



OFFLU guidance on avian influenza sequence databases

Genetic sequences provide key information about the evolutionary, clinical and epidemiological characteristics of influenza viruses; therefore timely deposition of sequence data is a crucial component in protecting animal and human health.

A Resolution has been unanimously voted by national representatives of 172 OIE Members for that purpose (<http://www.offlu.net/OFFLU%20Site/reso.pdf>).

OFFLU urges laboratories and scientific institutions to deposit sequence data into publicly available databases.

Currently, OFFLU recommends that data are deposited in any 'publicly available database' of the submitter's choice.

The following list provides links to several available influenza sequence databases:

- ✓ International Nucleotide Sequence Database Collaboration
(GenBank/DDBJ/EMBL)
<http://www.ncbi.nlm.nih.gov/projects/collab/>

- ✓ GISAID
<http://platform.gisaid.org/>

- ✓ SIB OpenFlu
<http://epiflu.vital-it.ch/>

- ✓ NCBI Flu Resource
<http://www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html>

✓ BioHealthBase

<http://www.biohealthbase.org/GSearch/home.do?decorator=Influenza>

✓ Virus Repository at OIE Reference Laboratory for Avian Influenza at
Hokkaido University, Sapporo, Japan.

<http://virusdb.czc.hokudai.ac.jp/vbdportal/view/index.jsp>

✓ Influenza Sequence & Epitope Database (ISED)

<http://influenza.korea.ac.kr>

If you are aware of any other publicly available influenza genetic sequence databases please contact the OFFLU Secretariat to let them know.

OFFLU does not specifically endorse or recommend any particular database, the links are provided to enable scientists to choose the database that best suits their needs.