

REPORTING PROTOCOL

EpiPulse Cases

Reporting Protocol for integrated
respiratory virus surveillance - Version 1.1

June 2026

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Introduction

This reporting protocol describes data collection in [EpiPulse Cases](#) for respiratory virus surveillance (including influenza-like illness (ILI), acute respiratory infection (ARI), severe acute respiratory infection (SARI), Influenza, SARS-CoV-2 and RSV) in the European Union/European Economic Area (EU/EEA) and World Health Organization European Region. From June 2026, all respiratory virus surveillance data are reported to EpiPulse Cases, with the exception of virus characterisation data which can still be reported via the TESSy record types INFLANTIVIR and, optionally, NCOVVARIANT (see [related reporting protocol](#)).

Reporting protocols are data collection guidelines for the data managers of reporting countries, and the protocol design is intended to improve user-friendliness by:

- introducing a uniform structure to make it easier for data managers to find data collection information across different subjects;
- removing information which is not relevant for data managers.

Since the data managers in reporting countries often have multiple roles, subject-specific material is distributed in the multiple annexes together with the reporting protocol.

How to use this document

This reporting protocol provides information for the data managers of reporting countries in three main sections:

- Reporting to EpiPulse Cases which contains guidelines on how to prepare data for submission to EpiPulse Cases and links to further information.
- Annex 1 which provides an introduction and overview of reporting for the PISA framework
- Annex 2 which contains the metadata for RESPIQUAL

Finding further information

Updated links to all the schedules, documentation and training materials mentioned in this reporting protocol are included in the [EpiPulse Help](#), including:

- EpiPulse Cases Metadata
- EpiPulse Cases Machine to Machine Technical Documentation

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Reporting to EpiPulse Cases

EpiPulse Cases was built as a replacement for TESSy, with the aim of improving the process of reporting, reviewing, and updating surveillance data. This section provides both an overview of the EpiPulse Cases reporting process and tips on where you can find useful information.

The overall process is as follows:

- Familiarise yourself with the data collection deadlines.
- Prepare (export and transform) your data.
- Check that your data complies with the EpiPulse Cases metadata– see [EpiPulse Help](#).
- Check that your data sources are up to date.
- Submit your file(s) to EpiPulse Cases.
- Finalise and approve your submission.

Checking the data collection schedule

A link to the current data collections schedule can be found the [EpiPulse Help](#) section.

Preparing data

After you have exported the data from your national database, you need to ensure that the data are in a format that EpiPulse Cases can accept. EpiPulse Cases accepts only CSV and XML files, optionally ZIP-compressed. The EpiPulse Cases metadata has been developed from the TESSy Metadata, with the aim to make only the minimal number of changes necessary, and to hopefully provide a better experience when reporting your datasets to ECDC.

A file converter tool is also available in EpiPulse Cases to support users in the transition period with the conversion of files in TESSy format to a format that would be compatible to EpiPulse Cases, see Section 18 in the EpiPulse Cases Guide – see [EpiPulse Help](#).

Specific guidelines for data collection and preparation for EpiPulse Cases are provided in the annexes.

Using latest metadata

The metadata defines the fields and data formats that are valid as input to EpiPulse Cases for a given subject. The EpiPulse Cases metadata includes a section that compares and highlights the changes between TESSy and EpiPulse Cases, to facilitate the transition.

As the requirements for data to be shared among ECDC stakeholders can change, the data format changes needed to support the new requirements are identified and agreed upon between the National Surveillance Contact Points, the Network Coordination Groups and ECDC's disease experts. These changes are then implemented to the EpiPulse Cases metadata.

The metadata for the subject of this reporting protocol are described in Annex 2.

It is especially important to focus on:

- **Field formats**
Many fields require the data to be 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.
- **Reference Values (the equivalent of TESSy Coded Values)**
Some fields only permit the use of specific values (reference values). For example, **M**, **F** or **OTH** are the coded values for 'Sex' and any other value in a 'Sex' field will be rejected. Please note that **UNK** is no longer a valid code, you may leave the field empty instead.

The EpiPulse Cases metadata Excel file contains all the definitions and rules necessary to format data correctly. The **READ ME** sheet of the Excel document explains how to work with the metadata. It can be downloaded from the [EpiPulse Help](#).

Filtering the fields in the file by subject will enable you to see the fields required for your subject and the rules that apply to these fields.

Checking your surveillance system descriptors

Before submitting file(s), please review your data source(s) in EpiPulse (in the menu, go to 'Report' -> '[Surveillance systems descriptors](#)') and update the information as necessary.

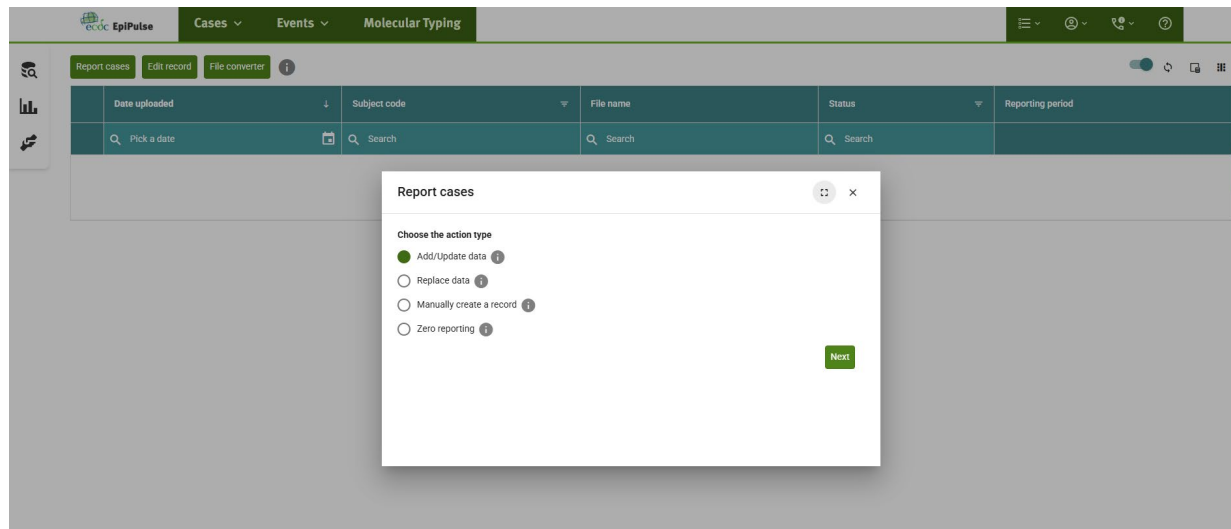
Complete and up-to-date data source information for each subject is important for improving the interpretation of data – each surveillance system has different features that need to be considered when comparing data at European level.

If your data source information is out-of-date and you do not have access rights to update it, please ask your National Focal Point for Surveillance or National Coordinator to do so.

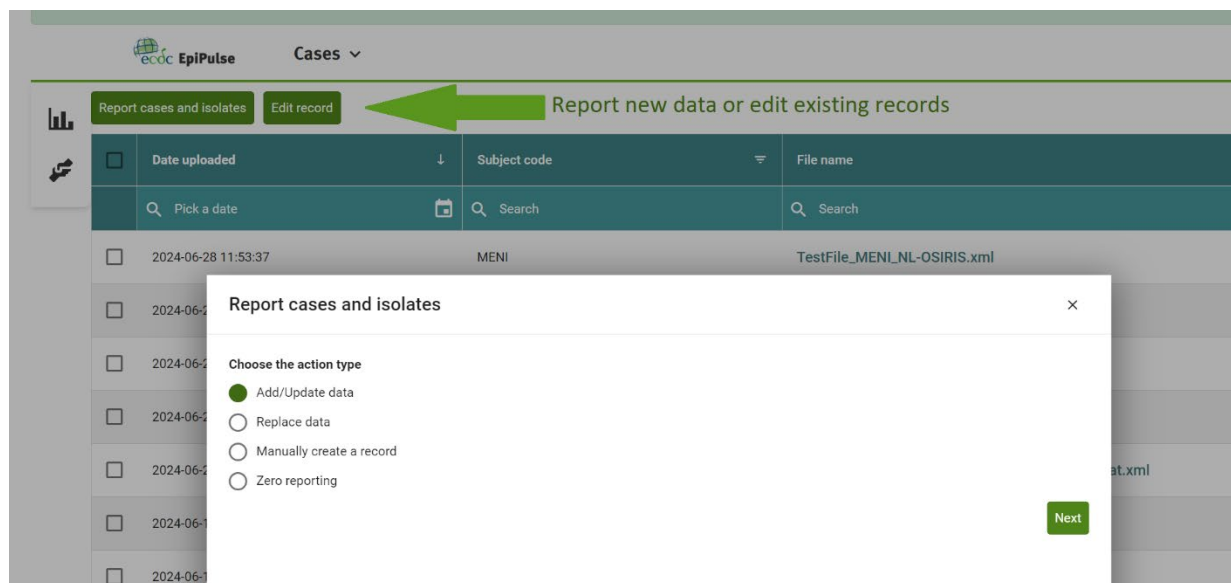
Information on data sources is available in the EpiPulse Cases Guide – see [EpiPulse Help](#).

