

REPORTING PROTOCOL

EpiPulse Cases

Reporting Protocol for zoonotic influenza virus

Contents

Introduction	3
How to use this document.....	3
Finding further information	3
Copyright.....	3
Reporting to EpiPulse Cases	4
Checking the data collection schedule.....	4
Preparing data.....	4
Using latest metadata	4
Checking your Surveillance System Descriptors	5
Uploading your data.....	5
Finalising your submission	6
EpiPulse Cases Helpdesk	8
Annex 1. Objectives.....	9
Annex 2. Metadata.....	9
<i>INFLZOO</i>	9
General	9
Epidemiological information	10
Clinical information.....	13
Prophylaxis and treatment	15
Vaccination.....	16
Exposure and transmission.....	17
Occupation	20
Contact tracing	21
Data information link	21
Other information.....	21
<i>INFLZOOCONTACT</i>	21
General	21
Epidemiological information	22

Introduction

This reporting protocol describes data collection for human cases of zoonotic influenza (subject code INFLZOO) and outcomes of contact tracing for zoonotic influenza cases (subject code INFLZOOCONTACT) to [EpiPulse Cases](#).

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 includes the objectives for data collection of human cases of zoonotic influenza
- Annex 2 which contains the metadata for the following subject codes:
 - INFLZOO for reporting of case-based data of zoonotic influenza virus
 - INFLZOOCONTACT for reporting outcomes of contact tracing for human cases of zoonotic influenza

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](#).

Using latest metadata

The metadata defines the fields and data formats that are valid as input to EpiPulse Cases for a given subject.

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 'Gender' and any other value in a 'Gender' 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.

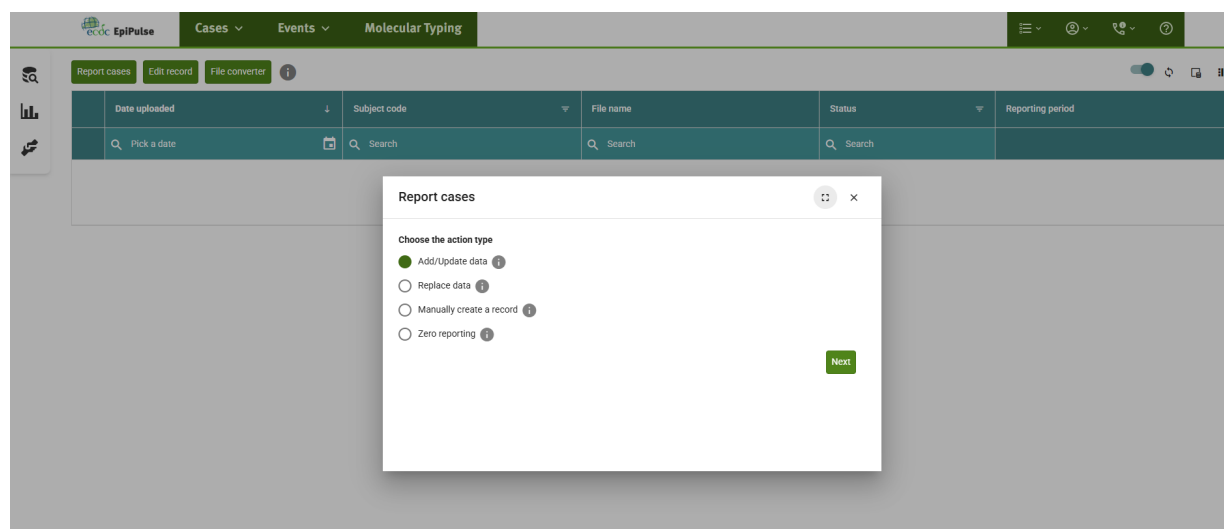
Complete and up-to-date data source information for each subject is important for improving the interpretation of data – each surveillance system has different features that need to be considered when comparing data at European level.

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](#).

