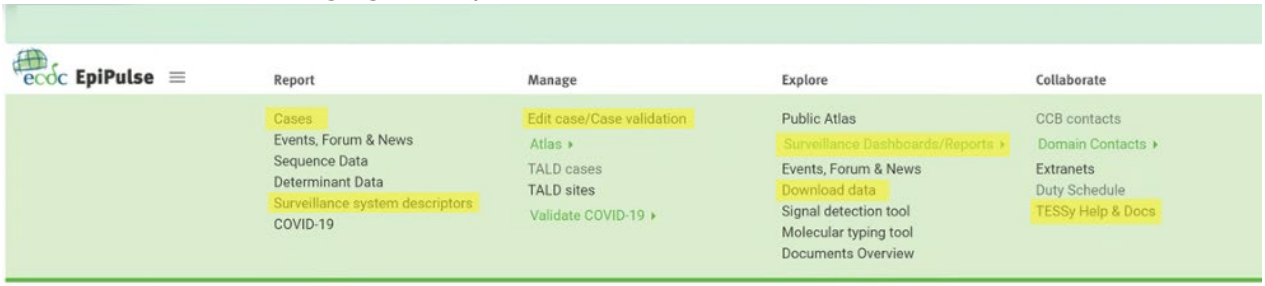
- The EpiPulse Cases (TESSy) user documentation provides information on reviewing validation results and adjusting reporting periods to avoid overwriting existing records.
- General training and guidance on reporting is available on the *EpiPulse Cases (TESSy) website*. A training video on reporting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

Navigating EpiPulse cases platform

Below is presented a mapping of the pages from TESSy to the EpiPulse Portal menu:

The TESSy / Upload page: **Report** > **Cases menu**.
The TESSy / Review page: **Manage** > **Edit case / Case validation** menu.
The TESSy / Query page: **Explore** > **Download data** menu.
The TESSy / Reports page: **Explore** > **Surveillance Dashboards / Reports** > **Legacy reports**
The TESSy / Data Sources: **Report** > **Surveillance system descriptors**
The TESSy / My profile page: **My profile and preference**
TESSy / Documents page: **Collaborate** > **TESSy Help & Docs**

Relevant menu items are highlighted in yellow below.



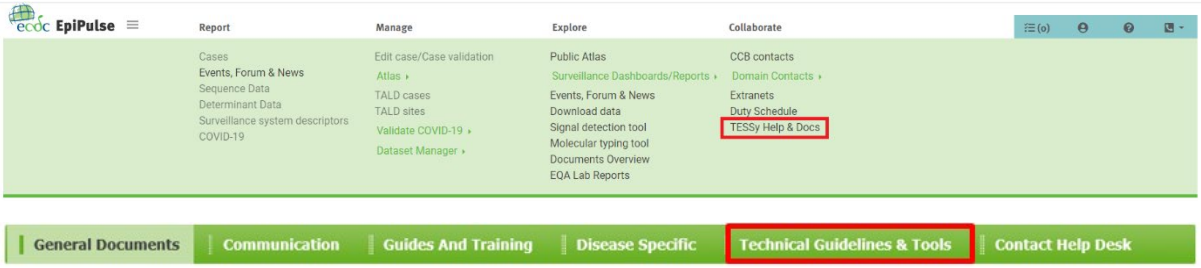
TESSy/EpiPulse Cases Help Desk

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

Revisions of metadata sets

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



Current record type versions

Table 2 shows the current record type versions in use for reporting data to TESSy.

Table 2: RESPISURV, RESPISEVERE, and RESPIAGGR, SARISURV, SARISURVDENOM, INFLSARIAGGR, INFLCLINAGGR, INFLANTIVIR and NCOVVARIANT record type version

Record type	Type of data	Record type version
RESPIAGGR	Aggregated	1
RESPISURV	Case-based	2
RESPISEVERE	Aggregated	1
SARISURV	Case-based	4
SARISURVDENOM	Aggregated	2
INFLSARIAGGR	Aggregated	4
INFLCLINAGGR	Aggregated	5
INFLANTIVIR	Case-based	9
NCOVVARIANT	Aggregated	2

RESPIAGGR metadata

RESPIAGGR 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.

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 (Table 2). 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 reported 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 reported 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

DETECTIONS

Selected indicator to report.

NOTE: Particularly for sentinel data, please ensure that you report a row for DETECTIONS for each pathogen for which TESTS are reported, including for zero detections. This way then zero detections (and 0%) positivity can be correctly reported in surveillance outputs. Similarly, if reporting sentinel DETECTIONS please be sure to also report TESTS.

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: 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 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

Coded value list: InfluenzaTypeSubtype

Coding:

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
AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
UNK = Unknown

Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection. If a zoonotic virus variant is detected, please report through record types INFLZOO (case-based data) or INFLZOOAGGR (aggregated).

RSV type

Field: RSVType

Coded value list name: RSVType

Coding: A = RSV type A
B = RSV type B
UNK = RSV unknown type

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

RESPISEVERE metadata

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 (Table 2). 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.

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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.

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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, ICU or the date of death.

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

DEATHS = 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.

Influenza Type Subtype

Field: InfluenzaTypeSubtype

Coded value list: InfluenzaTypeSubtype

Coding:

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
AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
UNK = Unknown

Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection. If a zoonotic virus variant is detected, please report through record types INFLZOO (case-based data) or INFLZOOAGGR (aggregated).

RSV type

Field: RSVType

Coded value list name: RSVType

Coding: A = RSV type A
B = RSV type B
UNK = RSV unknown type

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

RESPISURV metadata

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 (Table 2). 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 can be used instead. Where date of onset is available then please also report this field separately as it is 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 = AstraZeneca - Vaxzevria

BECNBG = Beijing CNBG - BBIBP-CorV

BECOV2A = Biological E – Corbeva

BHACOV = Bharat - Covaxin

BIMER = Hipra - Bimervax

CAN = CanSino - Convidecia

CHU = Chumakov - Covi-Vac

COM = Pfizer BioNTech - Comirnaty

COMBA.1 = Pfizer BioNTech - Comirnaty Original/Omicron BA.1

COMBA.4-5 = Pfizer BioNTech - Comirnaty Original/Omicron BA.4/BA.5

COMBIV = Pfizer BioNTech-Comirnaty Bivalent (Orig/Omicron BA.1 or Orig/Omicron BA.4/BA.5)

COMXBB = Pfizer BioNTech - Comirnaty Omicron XBB.1.5

CVAC = Curevac - CVnCOV

HAYATVAC = Julphar- Hayat-Vax

JANSS = Janssen - Jcovden

MOD = Moderna - Spikevax

MODBA.1 = Moderna - Spikevax Bivalent Original/Omicron BA.1

MODBA.4-5 = Moderna - Spikevax Bivalent Original/Omicron BA.4/BA.5

MODBIV = Moderna-Spikevax Bivalent (Original/Omicron BA.1 or Original/Omicron BA.4/BA.5)

MODXBB = Moderna - Spikevax XBB.1.5

NVX = SII – Covovax

NVXD = Novavax – Nuvaxovid

NVXDXBB = Novavax – Nuvaxovid XBB.1.5

OTHER = Other vaccine products

QAZVAQ = RIBSP - QazVac

SGSK = Sanofi GSK - Vidprevtyn

SIICOV = SII - Covishield

SIN = Sinovac - CoronaVac

SPU = Gamaleya - Sputnik-V

SPUL = Gamaleya - Sputnik-Light

SRCVB = SRCVB - EpiVacCorona

TUR = Health Institutes of Turkey - Turkovac

UNK = Unknown

VLA = Valneva – VLA2001

WUCNBG = Wuhan CNBG - Inactivated

ZFUZ = 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 = UnknownSpecified pathogen not captured in the coded values for Coinfection.

Complications

Field: Complications

Coded value list name: ComplicationsRESPI

Coding: AKI = Acute renal injury
ARDS = Acute respiratory distress syndrome
BRONCH = Bronchiolitis
ENCEPH = Encephalitis
HEARTFAIL = Heart failure
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 or unknown, 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 RSV

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: DrugUsedRESPI

Coding: J05AB16 = Remdesivir

J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
J06BD01 = Palivizumab
J06BD03 = Tixagevimab/cilgavimab (Evusheld)
J06BD07 = Casirivimab/imdevimab (Ronapreve)
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: DrugUsedRESPI

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
J05AB18 = Molnupiravir (Lagevrio)
J05AE30 = Nirmatrelvir/ritonavir (Paxlovid)
J06BD03 = Tixagevimab/cilgavimab (Evusheld) = Tixagevimab/cilgavimab (Evusheld)
J06BD05 = Sotrovimab (Xevudy)
J06BD06 = Regdanvimab (Regkirona) J06BD07 = Casirivimab/imdevimab (Ronapreve)
J06BD08 = Nirsevimab (Beyfortus)
J06BD01 = Palivizumab (Synagis)
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: InfluenzaTypeSubtype

Coding: 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
AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
UNK = Unknown

Influenza type, subtype, or lineage to be reported where Influenza is reported for the variables Pathogen or Coinfection. If a zoonotic virus variant is detected, please report through record types INFLZOO (case-based data) or INFLZOOAGGR (aggregated).

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 known cause
DIEDUNK = Died, cause of death unknown
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

DOWNS = Down's Syndrome

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 disorder (e.g., dementia, Parkinson’s disease, Alzheimer’s disease, amyotrophic lateral sclerosis (ALS))

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)
PREM = Prematurity
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 positive pressure vent

Level of respiratory support given to patient.

RSV type

Field: RSVType

Coded value list name: RSVType

Coding: A = RSV type A
B = RSV type B
UNK = RSV unknown type

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

RSV vaccination status

Field: RSVVaccinated

Coding: N = No
Y = Yes
UNK = Unknown

Received RSV vaccination in the most recent season.

RSV vaccination status (mother)

Field: RSVVaccinatedMother

Coding: N = No
Y = Yes
UNK = Unknown

If infant case, mother received RSV vaccination in the last trimester of pregnancy.

Date of RSV vaccine in the most recent season (if vaccinated)

Field:RSVVacDate

Coding: yyyy-mm-dd (preferred)
yyyy-Www
UNK= Unknown
NA=Not applicable

Date on which the case received the latest RSV vaccine (preferably exact date, formatted as yyyy-mm-dd).

RSV vaccine product

Field:RSVVacProduct

CodedValueList: [RSVvacProducts]

Coding: Arexvy
Abrysvo
UNK
Other

RSV vaccine product received in the most recent season.

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 S486P. 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

BA.2.86 = Pango lineage BA.2.86 and sub-lineages (excluding KP.3 and sub-lineages)

KP.3 = Pango lineage KP.3 and sub-lineages

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

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: This variable is used for linking RESPISURV and INFLANTIVIR entries.

