

## GISAID Single Upload Field Tutorial

### Isolate detail

#### **Isolate ID**

The ID that is assigned to the isolate by the EpiFlu database. It cannot be chosen by the submitter.

#### **Isolate name-REQUIRED**

The name you want to assign to the isolate. There are two naming conventions for isolates, one for human hosts and another for all other hosts. The format for humans is [influenza type]/[region]/[internal reference number]/[year of collection] and for all other hosts [influenza type]/[host]/[region]/[internal reference number]/[year of collection]. An example for a human host is A/Wisconsin/2145/2001 and for another host A/chicken/Rostov/864/2007. This field is mandatory.

#### **Passage details/history**

Information on the passage of the influenza virus, i.e. the host organisms that were employed to create the virus. This category is only eligible for laboratory-derived viruses. Examples for field entries include egg, MCDK1, C1 cell group, and so on.

#### **Type**

The type of the virus is determined by multiple parameters, depending on its genus. It is mandatory to specify the influenza virus type, either A, B, or C.

#### **Subtype H**

Choose between the 17 hemagglutinin subtypes of influenza virus A.

#### **Subtype N**

Choose between the 10 neuraminidase subtype of influenza virus A.

#### **Lineage**

The evolutionary group the virus belongs to. Each lineage is characterized by a common, distinct antigen and accordingly a specific pattern in their genomic sequence.

For influenza virus A subtype H1N1 one differentiates between the lineages pdm09 and seasonal. Viruses that belong to the pdm09 lineage were initially present in pigs only, but are now present in humans too. The seasonal lineage refers to H1N1 viruses that are the cause of the typical human seasonal flu. The category unknown is intended for viruses for whom the lineage is not known.

There are two main lineages that influenza B viruses diverged into, Victoria, and Yamagata. Both are based on differences in hemagglutinin. The category unknown should be used if another lineage is present or the lineage is unknown.

### Sample information

#### **Collection date-REQUIRED**

The date on which the sample was collected. You can enter the date by hand in the format YYYY-MM-DD where Y refers to year, M to month, and D to day or you can select a date using the calendar function by clicking on the button.

#### **Location-REQUIRED**

Specify the continent and location the virus was found in, then country, province/district/state, then county.

#### **Additional location information**

Additional information on the location of the virus, e.g. more comprehensive information on the location such as city.

#### **Host-REQUIRED**

Specify the host from which the sample was extracted. Hosts include human, animal, environment, laboratory derived, and Unknown. Depending on the type of host, different options are available.

Human -No further specification necessary.

Animal -Specify the type of animal the sample was taken from. Animals are differentiated into birds and mammals. For each of these two further classification is possible.

Environment -Category that is used for viruses that were found in the environment in contrary to host organisms. It is possible to further specify the environmental source.

Laboratory derived -Category for laboratory derived viruses, i.e. viruses that have been grown in a laboratory and do not stem from natural sources.

Unknown - Select this host category if the viral host is not known.

#### **Additional host information**

Supply additional information on the host, i.e. specifics like age or peculiarities, if present.

#### **Parameters for human hosts**

##### **Patient age**

The age of the host. You can choose to enter the age of the patient either in years or in months by selecting the corresponding bullet point.

##### **Gender**

The gender of the patient, i.e. male or female.

##### **ZIP code**

The ZIP code of the patient's place of residence.

##### **Patient status**

Options include Deceased, Recovered, In-patient, Out-patient, and Long-term resident.

##### **Last vaccinated**

The year in which the patient was vaccinated last against influenza pathogens.

##### **Outbreak**

This category gives information about influenza activity according. Sporadic, Regional or Wide-spread

##### **Treatment**

The treatment regimen the patient is subject to. It is possible to select multiple types of treatments from the list by holding down the Ctrl-key and clicking on multiple entries in the list.

##### **Specimen source**

The source of the specimen, i.e. the bodily compartment or liquid the sample was extracted from.

##### **In-vivo pathogenicity test**

The in-vivo test used to determine the extent to which the virus is able to generate infectious diseases.

#### **Parameters for animals**

##### **Domestic status**

The domestic status of the animal, i.e. are we dealing with a pet or a wild animal.

##### **Health status**

Information about the constitution of the animal. There are three categories: healthy, sick, and dead.

