



THE IMPORTANCE OF INFLUENZA DIAGNOSTIC SURVEILLANCE AND THE ROLE OF ATCC IN PROVIDING RELIABLE AND AUTHENTICATED ANALYTICAL REFERENCE MATERIALS

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Abstract

Influenza, particularly zoonotic transmissions like avian influenza, poses a global health threat due to its rapidly mutating RNA genome; this rapid evolution can lead to significant public health and economic consequences. Therefore, effective surveillance systems and diagnostic tools are vital for monitoring and controlling influenza outbreaks. To support these crucial efforts, ATCC® provides highly authenticated analytical reference materials that facilitate the development of reliable diagnostic and surveillance tools. This article captures the critical importance of accuracy and consistency in influenza diagnostic surveillance and highlights ATCC®'s contributions to this field.

1. Understanding Influenza and Its Impact

Influenza is an acute respiratory illness caused by influenza viruses, classified into types A, B, C, and D. Types A and B cause seasonal epidemics, type C causes mild illness, and type D affects cattle. The severity of the disease ranges from mild symptoms like fever, muscle aches, and congestion to severe complications like pneumonia and death.¹

Human and avian influenza pose major public health risks due to their potential for widespread illness and economic impact.¹⁻⁴ Human influenza (types A and B) causes seasonal epidemics, while avian influenza primarily affects birds but can sometimes infect humans, leading to severe disease. Early detection and control of outbreaks rely on effective surveillance and diagnostic testing.

1.1. Human Influenza

Human influenza is a contagious respiratory illness caused by viruses that can lead to mild to severe symptoms and even death. Annual vaccination is the best preventive measure. Human influenza viruses are categorized into types A, B, and C. Types A and B cause seasonal epidemics almost every winter in the United States. In contrast, type C causes mild illness and does not lead to epidemics.^{1,5}

The virus spreads through respiratory droplets when infected individuals cough, sneeze, or talk. Less commonly, touching a contaminated surface and then touching the mouth, nose, or eyes can spread the flu.⁵ Symptoms of this illness can include fever, cough, sore throat, body aches, and fatigue; in some cases, particularly in children, vomiting and diarrhea may occur. High-risk groups, such as young children, the elderly, pregnant people, and those with chronic conditions, face severe complications like bacterial pneumonia, ear and sinus infections, dehydration, and worsening of chronic illnesses.

The economic impact of influenza is significant, including inpatient and outpatient care settings and indirect costs related to lost productivity. In the United States, total annual direct medical costs are estimated at \$3.2 billion, whereas indirect costs account for \$8.0 billion. In the European Union, costs of seasonal influenza are estimated at €6 billion to €14 billion annually.⁷⁻¹⁰

1.2. Avian Influenza

Avian influenza, or bird flu, is caused by avian influenza type A viruses. These viruses naturally occur among wild aquatic birds worldwide and can infect domestic poultry and other bird and animal species. Although avian influenza viruses do not typically infect humans, sporadic human infections have occurred.^{2-4,6,11}

Human infections with avian influenza viruses can range from mild to severe. Symptoms can include conjunctivitis, influenza-like illness (e.g., fever, cough, sore throat, muscle aches), severe respiratory illness (e.g., shortness of breath, difficulty breathing, pneumonia, acute respiratory distress, viral pneumonia), and even death. Most human infections with avian influenza viruses have occurred after prolonged and close contact with infected birds.⁵

Avian influenza virus can jump from birds to humans through two main pathways: direct transmission or through an intermediate host.^{4,11-12}

Direct transmission happens when humans come into close contact with infected birds or contaminated environments. The virus spreads through exposure to infected birds' saliva, mucus, or feces. Human infections, though rare, can occur if the virus enters a person's eyes, nose, mouth, or lungs. Certain avian influenza subtypes can infect humans without adaptation. People with prolonged, unprotected contact with infected birds or areas are at higher risk.

Intermediate hosts, like pigs, can transmit viruses to humans. When a pig is infected with both human and avian influenza viruses, these can combine to form a new variant capable of infecting humans and spreading. This new virus variant can bind to human cell receptors and replicate efficiently at body temperatures lower than in birds—consequently, this results in a new niche (host) adaptation and expansive evolution.