Uploading your data

Data is submitted through the [EpiPulse web interface](#) (in the menu, go to Cases -> EpiPulse Cases).



The visual interface for reporting new data and editing existing records has remained very similar to that of TESSy. Similar to TESSy, you can Add/Update or Replace data with new uploads, using either CSV or XML files. You can also manually create records for some diseases, and report zero cases where appropriate.



The functionality for manually editing existing records is also a familiar experience. Search for the record you wish to edit and modify the existing information as needed.

Finalising your submission

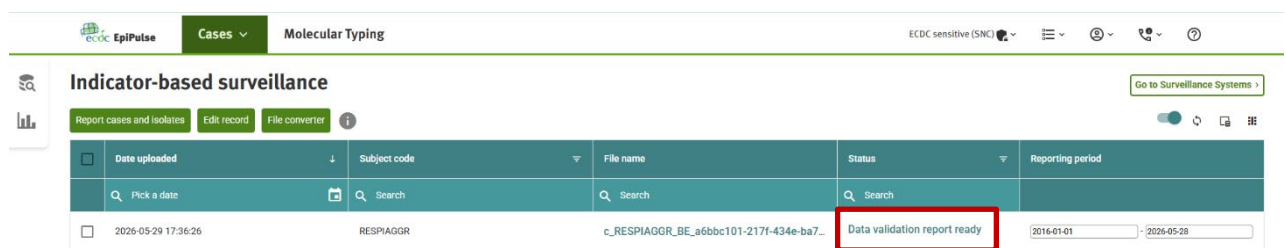
The compliance of your data with the validation rules in the metadata is checked automatically during the data upload process. In EpiPulse Cases this process is called "Technical Validation", and it is the only step where your upload can be rejected by the system, for severe data quality issues, such as the file format not being readable by the system, or (one of the few) technically required variables having missing values.

If your file has been rejected, there will be a message explaining each instance of non-compliance with the metadata that needs correcting.

The significant new feature in EpiPulse Cases is the Data Validation Report, which puts your data in the context of the already existing information for the same disease. It provides you a detailed overview of the new data in the file you have just uploaded, as well as an overall epidemiological situation showed with the existing (past) data together with the newly uploaded file(s). This means much more timely feedback on your uploads, including details on data quality, as well as outputs (graphs, charts, and tables) on some of epidemiological indicators. The Data Validation reports will evolve and grow based on your feedback in collaboration with our Disease Experts. These reports will provide a new and better way of understanding and updating the information collected at European level and will hopefully increase the quality and timeliness of the data, while reducing workloads.

Below you can find a few screenshots of the Data Validation Report.

1. Begin by opening the report:



2. View the report in a window, download the list of eventual validation messages, or download the report

Cross-field Validation

Total number of inconsistencies: 20

[Click here to download all inconsistencies](#)

RESPIAGGR

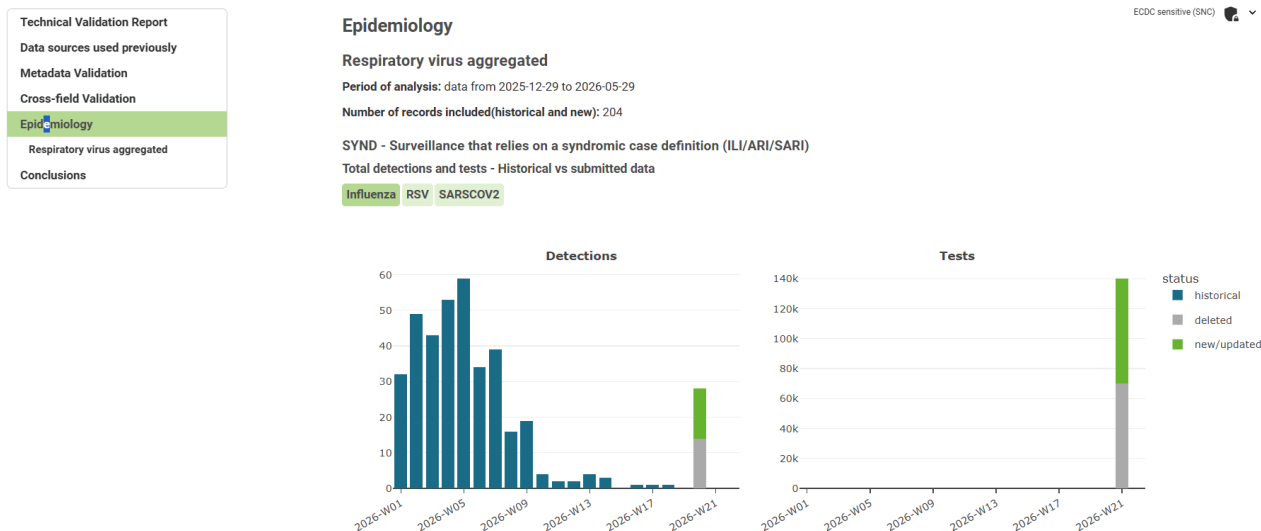
Number of inconsistencies: 20

Show entries Search:

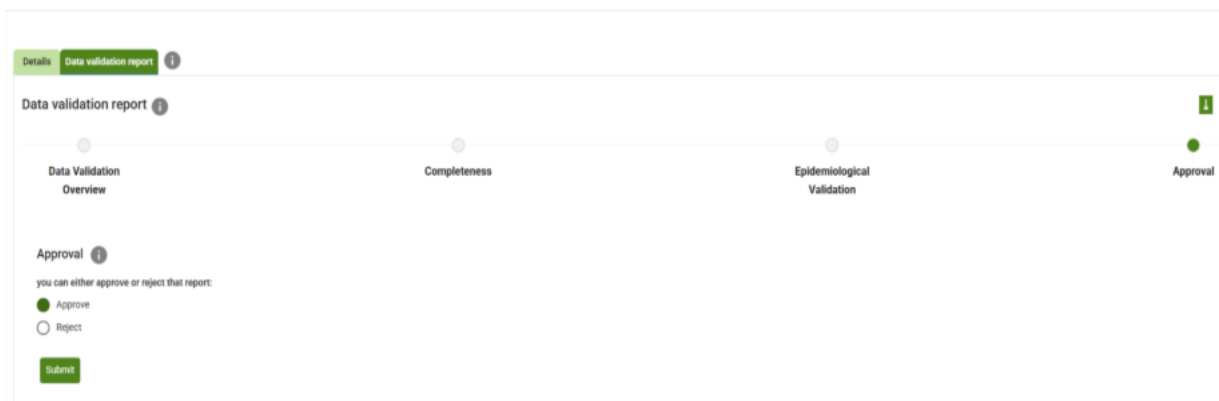
Filename	Issue/Inconsistency	Occurrences
RESPIAGGR_RO_V1_20260530.csv	Please avoid reporting overlapping age groups. If reporting Age15_29, do not additionally report Age30_64, as it overlaps with the previously reported variable.	5
RESPIAGGR_RO_V1_20260530.csv	Please avoid reporting overlapping age groups. If reporting Age30_64, do not additionally report Age15_29, as this overlaps with the previously reported variable.	5
RESPIAGGR_RO_V1_20260530.csv	Please avoid reporting overlapping age groups. If reporting Age65_79, do not additionally report Age65plus, as this overlaps with the previously reported variable.	5
RESPIAGGR_RO_V1_20260530.csv	Please avoid reporting overlapping age groups. If reporting Age80plus, do not additionally report Age65plus, as this overlaps with the previously reported variable.	5

Showing 1 to 4 of 4 entries Previous Next

3. The downloaded report can be opened full screen for easier viewing and navigation.



4. After reviewing the information in the Data Validation Report you can choose to approve or reject it. You can download the Data Validation Report file and email it to anyone who needs to check it before approval.



If you choose to reject it, no data will be saved in the EpiPulse Cases system, but your file will remain visible should you wish to re-download it or resubmit it for a new data validation at a later date or after further checks. Please check the Data Validation Report carefully, there might be warnings and remarks relating to possible data quality issues or potential overwriting of existing records that you should consider.

When your file has been validated and you are satisfied that all corrections have been made, please ensure prompt approval or rejection. Unapproved uploads will block the approval of other related uploads for the same disease.

EpiPulse Cases Helpdesk

Email: EpiPulseCases@ecdc.europa.eu

Telephone number: +46-(0)8-5860 1601

Availability: 9:00 – 16:00 Stockholm time, Monday to Friday (except ECDC holidays).

Annex 1. Overview of reporting

Data for routine respiratory surveillance is collected in seven integrated subject codes. These are outlined below together with information on case definitions, reporting deadline and data sharing.