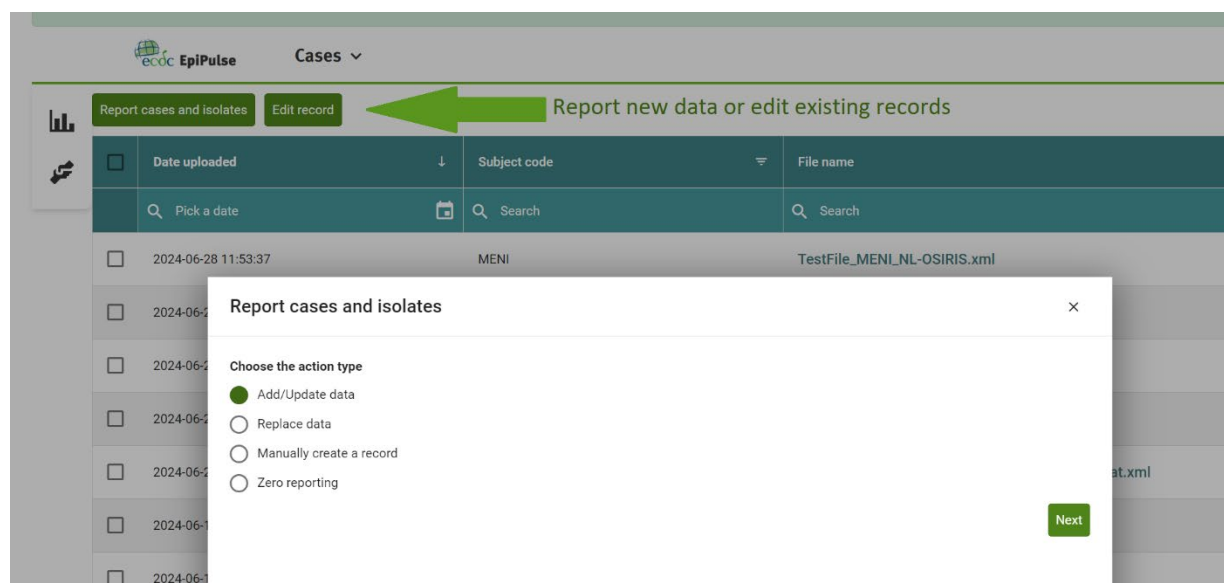
Uploading your data

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.

Disease:
 Health topic:
 Subject code *:

National record ID:
 Data source:

Date used for statistics(from):
 Date used for statistics(to):
 Uploaded on (from):
 Uploaded on (to):

Uploaded by:
 Approved on:
 Approved by:
 Age Group:

☐	National record ID	Data source ↓	Date used for statistics	Uploaded on	Uploaded by	Approved on	Approved by
☐	NationalRecordId09581235...	INFLZOO	2024-01-19	2025-09-22 09:35:31	ECDCDMZ\EPC_HD...	2025-09-22 11:22:14	ECDCDMZ\EPC_HD_CY
☐	NationalRecordId09581335...	INFLZOO	2024-01-24	2025-09-22 09:35:31	ECDCDMZ\EPC_HD...	2025-09-22 11:22:14	ECDCDMZ\EPC_HD_CY
☐	NationalRecordId09581335...	INFLZOO	2024-01-08	2025-09-22 09:35:31	ECDCDMZ\EPC_HD...	2025-09-22 11:22:14	ECDCDMZ\EPC_HD_CY
☐	NationalRecordId09581335...	INFLZOO	2024-01-28	2025-09-22 09:35:31	ECDCDMZ\EPC_HD...	2025-09-22 11:22:14	ECDCDMZ\EPC_HD_CY

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:

EpiPulse **Cases** Molecular Typing

☐	Date uploaded	Subject code	File name	Status	Reporting period
☐	2025-09-22 14:46:36	INFLZOO	INFLZOO_testdata.CSV	Data validation report ready	2024-01-01 - 2024-12-31