Avian Influenza can severely impact the poultry industry by causing large-scale bird deaths, leading to significant economic losses for farmers, disruptions in the food supply chain, and potential impacts on international trade due to the need to cull infected flocks. Consequently, such outbreak events can result in higher consumer poultry and egg prices. The 2022 avian flu outbreak in the United States has resulted in about 40 million animal losses and economic costs ranging from \$2.5 to \$3 billion.¹¹⁻¹³ Since then, the Centers for Disease Control and Prevention (CDC) reports that the number of affected birds—including wild aquatic birds, commercial poultry, and backyard or hobbyist flocks—in the United States has increased to over 130 million as of January 2025.⁶

The social implications of avian influenza outbreaks are also significant. The disease can lead to fear and panic among the public, leading to the stigmatization of affected communities and a breakdown in social cohesion. Furthermore, the disease can also impact food security, particularly in developing countries where poultry is a major protein source.^{14,15} According to the United States Bureau of Labor and Statistics, in November of 2024, the price of a dozen eggs increased to \$3.60 from \$2.10 the previous year, primarily due to avian influenza.¹⁶⁻¹⁹

The economic impact of avian influenza on poultry can be summarized as follows:

- **High mortality rates:** Highly pathogenic avian influenza (HPAI) strains can rapidly kill entire flocks, causing significant losses for farmers.
- **Culling practices:** To control viral transmission, infected and sometimes even healthy flocks nearby are often culled, leading to large-scale bird losses.
- **Economic losses:** Culling operations and production disruptions result in substantial economic losses for poultry producers.
- **Market disruption:** Outbreaks can lead to fluctuations in poultry prices due to reduced supply, impacting consumers.
- **Trade restrictions:** Countries may impose trade restrictions on poultry products from regions experiencing outbreaks, affecting international markets

1.3. Recent Global Spread of Avian Influenza Infection in Humans and Cattle

The recent global spread of avian influenza, specifically the H5N1 clade 2.3.4.4b, has raised significant concerns.^{20,21} Outbreaks of H5N1 in wild birds and poultry are no longer seasonal in Europe as clade 2.3.4.4b viruses have become endemic.^{21,22} Increased detection of avian influenza has also been reported in Africa.^{21,23-25} In late 2021, the virus was found in wild birds on the east coast of North America^{26,27} and it subsequently spread to South America.^{21,28,29}

Since February 2022, outbreaks of the HPAI H5N1 virus clade 2.3.4.4b in poultry and backyard bird flocks have affected over 130 million birds (either deceased or depopulated to control the spread) in the United States.⁶ By December 2024, the outbreak had spread to all 50 states, affecting 591 counties.⁶ Notably, most human cases in the United States have been observed on dairy farms, with the majority occurring in California. In response, California officials declared a state of emergency on December 18, 2022, indicating the need to expand monitoring and enhance the coordinated statewide approach to contain and mitigate the spread of the virus.³⁰

Since the summer of 2024, concerns about H5N1 in milk have led the United States Department of Agriculture (USDA) and Food and Drug Administration (FDA) to test milk for the virus' presence. On December 6, 2024, the USDA announced a federal order to collect and share milk samples for testing, aiming for comprehensive surveillance of H5N1, which has been detected in dairy cattle throughout the United States since March 2024.^{31,32} These measures are vital to ensure food safety and prevent virus transmission through dairy products.

The United States dairy industry contributes 3.5% of the nation's Gross Domestic Product (GDP) with 3.3 million total jobs.³³ The finding in mid-April 2024 that one in five milk samples from grocery stores across the country tested positive for fragments of the H5N1 avian flu virus has added more anxiety to shoppers on the safety of our food supply, significantly affecting the dairy industry.^{32,34,35} Accordingly, the economic estimates are highly concerning. In affected cowherds, the illness impacts nearly 10% of the animals, causing reduced feed consumption and a 10% to 20% decline in milk production.³⁶ The American Association of Bovine Practitioners (AABP) has estimated the economic impact of H5N1 for dairy cattle to be \$100 to \$200 per cow. This translates into a \$100,000 to \$200,000 loss within a two- to three-week period for a 1,000-cow dairy, and such loss does not include the long-term impact of the disease, decreased herd size, or other potential effects.³⁷

Public health experts are concerned about whether the H5N1 variant virus will jump to swine as the outbreaks continue to expand in dairy cattle, poultry, and other wild and domesticated animals. If that happens, it indicates a significant adaptation leap in the virus' evolution. The first confirmed infection in a pig would pose major public health unease.³⁸