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 database (except ENA). GISAID isolate sequence accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in EnaId variable.

SARISURV metadata

SARISURV is used for reporting case-based data on SARI cases.

Common TESSy variables

Record Identifier (mandatory)
Field: RecordId
Coding: Text (max 80 characters)

The record identifier is provided by the Member State. It should be useful for the country to identify readmission cases, by including a suffix with the date of admission with the format "*_yyyymmdd*" (for example, two separate admissions of case *1234* could have as record identifiers *1234_20210101* and *1234_20210115*). The complete record identifier must be:

- unique within the SARISURV surveillance system;
- anonymous.

Record type (mandatory)
Field: RecordType
Coding: SARISURV

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: SARISURV

The subject describes the disease to be reported.

Status (mandatory)
Field: Status
Coded value list: [Statuses]
Coding: NEW/UPDATE
DELETE

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.

Data source (mandatory)
Field: DataSource

Coded value list: [Data sources]

Coding: Pre-assigned as CountryCode-SARISURV to each country; CountryCode-SARISURV-VE if data collected only in the context of vaccine effectiveness studies (relevant when VE data collection will be implemented); can be modified by National Focal Point.

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national focal point in each Member State. The descriptions of the surveillance systems submitted to TESSy (*section Data Sources*) should include details about case definition used and should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)
Field: ReportingCountry
Coded value list: [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-mm-dd (preferred)
yyyy-Www

The reference date used for standard reports that is compared to the reporting period. The date used for statistics should be date of admission to hospital or diagnosis of respiratory infection (if admitted by other cause).

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 hospital admission. If child aged 0 or 1, please provide age in months in the variable AgeMonths (0-23 months). If no precise age is available, please use the variable AgeGroup.

Age months
Field: AgeMonth
Coding: Numerical (0-23)
UNK = Unknown

Age of patient in months as reported in the national system for cases < 2 years of age at the time of hospital admission. If the age of the patient is >= 2 years, AgeMonth should be reported as NA.

Age class (alternative)
Field: AgeClass
Coded value list: [AgeClass3]
Coding: Age00-04 = Less than 5 years of age
Age05-14 = Between 5 and 14 years of age

Age15-29 = Between 15 and 29 years of age
Age30-64 = Between 30 and 64 years of age
Age65-79 = Between 65 and 79 years of age
Age80+ = 80 years and older
UNK = Unknown

Age class of patient as reported in the national system at the time of hospital admission. This is an alternative variable, to be completed only if "Age" and/or "AgeMonths" not reported.

Gender
Field: Gender
Coded value list: [Gender]
Coding: F = Female
M = Male
O = Other
UNK = Unknown

Gender of the reported case.

Healthcare worker
Field: HealthCareWorker
Coded value list: [YesNoUnk]
Coding: N = No
Y = Yes
UNK = Unknown
The definition of a healthcare worker for the purposes of this reporting protocol is anyone working (paid or on a regular voluntary basis) in healthcare who has contact with any type of patient during his/her work, including (but not limited to): doctors; nurses; therapists; technicians; emergency medical personnel; medical and nursing students with patient contact; porters; and cleaners. Employees or volunteers at nursing/residential homes for the elderly also are also included as healthcare workers in this protocol.

Place of residence
Field: PlaceOfResidence
Coded value list: NUTS

Place of residence of patient at the time of hospital admission. Select the most detailed NUTS level possible. UNK is allowed.

Symptoms / clinical presentation

Date of onset of symptoms
Field: DateOfOnset
Coding: yyyy-mm-dd (preferred)
yyyy-Www
UNK= Unknown

Date of onset of symptoms.

Fever
Field: FEVER

Coding: N = No
Y = Yes
UNK = Unknown

History of fever or measured fever >=38 ºC within the 10 days before admission to hospital.

Cough
Field: COUGH
Coding: N = No
Y = Yes
UNK = Unknown

History of cough within the 10 days before admission to hospital.

Apnoea
Field: APNOEA
Coding: N = No
Y = Yes
UNK = Unknown

Patient presenting with apnoea.

Sepsis
Field: SEPSIS
Coding: N = No
Y = Yes
UNK = Unknown

Patient presenting with sepsis.

Other symptoms (Repeatable)
Field:OtherSymptoms
Coded value list: SymptomsOtherSARI
Coding: ANOS = Anosmia
AGEUS = Ageusia
DIARR = Diarrhoea
HEAD = Headaches
O = Other
PAINMUSC = Muscular pain
RUNOS = Runny nose
SBREATH = Shortness of breath
SORETHR = Sore throat
VOMIT = Vomiting
GENERALDETER = General deterioration

Other reported symptoms or clinical presentation not previously specified. If multiple other symptoms, separate by a semicolon (;) within the same field.

Hospitalisation and outcome

Date of admission to hospital
Field:DateOfHosp
Coding: yyyy-mm-dd (preferred)
Yyyy-Www
UNK= Unknown

Date of admission to hospital.

Admission to Intensive care/high dependency unit
Field: ICUHDU
Coding: N = No
Y = Yes
UNK = UnknownCase 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).

Date of admission to Intensive Care Unit/High Dependency Unit
Field: DateOfICUHDU
Coding: yyyy-mm-dd (preferred)
Yyyy-Www
UNK= Unknown

Date of admission to intensive care unit or high dependency unit. If admitted more than once to ICU/HDU, please report the date of first admission to ICU/HDU.

Length of stay in ICU/HDU
Field: NumberDaysICUHDU
Coding: Number

Number of days in ICU or HDU.

Respiratory Support
Field:RespSupport
Coded value list: [RespSupportSARI2]
Coding: NONE = No respiratory support given
OXYGEN = High-flow oxygen therapy (non-invasive ventilation)
VENT = Invasive Ventilation
ECMO = Extra Corporeal Membrane Oxygenation
O = Other respiratory support
UNK = Respiratory support given unknown

Level of respiratory support given to patient. Please indicate the most invasive that applied.

Outcome
Field: Outcome
Coded value list: [OutcomeRESPI]
Coding: ALIVE = Alive, recovered, cured, discharged from hospital
DIED = Died, as a result of viral respiratory infection
DIEDOTH = Died, other known cause
DIEDUNK = Died, cause of death unknown

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.

Date of outcome
Field: DateOfOutcome
Coding: yyyy-mm-dd (preferred)
Yyyy-Www
UNK= Unknown

Exact date of outcome. If discharged, date of discharge from hospital. If patient still hospitalised or not applicable, please use 'UNK'.

Preconditions and complications

Precondition (repeatable)
Field: Precondition
Coded value list: Preconditions
Coding: ASPL = Asplenia
ASTH = Asthma
CANC = Cancer, malignancy
CARDIACDIS = Cardiac disorder, excluding hypertension
DIAB = Diabetes
DOWNS = Down's Syndrome
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 disorder (e.g., dementia, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS))
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)
PREM = Prematurity
SMOKE = Smoke
TB = Tuberculosis
UNK = Unknown precondition

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

Other preconditions
Field: PreconditionOther
Coding: Text

Details of underlying conditions, or additional preconditions not previously specified. If multiple other preconditions, separate by a semicolon (;) within the same field.

Complications (Repeatable)

Field: Complications

Coded value list name: ComplicationsRESPI
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.

Other clinical presentation or complications
Field: PresentationComplicationOther
Coding: Text
UNK = Unknown

Other clinical presentations or complications not previously specified. If multiple, separate by a semicolon (;) within the same field.

Diagnosis and laboratory results

Date of specimen collection
Field: DateOfSpecCollection
Coding: yyyy-mm-dd (preferred)
Yyyy-Www

UNK= Unknown

Date of specimen collection. First date of collection in the current episode if multiple swabs.

Laboratory results for influenza
Field: ResultInfluenza
Coding: N = Negative
NT = Not tested
P = Positive
UNK = Tested but result Unknown

Result for influenza during this SARI admission episode.

Influenza type and subtype

Field: InfluenzaTypeSubtype

Coded value list: InfluenzaTypeSubtype

Coding:

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
AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
UNK = Unknown

Influenza virus type and subtype. If not available in the list or specific variants from a subtype, please describe in the variable "Laboratory results for other pathogens" (see below). If influenza negative or not tested, please select "NA".

Laboratory results for SARS-CoV-2
Field: ResultSARSCoV2
Coded value list: ResultSARSCoV2
Coding: N = Negative
NT = Not tested
P = Positive
UNDET = Undetermined/inconclusive
UNK = Tested, but result unknown

Laboratory result for SARS-CoV-2 in the current SARI admission episode.

Previous SARS-CoV-2 infection
Field: PreviousNCoV
Coding: N = No
Y = Yes
UNK = Unknown

Previously infected with SARS-CoV-2.

Date of previous SARS-CoV-2 infection
Field: DateOfPreviousNCoV
Coding: yyyy-mm-dd (preferred)
yyyy-Www
UNK= Unknown

Date of previous SARS-CoV-2 infection. If no exact date available, please provide an estimate.

Laboratory results for MERS-CoV
Field: ResultMERSCoV
Coded value list: [ResultMERSCoV]
Coding: N = Negative
NT = Not tested
P = Positive
UNK = Tested for MERS-CoV, but result unknown

Laboratory results for Middle East respiratory syndrome coronavirus (MERS-CoV) in the current SARI admission episode.

Laboratory results for RSV
Field: ResultRSV
Coded value list: [ResultRSV]
Coding: N = Negative
NT = Not tested
P = Positive
UNK = Tested for RSV, but result unknown

Result for RSV in the current SARI admission episode.

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

RSV type to be reported for RSV cases.

Laboratory results for Streptococcus pneumoniae
Field: ResultPneu
Coded value list: [ResultPneu]
Coding: N = Negative
NT = Not tested
P = Positive
UNK = Tested for Streptococcus pneumoniae, but result unknown

Result for Streptococcus pneumoniae in the current SARI admission episode.

Laboratory results for Legionella pneumophila
Field: ResultLegi
Coded value list: [ResultLegi]

Coding: N = Negative
NT = Not tested
P = Positive
UNK = Tested for Legionella pneumophila, but result unknown

Result for Legionella pneumophila in the current SARI admission episode.

Laboratory results for other pathogens
Field: OtherPathResults
Coding: Text

Laboratory positive results for other pathogens, other influenza subtypes (if coded as 'other' but known) or coronaviruses other than SARS-CoV-2, in the current SARI admission episode.

SARS-CoV-2 Variant
Field: VirusVariantCOVID
Coded value list: [VirusVariantNCOV]
Coding: VirusVariantNCOV:
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 S486P. 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
BA.2.86 = Pango lineage BA.2.86 and sub-lineages (excluding KP.3 and sub-lineages)
KP.3 = Pango lineage KP.3 and sub-lineages
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 VirusVariantOtherCOVID. 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 VirusVariantOtherCOVID. If typing results are inconclusive, report UNK.