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

Details

Data validation report

Data validation report

Download the report for full-screen viewing and sharing

Data Validation Overview

Completeness

Epidemiological Validation

Approval

Cross-field Validation

Total number of inconsistencies: 20

Click here to download all inconsistencies

Download all error messages for easier investigation

INFLZOO

Number of inconsistencies: 20

Show 5 entries

Search:

Filename	Issue/Inconsistency	Occurrences
INFLZOO_fictional_data 1 1.CSV	DateOfTreatment should be reported if DrugUsedTreatment is reported different than "NONE". Please fill in the DateOfTreatment.	1
INFLZOO_fictional_data 1 1.CSV	Please check the DateOfDeath variable.	1
INFLZOO_fictional_data 1 1.CSV	DateOfNotification is before DateOfOnset.	1
INFLZOO_fictional_data 1 1.CSV	DateOfNotification is before DateOfSpecimen.	2
INFLZOO_fictional_data 1 1.CSV	Please report DateOfInfluenzaVaccination.	3

Showing 1 to 5 of 6 entries

Previous12Next

3. Check data completeness; both for the new upload, and in the context of historical data

Data Validation Overview

Completeness

Epidemiological Validation

Approval

Completeness

- Completeness in the last year only (first button) and compared to earlier years.
- Different colours represent different levels of completeness.
- Compare this year's data submission to earlier years. If completeness has gone down for any variables, consider why this may be, whether there is an error or whether you can improve the completeness and resubmit.

Zoonotic influenza virus

Period of analysis: data from 2023-01-01 to 2023-12-31

Number of records included: 24

Epidemiological information

Clinical Information

Exposure and transmission

Prophylaxis and treatment

Vaccination

New data submitted

New and historical data combined

Completeness % by selected variables - Epidemiological information

Age

Gender

DateOfOnset

DateOfSpecimen

DateOfNotification

SettingClinical

CasePrescription

Imported

PlaceOfInfection

2023-01

2023-02

2023-03

2023-04

2023-05

2023-06

2023-07

2023-08

2023-09

2023-10

2023-11

2023-12

0% - 25%

26% - 50%

51% - 75%

76% - 100%

Zero cases reported

No data reported

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

7

Technical Validation Report

Data sources used previously

Metadata Validation

Cross-field Validation

Completeness

Zoonotic influenza virus

Epidemiology

Conclusions

Completeness

- Completeness in the last year only (first button) and compared to earlier years.
- Different colours represent different levels of completeness.
- Compare this year's data submission to earlier years. If completeness has gone down for any variables, consider why this may be, whether there is an error or whether you can improve the completeness and resubmit.

Zoonotic influenza virus

Period of analysis: data from 2023-01-01 to 2023-12-31

Number of records included: 24

Epidemiological information

Clinical Information

Exposure and transmission

Prophylaxis and treatment

Vaccination

New data submitted

New and historical data combined

Completeness % by selected variables - Epidemiological information

Epidemiology

Zoonotic influenza virus

Period of analysis: data from 2023-01-01 to 2023-12-31

Number of records included(historical and new): 24

Overview of INFLZOO data

New data submitted

Historical data

Show entries

Search:

Subtype	Total Cases	Hospitalisation	IntensiveCare	Death
AH5N1	9	1 (11.1%)	1 (11.1%)	1 (11.1%)
AH5NAUNK	1	1 (100.0%)	0 (0.0%)	0 (0.0%)
AH1N1	2	0 (0.0%)	0 (0.0%)	0 (0.0%)

Showing 1 to 3 of 3 entries

Previous **1** Next

5. 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 whomever needs to check it before approval.

Details

Data validation report

Data validation report

Data Validation Overview

Completeness

Epidemiological Validation

Approval

Approval

you can either approve or reject that report:

Approve

Reject

Submit

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)

8

Annex 1. Objectives

To complement event-based surveillance of zoonotic influenza in EpiPulse Events, reporting to EpiPulse Cases allows for indicator-based surveillance. Cases of zoonotic influenza should be reported to EpiPulse Cases as soon as feasible to avoid major delays. Submitted data can be updated retrospectively when additional information becomes available.