##### **Is vaccinated**

Vaccination status of the animal host: Yes if the animal has been vaccinated against influenza, otherwise No.

##### **Specimen source**

The specific source of the sample, i.e. where from which cellular location the specimen originates from.

##### **Strain or commercial product name used for vaccination**

##### **In-vivo pathogenicity test**

The in-vivo test used to determine the extent to which the virus is able to generate infectious diseases.

#### **Institute information**

##### **Originating lab**

The laboratory that provided the clinical specimen(s) or virus isolate(s). To choose a laboratory from the list it is first necessary to specify the continent and location the laboratory is located in. If the originating laboratory of your sample is not present in the list, then you can add a new institute to the list.

##### **Address**

The address of the institute is automatically entered by selecting the originating laboratory.

**Sample ID given by the sample provider**

The identification number that was assigned to the isolate by the originating laboratory.

**Submitting Lab**

Enter the laboratory that generated the sequential data of the virus specimen from a drop-down list. Entries in this list are sorted according to location, city, and laboratory name.

**Address**

The address of the laboratory that generated the viral segments' sequences. This field is set to the institute the user belongs to by default. It is possible to select another submitting laboratory, however. When a submitting laboratory has been selected, it will be inputted into the address field automatically.

**Sample ID given by the submitting laboratory**

The ID of the sample that has been assigned internally by the sequencing laboratory.

**Authors**

Researchers involved in sample curation and sequencing.

**Publication****Publication listing**

To add one or multiple publications to the isolate you can use the add publication hyperlink. The added publications should contain additional information on the isolate in question, e.g. by providing research results that pertain that isolate. Do note that it is only possible to add a publication to the isolate after it has been created.

You can edit existing publications by clicking on the Edit button that is shown next to the publication. A publication can be deleted by clicking on the Delete button.

**In vivo antiviral resistances**

There are three types of antiviral resistance testing approaches you can choose from: Unspecified, Genotype, and Phenotype.

**Unspecified resistance testing**

The category Unspecified merges all resistance testing results for whom the exact procedure is not known.

**Genotypic resistance testing**

Genotypic resistance testing refers to methods that predict viral resistance based on the sequence of the relevant viral segments.

**Phenotypic resistance testing**

Phenotypic resistance testing refers to methods that determine viral drug resistance by experimental means.

**Additional information****Antigenic characterization**

Antigenicity describes the ability of antigens to bind to certain products of the immune system. Antigen characterization is about determining the degree of antigenicity, e.g. by performing hemagglutination inhibition assays. The degree of antigenicity in hemagglutination inhibition assays is given by the smallest concentration of antiserum that is necessary to inhibit hemagglutination.

**Note**

Room for any piece of information that did not fit into the predefined isolate attributes.

**Segments**

Listing of isolate segments showing segment release status, if a segment is public domain or not, the type of segment, its corresponding isolate identifier, its length, the segment's EpiFlu accession number, and its INSDC accession number. Segments that are also available via other database are considered to be public domain segments. As a consequence, only public domain segments have an associated INSDC accession number.

Do note that it is not possible to add segments to an isolate at the time of its creation. You can only add segments to an isolate after having created the isolate. To edit a segment, you can click on the Pencil symbol in the second column of the table. You can select all isolates by clicking on the box in the first column of the first row or you can select individual segments by clicking on their corresponding boxes in the table's first column. Segment selection is necessary in order to delete, release or copy segments.

### **Segment release**

A single or multiple segments can be publicly released to the database by selecting them and clicking on the Release button. It is important to note two things regarding segment release: the first one is that segment release is instantaneous, i.e. once you click on the release button, the selected segments will be released. This means that there is no time for you to reconsider your choice. The second thing is that it is not possible to delete a segment from the database once it has been released to the public. However, in case of errors, it is possible to edit segment sequences after their release.

Once a single segment from an isolate has been released, that isolate will also be accessible when searching for released files in the EpiFlu isolate browser. However, when searching this way, you have to consider that the EpiFlu browser will only display those isolate segments that have been released. Unreleased segments are not shown. This is because every user shares the same view on released isolates. In order to view all segments, including the unreleased ones, you have to initiate a search for unreleased files.

### **Segment delete**

Selected segments can be deleted by clicking on the Delete segments button. Do note that a deletion is only performed if all of the selected isolates are still unreleased.