SARS-CoV-2 other variant
Field: VirusVariantOtherCOVID
Coding: Text

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

Wgs Sequence RA identifier
Field: WgsSequenceId
Coding: Text

Sequence identifier for whole genome or gene sequence, based on which the sequence read data can be retrieved from external database such as GISAID, GenBank or other database (except ENA). GISAID isolate sequence accession number should be reported in format EPI_ISL_402123, GenBank MK334047.1. Please report ENAId in WgsEnaId variable. If multiple pathogens/strains detected, please separate by a semicolon (;) within the same field.

Vaccination

Number of COVID-19 vaccination doses received

Field: NumberOfCovid19VaccDose

Coding: Numeric

Number of COVID-19 vaccination doses received.

Brand of last received COVID-19 vaccination dose

Field: BrandLastCOVID19Dose

Coded value list name: VaccineCOVID

Coding: AZ = AstraZeneca - Vaxzevria
BECNBG = Beijing CNBG - BBIBP-CorV
BECOV2A = Biological E – Corbeva
BHACOV = Bharat - Covaxin
BIMER = Hipra - Bimervax
CAN = CanSino - Convidecia
CHU = Chumakov - Covi-Vac
COM = Pfizer BioNTech - Comirnaty
COMBA.1 = Pfizer BioNTech - Comirnaty Original/Omicron BA.1

COMBA.4-5 = Pfizer BioNTech - Comirnaty Original/Omicron BA.4/BA.5

COMBIV = Pfizer BioNTech-Comirnaty Bivalent (Orig/Omicron BA.1 or Orig/Omicron BA.4/BA.5)

COMXBB = Pfizer BioNTech - Comirnaty Omicron XBB.1.5

CVAC = Curevac - CVnCOV

HAYATVAC = Julphar- Hayat-Vax

JANSS = Janssen - Jcovden

MOD = Moderna - Spikevax

MODBA.1 = Moderna - Spikevax Bivalent Original/Omicron BA.1

MODBA.4-5 = Moderna - Spikevax Bivalent Original/Omicron BA.4/BA.5

MODBIV = Moderna-Spikevax Bivalent (Original/Omicron BA.1 or Original/Omicron BA.4/BA.5)

MODXBB = Moderna - Spikevax XBB.1.5

NVX = SII – Covovax

NVXD = Novavax – Nuvaxovid

NVXDXBB = Novavax – Nuvaxovid XBB.1.5

OTHER = Other vaccine products

QAZVAQ = RIBSP - QazVac

SGSK = Sanofi GSK - Vidprevtyn

SIICOV = SII - Covishield

SIN = Sinovac - CoronaVac

SPU = Gamaleya - Sputnik-V

SPUL = Gamaleya - Sputnik-Light

SRCVB = SRCVB - EpiVacCorona

TUR = Health Institutes of Turkey - Turkovac

UNK = Unknown

VLA = Valneva – VLA2001

WUCNBG = Wuhan CNBG - Inactivated

ZFUZ = Anhui ZL – Zifivax

Brand/Type of last received COVID-19 vaccination dose.

Date last received COVID-19 vaccination dose

Field: DateLastCOVID19VaccDose

Coding: yyyy-mm-dd

UNK= Unknown

Date of last received COVID-19 vaccination dose.

Influenza vaccination status

Field: InfluenzaVaccinated

Coding: N = No

Y = Yes
UNK = Unknown

Received influenza vaccination in the most recent influenza season.

Date of influenza vaccine in the most recent season (if vaccinated)
Field:InfluenzaVacDate
Coding: yyyy-mm-dd (preferred)
yyyy-Www
UNK= Unknown
NA=Not applicable

Date on which the case received influenza season (preferably exact date, formatted as yyyy-mm-dd).

Influenza vaccine product
Field:InfluenzaVacProduct
Coding: Text

Type of vaccine received in the most recent season (product name/brand). If unknown, type "Unk".

Influenza vaccination season n-1
Field: InfluenzaVaccinatedPrevSeason
Coding: N = No
Y = Yes
UNK = Unknown

Seasonal influenza vaccination in the previous season (n-1). If the case is being reported during interseason (w21-w39), consider most recent season-1.

Influenza vaccination season n-2
Field: InfluenzaVaccinatedSecLastSeason
Coding: N = No
Y = Yes
UNK = Unknown

Seasonal influenza vaccination in the season two years before (n-2). If the case is being reported during interseason (w21-w39), consider most recent season-2.

RSV vaccination status
Field: RSVVaccinated
Coding: N = No
Y = Yes
UNK = Unknown

Received RSV vaccination in the most recent season.

RSV vaccination status (mother)
Field: RSVVaccinatedMother
Coding: N = No
Y = Yes
UNK = Unknown

If infant case, mother received RSV vaccination in the last trimester of pregnancy.

Date of RSV vaccine in the most recent season (if vaccinated)
Field:RSVVacDate
Coding: yyyy-mm-dd (preferred)
yyyy-Www
UNK= Unknown
NA=Not applicable

Date on which the case received the latest RSV vaccine (preferably exact date, formatted as yyyy-mm-dd).

RSV vaccine product
Field:RSVVacProduct
CodedValueList: [RSVvacProducts]
Coding: Arexvy
Abrysvo
UNK
Other

RSV vaccine product received in the most recent season.

Pneumococcal vaccination
Field: PneumoVaccinated
Coding: N = No
Y=Yes
UNK = Unknown

Pneumococcal vaccination received (any type, ever).

Year of last PCV10/13 vaccination
Field: YearLastPCV
Coding: yyyy
UNK = Unknown
NA = Never administered

Year of administration of the last PCV10/13 vaccine.

Year of last PPV23 pneumococcal vaccination
Field: YearLastPPV
Coding: yyyy
UNK = Unknown
NA = Never administered

Year of administration of the last PPV23 vaccine.

Antiviral prophylaxis/therapy

Drug Used for Prophylaxis
Field: DrugUsedProphylaxis

Coded value list name: DrugUsedRESPI

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
J06BD01 = Palivizumab
J06BD03 = Tixagevimab/cilgavimab (Evusheld)
J06BD07 = Casirivimab/imdevimab (Ronapreve)
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: DrugUsedRESPI

Coding: J05AB16 = Remdesivir
J05AC02 = Rimantadine
J05AH01 = Zanamivir
J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
N04BB01 = Amantadine
O = Other
UNK = Unknown
J05AB18 = Molnupiravir (Lagevrio)
J05AE30 = Nirmatrelvir/ritonavir (Paxlovid)
J06BD07 = Casirivimab/imdevimab (Ronapreve)
J06BD03 = Tixagevimab/cilgavimab (Evusheld)
J06BD05 = Sotrovimab (Xevudy)
J06BD06 = Regdanvimab (Regkirona)
J06BD08 = Nirsevimab (Beyfortus)
J06BD01 = Palivizumab (Synagis)

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

Other drugs used for prophylaxis or treatment
Field:DrugsOther
Coding: Text
UNK=Unknown

Other drugs used for prophylaxis or treatment not previously specified. If multiple, separate by a semicolon (;) within the same field.

SARISURVDENOM metadata

SARISURVDENOM is used for reporting of **weekly denominators for the record type SARISURV** (hospital catchment population and admissions, by age group).
Several options may be used to determine the proportion of the population covered by the selected sentinel hospitals:

1. If the information on the hospitals' catchment population is available, it should be provided directly.
2. If the information on hospitals' catchment population is not available, it should be estimated. Two approaches to calculating denominators are provided below.
    a. Estimate based on the median weekly number of all-cause hospitalisations in the previous years: Proportion of patients discharged from the selected hospitals among all hospitals in the region multiplied by the region population. Catchment population = region population * (number patients discharged from selected hospitals/number of patients discharged from all hospitals in region). The catchment population estimation should first be done for each hospital and estimates from hospitals should be summed up, so that the estimates apply to the full surveillance system.
    b. Estimate based on the number of beds: in an urban area, the catchment population can be estimated by taking into account the population of the city, the number of hospitals in the city and the number of beds in a hospital. Coefficients should be attributed to each hospital in the city depending on their activity estimated by the number of beds. For example, in a city with 3 hospitals, if hospital A has 50 beds, the coefficient to be applied will be 0.5, if hospital B has 125 beds, the coefficient will be 1.25 and if hospital C has 75 beds, the coefficient will be 0.75, so:

    Catchment population = City population*coefficient (based on the number of beds)/Number of hospitals in the city.

In this approach, the estimation of population coverage of hospitals should first be done for each hospital and estimates from hospitals should be summed up, so that the estimates apply to the full surveillance system.

Common TESSy variables

Record type (mandatory)
Field: RecordType
Coding: SARISURVDENOM

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: SARISURVDENOM

The subject describes the disease to be reported.

Data source (mandatory)
Field: DataSource
Coding: Pre-assigned as CountryCode-SARISURV to each country; can be modified by National Focal Point.

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national focal point in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation. The code should be the same as used for SARISURV.

Reporting country (mandatory)
Field: ReportingCountry
Coded values list: [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 date used for statistics should match the case-based SARISURV submissions, in order to provide the denominators needed to calculate rates and proportions.

Denominator variables

Total number of SARI reporting sites
Field: NumSariRepSites
Coding: Numeric

Total number of sites reporting SARI hospitalisations. Should be adjusted according to the number of hospitals reporting case-based data in the current week. (E.g. if a country has 2 hospitals each with 50,000 catchment population and in week X only 1 hospital reports, please report NumSariRepSites = 1 and the variable TotalDenominator = 50,000 and not 100,000).
Required: True (warning)

Description of SARISURV
Field: DescriptionSARISURV
Coding: Text

Additional information regarding the current week's case-based SARISURV data, not captured by the variable Data Source.

SARI admissions by age group

Number of hospital SARI admissions age 0-4
Field: NumSariHospitalisationsAge00-04
Coding: Numeric

Number of hospital SARI admissions in patients aged 0-4 (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 5-14
Field: NumSariHospitalisationsAge05-14
Coding: Numeric

Number of hospital SARI admissions in patients aged 05-14 (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 15-29
Field: NumSariHospitalisationsAge15-29
Coding: Numeric

Number of hospital SARI admissions in patients aged 15-29 (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 30-64
Field: NumSariHospitalisationsAge30-64
Coding: Numeric

Number of hospital SARI admissions in patients aged 30-64 (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 65-79
Field: NumSariHospitalisationsAge65-79
Coding: Numeric

Number of hospital SARI admissions in patients aged 65-79 (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 80+
Field: NumSariHospitalisationsAge80+
Coding: Numeric

Number of hospital SARI admissions in patients aged 80+ (numerator) in the indicated reporting period.

Number of hospital SARI admissions age 15-64 (alternative)
Field: NumSariHospitalisationsAge15-64
Coding: Numeric

Number of hospital SARI admissions in patients aged 15-64 (numerator), to submit only if data for the age groups 15-29 and 30-64 are not available in the indicated reporting period.

