

## EpiFluDB Batch Uploader Tutorial

1. From the Batch Upload Page in EpiFLUDB – Read the agreement and select Yes, I agree to the above EULA and to be bound by the terms of such EULA. Download the Excel file version and save it on your local hard drive for future use.
2. Open in Excel and Enable Excel macros
3. Enter your data into the spreadsheets

Fill out both the sheet "Isolates" and the sheet "Sequences".

"Sequences" need to be in Fasta format. The Fasta sequence header contains the name of your segment and needs to correspond exactly to what you entered into the Seq\_Id columns in the "Isolates" sheet.

If you want to copy data from an Excel file you generated during the workshop, make sure you select, copy and paste just the columns that you need, but don't copy entire spreadsheets because this may lead to problems.

4. Upload your data to EpiFluDB

In the Excel toolbar, select "GISAID (1.1.3)". If you are using Excel 2007, go to "Add-Ins" and then select "GISAID (1.1.3)".

Green row(s): isolates have been uploaded successfully

Orange row(s): isolates have errors and need to be corrected before upload is possible; look for the red cells and check the content of the error message by hovering over the cell or clicking on the red triangle in the top right corner of the cell.

White row(s): isolates have not been changed

5. Troubleshooting the upload

If the Excel file should behave in an unexpected way, save and close all Excel files you have open, shut down Excel completely and restart it.

6. Check and release your data all users of EpifluDB

Go to EpifluDB and check your newly uploaded data in "My unreleased files". If you are happy with the isolate(s), release them to all users of EpifluDB, by selecting the relevant isolates and then selecting "Release selected isolates (without errors)".