Over-arching objective

- To inform risk assessments, targeted prevention strategies, and public health responses.

Individual cases

- Identification and characterisation of human infections and rule out human-to-human transmission.
 - Record individual case data, including virus subtype, clinical presentation, exposure history, treatment, and outcome.
 - Record the number of case contacts.

Multiple cases

- Monitor temporal and geographic trends in zoonotic influenza infections.
- Identify possible risk factors for *infection/case identification*, including exposure (e.g. virus, setting, animal, geography), intervention (e.g. PPE, PEP, vaccination) and clinical factors (e.g. preconditions)
- Identify possible risk factors for *severe disease*, including exposure (e.g. virus, setting, animal, geography), intervention (e.g. PPE, PEP, vaccination) and clinical factors (e.g. preconditions)

Annex 2. Metadata

INFLZOO

General

Subject code (required)

Field: SubjectCode

Coding: INFLZOO=Zoonotic influenza virus

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

Health topic

Field: HealthTopic

Coding: RESPI=Respiratory viruses

Description: The code of the health topic that is being reported.

Reporting country (required)

Field: ReportingCountry

Coding: [Countries]

Description: The country reporting the record.

Status

Field: Status

Coding: DELETE=Delete a previously reported record.

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

Description: 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

Description: 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: [Data sources]

Description: 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-mm-dd

yyyy-Www

Description: Earliest date associated with the case. Please use date of onset if available and preferentially to date of sample collection and to date of reporting to national health authority. If asymptomatic, use date of sample collection.

Epidemiological information

Age

Field: Age

Coding: Numeric (0-125)

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

Age in months

Field: AgeMonth

Coding: Numeric (0-23)

Description: 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: F=Female

M=Male

OTH=Other

Description: Gender of the reported case.

Date of onset of disease

Field: DateOfOnset

Coding: yyyy-mm-dd

Description: Date of onset of disease. Leave empty for asymptomatic cases.

Date of specimen collection

Field: DateOfSpecimen

Coding: yyyy-mm-dd

Description: Date of first specimen collection. If initial specimen collection did not result in case confirmation, please report the date of specimen collection linked to positive result.

Date of notification

Field: DateOfNotification

Coding: yyyy-mm-dd

Description: Date of notification to a regional or national public health agency.

Setting

Field: SettingClinical

Coding: HOSP_OTH=Hospital (not SARI surveillance)

HOSP_SARI=Hospital (SARI surveillance)

I=Investigation of outbreak in animals

OTH=Other

PC_ILIARI=Primary care (ILI/ARI surveillance)

PC_OTH=Primary care (not ILI/ARI surveillance)

T=Contact tracing

Description: Specification of the setting of diagnosis or case identification.

Pathogen detection method

Field: PathogenDetectionMethod

Coding: ANTIGEN=Antigen detection

GENOSEQ=Genotyping/Sequencing

ISOV=Isolation of virus

NEU=Neutralisation

NUC=Nucleic acid amplification

OTH=Other

SCONV=Seroconversion or fourfold titre rise

SIGG=Specific IgG-antibodies

SIGM=Specific IgM-antibodies

SIGMG=Specific IgM- and IgG-antibodies

Description: Laboratory method used for diagnosis of the case. This field is repeatable to allow reporting of all laboratory methods that were used and resulted in a positive result.

Virus HA subtype (required)

Field: HAsubtype

Coding: AH1=A(H1)

AH10=A(H10)

AH11=A(H11)
AH12=A(H12)
AH13=A(H13)
AH14=A(H14)
AH15=A(H15)
AH16=A(H16)
AH17=A(H17)
AH18=A(H18)
AH2=A(H2)
AH3=A(H3)
AH4=A(H4)
AH5=A(H5)
AH6=A(H6)
AH7=A(H7)
AH8=A(H8)
AH9=A(H9)
HAUNK=HA unknown
OTH=Other

Description: Influenza virus HA subtype.