Subject codes

The following subject codes exist in EpiPulse Cases:

1. **RESPICLINPC** for reporting weekly age-disaggregated primary care syndromic data (ILI/ARI).
2. **RESPIAGGR** for reporting of age-disaggregated counts of detections and tests from ILI/ARI surveillance and pathogen-specific laboratory-based surveillance system.
3. **RESPICLINSC** for reporting weekly age-disaggregated secondary care syndromic data (SARI). This subject code can also be used for reporting weekly denominator data for countries reporting case-based SARI data to RESPICASE.
4. **RESPISEVERE** for reporting age-disaggregated counts of detections and tests from SARI surveillance and counts from pathogen-specific laboratory-based surveillance of hospital admission, ICU admissions and deaths due to respiratory illness.
5. **RESPICASE** for reporting case-based data for severe cases capturing both syndromic and virological data for a single case. Both SARI cases and severe cases captured through pathogen-specific laboratory-based surveillance can be reported to this subject code.
6. **RESPIQUAL** for reporting weekly qualitative indicators
7. **RESPITHRESHOLD** for reporting threshold data collected for ILI, ARI and SARI

All subject codes allow integrated reporting of syndrome (ILI, ARI or SARI) and/or lab-confirmed infections by pathogen(s).

Further considerations for reporting quantitative and qualitative data are described in annex 2 and 3 respectively. Instructions for reporting threshold data will be provided at a later stage in annex 4. Included variables for each subject codes are outlined below in the annex 5.

Please note that INFLANTIVIR and NCOVVARIANT record types will continue to be collected in TESSy until further notice. A separate reporting protocol will remain available. Case-based data on human infections with zoonotic influenza viruses should be reported to the subject code INFLZOO in EpiPulse Cases. A separate reporting protocol is available.

Case definitions

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

Deadline for reporting

Wednesday 23:59 CET for all subject codes except for RESPITHRESHOLD.

RESPITHRESHOLD submission deadline will be communicated separately via email. Annual updates are expected.

Data that have not been uploaded and approved in EpiPulse Cases on time will not be included in weekly reports. If you are unable to meet this deadline, please contact the ECDC Respiratory Viruses surveillance team (ecdc.influenza@ecdc.europa.eu).

Data sharing

Please refer to the ECDC's policy on data governance to be published on the ECDC website for information on data protection governance for EpiPulse including data sharing: [Data protection governance for EpiPulse-final.pdf](#). All data collected are shared with the World Health Organisation – Regional Office for Europe (WHO/Europe) on a weekly basis and therefore duplicate reporting to WHO HQ is therefore not required.

Annex 2. Reporting quantitative data

This annex outlines considerations for submitting data to the following subject codes: RESPICLINPC, RESPIAGGR, RESPICLINS, RESPISEVERE or RESPICASE and is organised per topic. Please note that this is a living document to which additional considerations will be added over time. ECDC is actively working to expand this section within the next year.

Surveillance Type

The `SurvType` variable, with values `SYND` and `PATH`, is used to divide surveillance systems into two broad types, described below. Examples are provided in Table 1.

SYND

In systems where surveillance type = `SURV`, cases are identified using a syndromic case definition such as `ILI`, `ARI`, `SARI`, including where data derived from electronic health records (EHR) are used to try to replicate the traditional case definition.

When reporting aggregate data to EpiPulse Cases, the syndromic component should be reported to `RESPICLINPC` (`ILI/ARI`) or `RESPICLINS` (`SARI`) and virological data reported to `RESPIAGGR` (`ILI/ARI`), or `RESPISEVERE` (`SARI`). Alternatively, case-based syndromic and virological `SARI` data can be reported to `RESPICASE`.

These data were previously reported as 'sentinel' (`STL`) in `TESSy`.

PATH

In systems where surveillance type = `PATH`, case identification occurs on the basis of a positive test for a pathogen (influenza, `RSV`, `SARS-CoV-2`), or EHR-based diagnostic codes that reflect pathogen-specific diagnoses.

When it is clearly known that a laboratory-confirmed detection of influenza, `RSV` or `SARS-CoV-2` originates from a patient admitted to hospital/ICU or who has died, these data should be reported to `RESPISEVERE` (aggregate) or `RESPICASE` (case-based).

Where patients are tested outside of hospital settings, where the setting for testing is not known or if the data include a mix of hospital and non-hospital settings, only aggregate data should be reported, using `RESPIAGGR`.

These data were previously reported as 'non-sentinel' (`NONSTL`) in `TESSy`.

Table 1. Examples of different surveillance systems within each of the surveillance types and the linked reporting of syndromic and virological data

Care level	Surveillance type	Examples of systems	Data type	Syndromic data	Virological data
Primary care	SYND	a. Sentinel ILI/ARI surveillance network of GP practices from which a subset of cases is tested.	Aggregate	RESPICLINPC	RESPIAGGR
		b. EHR-based ARI/ILI surveillance covering most GP practices in the country paired with a sentinel GP network that tests ARI/ILI cases			
Primary care or unknown	PATH	a. Laboratory-based surveillance of all SARS-CoV-2, influenza, RSV detections and (tests)	Aggregate	NA	RESPIAGGR
Secondary care	SYND	a. Questionnaire-based SARI system	Case-based	RESPICASE (numerator) and RESPICLINSC (denominator)	RESPICASE
		b. SARI system that applies an EHR-based case definition for SARI using ICD codes.	Aggregate	RESPICLINSC	RESPISEVERE
Secondary care	PATH	a. Hospital laboratory surveillance of SARS-CoV-2 positives.	Case-based	NA	RESPICASE
		b. ICU surveillance of all patients positive for influenza, RSV or SARS-CoV-2	Aggregate	NA	RESPISEVERE
		c. EHR-based data indicating detection of a specific pathogen for patients not included within a SARI case definition.			
Mortality	PATH	a. Deaths occurring among patients who recently tested positive for influenza, RSV or SARS-CoV-2 and who are not captured through SARI surveillance	Aggregate	NA	RESPISEVERE
		b. Cause-specific death registry data.			

Denominators for syndromic data

In systems where surveillance type = SURV, two different denominators can be reported.

For primary care ILI/ARI-based systems (RESPICLINPC), all-cause consultations are reported using Indicator = DENOMCONSULT and the catchment population is reported using Indicator = DENOMPOP.

For secondary care SARI systems (RESPICLINSC), all-cause admissions are reported using Indicator = DENOMADMIT and the catchment population is reported using Indicator = DENOMPOP.

One or both denominators can be reported depending on data availability and system design. Where possible, catchment populations are preferable since they allow incidence of ILI/ARI/SARI to be estimated.

In systems where surveillance type = PATH, the above denominators cannot be reported.

Testing denominators

Testing denominators can be reported irrespective of SurvType. They can be used to calculate test positivity. For ERVISS, in instances where countries report more detections than tests, data for that week are excluded, test positivity is not calculated, and country data are excluded from aggregations.

In case-based data (RESPICASE), the variables TestRSV, TestInfluenza and TestSARSCOV2 are used to report individuals who are tested. This allows for reporting of patients who are tested, irrespective of the result. Where test-negative patients are reported as well as patients with a positive detection, the sum of tests reported per pathogen is the testing denominator to use for calculating test positivity.

In aggregate subject codes (RESPISEVERE, RESPIAGGR), the testing denominator (total number of tests performed per pathogen) is reported directly. In RESPIAGGR using Indicator = TESTS. In RESPISEVERE using Indicator = HOSAD_TESTS (hospital admissions) or Indicator = ICU_TESTS (among ICU admissions). One testing denominator should be reported (where available) for each country-week-pathogen-indicator combination. Even if using multiplex PCR, separate rows for tests for RSV, influenza and SARS-CoV-2 should be reported. The reporting of RSVType or InfluenzaTypeSubtype is not valid when Indicator = TESTS.

Age groups

Within RESPICLINS, RESPIAGGR, and RESPIERVE, countries may report data using two alternative sets of age groups.

Where possible, please report the narrow age groups: 00–04, 05–14, 15–29, 30–64, 65–79, and 80+ years. Countries that are unable to report these can use the broader age groups: 00–04, 05–14, 15–64, and 65+ years. Countries that cannot report any age-disaggregated data may report all data under AgeUnk. The total across all age groups, including AgeUnk, is used to calculate overall totals for displays in ERVISS.

Please ensure that the same age group structure is applied consistently to numerator and denominator data.

Co-infections

Co-infections are reported differently for case-based (RESPICASE) and aggregate (RESPIAGGR, RESPISEVERE) subject codes.

Case-based data

Co-infections involving more than one of influenza, RSV and SARS-CoV-2, e.g. RSV and Influenza, should be reported using TestRSV = 1, TestInfluenza = 1, DetectionRSV = 1, DetectionInfluenza = 1.

Co-infections with two types or subtypes of the same pathogen makes use of InfluenzaTypeSubtype and RSVType being repeatable in RESPICASE. e.g., Influenza A(H1N1)pdm09 and influenza B/Vic, would be reported using TestInfluenza = 1, DetectionInfluenza = 1, InfluenzaTypeSubtype = AH1N1pdm09, InfluenzaTypeSubtype = BVic.