Number of hospital SARI admissions age 65+ (alternative)
Field: NumSariHospitalisationsAge65+
Coding: Numeric

Number of hospital SARI admissions in patients aged 65+ (numerator), to submit only if data for the age groups 65-79 and 80+ are not available in the indicated reporting period.

Total number of hospital SARI admissions of age unknown
Field: NumSariHospitalisationsAgeUNK
Coding: Numeric

Number of hospital SARI admissions of unknown age in the indicated reporting period. The sum of the age-specific variables and this variable should be equal to the total number of hospital SARI admissions.

All-cause admissions to hospital by age group

Number of patients aged 0-4 admitted to hospital
Field: HospAdmissionsAge00-04
Coding: Numeric

Number of all-cause hospital admissions in patients aged 0-4 in the indicated reporting period.

Number of patients aged 5-14 admitted to hospital
Field: HospAdmissionsAge05-14
Coding: Numeric

Number of all-cause hospital admissions in patients aged 5-14 in the indicated reporting period.

Number of patients aged 15-29 admitted to hospital
Field: HospAdmissionsAge15-29
Coding: Numeric

Number of all-cause hospital admissions in patients aged 15-29 in the indicated reporting period.

Number of patients aged 30-64 admitted to hospital
Field: HospAdmissionsAge30-64
Coding: Numeric

Number of all-cause hospital admissions in patients aged 30-64 in the indicated reporting period.

Number of patients aged 65-79 admitted to hospital
Field: HospAdmissionsAge65-79
Coding: Numeric

Number of all-cause hospital admissions in patients aged 65-79 in the indicated reporting period.

Number of patients aged 80+ admitted to hospital
Field: HospAdmissionsAge80+
Coding: Numeric

Number of all-cause hospital admissions in patients aged 80+ in the indicated reporting period.

Number of patients aged 15-64 admitted to hospital (alternative)
Field: HospAdmissionsAge15-64
Coding: Numeric

Number of all-cause hospital admissions in patients aged 15-64 in the indicated reporting period. Alternative, to submit if data for the age groups 15-29 and/or 30-64 are not available.

Number of patients aged 65+ admitted to hospital (alternative)
Field: HospAdmissionsAge65+
Coding: Numeric

Number of all-cause hospital admissions in patients aged 65+ in the indicated reporting period. Alternative, to submit if data for the age groups 65-79 and/or 80+ are not available.

Number of patients of unknown age admitted to hospital
Field: HospAdmissionsAgeUNK
Coding: Numeric

Number of hospital admissions of unknown age in the indicated reporting period. The sum of the age-specific variables and this variable should be equal to the total number of all-cause hospital admissions.

Hospital catchment population by age group

Population aged 0-4 served by the participating hospitals
Field: DenomHospPopulationAge00-04
Coding: Numeric

Population with less than five years of age under surveillance by participating hospitals (catchment population).

Population aged 5-14 served by the participating hospitals
Field: DenomHospPopulationAge05-14
Coding: Numeric

Population aged 5-14 under surveillance by participating hospitals (catchment population).

Population aged 15-29 served by the participating hospitals
Field: DenomHospPopulationAge15-29
Coding: Numeric

Population aged 15-29 under surveillance by participating hospitals (catchment population).

Population aged 30-64 served by the participating hospitals
Field: DenomHospPopulationAge30-64
Coding: Numeric

Population aged 30-64 under surveillance by participating hospitals (catchment population).

Population aged 65-79 served by the participating hospitals
Field: DenomHospPopulationAge65-79
Coding: Numeric

Population aged 65-79 under surveillance by participating hospitals (catchment population).

Population aged 80+ served by the participating hospitals

Field: DenomHospPopulationAge80+
Coding: Numeric

Population aged 80+ under surveillance by participating hospitals (catchment population).

Population aged 15-64 served by the participating hospitals (alternative)
Field: DenomHospPopulationAge15-64
Coding: Numeric

Population aged 15-64 under surveillance by participating hospitals (catchment population). Alternative, to submit if data for the age groups 15-29 and/or 30-64 are not available.

Population aged 65+ served by the participating hospitals (alternative)
Field: DenomHospPopulationAge65+
Coding: Numeric

Population aged 65+ under surveillance by participating hospitals (catchment population). Alternative, to submit if data for the age groups 65-79 and/or 80+ are not available.

Population of age unknown served by the participating hospitals
Field: DenomHospPopulationAgeUNK
Coding: Numeric

Population of age unknown under surveillance by participating hospitals (catchment population). The sum of the age-specific variables and this variable should be equal to the total hospital catchment population.

INFLSARIAGGR metadata

INFLSARIAGGR is used for reporting of aggregated data on SARI cases and underlying population denominators for calculation of total and age-specific notification rates and proportions. Aggregated data should be reported weekly.
The epidemiological variables to collect include:

- All-cause hospital admissions, by age group (denominator);
- Hospital catchment population, by age group (denominator);
- SARI hospitalisations, by age group (numerator);
- SARI hospitalisation deaths, by age group (numerator);
- SARI admissions to intensive care, by age group (numerator);
- SARI specimens tested for influenza, respiratory syncytial virus (RSV) and SARS-CoV-2, by age group (denominator);
- SARI specimens positive for influenza, RSV and SARS-CoV-2, by age group (numerator);
- SARI specimens positive for influenza by virus (sub)type and lineage (numerator).

Common TESSy variables

Record type (mandatory)
Field: RecordType
Coding: INFLSARIAGGR

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: INFLSARI

The subject describes the disease to be reported.

Data source (mandatory)
Field: DataSource
Coding: Pre-assigned as CountryCode-INFLSARIAGGR to each country; can be modified by National Coordinator; countries reporting aggregated data through the new SARI surveillance stream should change data source to "CountryCode-SARISURVAGGR"

The data source specifies the surveillance system from which the data originate and is generated and revised/updated by the national focal point in each Member State. The descriptions of the surveillance systems submitted to TESSy (*section Data Sources*) should include details about case definition used and should be kept up to date and will be used to assist with data interpretation. If country is reporting

cases that do not follow strict WHO case definition (see *Definitions*), that should be stated in DataSource.

Reporting country (mandatory)
Field: ReportingCountry
Coded value list: [Countries]

Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)
This variable identifies the country reporting the aggregate dataset.

Date used for statistics (mandatory)
Field: DateUsedForStatistics
Coding: yyyy-Www

The reference date used for standard reports that is compared to the reporting period. The date used for statistics should be preferably the week of admission to hospital, but can be any date that the reporting country finds applicable, e.g. date of admission, date of notification, date of diagnosis or any other date.

Epidemiological variables

Total number of SARI reporting sites
Field: NumSariRepSites
Coding: Numeric

Total number of sites reporting SARI hospitalisations. Should be adjusted according to the number of hospitals reporting. (E.g. if a country has 2 hospitals each with 50,000 catchment population and in week X only 1 hospital reports, please report NumSariRepSites = 1 and the denominator to be 50,000 and not 100,000)
Required: True (warning)

Reporting fraction (alternative)
Field: ReportingFraction
Coding: Numeric (decimal)

Proportion of SARI admissions at the participating hospitals that are reported in the current week. This is an alternative variable, to account for the fact that some hospitals might report only a fraction of the SARI cases (eg. Only cases admitted on two specific days of the week). Catchment population and all-cause admissions should not be adjusted for this reporting fraction (e.g. if a hospital has a catchment population of 50,000, the reported catchment population should be 50,000, even if SARI admissions reported cover only specific days of the week).

Description of SARI system
Field: DescriptionSARI
Coding: Text

Description of SARI surveillance system.

SARI admissions by age group

Number of hospital SARI admissions age 0-4
Field: NumSariHospitalisationsAge00-04STL

Coding: Numeric

Number of hospital SARI admissions in patients aged 0-4 (numerator).

Number of hospital SARI admissions age 5-14
Field: NumSariHospitalisationsAge05-14STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 05-14 (numerator).

Number of hospital SARI admissions age 15-29
Field: NumSariHospitalisationsAge15-29STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 15-29 (numerator).

Number of hospital SARI admissions age 30-64
Field: NumSariHospitalisationsAge30-64STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 30-64 (numerator).

Number of hospital SARI admissions age 65-79
Field: NumSariHospitalisationsAge65-79STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 65-79 (numerator).

Number of hospital SARI admissions age 80+
Field: NumSariHospitalisationsAge80+STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 80+ (numerator).

Number of hospital SARI admissions age 15-64 (alternative)
Field: NumSariHospitalisationsAge15-64STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 15-64 (numerator), to submit if data for the age groups 15-29 and 30-64 are not available.

Number of hospital SARI admissions age 65+ (alternative)
Field: NumSariHospitalisationsAge65+STL
Coding: Numeric

Number of hospital SARI admissions in patients aged 65+ (numerator), to submit if data for the age groups 65-79 and 80+ are not available.

Number of hospital SARI admissions with unknown age
Field: NumSariHospitalisationsAgeUnkSTL
Coding: Numeric

Number of hospital SARI admissions in patients with unknown age (numerator). The sum of the age-specific variables and this variable should be equal to the total number of hospital SARI admissions.

SARI admissions to ICU/HDU by age group

Number of hospital SARI admissions to ICU/HDU age 0-4
Field: NumSariICUadmissionsAge00-04
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 0-4 (numerator).

Number of hospital SARI admissions to ICU/HDU age 5-14
Field: NumSariICUadmissionsAge05-14
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 05-14 (numerator).

Number of hospital SARI admissions to ICU/HDU age 15-29
Field: NumSariICUadmissionsAge15-29
Coding:Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 15-29 (numerator).

Number of hospital SARI admissions to ICU/HDU age 30-64
Field: NumSariICUadmissionsAge30-64
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 30-64 (numerator).

Number of hospital SARI admissions to ICU/HDU age 65-79
Field: NumSariICUadmissionsAge65-79
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 65-79 (numerator).

Number of hospital SARI admissions to ICU/HDU age 80+
Field: NumSariICUadmissionsAge80+
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 80+ (numerator).

Number of hospital SARI admissions to ICU/HDU age 15-64 (Alternative)
Field: NumSariICUadmissionsAge15-64
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 15-64 (numerator), to submit if data for the age groups 15-29 and 30-64 are not available.

Number of hospital SARI admissions to ICU/HDU age 65+ (Alternative)
Field: NumSariICUadmissionsAge65+
Coding: Numeric

Number of hospital SARI admissions to Intensive Care/High Dependency Care Units in patients aged 65+ (numerator), to submit if data for the age groups 65-79 and 80+ are not available.