Virus NA subtype (required)

Field: NAsubtype

Coding: N1=A(HxN1)

N10=A(HxN10)
N11=A(HxN11)
N2=A(HxN2)
N3=A(HxN3)
N4=A(HxN4)
N5=A(HxN5)
N6=A(HxN6)
N7=A(HxN7)
N8=A(HxN8)
N9=A(HxN9)
NAUNK=NA unknown
OTH=Other

Description: Influenza virus NA subtype.

Viral coinfection

Field: ViralCoinfection

Coding: INFL_A=Seasonal influenza virus (A)

INFL_B=Seasonal influenza virus (B)

INFLZOO=Other zoonotic influenza virus

Description: Presence of viral co-infection with other influenza viruses. Please provide additional information on other co-infections in the comment field as open text.

Clinical information

Clinical presentation (criteria)

Field: ClinicalCriteria

Coding: ASY=Asymptomatic

CONJ=Conjunctival presentation

COUGH=Dry or productive cough

DIARR=Diarrhoea

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

HEAD=Headache

IRR=Irritability/confusion

NEURO=Neurological symptom(s)

OTH=Other

PAIN=Pain

PAINABDO=Pain - abdominal

PAINCHEST=Pain - chest

PAINJOINT=Pain - joint

PAINMUSC=Pain - muscular

PAINOTH=Pain - other

RUNOS=Runny nose

SBREATH=Shortness of breath

SORETHR=Sore throat

VOMIT=Nausea/vomiting

WEAK=General weakness

Description: Clinical presentation (criteria) of the case.

Case precondition

Field: CasePrecondition

Coding: ASPL=Asplenia

ASTH=Asthma

CANC=Cancer, malignancy

CARDIACDIS=Cardiac disorder, excluding hypertension

DIAB=Diabetes

DOWNS=Down's syndrome

HIV=HIV/other immune deficiency

HYPERT=Hypertension

IMMUNODEF=Immunodeficient

KIDNEY=Kidney-related condition, renal disease

LIVER=Liver-related condition, liver disease

LUNG=Chronic lung disease, excluding asthma

NEUROMUS=Neuromuscular disorder, chronic neurological

NONE=No underlying condition

OBESITY=Obesity

OTH=Other precondition

PREG=Pregnancy

PREG1=Pregnancy, 1st trim, the 1st trim is from week 1 to the end of week 12

PREG2=Pregnancy, 2nd trim, the 2nd trim is from week 13 to the end of week 26

PREG3=Pregnancy, 3rd trim, the 3rd trim is from week 27 to the end of the pregnancy

PREGPOST=Post-partum (<6 weeks)

SMOKE=Current smoking

TB=Tuberculosis

Description: Patient's underlying condition or conditions.

Complications

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

NONE=None

OTH=Other

OTHBAC=Other secondary bacterial infection

PNEU=Bacterial pneumonia

SEPSIS=Sepsis

STILLBIRTH=Still birth as pregnancy outcome in a case

Description: Complications at any time.

Admisssion to hospital

Field: Hospitalisation

Coding: 0 = No

1 = Yes

Description: Hospitalisation in the 4 weeks after onset of illness.

Date of hospitalisation

Field: DateOfHospitalisation

Coding: yyyy-mm-dd

Description: Date of hospitalisation (exact date only).

Intensive care

Field: IntensiveCare

Coding: 0 = No

1 = Yes

Description: 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).

Date of admission to ICU or HDU

Field: DateOfICUHDU

Coding: yyyy-mm-dd

Description: Date of admission to intensive care unit or high dependency unit (exact date only).

Number of days in ICU or HDU

Field: NumberOfDaysICUHDU

Coding: Numeric

Description: Total number of days patient spent in IDU or HDU.

Date of discharge

Field: DateOfDischarge

Coding: yyyy-mm-dd

Description: Date of hospital discharge (exact date only).