Co-infections between influenza, RSV, SARS-CoV-2 and other respiratory pathogens can be reported using the relevant Test and Detection variables for the pathogen, together with PathogenOther to report the detection of the other respiratory pathogen. PathogenOther is repeatable for RESPICASE, so co-infections involving two other respiratory pathogens can be reported in a similar way.

Aggregate data

Co-infections are reported across multiple rows, e.g. a patient aged 66 years co-infected with RSV-A and Influenza A(H1N1)pdm09 should be reported to RESPIAGGR as:

- Pathogen = RSV, Indicator = DETECTIONS, RSVType = RSV_A, Age65_79 = 1
- Pathogen = RSV, Indicator = TESTS, Age65_79 = 1
- Pathogen = INFL, Indicator = DETECTIONS, InfluenzaTypeSubtype = AH1N1pdm09, Age65_79 = 1
- Pathogen = INFL, Indicator = TESTS, Age65_79 = 1

Co-infections with two types or subtypes of the same pathogen can be reported as above using multiple rows, e.g. a patient aged 66 years co-infected with Influenza B/Vic and Influenza A(H1N1)pdm09 should be reported to RESPIAGGR as:

- Pathogen = INFL, Indicator = DETECTIONS, InfluenzaTypeSubtype = BVic, Age65_79 = 1
- Pathogen = INFL, Indicator = DETECTIONS, InfluenzaTypeSubtype = AH1N1pdm09, Age65_79 = 1
- Pathogen = INFL, Indicator = TESTS, Age65_79 = 2.

The resulting double-counting of tests for patients with these coinfections is necessary to avoid potential exclusion from ERVISS (records are excluded where detections > tests) and we do not expect this to significantly impact interpretation of trends.

It is also possible to report co-infections between influenza, RSV or SARS-CoV-2 and other respiratory pathogens. Detections of other respiratory pathogens here are reported in the same row as the main pathogen detection – e.g. a patient aged 66 years co-infected with RSV-A and Human metapneumovirus should be reported to RESPIAGGR as:

- Pathogen = RSV, Indicator = DETECTIONS, RSVType = RSV_A, PathogenOther = HMPV, Age65_79 = 1
- Pathogen = RSV, Indicator = TESTS, Age65_79 = 1.

PathogenOther is not repeatable for aggregate data, so co-infections involving two other respiratory pathogens will need to be reported as Indicator = DETECTIONS across multiple rows, similar to the second example above but using Pathogen = OTH.

UNK vs missing

In EpiPulse Cases, where there is no data to report for a variable or its value is unknown, the field should be left blank. UNK cannot be reported unless it is explicitly included in the reference list for a variable. This only occurs where the reporting of UNK is meaningful.

Within the RESPI subject codes, the following variables still include an UNK value in their reference lists:

- InfluenzaTypeSubtype (INFL_UNK = Influenza untyped)
- RSVType (RSV_UNK = RSV untyped).

Zero vs missing

In ERVISS, no assumptions are made about missing data. This means that zeros must be explicitly reported since missing values are not recoded to zero. For example, in weeks where testing was performed for a pathogen but all were negative, please ensure that a value of 0 is reported for Indicator = DETECTIONS to ensure that this is included in ERVISS and 0% positivity is calculated. This requires submitting an additional row of data in RESPIAGGR and RESPISEVERE to capture the zero detections.

EHR diagnostic codes

EHR diagnostic codes can be reported to RESPICASE in the variable EHRDiagnosticCodes. These can be reported to indicate which codes apply to each patient, including those that are used to define the respiratory diagnosis to meet a case definition or that relate to underlying health conditions, using the format described below. The variable is free text, but to allow validation of the submitted codes please submit codes using the following format: Code System: Code System Version: Code: Primary (P)/Secondary (S). For example: "ICD10:2019:J12.1:P".

Only one code should be primary, capturing the principal medical condition that prompted the admission. All others should be marked as secondary.

If Code System Version is not applicable, please leave this blank: e.g. SNOMEDCT::86406008:S. For multiple codes, please ensure each code adheres to this formatting and separate codes with a semi-colon ";" within the same character string.

Currently, codes from the following systems will be accepted: ICD9, ICD10, ICD11, SNOMED_CT, LOINC and ICPC.

Annex 3. Reporting qualitative indicators

Qualitative indicators (QI) provide an overview of the transmissibility, severity and impact of respiratory illness, assessed using thresholds that allow for the qualitative categorisation of intensity levels. Reporting of QI to RESPIQUAL is based on the [WHO Pandemic Influenza Severity Assessment \(PISA\) guide \(2025\)](#) with some adaptations to allow for reporting of RSV and SARS-CoV-2. The PISA framework includes four indicators: transmissibility, morbidity and mortality, seriousness of disease and impact on healthcare capacity.

We prioritise the collection of a set of six core QI for use in weekly integrated situational assessment and communication: transmissibility (TRANS) and morbidity & mortality (MORB, with a preference for hospitalisations) for influenza, SARS-CoV-2 and RSV. These are shown in blue text in Table 2. For influenza this should be a continuation of the Intensity and Impact variables previously reported in TESSy INFLCLINAGGR. Additional guidance for reporting these for RSV and SARS-CoV-2 will follow.

In ERVISS, display of the following qualitative indicators will be prioritised:

- Six pathogen-specific QIs: transmissibility and morbidity & mortality (with a preference for hospitalisations) for influenza, SARS-CoV-2 and RSV.
- Syndromic intensity levels based on thresholds for reported ILI, ARI and SARI rates. Note that these are not reported to RESPIQUAL. They are calculated each week using thresholds approved by countries and submitted via RESPITHRESHOLD.

PISA requirements can be fulfilled by reporting seriousness of disease (SERIOUS, twice a season) and impact on healthcare capacity (IMPACT, weekly), based on influenza-specific and/or syndromic data (Table 2). Qualitative indicators reported where Surveillance Type = PISA submitted via EPC are transferred weekly to a [global WHO platform](#), where they are visualised and made publicly available, including associated confidence and comment information.

Table 2. Overview of reporting QI in RESPIQUAL

Qualitative indicator	Surveillance type	Pathogen / syndrome	Description (adapted from PISA)	Frequency
TRANS	PISA	INFL	Measure of how many people get sick with the virus and therefore reflects the ease of movement of the virus between individuals and communities	Weekly
	OTH	RSV SARSCOV2		
	PISA	SYND	Measure of how many people get sick with acute respiratory diseases	
MORB	PISA	INFL	Measures of the level of serious disease and death in the population due to influenza. (<i>Preference for hospitalisations</i>)	Weekly
	Other	RSV SARSCOV2		
	PISA	SYND	Measure of the level of serious disease and death in the population due to acute respiratory disease	
SERIOUS	PISA	INFL	The seriousness of disease indicator describes the extent to which individuals become ill when infected with an influenza virus	Twice per season (peak and end)
IMPACT	PISA	INFL	Describes how the influenza epidemic or pandemic is affecting health care system capacity	Weekly
		SYND	This indicator describes how acute respiratory diseases are affecting health care system capacity	

Integrated reporting of influenza, SARS-CoV-2 and RSV

Similar methods should ideally be used for deriving qualitative indicators for each pathogen to facilitate an integrated assessment of data reported for transmissibility and morbidity and mortality. Further methodological guidance on the most appropriate methods to assess these, including for RSV and SARS-CoV-2, will follow.

In the interim, reporting for influenza can continue using a 5-point scale based on the definitions used for INFLCLINAGGR as outlined below. Data previously reported to TESSy (INFLCLINAGGR) as: Intensity (influenza) can be reported directly to RESPIAGGR as transmissibility for influenza; Impact (influenza) can be reported directly to RESPIAGGR as morbidity and mortality for influenza. The latter is in line with the split of the old PISA impact indicator into 'morbidity and mortality' and 'impact on healthcare capacity' in the 2025 PISA guidance.

Transmissibility for influenza

Transmissibility for influenza summarises influenza activity within the country, using either qualitative expert assessment of weekly ILI/ARI trends compared with previous seasons, or semi-quantitative methods based on historical thresholds (e.g. MEM or WHO), with consideration of influenza virus detections alongside syndromic data. Categories for a semi-quantitative method:

1 = No activity or below epidemic threshold: ILI or ARI rates that are very low and at levels usually seen throughout the inter-epidemic period.

2 = 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.

3 = Moderate: ILI or ARI rates that are similar to rates usually observed, based on historical data. Influenza virus detections have been reported.

4 = High: ILI or ARI rates that are higher than rates usually observed, based on historical data. Influenza virus detections have been reported.

5 = Extraordinary: ILI/ARI rates that are much higher than rates usually observed, based on historical data. Influenza virus detections have been reported.

Morbidity and mortality for influenza

Morbidity and mortality for influenza captures the impact of influenza on severe outcomes. To aid historical and between-country comparison we recommend that countries use indicators of hospitalisations instead of mortality. If this is not possible, the free text comment field may be used to specify which data form the basis of the qualitative assessment (e.g. ICU admissions, mortality).

Qualitative assessment of influenza related hospitalisations can be based on SARI or laboratory-confirmed hospitalisations, expressed as counts, rates, or percentage positivity:

1 = No activity or below epidemic threshold: influenza related hospitalizations at levels usually seen throughout the inter-epidemic period.