Number of hospital SARI admissions to ICU/HDU age unknown
Field: NumSariICUadmissionsAgeUnk
Coding: Numeric
Total number of hospital SARI admissions to ICU/HDU in patients of age unknown (numerator).
The sum of the age-specific variables and this variable should be equal to the total number of hospital SARI admissions to ICU/HDU.

SARI deaths by age group

Number of hospital SARI deaths aged 0-4
Field: NumSariDeathsAge00-04STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 0-4 (numerator).

Number of hospital SARI deaths aged 5-14
Field: NumSariDeathsAge05-14STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 05-14 (numerator).

Number of hospital SARI deaths aged 15-29
Field: NumSariDeathsAge15-29STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 15-29 (numerator).

Number of hospital SARI deaths aged 30-64
Field: NumSariDeathsAge30-64STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 30-64 (numerator).

Number of hospital SARI deaths aged 65-79
Field: NumSariDeathsAge65-79STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 65-79 (numerator).

Number of hospital SARI deaths aged 80+
Field: NumSariDeathsAge80+STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 80+ (numerator).

Number of hospital SARI deaths aged 15-64 (Alternative)
Field: NumSariDeathsAge15-64STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 15-64 (numerator), to submit only if data for the age groups 15-29 and 30-64 are not available.

Number of hospital SARI deaths aged 65+ (Alternative)
Field: NumSariDeathsAge65+STL
Coding: Numeric

Total hospital SARI admissions that resulted in death in patients aged 65+ (numerator), to submit only if data for the age groups 65-79 and 80+ are not available.

Number of hospital SARI deaths unknown age
Field: NumSariDeathsAgeUnkSTL
Coding: Numeric
Number of SARI deaths in patients of unknown age (numerator). The sum of the age-specific variables and this variable should be equal to the total number of hospital SARI deaths.

Hospital admission denominators by age group

Number of hospital admissions age 0-4
Field: DenomHospAdmissionsAge00-04STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 0-4 (denominator).

Number of hospital admissions age 5-14
Field: DenomHospAdmissionsAge05-14STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 5-14 (denominator).

Number of hospital admissions age 15-29
Field: DenomHospAdmissionsAge15-29STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 15-29 (denominator).

Number of hospital admissions age 30-64
Field: DenomHospAdmissionsAge30-64STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 30-64 (denominator).

Number of hospital admissions age 65-79
Field: DenomHospAdmissionsAge65-79STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 65-79 (denominator).

Number of hospital admissions age 80+
Field: DenomHospAdmissionsAge80+STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 80+ (denominator).

Number of hospital admissions age 15-64 (Alternative)
Field: DenomHospAdmissionsAge15-64STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 15-64 (denominator), to submit if data for the age groups 15-29 and 30-64 are not available.

Number of hospital admissions age 65+ (Alternative)
Field: DenomHospAdmissionsAge65+STL
Coding: Numeric

Number of hospital admissions (all causes) in patients aged 65+ (denominator), to submit if data for the age groups 65-79 and 80+ are not available.

Number of hospital admissions age unknown
Field: DenomHospAdmissionsUnkSTL
Coding: Numeric

Number of hospital admissions (all causes) in patients of unknown age (denominator). The sum of the age-specific variables and this variable should be equal to the total hospital admissions (denominator).

Catchment population denominators by age group

Population aged 0-4 covered by the hospitals submitting SARI data
Field: DenomHospPopulationAge00-04STL
Coding: Numeric

Population aged 0-4 covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 5-14 covered by the hospitals submitting SARI data
Field: DenomHospPopulationAge05-14STL
Coding: Numeric

Population aged 5-14 covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 15-29 covered by the hospitals submitting SARI data

Field: DenomHospPopulationAge15-29STL
Coding: Numeric
Population aged 15-29 covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 30-64 covered by the hospitals submitting SARI data
Field: DenomHospPopulationAge30-64STL
Coding: Numeric

Population aged 30-64 covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 65-79 covered by the hospitals submitting SARI data
Field: DenomHospPopulationAge65-79STL
Coding: Numeric

Population aged 65-79 covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 80+ covered by the hospitals submitting SARI data
Field: DenomHospPopulationAge80+STL
Coding: Numeric

Population aged 80+ covered by the hospitals submitting aggregated SARI data (denominator).

Population aged 15-64 covered by the hospitals submitting data (alternative)
Field: DenomHospPopulationAge15-64STL
Coding: Numeric

Population aged 15-64 covered by the hospitals submitting aggregated SARI data (denominator), to submit if data for the age groups 15-29 and 30-64 are not available.

Population aged 65+ covered by the hospitals submitting data (alternative)
Field: DenomHospPopulationAge65+STL
Coding: Numeric

Population aged 65+ covered by the hospitals submitting aggregated SARI data (denominator), to submit if data for the age groups 65-79 and 80+ are not available.

Population of unknown age covered by the hospitals submitting data
Field: DenomHospPopulationUnkSTL
Coding: Numeric
Population of unknown age covered by the hospitals submitting aggregated SARI data (denominator). The sum of the age-specific variables and this variable should be equal to the total hospital population (denominator).

Specimens tested for influenza

Number of SARI specimens tested for influenza age 0-4
Field: NumSpecimensTestedFluAge00-04
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 0-4.

Number of SARI specimens tested for influenza age 5-14
Field: NumSpecimensTestedFluAge05-14
Coding: Numeric
Number of SARI specimens tested for influenza from patients aged 5-14.

Number of SARI specimens tested for influenza age 15-29
Field: NumSpecimensTestedFluAge15-29
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 15-29.

Number of SARI specimens tested for influenza age 30-64
Field: NumSpecimensTestedFluAge30-64
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 30-64.

Number of SARI specimens tested for influenza age 65-79
Field: NumSpecimensTestedFluAge65-79
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 65-79.

Number of SARI specimens tested for influenza age 80+
Field: NumSpecimensTestedFluAge80+
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 80+.

Number of SARI specimens tested for influenza age 15-64 (Alternative)
Field: NumSpecimensTestedFluAge15-64
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens tested for influenza age 65+ (Alternative)
Field: NumSpecimensTestedFluAge65+
Coding: Numeric

Number of SARI specimens tested for influenza from patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens tested for influenza age unknown
Field: NumSpecimensTestedFluAgeUnk
Coding: Numeric
Number of SARI specimens tested for influenza from patients of unknown age. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens tested for influenza.

Specimens positive for influenza

Number of SARI specimens positive for influenza age 0-4
Field: NumSpecimensFluDetectAge00-04
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 0-4.

Number of SARI specimens positive for influenza age 5-14
Field: NumSpecimensFluDetectAge05-14
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 5-14.

Number of SARI specimens positive for influenza age 15-29
Field: NumSpecimensFluDetectAge15-29
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 15-29.

Number of SARI specimens positive for influenza age 30-64
Field: NumSpecimensFluDetectAge30-64
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 30-64.

Number of SARI specimens positive for influenza age 65-79
Field: NumSpecimensFluDetectAge65-79
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 65-79.

Number of SARI specimens positive for influenza age 80+
Field: NumSpecimensFluDetectAge80+
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 80+.

Number of SARI specimens positive for influenza age 15-64 (Alternative)
Field: NumSpecimensFluDetectAge15-64
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens positive for influenza age 65+ (Alternative)
Field: NumSpecimensFluDetectAge65+
Coding: Numeric

Number of SARI specimens positive for influenza from patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens positive for influenza age unknown

Field: NumSpecimensFluDetectAgeUnk

Coding: Numeric

Number of SARI specimens positive for influenza from patients of unknown age. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens positive for influenza.

Number of SARI specimens positive for influenza A not subtyped

Field: NumSpecimensAUnkDetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza A (not subtyped).

Number of SARI specimens positive for influenza A(H1)pdm09 not N subtyped

Field: NumSpecimensAH1pdm09DetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza A(H1)pdm09.

Number of SARI specimens positive for influenza A(H1N1)pdm09

Field: NumSpecimensAH1N1pdm09DetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza A(H1N1)pdm09.

Number of SARI specimens positive for influenza A(H3) not N subtyped

Field: NumSpecimensAH3DetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza A(H3) (not N subtyped).

Number of SARI specimens positive for influenza A(H3N2)

Field: NumSpecimensAH3N2DetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza A(H3N2).

Number of SARI specimens positive for influenza B (no lineage determined)

Field: NumSpecimensBDetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza type B without lineage determination.

Number of SARI specimens positive for influenza B Victoria

Field: NumSpecimensBVICDetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza B/Victoria.

Number of SARI specimens positive for influenza B Yamagata
Field: NumSpecimensBYAMDetectSARI
Coding: Numeric

Number of SARI specimens positive for influenza B/Yamagata.

Specimens tested for SARS-CoV-2

Number of SARI specimens tested for SARS-CoV-2 age 0-4
Field: SARITestedSARSCoV2Age00-04
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 0-4.

Number of SARI specimens tested for SARS-CoV-2 age 5-14
Field: SARITestedSARSCoV2Age05-14
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 5-14.

Number of SARI specimens tested for SARS-CoV-2 age 15-29
Field: SARITestedSARSCoV2Age15-29
Coding: Numeric
Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 15-29.

Number of SARI specimens tested for SARS-CoV-2 age 30-64
Field: SARITestedSARSCoV2Age30-64
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 30-64.

Number of SARI specimens tested for SARS-CoV-2 age 65-79
Field: SARITestedSARSCoV2Age65-79
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 65-79.

Number of SARI specimens tested for SARS-CoV-2 age 80+
Field: SARITestedSARSCoV2Age80+
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 80+.

Number of SARI specimens tested for SARS-CoV-2 age 15-64 (Alternative)
Field: SARITestedSARSCoV2Age15-64
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens tested for SARS-CoV-2 age 65+ (Alternative)
Field: SARITestedSARSCoV2Age65+
Coding: Numeric

Number of tests for SARS-CoV-2 in hospitalised SARI patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens tested for SARS-CoV-2 age unknown
Field: SARITestedSARSCoV2AgeUnk
Coding: Numeric
Number of tests for SARS-CoV-2 in hospitalised SARI patients with unknown age. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens tested for SARS-CoV-2.

Specimens positive for SARS-CoV-2

Number of SARI specimens positive for SARS-CoV-2 aged 0-4
Field: NumSpecimensSARSCoV2DetectSARIAge00-04
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 0-4.

Number of SARI specimens positive for SARS-CoV-2 aged 5-14
Field: NumSpecimensSARSCoV2DetectSARIAge05-14
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 5-14.

Number of SARI specimens positive for SARS-CoV-2 aged 15-29
Field: NumSpecimensSARSCoV2DetectSARIAge15-29
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 15-29.

Number of SARI specimens positive for SARS-CoV-2 aged 30-64
Field: NumSpecimensSARSCoV2DetectSARIAge30-64
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 30-64.