Outcome of case

Field: Outcome

Coding: A=Alive

D=Died

STILLTREATMENT=Still on medical treatment

Description: Information on the outcome of the case 4 weeks after onset of illness or, if asymptomatic, after laboratory confirmation of infection.

Date of death

Field: DateOfDeath

Coding: yyyy-mm-dd

Description: Date of death (exact date only).

Prophylaxis and treatment

Drug used for prophylaxis

Field: DrugUsedProphylaxis

Coding: BALO=Baloxavir marboxil

M2=M2 inhibitors

NONE=None

OSEL=Oseltamivir

OTH=Other (or any other combination)

ZANA=Zanamivir

Description: If symptomatic, antivirals used as prophylaxis in the 14 days following exposure (if known) and prior to symptom onset. If asymptomatic, antivirals used as prophylaxis in the 14 days prior to laboratory confirmation of infection.

Starting date of treatment

Field: DateOfTreatment

Coding: yyyy-mm-dd

Description: Starting date for anti-viral treatment of the case during illness phase

Drug used for treatment

Field: DrugUsedTreatment

Coding: BALO=Baloxavir marboxil

M2=M2 inhibitors

NONE=None

OSEL=Oseltamivir

OTH=Other (or any other combination)

ZANA=Zanamivir

Description: Antivirals used as treatment of the case during illness phase or, if asymptomatic, following laboratory confirmation of infection.

Resistance

Field: Resistance

Coding: BALO=Baloxavir marboxil

M2=M2 inhibitors

NONE=None

OSEL=Oseltamivir

OTH=Other (or any other combination)

ZANA=Zanamivir

Description: Resistance to antiviral treatment as assessed by virologists. Report whether resistance has been detected to any antivirals in the coded value list.

Respiratory support

Field: RespiratorySupport

Coding: ECMO=Extracorporeal membrane oxygenation

NOTAVAIL=No respiratory support available

NOTNEC=No respiratory support necessary

OTH=Other respiratory support

OXYGEN=Oxygen therapy

VENT=Ventilator including non-invasive positive pressure ventilation

Description: Level of respiratory support given to patient.

Vaccination

Influenza vaccination

Field: InfluenzaVaccination

Coding: 0 = No

1 = Yes

Description: Current seasonal influenza vaccination.

Date of influenza vaccination

Field: DateOfInfluenzaVaccination

Coding: yyyy-mm-dd

Description: Date of last received seasonal influenza vaccination.

Zoonotic influenza A(H5) vaccination status

Field: VaccinationStatusINFLZOO

Coding: 1DOSE=1 dose

2DOSE=2 doses

3DOSE=3 doses

4DOSE=4 doses

NOTVACC=Not vaccinated

UNKDOSE=Vaccinated, dose unknown

Description: Indicates if the case is vaccinated against zoonotic influenza A(H5) and number of vaccine doses received.

Date of zoonotic influenza A(H5) vaccination

Field: DateOfINFLZOOVaccination

Coding: yyyy-mm-dd

Description: If vaccinated, date of last received zoonotic influenza A(H5) vaccine dose.

Zoonotic influenza A(H5) vaccine

Field: VaccineINFLZOO

Coding: AFLUNOV=Aflunov egg-based vaccine

CELLEMIC=Celldemic cell-based vaccine

OTH=Other

SEQIRUS=Zoonotic influenza vaccine Seqirus

Description: If vaccinated, zoonotic influenza A(H5) vaccine received.

Exposure and transmission

Imported

Field: Imported

Coding: 0 = No

1 = Yes

Description: Patient travelled outside the reporting country in the 14 days prior to symptom onset.

Place of infection

Field: PlaceOfInfection

Coding: [NUTS/GAUL]

Description: Most likely place where the case was infected (e.g. place of exposure). Select the most detailed NUTS level possible. If place of infection is unknown, place of residence or place of notification can be provided as a proxy. If the place of infection is not an EU/EEA country, then use GAUL nomenclature.