2 = Low: influenza related hospitalizations that are relatively low compared to rates from historical data but higher than the baseline.

3 = Moderate: influenza related hospitalizations that are similar to rates usually observed, based on historical data.

4 = High: influenza related hospitalizations that are higher than rates usually observed, based on historical data.

5 = Extraordinary: influenza related hospitalizations that are much higher than rates usually observed, based on historical data.

Other reporting considerations

The PISA guidance lists numerous examples of parameters that can be used for the reporting of each indicator.

Reporting countries may choose which indicators to report based on the surveillance systems in place. For each indicator, non-mandatory comment and confidence variables are available.

Not all combinations of Indicator & Value and, separately, Indicator & Pathogen/Syndrome are valid. Specifically, 'No activity or below epidemic threshold' is not a valid entry for 'Seriousness of disease' and the combination of 'Seriousness of disease' with 'SYND = Syndromic' is not valid.

Although all combinations can be technically submitted to EPC, invalid combinations will be flagged as inconsistencies in the Data Validation Report. Data submitted with invalid combinations will not be used in subsequent analyses or visualisations.

Qualitative indicators referring to the PISA surveillance type (all four indicators on Influenza and/or Syndromic) submitted via EPC are transferred weekly to a [global WHO platform](#), where they are visualised and made publicly available, including associated confidence and comment information.

Annex 4. Reporting thresholds

RESPITHRESHOLDS has been introduced to allow countries to report and update calculated threshold data. Currently ILI, ARI and SARI threshold data can be reported. Ahead of the 2026/2027 season, ECDC and WHO's Regional Office for Europe will calculate thresholds which will be sent to countries for validation in a EpiPulse Cases compatible metadata format. Countries are responsible for uploading and validating the thresholds in the EpiPulse Cases platform. Further guidance will be provided on the upload process and the ability to change thresholds in July 2026.

Annex 5. Metadata

RESPICLINPC

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPICLINPC = Primary care consultation data (ILI/ARI syndromic)

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

The record identifier is provided by the reporting country. It must be unique within the national respiratory virus disease surveillance system and anonymous. For aggregate datasets, countries may choose to concatenate multiple variables to create a unique identifier (e.g. ReportingCountry-DateUsedForStatistics-ClinicalSyndrome-Indicator).

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week assigned to the reported data. This should correspond to the date used by the national surveillance institute or organisation in its reports and official statistics, to ensure coherence between national and supranational outputs. The reference date used for statistics may differ between countries. For RESPICLINPC, it is preferably the date the case was medically attended.

Clinical syndrome (required)

Field: ClinicalSyndrome

Coding: ARI = Acute respiratory infection

ILI = Influenza-like illness

Specify the clinical syndrome captured by the system. If an electronic health record (EHR) based case definition is applied, please describe which clinical syndrome it corresponds to.

Indicator (required)

Field: Indicator

Coding: CASES = Cases

DENOMCONSULT = All-cause consultations

DENOMPOP = Catchment population

Select the indicator to report. You may report all-cause consultations, catchment population, or both.

Age group 0–4 years

Field: Age00_04

Coding: NUM

Number of patients in the age group 0–4 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 5–14 years

Field: Age05_14

Coding: NUM

Number of patients in the age group 5–14 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–64 years

Field: Age15_64

Coding: NUM

Number of patients in the age group 15–64 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 65+ years

Field: Age65plus

Coding: NUM

Number of patients in the age group 65+ years corresponding to the reported indicator (newly reported for the week of reporting).

Age unknown

Field: AgeUnk

Coding: NUM

Number of patients with an unknown age corresponding to the reported indicator (newly reported for week of reporting).

RESPIAGGR

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPIAGGR = Respiratory virus aggregated

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

The record identifier is provided by the reporting country. It must be unique within the national respiratory virus disease surveillance system and anonymous. For aggregate datasets, countries may choose to concatenate multiple variables to create a unique identifier (e.g. ReportingCountry-DateUsedForStatistics-SurveillanceType-ClinicalSyndrome-Pathogen-PathogenOther-InfluenzaTypeSubtype-RSVType-Indicator).

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week assigned to the reported data. This should correspond to the date used by the national surveillance institute or organisation in its reports and official statistics, to ensure coherence between national and supranational outputs. The reference date used for statistics may differ between countries. For RESPIAGGR, the preferred reference date is the date of specimen collection.

Pathogen (required)

Field: Pathogen

Coding: INFL = Influenza virus, not specified

MERSCOV = Middle East respiratory syndrome-related coronavirus (MERS-CoV)

OTH = Other pathogen, not specified

RSV = Respiratory Syncytial Virus

SARSCOV2 = Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2)

Specify the pathogen associated with the indicator. If selecting OTH, please specify which pathogen in the PathogenOther variable.

Pathogen other

Field: PathogenOther

Coding: ADEV = Adenovirus

BORDHOL = *Bordetella holmesii*

BORDPAR = *Bordetella parapertussis*

BORDPER = *Bordetella pertussis*

BORDSPP = *Bordetella* species, not specified

CHLPNE = *Chlamydia pneumoniae*

COV229E = Human coronavirus 229E

COVHKU1 = Human coronavirus HKU1
COVNL63 = Human coronavirus NL63
COVOC43 = Human coronavirus OC43
COVOTH = Coronavirus, not specified
COXBUR = *Coxiella burnetii*
ENTEROVOTH = Enterovirus (not polio), including rhinovirus
HAEINF = *Haemophilus influenzae* (non-typeable)
HAEINFB = *Haemophilus influenzae* type b
HBOV = Human bocavirus
HMPV = Human metapneumovirus
HPIV = Human parainfluenza virus
HPIV1 = Human parainfluenza virus type 1
HPIV2 = Human parainfluenza virus type 2
HPIV3 = Human parainfluenza virus type 3
HPIV4 = Human parainfluenza virus type 4
LLONG = *Legionella longbeachae*
LPNE = *Legionella pneumophila*
MORCAT = *Moraxella catarrhalis*
MYCPNE = *Mycoplasma pneumoniae*
PAREV = Parechovirus
STRADGA = Streptococcus Group C/G
STRAGA = *Streptococcus agalactiae*
STRPNE = *Streptococcus pneumoniae*
STRPYO = *Streptococcus pyogenes*.

Specify any pathogen that was not captured in the Pathogen variable. Reporting of additional pathogens is optional and these data are currently not used in weekly outputs.

Influenza type and subtype

Field: InfluenzaTypeSubtype

Coding: AH1N1pdm09 = A(H1N1)pdm09

AH1pdm09 = A(H1)pdm09

AH3 = A(H3) AH3N2 = A(H3N2)

AUNK = A unknown

BNoLineage = B lineage not determined

BVic = B/Vic

BYam = B/Yam

INFL_UNK = Influenza untyped

Influenza type and subtype should be reported when INFL (Influenza) is reported for the Pathogen variable. Note: When reporting TESTS, please leave this field blank.

RSV type

Field: RSVType

Coding: RSV_A = RSV Type A

RSV_B = RSV Type B

RSV_UNK = RSV unknown type

Report RSV type when RSV is reported for the variable Pathogen. Note: When reporting TESTS, please leave this field blank.

Surveillance type (required)

Field: SurveillanceType

Coding: PATH = Virological data from pathogen-specific laboratory-based surveillance

SYND = Virological data from surveillance that relies on a syndromic case definition (ILI/ARI/SARI)

Indicate whether you are reporting virological data from: (i) Surveillance that relies on a syndromic case definition (such as ILI, ARI, SARI or electronic health record (EHR) based case definitions); or (ii) Pathogen-specific laboratory-based surveillance (e.g. for influenza, RSV, SARS-CoV-2) or EHR diagnostic codes that reflect pathogen-specific diagnoses (e.g., cases not included in the EHR-based case definition). Surveillance that relies on a syndromic case definition (ILI/ARI/SARI) was previously coded as sentinel (STL) in TESSy, reflecting how many of these systems were historically designed and implemented. Pathogen-specific laboratory-based surveillance was previously coded as nonsentinel (NONSTL). Please note that both (i) and (ii) can be sentinel or universal depending on the system design.

Clinical syndrome

Field: ClinicalSyndrome

Coding: ARI = Acute respiratory infection

ILI = Influenza-like illness

Specify the clinical syndrome of the tested patients and corresponding detections. If an electronic health record (EHR)-based case definition is applied, please select the clinical syndrome that it represents. If you cannot differentiate tests and detections by clinical syndrome, you can leave this field blank.

Indicator (required)

Field: Indicator

Coding: DETECTIONS = Number of detections

TESTS = Number of tests

Select the indicator to report. Where SurveillanceType = SYND ensure to report both DETECTIONS and TESTS per pathogen.

Age group 0–4 years

Field: Age00_04

Coding: NUM

Number of patients in the age group 0–4 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 5–14 years

Field: Age05_14

Coding: NUM

Number of patients in the age group 5–14 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–29 years

Field: Age15_29

Coding: NUM

Number of patients in the age group 15–29 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–64 years

Field: Age15_64

Coding: NUM

Number of patients in the age group 15–64 years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 15–29 and 30–64 years.