Number of SARI specimens positive for SARS-CoV-2 age 65-79
Field: NumSpecimensSARSCoV2DetectSARIAge65-79
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 65-79.

Number of SARI specimens positive for SARS-CoV-2 age 80+
Field: NumSpecimensSARSCoV2DetectSARIAge80+
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 80+.

Number of SARI specimens positive for SARS-CoV-2 age 15-64 (Alternative)
Field: NumSpecimensSARSCoV2DetectSARIAge15-64
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens positive for SARS-CoV-2 age 65+ (Alternative)
Field: NumSpecimensSARSCoV2DetectSARIAge65+
Coding: Numeric

Number of SARI specimens positive for SARS-CoV-2 in patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens positive for SARS-CoV-2 age unknown
Field: NumSpecimensSARSCoV2DetectSARIAgeUnk
Coding: Numeric
Number of SARI specimens positive for SARS-CoV-2 in patients with unknown age. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens positive for SARS-CoV-2.

Specimens tested for MERS-CoV

Number of SARI specimens tested for MERS-CoV
Field: NumSpecimensTestedMERS
Coding: Numeric

Number of SARI specimens tested for MERS-CoV.

Specimens positive for MERS-CoV

Number of SARI specimens positive for MERS-CoV
Field: NumSpecimensMERSDetectSARI
Coding: Numeric

Total number of SARI specimens positive for MERS-CoV.

Specimens tested for RSV

Number of SARI specimens tested for RSV age 0-4
Field: NumSpecimensTestedRSVAge00-04
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 0-4.

Number of SARI specimens tested for RSV age 5-14
Field: NumSpecimensTestedRSVAge05-14
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 5-14.

Number of SARI specimens tested for RSV age 15-29

Field: NumSpecimensTestedRSVAge15-29
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 15-29.

Number of SARI specimens tested for RSV age 30-64
Field: NumSpecimensTestedRSVAge30-64
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 30-64.

Number of SARI specimens tested for RSV age 65-79
Field: NumSpecimensTestedRSVAge65-79
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 65-79.

Number of SARI specimens tested for RSV age 80+
Field: NumSpecimensTestedRSVAge80+
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 80+.

Number of SARI specimens tested for RSV age 15-64 (Alternative)
Field: NumSpecimensTestedRSVAge15-64
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens tested for RSV age 65+ (Alternative)
Field: NumSpecimensTestedRSVAge65+
Coding: Numeric

Number of SARI specimens tested for RSV from patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens tested for RSV age unknown
Field: NumSpecimensTestedRSVAgeUnk
Coding: Numeric
Number of SARI specimens tested for RSV from patients aged unknown. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens tested for RSV.

Specimens positive for RSV

Number of SARI specimens positive for RSV age 0-4
Field: NumSpecimensRSVDetectAge00-04
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 0-4.

Number of SARI specimens positive for RSV age 5-14

Field: NumSpecimensRSVDetectAge05-14
Coding: Numeric
Number of SARI specimens positive for RSV from patients aged 5-14.

Number of SARI specimens positive for RSV age 15-29
Field: NumSpecimensRSVDetectAge15-29
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 15-29.

Number of SARI specimens positive for RSV age 30-64
Field: NumSpecimensRSVDetectAge30-64
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 30-64.

Number of SARI specimens positive for RSV age 65-79
Field: NumSpecimensRSVDetectAge65-79
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 65-79.

Number of SARI specimens positive for RSV age 80+
Field: NumSpecimensRSVDetectAge80+
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 80+.

Number of SARI specimens positive for RSV age 15-64 (Alternative)
Field: NumSpecimensRSVDetectAge15-64
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 15-64, to submit if data for the age groups 15-29 and 30-64 are not available.

Number of SARI specimens positive for RSV age 65+ (Alternative)
Field: NumSpecimensRSVDetectAge65+
Coding: Numeric

Number of SARI specimens positive for RSV from patients aged 65+, to submit if data for the age groups 65-79 and 80+ are not available.

Number of SARI specimens positive for RSV age unknown
Field: NumSpecimensRSVDetectAgeUnk
Coding: Numeric
Number of SARI specimens positive for RSV from patients with age unknown. The sum of the age-specific variables and this variable should be equal to the total number of SARI specimens positive for RSV.

Number of SARI specimens positive for RSV type A (all ages)
Field: NumSpecimensRSVTypeA

Coding: Numeric

Number of SARI specimens positive for RSV type A.

Number of SARI specimens <u>positive</u> for RSV type B (all ages)
Field: NumSpecimensRSVTypeB
Coding: Numeric

Number of SARI specimens positive for RSV type B.

INFLCLINAGGR metadata

Common TESSy variables

Record type (mandatory)
Field: RecordType
Coding: INFLCLINAGGR

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: INFLCLIN

Subject of the data reported.

Data source (mandatory)
Field: DataSource
Coded value list: [Data sources]

The data source (surveillance system) that the record originates from.

Reporting country (mandatory)
Field: Reportingcountry
Coded value list: [Countries]
Coding: International organization for standardization (ISO) 3166-1-alpha-2, (two-letter code)

The country reporting the record.

Date used for statistics (mandatory)
Field: DateUsedForStatistics
Coding: yyyy-mm-dd

The reference date used for standard reports that is compared to the reporting period. The date used for statistics can be any date that the reporting country finds applicable, e.g. date of notification, date of diagnosis or any other date.

Epidemiological variables

ARI_Denominator: Age 0-4

Field: ARI_Denominator00-04
Coding: Number

Number of ARI_Denominator in the age 0-4. For type, see data source property 'Type of denominator'.

ARI_Denominator: Age 5-14
Field: ARI_Denominator05-14
Coding: Number

Number of ARI_Denominator in the age 5-14. For type, see data source property 'Type of denominator'.

ARI_Denominator: Age 15-64
Field: ARI_Denominator15-64
Coding: Number

Number of ARI_Denominator in the age 15-64. For type, see data source property 'Type of denominator'.

ARI_Denominator: Age 65+
Field: ARI_Denominator65+
Coding: Number

Number of ARI_Denominator in the age >= 65. For type, see data source property 'Type of denominator'.

ARI_Denominator: Total
Field: ARI_DenominatorNumberOfCases
Coding: Number

Total number of ARI_denominator. For type, see data source property 'Type of denominator'.

ARI_Denominator: Age unknown
Field: ARI_DenominatorUnk
Coding: Number

Number of ARI_Denominator with unknown age. For type, see data source property 'Type of denominator'.

ARI: Age 0-4
Field: ARI00-04
Coding: Number

Number of ARI observed in the age 0-4.

ARI: Age 5-14
Field: ARI05-14
Coding: Number

Number of ARI observed in the age 5-14.

ARI: Age 15-64
Field: ARI15-64

Coding: Number

Number of ARI observed in the age 15-64.

ARI: Age 65+
Field: ARI65+
Coding: Number

Number of ARI observed in the age >= 65.

ARI: Total number of observed
Field: ARINumberOfCases
Coding: Number

Number of ARI observed.

ARI: Age unknown
Field: ARIUnk
Coding: Number

Number of ARI observed - age unknown.

ILI_Denominator: Age 0-4
Field: ILI_Denominator00-04
Coding: Number

Number of ILI_Denominator in the age 0-4. For type, see data source property 'Type of denominator'.

ILI_Denominator: Age 5-14
Field: ILI_Denominator05-14
Coding: Number

Number of ILI_Denominator in the age 5-14. For type, see data source property 'Type of denominator'.

ILI_Denominator: Age 15-64
Field: ILI_Denominator15-64
Coding: Number

Number of ILI_Denominator in the age 15-64. For type, see data source property 'Type of denominator'.

ILI_Denominator: Age 65+
Field: ILI_Denominator65+
Coding: Number

Number of ILI_Denominator in the age >= 65. For type, see data source property 'Type of denominator'.

ILI_Denominator: Total
Field: ILI_DenominatorNumberOfCases
Coding: Number

Total number of ILI_denominator. For type, see data source property 'Type of denominator'.

ILI_Denominator: Age unknown
Field: ILI_DenominatorUnk
Coding: Number

Number of ILI_Denominator with unknown age. For type, see data source property 'Type of denominator'.

ILI: Age 0-4
Field: ILI00-04
Coding: Number

Number of ILI observed in the age 0-4.

ILI: Age 5-14
Field: ILI05-14
Coding: Number
Number of ILI observed in the age 5-14.

ILI: Age 15-64
Field: ILI15-64
Coding: Number

Number of ILI observed in the age 15-64.

ILI: Age 65+
Field: ILI65+
Coding: Number

Number of ILI observed in the age >= 65.

ILI: Total number of observed
Field: ILINumberOfCases
Coding: Number

Number of ILI observed.

ILI: Age unknown
Field: ILIUnk
Coding: Number

Number of ILI observed - age unknown.

Geographic spread of influenza (mandatory)
Field: GeographicSpread
Coded value list: [GeographicSpread]
Coding: L = Local
NO = No activity
R = Regional
S = Sporadic
UNK = Unknown (no information available)
W = Widespread

Geographic spread is a measure of the geographic distribution of reported detections of influenza viruses in specimens from sentinel or non-sentinel sources.

- No activity: No influenza viruses detected (other than detections from cases with recent known history of travel).
- Sporadic: Influenza viruses sporadically detected.
- Local(ised): Circulation of influenza viruses limited to one administrative unit in the MS (or reporting site);
- Regional: Circulation of influenza viruses appearing in multiple but less than 50% of the administrative units of the MS (or reporting sites)*.
- Widespread: Circulation of influenza viruses appearing in 50% or more of the administrative units of the MS (or reporting sites).

*Regional activity is generally not used for MS with a small population (<5 M) and covering a small geographic area."

Intensity of influenza

Field: Intensity
Coded value list: [Intensity]
Coding: B = Baseline
H = High
L = Low
M = Medium
UNK = Unknown (no information available)
VH = Very High

Intensity is a measure of influenza activity within individual MS.

- Baseline or below epidemic threshold: ILI or ARI rates that are very low and at levels usually seen throughout the inter-epidemic period.
- Low: ILI or ARI rates that are relatively low compared to rates from historical data but higher than the baseline. Influenza virus detections have been reported.
- Medium: ILI or ARI rates that are similar to rates usually observed, based on historical data. Influenza virus detections have been reported.
- High intensity: ILI or ARI rates that are higher than rates usually observed, based on historical data. Influenza virus detections have been reported.
- Very high: ILI/ARI rates that are much higher than rates usually observed, based on historical data. Influenza virus detections have been reported.

Intensity level can be defined using two approaches:
a) Qualitative indicator based on a national expert evaluation of intensity. For MS that report intensity as a qualitative indicator using an expert evaluation of intensity, they can do so by reviewing the weekly ILI or ARI rates and comparing them to rates in previous seasons. It is recommended to take influenza virus detections into account as well.

b) Semi-quantitative indicator using historical data (e.g. Moving Epidemic Method, WHO or other methods). For MS that report intensity as a semi-quantitative indicator, they can do so by a predefined method. It is recommended to take influenza virus detections into account as well as syndromic data.