Mode of transmission

Field: ModeOfTransmission

Coding: ANIMAL=Animal to human transmission

ENV=Transmission from contaminated environment

FOOD=Food including drinking water

HAI=Healthcare-associated

LAB=Transmission in a laboratory due to occupational exposure

OTH=Other

PTP=Person-to-person

Description: Suspected main mode of transmission.

Exposure setting

Field: ExposureSetting

Coding: BACKYARD=Backyard or household

FAIR=Agricultural fair, live animal show or zoo

FARM=Farm (excluding backyard or household)

HEALTHCARE=Healthcare setting

LAB=Laboratory

MARKET=Live animal/bird market, wet market or wholesale market

OTH=Other

RESCUE=Animal rescue/rehabilitation centre

VET=Veterinary practice/hospital

Description: Likely setting of exposure of the human case to zoonotic influenza virus.

Exposure activity

Field: ExposureActivity

Coding: EAT=Eating raw or unpasteurised animal products (please specify products under ExposureComment)

FOODPREP=Food preparation

HAND=Handling animals

HUMANCONTACT=Close contact with confirmed human case

HUNT=Hunting

LAB=Handling samples containing zoonotic influenza virus

OTH=Other

SHOP=Purchasing live animals

SLAUGH=Slaughtering, butchering, skinning or pelting

TRADMED=Traditional medicine

Description: Exposure activity

Exposure to animal species

Field: ExposureAnimal

Coding: A=Avian (all species, if details or species unknown)

B=Bat

C=Chicken or other domestic birds (poultry, turkey, ...)

D=Dog

E=Cat and other domestic felines

F=Ferret or mink

G=Small ruminant (goat, sheep)

NONE=No animal exposure was established from epidemiological investigation

OTH=Other

P=Pig

R=Cattle

S=Seal

W=Wild bird

Description: Exposure of the human case infected with a zoonotic influenza virus to an animal.

Exposure comment

Field: ExposureComment

Coding: Text

Description: Please provide further detail on exposure to animal species, animal product, exposure activity, occupation.

Influenza A in animals, environment or animal products

Field: ExposureInfluenzaA

Coding: N=No

NOTINVEST=Not investigated

Y=Yes

Description: Detection of influenza A in the animals, environment or animal products the case had exposure to.

Virus HA subtype in animals, environment or animal products

Field: ExposureHASubtype

Coding: AH1=A(H1)

AH10=A(H10)

AH11=A(H11)

AH12=A(H12)

AH13=A(H13)

AH14=A(H14)

AH15=A(H15)

AH16=A(H16)

AH17=A(H17)

AH18=A(H18)

AH2=A(H2)

AH3=A(H3)

AH4=A(H4)

AH5=A(H5)

AH6=A(H6)

AH7=A(H7)

AH8=A(H8)

AH9=A(H9)

HAUNK=HA unknown

OTH=Other

Description: Influenza A virus HA subtype in the animals, environment or animal products the case had exposure to.

Virus NA subtype in animals, environment or animal products

Field: ExposureNASubtype

Coding: N1=A(HxN1)

N10=A(HxN10)

N11=A(HxN11)

N2=A(HxN2)

N3=A(HxN3)

N4=A(HxN4)

N5=A(HxN5)

N6=A(HxN6)

N7=A(HxN7)

N8=A(HxN8)

N9=A(HxN9)

NAUNK=NA unknown

OTH=Other

Description: Influenza A virus NA subtype in the animals, environment or animal products the case had exposure to.

Use of personal protective equipment

Field: PPEUsage

Coding: BREACH=PPE used with known breach or improper use, including inconsistent use

N=No use of PPE

Y=Appropriate use of PPE

Description: Use of personal protective equipment (PPE) by the case during exposure to animals presumably infected with zoonotic influenza virus or a contaminated environment within 10 days of onset of symptoms and/or date of sampling.

Occupation

Field: Occupation

Coding: BYF=Backyard or hobby farmer

COF=Commercial farmer

CUL=Culler

HCW=Healthcare worker

OTH=Other occupation

RIN=Bird ringer or wildlife worker

VET=Veterinarian

Description: Information on the occupation of the case.

