

Table 1. Detection of antiviral drug-resistant viruses in Japan during the 2024/2025 influenza season

as of February 6, 2026

|                                   | A(H1N1)pdm09 |              |              |           |             |               | A(H3N2)     |             |           |           |             |               | B         |             |           |           |             |
|-----------------------------------|--------------|--------------|--------------|-----------|-------------|---------------|-------------|-------------|-----------|-----------|-------------|---------------|-----------|-------------|-----------|-----------|-------------|
|                                   | Baloxavir    | Oseltamivir  | Peramivir    | Zanamivir | Laninamivir | Amantadine    | Baloxavir   | Oseltamivir | Peramivir | Zanamivir | Laninamivir | Amantadine    | Baloxavir | Oseltamivir | Peramivir | Zanamivir | Laninamivir |
| <b>Resistant (%)</b>              | 3<br>(0.3%)  | 21<br>(1.0%) | 21<br>(1.0%) | 0         | 0           | 333<br>(100%) | 2<br>(0.8%) | 0           | 0         | 0         | 0           | 179<br>(100%) | 0         | 0           | 0         | 0         | 0           |
| <b>Number of viruses tested</b>   | 859          | 2,126        | 2,126        | 323       | 323         | 333           | 260         | 186         | 186       | 186       | 186         | 179           | 194       | 155         | 155       | 155       | 155         |
| <b>Number of viruses reported</b> | 3,866        |              |              |           |             |               | 648         |             |           |           |             |               | 647       |             |           |           |             |

Baloxavir was examined by focus reduction assay, rhPCR allelic discrimination and/or PA sequencing.

NA inhibitors were examined by fluorescence-based NA-Fluor assay, chemiluminescence-based NA-XTD assay, real time RT-PCR allelic discrimination and/or NA sequencing.

Amantadine was examined by M2 sequencing.