Trend of influenza

Field: Trend
Coded value list: [Trend]
Coding: D = Decreasing
I = Increasing
S = Stable

UNK = Unknown (no information available)

Trend is a measure of changes in influenza activity (based on ILI and/or ARI rates and lab-confirmed influenza cases) in comparison to the previous week or weeks.

• Increasing: ILI and/or ARI consultation rates are substantially higher compared to the previous week(s) and influenza viruses must have been detected in specimens from sentinel and/or non-sentinel sources[ab].

• Stable: ILI and/or ARI consultation rates are similar compared to the previous week(s). Influenza viruses must have been detected in specimens from sentinel and/or non-sentinel sources[b].

• Decreasing: ILI and/or ARI consultation rates are substantially lower compared to the previous week(s). Influenza viruses must have been detected in specimens from sentinel and/or non-sentinel sources ab.

a) Multiple prior weeks should be used to assign increasing or decreasing trend when intensity is "Baseline or below epidemic threshold" and in the absence of such evidence default to stable; b) Sentinel data are preferred but if these are not available non-sentinel data may be used.

Impact

Field: Impact
Coded value list: [Impact]
Coding: B = Baseline
H = High
L = Low
M = Medium
UNK = Unknown (no information available)
VH = Very High

Impact is a measure of resultant hospitalization of the epidemic within individual MS.

• Baseline: influenza related hospitalizations (SARI or laboratory confirmed hospitalizations, as counts, percentage positivity or rates) at levels usually seen throughout the inter-epidemic period.

• Low: influenza related hospitalizations (SARI or laboratory confirmed hospitalizations, as counts, percentage positivity or rates) that are relatively low compared to rates from historical data but higher than the baseline.

• Medium: influenza related hospitalizations (SARI or laboratory confirmed hospitalizations, as counts, percentage positivity or rates) that are similar to rates usually observed, based on historical data.

• High: influenza related hospitalizations (SARI or laboratory confirmed hospitalizations, as counts, percentage positivity or rates) that are higher than rates usually observed, based on historical data.

• Very high: influenza related hospitalizations (SARI or laboratory-confirmed hospitalizations, as counts, percentage positivity or rates) that are much higher than rates usually observed, based on historical data.

PISA indicator for impact of influenza

Field: PISA_Impact
Coded value list: [NoLowModHigExtUnk]
Coding: E = Extraordinary
H = High
L = Low
M = Moderate
N = No activity
UNK = Unknown

Suggested parameters that can be used for the assessment:

-Weekly number of hospital or ICU admissions for influenza, or rate per unit population
-Influenza-confirmed SARI proportion of all hospital or ICU admissions
-Number of patients currently in hospital or ICU with influenza, or rate per unit population
-Composite (product) of weekly SARI rate and weekly percentage positivity rates of SARI cases for influenza
-Weekly excess P&I or all-cause mortality
-Number of hospitalizations for influenza/ requiring oxygen support.

PISA Impact comment
Field: PISA_Impact_comment
Coding: Text

Comment field related to PISA Impact indicator.

Confidence of the PISA indicator Impact
Field: PISA_Impact_confidence
Coded value list: [LowMediumHighUnk]
Coding: H = High
L = Low
M = Medium
UNK = Unknown

Level of confidence for the indicator assessment.

PISA indicator for seriousness of influenza
Field: PISA_Seriousness
Coded value list: [LowMediumHighUnk]
Coding: E = Extraordinary
H = High
L = Low
M = Moderate
N = No activity
UNK = Unknown

Parameter to be used for the assessment (middle and end of season only):
-Cumulative death: hospitalization ratio (for respiratory hospitalizations or ideally for confirmed influenza cases and cases with outcome or discharge data)
-Cumulative ICU: hospitalization ratio (for respiratory hospitalizations or ideally for confirmed influenza)
-SARI:ILI or SARI:ARI ratios.

PISA Seriousness comment
Field: PISA_Seriousness_comment
Coding: Text

PISA Seriousness comment.

Confidence of the PISA indicator Seriousness
Field: PISA_Seriousness_confidence
Coded value list: [LowMediumHighUnk]
Coding: H = High
L = Low
M = Medium
UNK = Unknown

Level of confidence for the indicator assessment.

Pisa indicator for transmissibility of influenza
Field: PISA_Transmissibility
Coded value list: [NoLowModHigExtUnk]

Coding: E = Extraordinary
H = High
L = Low
M = Moderate
N = No activity
UNK = Unknown

Parameter to be used for the assessment:
-Weekly ILI or MAARI cases as a proportion of total visits or incidence rates
-Composite (product) of weekly ILI or MAARI rates and weekly percentage positivity for influenza
-Percentage positivity from specific syndromic presentations (e.g. ILI, ARI, MAARI)
-Number of influenza outbreaks reported in aged care facilities or other susceptible groups
-Other healthcare system usage for mild respiratory illness (e.g. health hotline calls, consultations for coughs/fever, searches on health advice website etc)
-Data from participatory surveillance (e.g. prevalence of symptomatic illness/health seeking behaviour and testing practices).

PISA Transmissibility comment
Field: PISA_Transmissibility_comment
Coding: Text

Comment field related to PISA transmissibility indicator.

Confidence of the PISA indicator Transmissibility
Field: PISA_Transmissibility_confidence
Coded value list: [LowMediumHighUnk]
Coding: H = High
L = Low
M = Medium
UNK = Unknown

Level of confidence for the indicator assessment.

Number of reporting physicians
Field: NumberOfPhysicians
Coding: Number

Number of reporting physicians.

Comments for the network only
Field: CommentNonPublic
Coding: Text

Comments for the network only.

Public comments
Field: CommentPublic
Coding: Text

Public comments provide additional relevant information that can be made public.

INFLANTIVIR metadata

The metadata includes information on virus, demographics, source of specimen, hospitalisation, underlying conditions, vaccination status and treatment. The reporting also includes the genetic clade and antigenic group to which the virus belongs, as well as phenotypic and/or genotypic antiviral susceptibility results.

Common TESSy variables

Record Identifier (mandatory)
Field: RecordId
Coding: Text

The name of the virus following WHO format rules: ?/?/?/yyyy - [A|B]/[country|region|city]/[number]/[year] (e.g. A/California/7/2009). If the sample is taken from an animal host, use A/?/?/?/yyyy - A/[animal host]/[country|region|city]/[number]/[year] (e.g. A/chicken/Netherlands/1/2003). IMPORTANT: As the database is based on virus isolate records, an isolate may already be entered. Be aware that data entered by the European reference laboratory and data entered by a country is linked using the strain number. It is therefore vital that the strain numbers on both records are equal and match.

Record type (mandatory)
Field: RecordType
Coding: INFLANTIVIR

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: INFLANTIVIR

Subject of the data reported.

Data source (mandatory)
Field: Data source

Coded value list name: [Data sources]

The data source (surveillance system) that the record originates from.

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: Reporting country

Coded value list name: [Countries]

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

The country reporting the record.

Date used for statistics (mandatory)

Field: Date used for statistics

Coding: yyyy-mm-dd

Date of specimen collected.

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.

Gender

Field: Gender

Coding: Gender:

F = Female

M = Male

O = Other

Unk = Unknown

Gender of the reported case.

Date of Onset of Disease
Field: DateOfOnset
Coding: yyyy-mm-dd
UNK = Unknown

Date of onset of disease. Not applicable in asymptomatic cases. If not applicable, please use 'Unk'.

Probable country of infection
Field: ProbableCountryOfInfection
Coded value list: Country
Country(ies) visited in the 2 weeks prior to onset of illness. If there is more than one country N/A should be used in the empty repeated fields.

Exposure to drugs in a household 2 weeks before onset of disease
Field: ExposureDrug2weeksHouse
Coded value list: [YesNoUnk]
Coding: N = No
Unk = Unknown
Y = Yes

Has anyone in the household been treated with antiviral drug in 14 days prior to onset of illness.

Exposure to type of drug in a household 2 weeks before onset of disease
Field: ExposureDrug2weeksHouseType
Coded value list: [ExposureDrugINFL]
Coding: A = Amantadine
B = Baloxavir marboxil
O = Oseltamivir
P = Peramivir
RIM = Rimantadine
Unk = Unknown
Z = Zanamivir

Kind of drug for household member(s) treatment in 14 days prior to onset of illness of the patient.

Patient exposure to drugs 2 weeks before onset of disease
Field: ExposureDrug2weeksPatient
Coded value list: [YesNoUnk]
Coding: N = No
Unk = Unknown
Y = Yes

Has the patient been treated with antiviral drug in 14 days prior to onset of illness.

Patient exposure to type of drug 2 weeks before onset of disease
Field: ExposureDrug2weeksPatientType
Coded value list: [ExposureDrugINFL]
Coding: A = Amantadine
B = Baloxavir marboxil

O = Oseltamivir
P = Peramivir
RIM = Rimantadine
Unk = Unknown
Z = Zanamivir

Kind of drug for patient treatment in 14 days prior to onset of illness.

Source virus (mandatory)
Field: VirusSource
Coded value list: [VirusSourceINFL]
Coding: N = Non-sentinel patient
S = Sentinel patient
Unk = Unknown

Of which system the patient of which the virus has been isolated is coming from, sentinel or non-sentinel.

Category (if non-sentinel) (mandatory)
Field: VirusCategoryIfNonSentinel
Coding value list: [VirusCategoryIfNonSentinelINFL]
Coding: C = Community
H = Hospital
I = Institution
NA = Not applicable
O = other
Unk = Unknown

Further specification of non-sentinel source.

Virus (sub)type (mandatory)
Field: Subtype
Coded value list: InfluenzaTypeSubtype
Coding:
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
AH1pdm09 = A(H1)pdm09
AH1N1pdm09 = A(H1N1)pdm09
UNK = Unknown
Virus type and subtype.

Vaccination status
Field: VaccStatus
Coding value list: [VaccStatusINFL]
Coding: NOTVACC = Not vaccinated
Unk = Unknown
VACCINFULL = Fully vaccinated

Vaccinated with vaccine for current season. Fully vaccinated is only applicable for young children. Majority of the patients only need one vaccination/season.

I-MOVE specimen
Field: IMOVE
Coding value list: [YesNoUnk]
Coding: N = No
NA = Not applicable
Unk = Unknown
Y = Yes

This specimen has been included in the I-MOVE vaccine effectiveness study.

Hospitalisation during the 4 weeks after onset of illness
Field: Hospitalisation
Coding value list: [YesNoUnk]
Coding: N = No
Unk = Unknown
Y = Yes

Hospitalisation in the 4 weeks after onset of illness.