Age group 30–64 years

Field: Age30_64

Coding: NUM

Number of patients in the age group 30–64 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 65+ years

Field: Age65plus

Coding: NUM

Number of patients in the age group 65+ years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 65–79 and 80+ years.

Age group 65–79 years

Field: Age65_79

Coding: NUM

Number of patients in the age group 65–79 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 80+ years

Field: Age80plus

Coding: NUM

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

Age unknown

Field: AgeUnk

Coding: NUM

Number of patients with an unknown age corresponding to the reported indicator (newly reported for week of reporting).

RESPICLINSC

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPICLINSC = Secondary care consultation data (SARI syndromic)

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

The record identifier is provided by the reporting country. It must be unique within the national respiratory virus disease surveillance system and anonymous. For aggregate datasets, countries may choose to concatenate multiple variables to create a unique identifier (e.g. ReportingCountry-DateUsedForStatistics-ClinicalSyndrome-Indicator).

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week assigned to the reported data. This should correspond to the date used by the national surveillance institute or organisation in its reports and official statistics, to ensure coherence between national and supranational outputs. The reference date used for statistics may differ between countries. For RESPICLINSC, the date should ideally be based on the date of admission to hospital or ICU, or the date of death.

Indicator (required)

Field: Indicator

Coding: DEATHS = Cases who have died

DENOMADMIT = All-cause hospital admissions

DENOMPOP = Catchment population

HOSAD = Hospitalised cases

ICUAD = Cases admitted to ICU

Select the indicator to report. Please note that more than one category can apply at the same time. This means you may need to report multiple categories for the same case (i.e. a case may be reported as hospitalised, in ICU, and deceased). If your surveillance system is ICU based, please do not report hospitalisations. You may report all-cause hospital admissions, catchment population, or both.

Age group 0–4 years

Field: Age00_04

Coding: NUM

Number of patients in the age group 0–4 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 5–14 years

Field: Age05_14

Coding: NUM

Number of patients in the age group 5–14 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–29 years

Field: Age15_29

Coding: NUM

Number of patients in the age group 15–29 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–64 years

Field: Age15_64

Coding: NUM

Number of patients in the age group 15–64 years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 15–29 and 30–64 years.

Age group 30–64 years

Field: Age30_64

Coding: NUM

Number of patients in the age group 30–64 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 65+ years

Field: Age65plus

Coding: NUM

Number of patients in the age group 65+ years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 65–79 and 80+ years.

Age group 65–79 years

Field: Age65_79

Coding: NUM

Number of patients in the age group 65–79 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 80+ years

Field: Age80plus

Coding: NUM

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

Age unknown

Field: AgeUnk

Coding: NUM

Number of patients with an unknown age corresponding to the reported indicator (newly reported for week of reporting).

RESPISEVERE

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPISEVERE = Respiratory virus severity indicators

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

The record identifier is provided by the reporting country. It must be unique within the national respiratory virus disease surveillance system and anonymous. For aggregate datasets, countries may choose to concatenate multiple variables to create a unique identifier (e.g. ReportingCountry-DateUsedForStatistics-SurveillanceType-Pathogen-PathogenOther-InfluenzaTypeSubtype-RSVType-Indicator).

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

The week assigned to the reported data. This should correspond to the date used by the national surveillance institute or organisation in its reports and official statistics, to ensure coherence between national and supranational outputs. The reference date used for statistics may differ between countries. For RESPISEVERE, the reference date should ideally be the date of admission to hospital or ICU, or the date of death. If the date of admission is unknown, or if the admission was due to another cause, the date of specimen collection may be used instead.

Pathogen (required)

Field: Pathogen

Coding: INFL = Influenza virus, not specified

MERSCOV = Middle East respiratory syndrome-related coronavirus (MERS-CoV)

OTH = Other pathogen, not specified

RSV = Respiratory Syncytial Virus

SARSCOV2 = Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2)

Specify the pathogen associated with the indicator. If selecting OTH, please specify which pathogen in the PathogenOther variable.

Pathogen other

Field: PathogenOther

Coding: ADEV = Adenovirus

BORDHOL = *Bordetella holmesii*

BORDPAR = *Bordetella parapertussis*

BORDPER = *Bordetella pertussis*

BORDSPP = *Bordetella* species, not specified

CHLPNE = *Chlamydia pneumoniae*

COV229E = Human coronavirus 229E

COVHKU1 = Human coronavirus HKU1

COVNL63 = Human coronavirus NL63

COVOC43 = Human coronavirus OC43

COVOTH = Coronavirus, not specified

COXBUR = *Coxiella burnetii*
ENTEROVOTH = Enterovirus (not polio), including rhinovirus
HAEINF = *Haemophilus influenzae* (non-typeable)
HAEINFB = *Haemophilus influenzae* type b
HBOV = Human bocavirus
HMPV = Human metapneumovirus
HPV = Human parainfluenza virus
HPV1 = Human parainfluenza virus type 1
HPV2 = Human parainfluenza virus type 2
HPV3 = Human parainfluenza virus type 3
HPV4 = Human parainfluenza virus type 4
LLONG = *Legionella longbeachae*
LPNE = *Legionella pneumophila*
MORCAT = *Moraxella catarrhalis*
MYCPNE = *Mycoplasma pneumoniae*
PAREV = Parechovirus
STRADGA = Streptococcus Group C/G
STRAGA = *Streptococcus agalactiae*
STRPNE = *Streptococcus pneumoniae*
STRPYO = *Streptococcus pyogenes*.

Specify any pathogen that was not captured in the Pathogen variable. Reporting of additional pathogens is optional and these data are currently not used in weekly outputs.

Influenza type and subtype

Field: InfluenzaTypeSubtype

Coding: AH1N1pdm09 = A(H1N1)pdm09

AH1pdm09 = A(H1)pdm09

AH3 = A(H3)

AH3N2 = A(H3N2)

AUNK = A unknown

BNoLineage = B lineage not determined

BVic = B/Vic

BYam = B/Yam

INFL_UNK = Influenza untyped

Influenza type and subtype should be reported when Influenza is reported for the Pathogen variable. Note: When reporting TESTS, please leave this field blank.

RSV type

Field: RSVType

Coding: RSV_A = RSV Type A

RSV_B = RSV Type B

RSV_UNK = RSV unknown type

Report RSV type when RSV is reported for the variable Pathogen. Note: When reporting TESTS, please leave this field blank.

Surveillance type (required)

Field: SurveillanceType

Coding: PATH = Virological data from pathogen-specific laboratory-based surveillance

SYND = Virological data from surveillance that relies on a syndromic case definition (ILI/ARI/SARI)

Indicate whether you are reporting virological data from: (i) Surveillance that relies on a syndromic case definition (such as ILI, ARI, SARI or electronic health record (EHR) case definitions); or (ii) Pathogen-specific laboratory-based surveillance (e.g. for influenza, RSV, SARS-CoV-2) or EHR diagnostic codes that reflect pathogen-specific diagnoses (e.g., cases not included in the EHR-based case definition). Surveillance that relies on a syndromic case definition (ILI/ARI/SARI) was previously coded as sentinel (STL) in TESSy, reflecting how many of these systems were historically designed and implemented. Pathogen-specific laboratory-based surveillance was previously coded as nonsentinel (NONSTL). Please note that both (i) and (ii) can be sentinel or universal depending on the system design.

Indicator (required)

Field: Indicator

Coding: DEATHS_DETECTIONS = Deaths among patients who recently tested positive

HOSAD_DETECTIONS = Detections among patients admitted to hospital

HOSAD_TESTS = Tests among patients admitted to hospital

ICUAD_DETECTIONS = Detections among patients admitted to ICU

ICUAD_TESTS = Tests among patients admitted to ICU

Select the indicator to report. Please note that more than one category can apply at the same time. This means you may need to report multiple categories for the same case (i.e. a case may be reported as hospitalised, in ICU, and deceased). If your surveillance system is ICU based, please do not report hospitalisations. Where SurveillanceType = SYND ensure to report both HOSAD_DETECTIONS and HOSAD_TESTS per pathogen.

Age group 0–4 years

Field: Age00_04

Coding: NUM

Number of patients in the age group 0–4 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 5–14 years

Field: Age05_14

Coding: NUM

Number of patients in the age group 5–14 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–29 years

Field: Age15_29

Coding: NUM

Number of patients in the age group 15–29 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 15–64 years

Field: Age15_64

Coding: NUM

Number of patients in the age group 15–64 years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 15–29 and 30–64 years.

Age group 30–64 years

Field: Age30_64

Coding: NUM

Number of patients in the age group 30–64 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 65+ years

Field: Age65plus

Coding: NUM

Number of patients in the age group 65+ years corresponding to the reported indicator (newly reported for the week of reporting). Please only use this reporting type if data are not reported separately for the age groups 65–79 and 80+ years.