Contact tracing

Contact tracing

Field: ContactTracing

Coding: 0 = No

1 = Yes

Description: Contact tracing performed for diagnosed zoonotic influenza case.

Data information link

Item code

Field: ItemCode

Coding: Text

Description: Code of related EpiPulse item.

Wgs accession identifier

Field: WgsAccession

Coding: Text

Description: Sequence identifier, 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 (;).

Other information

Comment

Field: Comment

Coding: Text

Description: Comment field. Please provide any additional comments relevant to the submitted data.

INFLZOOCONTACT

General

Status (required)

Field: Status

Coding: DELETE=Delete a previously reported record

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

Description: 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.

Health topic (required)

Field: HealthTopic

Coding: RESPI=Respiratory viruses

Description: The code of the health topic that is being reported.

Reporting country (required)

Field: ReportingCountry

Coding: [Countries]

Description: The country reporting the record.

Subject code (required)

Field: SubjectCode

Coding: INFLZOOCONTACT=Zoonotic influenza virus - contact tracing

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

National record identifier (required)

Field: NationalRecordId

Coding: Text

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

Date used for statistics (required)

Field: DateUsedForStatistics

Coding: yyyy-mm-dd

Description: Please report the same DateUsedForStatistics as used for reporting to INFLZOO. This should be the earliest date associated with the case. Please use date of onset if available and preferentially to date of sample collection and to date of reporting to national health authority. If asymptomatic, use date of sample collection.

Data source (required)

Field: DataSource

Coding: [Data sources]

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

Epidemiological information

Virus HA subtype (required)

Field: Hasubtype

Coding: AH1=A(H1)

AH2=A(H2)

AH3=A(H3)

AH4=A(H4)

AH5=A(H5)

AH6=A(H6)
AH7=A(H7)
AH8=A(H8)
AH9=A(H9)
AH10=A(H10)
AH11=A(H11)
AH12=A(H12)
AH13=A(H13)
AH14=A(H14)
AH15=A(H15)
AH16=A(H16)
AH17=A(H17)
AH18=A(H18)
HAUNK=HA unknown
OTH=Other

Description: Influenza virus HA subtype.

Virus NA subtype (required)

Field: NAsubtype

Coding: N1=A(HxN1)

N2=A(HxN2)

N3=A(HxN3)

N4=A(HxN4)

N5=A(HxN5)

N6=A(HxN6)

N7=A(HxN7)

N8=A(HxN8)

N9=A(HxN9)

N10=A(HxN10)

N11=A(HxN11)

NAUNK=NA unknown

OTH=Other

Description: Influenza virus NA subtype.

Report granularity (required)

Field: ReportGranularity

Coding: CASE=Case-based

Description: Granularity of reporting contact tracing information. Case-based refers to reporting of aggregated contact tracing results per reported INFLZOO case.

Epidemiological link case identification

Field: EpiLinkCaseId

Coding: Text

Description: Provide record identifier (NationalRecordId) of linked case in subject code INFLZOO.

Contact definition

Field: ContactDefinition

Coding: Text

Description: Definition used to define a contact of a diagnosed zoonotic influenza case.

Contact indicator (required)

Field: ContactIndicator

Coding: IDENTIFIED=Number of contacts identified for zoonotic influenza case

POSITIVE=Number of contacts of zoonotic influenza case that tested positive for zoonotic influenza virus during the 14 day follow-up period after last exposure

REACHED=Number of contacts of zoonotic influenza case identified for contact tracing that were reached (effectively contacted, i.e. answered call or email)

TESTED=Number of contacts of zoonotic influenza case that were tested for influenza A virus during the 14-day follow-up period after last exposure

Description: Selected indicator to report.

Indicator value (required)

Field: IndicatorValue

Coding: Numeric

Description: Please enter the value for the indicator selected (e.g. the number of contacts identified, reached, tested or positive).

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