Progression of the disease in the 4 weeks after the onset of illness
Field: Progress4weeks
Coding value list: [Progress4weeks]
Coding: C = Complicated
U = Uncomplicated
Unk = Unknown

Progression of the disease in the 4 weeks after onset of illness

ImmunoCompromised
Field: ImmunoCompromised
Coding value list: [ImmunoCompromised]
Coding: N = No
UNK = Unknown
YD = Yes, due to disease
YM = Yes, due to medication
YRU = Yes, reason unknown

Information, if case is immunocompromised.

Diagnosis of complication
Field: ComplicationDiagnosis
Coding value list: [ComplicationDiagnosisINFL]
Coding: OTH = Other
OTIT = Otitis
PNEU = Pneumonia

Complication diagnosis.

Other diagnosis of complication
Field: ComplicationDiagnosisOther
Coding: Text

Other complication diagnosis.

Outcome of case
Field: Outcome
Coding value list: [CaseReportOutcome]
Coding: A = Alive
D = Died
NA = Not applicable
Unk = Unknown

Death in the 4 weeks after onset of illness.

Laboratory variables

Antigenic group

Field: Antigenic group

Coded value list: AntigenicGroupINFL

Coding:

agAH1/Lisboa/188/2023 = A(H1)pdm09_5a.2a(C.1.9)_A/Lisboa/188/2023-like
agAH1/Sydney/5/2021 = A(H1)pdm09_5a.2a(C.1)_A/Sydney/5/2021-like
agAH1/Victoria/4897/2022 = A(H1)pdm09_5a.2a.1_A/Victoria/4897/2022-like
agAH1/Wisconsin/67/2022 = A(H1)pdm09_5a.2a.1_A/Wisconsin/67/2022-like
agAH1NOCAT = A(H1)pdm09 not attributed to category
agAH3/Croatia/10136RV/2023 = A(H3)_2a.3a.1(J.2)_A/Croatia/10136RV/2023-like
agAH3/Darwin/9/2021 = A(H3)_2a_A/Darwin/9/2021-like
agAH3/France/IDF-IPP29542/2023 = A(H3)_2a.3a.1(J.4)_A/France/IDF-IPP29542/2023-like
agAH3/Thailand/8/2022 = A(H3)_2a.3a.1_A/Thailand/8/2022-like
agAH3NOCAT = A(H3) not attributed to category
agBVicB/Austria/1359417/2021 = B(Vic)_V1A.3a.2(C)_B/Austria/1359417/2021-like
agBVicB/Stockholm/3/2022 = B(Vic)_V1A.3a.2(C.5)_B/Stockholm/3/2022-like
agBVicB/Washington/02/2019 = B(Vic)_V1A.3_B/Washington/02/2019-like
agBVicNOCAT = B(Vic) lineage not attributed to category
Coded list of reference strains for Antigenic group.

Genetic clade

Field: Genetic clade

Coded value list: GeneticCladeINFL

Coding:

genAH1/Lisboa/188/2023 = A(H1)pdm09_5a.2a(C.1.9)_A/Lisboa/188/2023
genAH1/Michigan/62/2023 = A(H1)pdm09_5a.2a(C.1.8)_A/Michigan/62/2023
genAH1/Netherlands/10468/2023 = A(H1)pdm09_5a.2a(C.1)_A/Netherlands/10468/2023
genAH1/Sydney/5/2021 = A(H1)pdm09_5a.2a(C.1)_A/Sydney/5/2021
genAH1/Victoria/4897/2022 = A(H1)pdm09_5a.2a.1(D)_A/Victoria/4897/2022
genAH1NOClade = A(H1)pdm09_NOClade
genAH1SubgroupNotListed = A(H1)pdm09_SubgroupNotListed
genAH3/Croatia/10136RV/2023 = A(H3)_2a.3a.1(J.2)_A/Croatia/10136RV/2023

genAH3/Darwin/9/2021 = A(H3)_2a_A/Darwin/9/2021
genAH3/France/IDF-IPP29542/2023 = A(H3)_2a.3a.1(J.4)_A/France/IDF-IPP29542/2023
genAH3/Lisboa/216/2023 = A(H3)_2a.3a.1(J.2.2)_A/Lisboa/216/2023
genAH3/Sydney/856/2023 = A(H3)_2a.3a.1(J.1)_A/Sydney/856/2023
genAH3/Thailand/8/2022 = A(H3)_2a.3a.1(J)_A/Thailand/8/2022
genAH3/West Virginia/51/2024 = A(H3)_2a.3a.1(J.2.1)_A/WestVirginia/51/2024
genAH3NOClade = A(H3)_NOClade
genAH3SubgroupNotListed = A(H3)_SubgroupNotListed
genBVicB/Austria/1359417/2021 = B(Vic)_V1A.3a.2(C)_B/Austria/1359417/2021
genBVicB/Catalonia/2279261NS/2023 = B(Vic)_V1A.3a.2(C.5.1)_B/Catalonia/2279261NS/2023
genBVicB/Guangxi-Beiliu/2298/2023 = B(Vic)_V1A.3a.2(C.5.7)_B/Guangxi-Beiliu/2298/2023
genBVicB/Stockholm/3/2022 = B(Vic)_V1A.3a.2(C.5)_B/Stockholm/3/2022
genBVicB/Switzerland/329/2024 = B(Vic)_V1A.3a.2(C.5.6)_B/Switzerland/329/2024
genBVicB/Washington/02/2019 = B(Vic)_V1A.3_B/Washington/02/2019
genBVicNOClade = B(Vic)_NOClade
genBVicSubgroupNotListed = B(Vic)_SubgroupNotListed
genBYamB/Phuket/3073/2013 = B(Yam)_Y3_B/Phuket/3073/2013
genBYamNOClade = B(Yam)_NOClade

Coded list of reference strains for Genetic clade.

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.

ISD: HA sequence number

Field: HAISD

Coding: Text

Accession number for sequence data HA, ISD or other.

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.

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.

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.

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.

M2 sequence aa resistance mutations

Field: M2AAMutations

Coding: Text

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

ISD: M2 sequence number

Field: M2ISD

Coding: Text

Accession number for sequence data M2, ISD or other.

NA sequence aa resistance mutations

Field: NAAAMutations

Coding: Text

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

ISD: NA sequence number

Field: NAISD

Coding: Text

Accession number for sequence data NA, ISD or other.

PA sequence aa resistance mutations

Field: PAAAMutations

Coding: Text

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 I38F.

ISD: PA sequence number

Field: PAISD

Coding: Text

Accession number for sequence data PA, ISD or other.

Sequence identifier

Field: SequenceId

Coding: Text

Sequence identifier for whole or partial genome, based on which the sequence read data can be retrieved from GISAID. GISAID isolate sequence accession number should be reported in format EPI_ISL_402123. Reporting of 'NA' or 'UNK' is not allowed.

IC50 Oseltamivir (MUNANA) nM

Field: OseltamivirMUNANA

Coding: Number (decimal number)

Sensitivity for oseltamivir with fluorescent assay using MUNANA in nM.

IC50 Oseltamivir (NA-Star) nM
Field: OseltamivirNAStar
Coding: Number (decimal number)

Sensitivity for oseltamivir with chemiluminescent assay using NAStar in nM.

IC50 Zanamivir (MUNANA) nM
Field: ZanamivirMUNANA
Coding: Number (decimal number)

Sensitivity for zanamivir with fluorescent assay using MUNANA in nM.

IC50 Zanamivir (NA-Star) nM
Field: ZanamivirNAStar
Coding: Number (decimal number)

Sensitivity for zanamivir with chemiluminescent assay using NAStar in nM.

IC50 Amantadine µM
Field: Amantadine
Coding: Number (decimal number)

Sensitivity for amantadine in µM.

IC50 Rimantadine µM
Field: Rimantadine
Coding: Number (decimal number)

Sensitivity for rimantadine in µM.

Weekly interpretive comment on antigenic characterisations
Field: CommentAG
Coding: Text

Weekly interpretive comment on antigenic characterisations.

Weekly interpretive comment on genetic characterisations
Fied: CommentGC
Coding: Text

Weekly interpretive comment on genetic characterisations.

Comment
Field: Comment
Coding: Text

Free comment on data, suggestion to fill in conclusion here.

NCOVVARIANT metadata

NCOVVARIANT is used for reporting of aggregated data on variants of interest and of concern per week.

Common TESSy variables

Record Identifier (mandatory)
Field: RecordId
Coding: Text (max 80 characters)

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

- unique within the national COVID-19 disease surveillance system
- anonymous.

Record type (mandatory)
Field: RecordType
Coding: NCOVVARIANT

The record type defines the structure and the format of the data reported. 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 (Table 2). 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: NCOVVARIANT

The subject describes the disease to be reported.

Data source (mandatory)
Field: DataSource
Coding: Pre-assigned as CountryCode-NCOVVARIANT to each country; can be modified by National Coordinator

The data source specifies the surveillance system from which the data originates and is generated and revised/updated by the national contact point for surveillance in each Member State. The descriptions of the surveillance systems submitted to TESSy should be kept up to date and will be used to assist with data interpretation.

Reporting country (mandatory)
Field: ReportingCountry
Coded value list: [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 of sampling.

Epidemiological variables

Virus variant of SARS-CoV-2
Field: VirusVariant
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 S486P. Mutational proxy: Spike: Q183E, F486P, F490S
BA.2.86 = Pango lineage BA.2.86 and sub-lineages (excluding KP.3 and sub-lineages)
KP.3 = Pango lineage KP.3 and sub-lineages
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 VirusVariantOther. 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 VirusVariantOther. If typing results are inconclusive, report UNK.

Virus variant type other specified
Field: VirusVariantOther
Coding: TEXT

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

Number of detections from representative surveillance – sentinel
Field: NumberRepresentativeSentinel
Coding: Numeric

Number of the specific variant detected from representative sentinel (primary care or SARI) surveillance. Refer to *https://www.ecdc.europa.eu/en/publications-data/operational-considerations-respiratory-virus-surveillance-europe* for more details.

Number of detections from representative surveillance – non-sentinel
Field: NumberRepresentativeNonSentinel
Coding: Numeric

Number of the specific variant detected from a carefully selected (representative) subset of non-sentinel specimens where this is needed to increase the volume of representative sequencing or genotyping to the desired detection threshold. Refer to *https://www.ecdc.europa.eu/en/publications-data/operational-considerations-respiratory-virus-surveillance-europe* for more details.

Number of detections from targeted surveillance
Field: NumberTargeted
Coding: Numeric

Number of the specific variant detected from targeted sequencing or genotyping, such as 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.

Number of detections with unknown reason for sequencing
Field: NumberUNK
Coding: Numeric

Number of the specific variant where the reason for sequencing or genotyping was not known.