Age group 65–79 years

Field: Age65_79

Coding: NUM

Number of patients in the age group 65–79 years corresponding to the reported indicator (newly reported for the week of reporting).

Age group 80+ years

Field: Age80plus

Coding: NUM

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

Age unknown

Field: AgeUnk

Coding: NUM

Number of patients with an unknown age corresponding to the reported indicator (newly reported for week of reporting).

RESPICASE

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPICASE = Case-based data for patients with severe disease capturing both syndromic and virological data

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

The record identifier is provided by the reporting country. It must be unique within the national respiratory virus disease surveillance system and anonymous.

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

yyyy-mm-dd

The date assigned to the reported data (the exact date is preferred). This should correspond to the date used by the national surveillance institute or organisation in its reports and official statistics, to ensure coherence between national and supranational outputs. The reference date used for statistics may differ between countries. For RESPICASE, the date of admission to hospital is preferred. If admitted due to cause other than a respiratory infection or date of admission is unknown, date of specimen collection or diagnosis of respiratory infection can be used.

Age

Field: Age

Coding: NUM

Age of patient in years at the time of hospital admission, as reported in the national system. For patients under two years old, please provide the age in months using the variable AgeMonth (0–23 months).

Age in months

Field: AgeMonth

Coding: NUM

Age of the patient in months for cases under two years old at the time of hospital admission. For patients two years old and above, AgeMonth should be left blank.

Sex

Field: Sex

Coding: F = Female

M = Male

OTH = Other

The sex of the reported case. Use OTH for individuals who do not identify strictly as male or female, including non-binary, intersex, or those who prefer to self-describe.

Healthcare worker

Field: HealthCareWorker

Coding: BOOL

Indicate whether the case occurred in a healthcare worker. For this reporting protocol, a healthcare worker is defined as any person working (paid or on a regular voluntary basis) in a healthcare setting who has contact with any type of patient. This includes but is not limited to: doctors; nurses; therapists; technicians; emergency medical personnel; medical and nursing students with patient contact; porters; and cleaners. Staff or volunteers working in nursing or residential care homes for older adults are also classified as healthcare workers.

Surveillance type (required)

Field: SurveillanceType

Coding: PATH = Virological data from pathogen-specific laboratory-based surveillance

SYND = Virological data from surveillance that relies on a syndromic case definition (ILI/ARI/SARI)

Indicate whether you are reporting virological data from: (i) Surveillance that relies on a syndromic case definition (such as ILI, ARI, SARI or electronic health record (EHR) based case definitions); or (ii) Pathogen-specific laboratory-based surveillance (e.g. for influenza, RSV, SARS-CoV-2) or EHR diagnostic codes that reflect pathogen-specific diagnoses (e.g., cases not included in the EHR-based case definition). Surveillance that relies on a syndromic case definition (ILI/ARI/SARI) was previously coded as sentinel (STL) in TESSy, reflecting how many of these systems were historically designed and implemented. Pathogen-specific laboratory-based surveillance was previously coded as nonsentinel (NONSTL). Please note that both (i) and (ii) can be sentinel or universal depending on the system design.

Date of specimen collection

Field: DateOfSpecimen

Coding: yyyy-mm-dd

The date of the first specimen collection for the current episode.

Test results influenza

Field: TestInfluenza

Coding: BOOL

Indicate the influenza test result for the patient during the current episode. This variable is boolean: 0 = Tested, influenza not detected (including unknown results), 1 = Tested, influenza detected. If left empty it will be interpreted as not tested for influenza.

Test results RSV

Field: TestRSV

Coding: BOOL

Indicate the influenza test result for the patient during the current episode. This variable is boolean: 0 = Tested, RSV not detected (including unknown results), 1 = Tested, RSV detected. If left empty it will be interpreted as not tested for RSV.

Test results SARSCoV2

Field: TestSARSCOV2

Coding: BOOL

Indicate the influenza test result for the patient during the current episode. This variable is boolean: 0 = Tested, SARS-CoV-2 not detected (including unknown results), 1 = Tested, SARS-CoV-2 detected. If left empty it will be interpreted as not tested for SARS-CoV-2.

Pathogen Other

Field: PathogenOther

Coding: ADEV = Adenovirus

BORDHOL = *Bordetella holmesii*

BORDPAR = *Bordetella parapertussis*

BORDPER = *Bordetella pertussis*

BORDSPP = *Bordetella* species, not specified

CHLPNE = *Chlamydia pneumoniae*

COV229E = Human coronavirus 229E

COVHKU1 = Human coronavirus HKU1

COVNL63 = Human coronavirus NL63

COVOC43 = Human coronavirus OC43

COVOTH = Coronavirus, not specified

COXBUR = *Coxiella burnetii*

ENTEROVOTH = Enterovirus (not polio), including rhinovirus

HAEINF = *Haemophilus influenzae* (non-typeable)

HAEINFB = *Haemophilus influenzae* type b

HBOV = Human bocavirus

HMPV = Human metapneumovirus

HPIV = Human parainfluenza virus

HPIV1 = Human parainfluenza virus type 1

HPIV2 = Human parainfluenza virus type 2

HPIV3 = Human parainfluenza virus type 3

HPIV4 = Human parainfluenza virus type 4

LLONG = *Legionella longbeachae*

LPNE = *Legionella pneumophila*

MERSCOV = Middle East respiratory syndrome-related coronavirus (MERS-CoV)

MORCAT = *Moraxella catarrhalis*

MYCPNE = *Mycoplasma pneumoniae*

PAREV = Parechovirus

STRADGA = Streptococcus Group C/G

STRAGA = *Streptococcus agalactiae*

STRPNE = *Streptococcus pneumoniae*

STRPYO = *Streptococcus pyogenes*.

Specify any pathogen other than influenza, RSV or SARSCoV2. This variable is repeatable. Reporting of additional pathogens is optional and these data are currently not used in weekly outputs.

Influenza type and subtype

Field: InfluenzaTypeSubtype

Coding: AH1N1pdm09 = A(H1N1)pdm09

AH1pdm09 = A(H1)pdm09

AH3 = A(H3)

AH3N2 = A(H3N2)

AUNK = A unknown

BNoLineage = B lineage not determined

BVic = B/Vic

BYam = B/Yam

INFL_UNK = Influenza untyped

If influenza was detected (as indicated in the DetectionInfluenza variable), provide the influenza type and subtype detected for the reported case. Multiple types or subtypes can be reported for this variable (repeatable variable) for reporting cases of co-infection.

RSV Type

Field: RSVType

Coding: RSV_A = RSV Type A

RSV_B = RSV Type B

RSV_UNK = RSV unknown type

If RSV was detected (as indicated in the DetectionRSV variable), provide the RSV type detected for the reported case. Multiple types can be reported for this variable (repeatable variable) for reporting cases of co-infection, submit separate entries for each detected type.

WGS accession identifier

Field: WgsAccession

Coding: TEXT

Provide the sequence identifier, which is used to retrieve sequence data (sequencing reads, genome assemblies, or gene sequences) from external databases such as GISAID, ENA, SRA, or GenBank. Report accession numbers as follows: GISAID isolate ID (e.g. EPI_ISL_402123), GenBank nucleotide sequence ID (e.g. MK334047) or ENA/SRA Run ID starting with ERR or SRR. Do not use sample or experiment IDs (ERS, ERX, SRS, SRX). If multiple pathogens or strains are present, list accession IDs separated by a semicolon (;).

Date of onset of disease

Field: DateOfOnset

Coding: yyyy-mm-dd

Date of onset of disease (exact date only).

Clinical criteria (symptoms)

Field: ClinicalCriteria

Coding: AGEUS = Ageusia/Dysgeusia

ANOS = Anosmia

APNOEA = Apnoea

COUGH = Dry or productive cough

DIARR = Diarrhoea

FEVER = Fever above 38C or history of fever (temp not measured)

GENERALDETER = General deterioration

HEAD = Headache

PAINMUSC = Pain - muscular

RUNOS = Runny nose

SBREATH = Shortness of breath

SEPSIS = Sepsis

SORETHR = Sore throat

VOMIT = Nausea/vomiting

Symptoms present at the time of hospital admission. This variable is repeatable.

Clinical criteria (symptoms) other

Field: ClinicalCriteriaOther

Coding: TEXT

Additional symptoms that were not captured in the ClinicalCriteria variable.

Case precondition

Field: CasePrecondition

Coding: DIAB = Diabetes

HEART = Chronic heart disease

HYPERT = Hypertension

IMMUNODEF = Immunodeficient

KIDNEY = Kidney-related condition, renal disease

LIVER = Liver-related condition, liver disease

LUNG = Chronic lung disease

NEURO = Neurological disorder

OBESITY = Obesity

PREG = Pregnancy

PREGPOST = Post-partum (<6 weeks)

PREM = Prematurity of infant (report only for cases aged < 2 years)

SMOKE = Current smoking

TB = Tuberculosis

Underlying medical conditions or pre-existing health factors. This variable is repeatable if multiple preconditions apply.

Case precondition other

Field: CasePreconditionOther

Coding: TEXT

Additional preconditions that were not captured in the CasePrecondition variable.

Complication diagnosis

Field: ComplicationDiagnosis

Coding: AKI = Acute renal injury

ARDS = Acute respiratory distress syndrome

BRONCH = Bronchiolitis

ENCEPH = Encephalitis

HEARTFAIL = Heart failure

MULTIFAIL = Multi-organ failure

MYOCARD = Myocarditis

PNEU = Pneumonia

SEPSIS = Sepsis

STILLBIRTH = Still birth as pregnancy outcome in a case

Complications associated with the illness. This variable is repeatable for cases experiencing multiple complications.

Complication diagnosis other

Field: ComplicationDiagnosisOther

Coding: TEXT

Additional complications that were not captured in the ComplicationDiagnosis variable.

Date of hospitalisation

Field: DateOfHospitalisation

Coding: yyyy-mm-dd

Date of hospitalisation (exact date only).

Intensive care

Field: IntensiveCare

Coding: BOOL

Indicate whether the case required care in an intensive care unit (ICU) or a high dependency unit (HDU), defined as a unit with capabilities for more intensive observation, treatment and nursing care than can be provided by a regular ward.

Date of ICU or HDU

Field: DateOfICUHDU

Coding: yyyy-mm-dd

Date of admission to an intensive care unit (ICU) or high dependency unit (HDU) (exact date only).

Invasive respiratory support

Field: RespiratorySupport

Coding: ECMO = Extracorporeal membrane oxygenation

VENT = Invasive mechanical ventilation

Indicate which form of invasive respiratory support the patient received during the clinical episode. If a patient received both VENT and ECMO, please indicate ECMO.

Date of discharge

Field: DateOfDischarge

Coding: yyyy-mm-dd

Date the patient was discharged from hospital (exact date only). Indicate this date for any kind of discharge (i.e. discharged alive or dead). If transferred to another hospital and follow-up information is available from the receiving hospital, please provide the actual date of discharge following the episode. If the date of discharge is unknown, this field should be left blank.

Date of death

Field: DateOfDeath

Coding: yyyy-mm-dd

Date of death (exact date only).

Outcome

Field: Outcome

Coding: A = Alive, recovered, cured, discharged from hospital

D = Died

STILLTREATMENT = Still on medical treatment related to viral respiratory infection (not recovered)

Indicate the clinical outcome of the case. This information should be recorded as accurately as possible. If the patient is still ill at the time of reporting, please code the outcome as STILLTREATMENT. Update this status once the final outcome is known. This includes patients that were transferred if follow-up information is available from the receiving hospital. If the outcome is unknown (e.g. if a patient was transferred to another hospital with unknown outcome), this field should be left blank.

EHR diagnostic code

Field: EHRDiagnosticCode

Coding: TEXT

Indicate the EHR diagnostic codes that apply to the patient, including those that are used to define the respiratory diagnosis to meet a case definition or that relate to underlying health conditions relevant to the medical condition that prompted the admission. Report the code system and code version first, followed by the diagnostic code and whether it is primary (P) or secondary (S, i.e. not primary) (e.g., ICD10:v2019:J45.9: P). Only one code should be primary, capturing the principal medical condition that prompted the admission. All others should be marked as secondary. If Code System Version is not applicable, please leave this field blank. For multiple codes, please ensure each code adheres to this formatting and separate codes with a semi-colon ";" within the same character string.

Drug used for prophylaxis

Field: DrugUsedProphylaxis

Coding: J05AB16 = Remdesivir

J05AC02 = Rimantadine

J05AH01 = Zanamivir

J05AH02 = Oseltamivir

J05AX25 = Baloxavir marboxil

J06BD03 = Tixagevimab and cilgavimab

J06BD07 = Casirivimab and imdevimab

N04BB01 = Amantadine

OTH = Other

Antiviral drugs administered as prophylaxis in the 14 days prior to illness onset. This variable is repeatable if multiple drugs were used.

Drug used for treatment

Field: DrugUsedTreatment

Coding: J05AB16 = Remdesivir

J05AB18 = Molnupiravir

J05AC02 = Rimantadine

J05AE30 = Nirmatrelvir and ritonavir

J05AH01 = Zanamivir

J05AH02 = Oseltamivir
J05AX25 = Baloxavir marboxil
J06BD01 = Palivizumab
J06BD03 = Tixagevimab and cilgavimab
J06BD05 = Sotrovimab
J06BD06 = Regdanvimab
J06BD07 = Casirivimab and imdevimab
J06BD08 = Nirsevimab
J06BD09 = Sipavibart
N04BB01 = Amantadine
OTH = Other

Antiviral drugs administered for treatment during the illness. This variable is repeatable if multiple drugs were used.

Influenza vaccination status

Field: InfluenzaVaccination

Coding: BOOL

Indicate whether the patient received an influenza vaccination during the most recent influenza season.

Influenza vaccination date

Field: DateOfInfluenzaVaccination

Coding: yyyy-mm-dd

Date of the most recent influenza vaccination (exact date only). If the exact date is unknown but the month is known, please enter the 15th of that month as an approximate date.

COVID19 vaccination status

Field: COVID19Vaccination

Coding: BOOL

Indicate whether the patient received a SARS-CoV-2 vaccination within the 12 months prior to admission.

COVID19 vaccination date

Field: DateOfCOVID19Vaccination

Coding: yyyy-mm-dd

Date of the most recent SARS-CoV-2 vaccination (exact date only). If the exact date is unknown but the month is known, please enter the 15th of that month as an approximate date.

RSV immunisation status

Field: RSVImmunisation

Coding: BOOL

Indicate whether the patient received immunisation against RSV within the recommended timeframe (the recommended timeframe is defined according to the type of RSV immunisation).

RSV immunisation type

Field: RSVImmunisationType

Coding: MAB = Monoclonal antibody

VACC = Vaccine

Type of RSV immunisation received.

RSV immunisation date

Field: DateOfRSVImmunisation

Coding: yyyy-mm-dd

Date of the most recent RSV immunisation (exact date only). If the exact date is unknown but the month is known, please enter the 15th of that month as an approximate date.

RSV mother vaccination status

Field: RSVMotherVaccination

Coding: BOOL

Vaccination status of the birth mother during current pregnancy, administered within the recommended time window. This variable should be reported only for cases <2 years of age at the time of disease onset.

RESPIQUAL

Health topic

Field: HealthTopic

Coding: RESPI = Respiratory viruses

The code of the health topic that is being reported.

Subject code (required)

Field: SubjectCode

Coding: RESPIQUAL = Respiratory virus - qualitative indicators

SubjectCode is a reporting model for a disease/health topic - identifies the reporting structure and format of a record (case based or aggregate reporting).

Reporting country (required)

Field: ReportingCountry

Coding: LOCATION

The country reporting the record.

Status

Field: Status

Coding: DELETE = Delete a previously reported record.

NEW/UPDATE = Update a previously reported record (default).

The Status value is used to provide the functionality for a record within EpiPulse Cases database. Default value: NEW/UPDATE. If set to DELETE, the record with the specified NationalRecordId is deleted (invalidated) from EpiPulse Cases database, if it exists. If set to NEW/UPDATE, the record is inserted into the database: If the same NationalRecordId already exists for the same data source and subject code, then the current submitted record updates (replace) the existing one.

National record identifier (required)

Field: NationalRecordId

Coding: TEXT

Unique identifier for each record within and across the specified surveillance system (data source) – selected and generated by the country reporting the record.

Data source (required)

Field: DataSource

Coding: DATASOURCE

The data source (surveillance system) that the record originates from. The DataSource value must be a special reference value from EpiPulse Cases metadata.

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-Www

The reference week (yyyy-Www) for the reported qualitative indicator.

Pathogen or syndrome (required)

Field: PathogenSyndrome

Coding: INFL = Influenza

RSV = Respiratory syncytial virus

SARSCOV2 = Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2)

SYND = Syndromic

Pathogen or syndrome that applies.

Surveillance type (required)

Field: SurveillanceType

Coding: OTH = Other

PISA = PISA

Type of surveillance system.

Qualitative indicator (required)

Field: QualitativeIndicator

Coding: IMPACT = Impact on healthcare capacity

MORB = Morbidity and mortality

SERIOUS = Seriousness of disease

TRANS = Transmissibility

Please select the qualitative indicator that you would like to report. The reporting protocol includes considerations for each qualitative indicator.

Qualitative value (required)

Field: QualitativeValue

Coding: 1 = No activity or below epidemic threshold

2 = Low

3 = Moderate

4 = High

5 = Extraordinary

Please select the value corresponding to the selected combination of pathogen/syndrome, surveillance type and qualitative indicator.

Confidence

Field: Confidence

Coding: H = High

L = Low

M = Medium

Level of confidence for the qualitative value reported for the selected combination of pathogen/syndrome, surveillance type and qualitative indicator.

Comment

Field: Comment

Coding: TEXT

Information should be included on any factors which may have influenced the assessment (for example, changes in health care seeking behaviour, testing practices and capacities and so on), and any differences in activity in certain age groups, at-risk groups or regions highlighted.

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