No instances of person-to-person virus transmission have been reported in the United States. Notably, the human cases have been mild, with most infected individuals having known exposure to infected cattle or poultry.³⁹ Rare hospitalized human cases of H5N1 have been documented in various regions, including the first hospitalized human cases in Louisiana and Canada; as of January 2025, health officials have reported that a Louisiana patient was the first individual in the United States to die from the illness.^{40,41} At the same time, another avian influenza variant (H9N2) in China continues to infect humans.^{42,43} These cases, overall, underscore the ongoing zoonotic transmission risk and the need for vigilant surveillance. The World Organization for Animal Health (WOAH/OIE) and World Health Organization (WHO) note the virus' rapid spread across continents, including North America, Europe, Asia, and the Middle East. Surveillance detects mutations that may enhance human transmission, requiring swift action to prevent outbreaks.^{3,44}

2. The Importance of Diagnostics and Surveillance Testing

Surveillance is crucial for infectious disease (ID) control and prevention, involving systematically collecting, analyzing, and interpreting data to detect and monitor activity. It enables the early identification of infectious agents, aids in understanding their transmission dynamics, and supports the implementation of control measures to prevent further spread.⁴⁴⁻⁴⁷ As such, reliable analytical reference materials (ARMs) are essential to ensure the accuracy and reliability of these tests.

2.1. Understanding the Role of Surveillance in Influenza Control

Given the evolving behavior of influenza viruses, surveillance testing remains indispensable. It allows public health authorities to monitor the dissemination of flu strains and identify early signs of potential pandemics. Here are key reasons why influenza diagnostic surveillance is essential:

- **Early detection and response:** Surveillance enables early detection of influenza outbreaks, allowing for timely public health interventions to prevent further spread.⁴⁴⁻⁴⁸
- **Monitoring virus evolution:** Influenza viruses constantly evolve through antigenic drift and shift. Surveillance helps track seasonal changes, informing vaccine composition and antiviral treatment strategies. The current global spread of avian influenza strains, particularly H5N1 variants, underscores the importance of surveillance in monitoring the spread and preventing human and animal infections.⁴⁴⁻⁴⁸
- **Assessing disease burden:** Surveillance data provide insights into the impact of influenza on different population groups, guiding resource allocation and public health policies.⁴⁴⁻⁴⁸
- **Informing vaccine development:** Surveillance findings are critical for updating and developing effective influenza vaccines, ensuring they target the most prevalent and virulent strains.⁴⁴⁻⁴⁸
- **Detecting antiviral resistance:** Laboratory surveillance helps identify resistance to antiviral medications, informs treatment guidelines, and ensures effective patient care.⁴⁴⁻⁴⁸

2.2. Accurate Diagnostic Surveillance Tools Need Reliable Analytical Reference Materials (ARMs)

Reliable ARMs are crucial for accurate diagnostic testing. Effective influenza surveillance needs high-quality ARMs to ensure test accuracy and reproducibility. These standardized reference materials calibrate tests, verify performance, and validate results. Diagnostic tests may produce false results without them, compromising surveillance data and public health responses.

The reliability of diagnostic tests is particularly crucial in the context of new or emerging strains of influenza, such as H5N1, H5N6, H7N7, H7N9, H9N2, and H10N8.^{4,11,12,49-52} These variants may exhibit subtle differences in their genetic makeup, making it more difficult to distinguish them from other strains without accurate reference materials. Here's why ARMs are crucial:

- **Ensuring test accuracy:** Reliable reference materials are critical for the accuracy and reproducibility of diagnostic tests. Reference materials help validate diagnostic tests for sensitivity, specificity, and accuracy, ensuring reliable results.

- **Standardization across laboratories:** They provide a standard against which diagnostic tests can be measured, facilitating comparability of results across different laboratories and over time.
- **Quality assurance:** High-quality reference materials ensure that diagnostic tests meet regulatory standards and guidelines, which is vital for public health surveillance and clinical diagnostics
- **Supporting research and development:** They are used in research to develop and improve diagnostic assays, contributing to advancements in influenza detection and control.

3. ATCC Contributes to Influenza Clinical Diagnostics and Surveillance with Reliable ARMs

With its rich historical collection of microorganisms combined with the implementation of innovative synthetic biology and preservation technologies, ATCC® has been at the forefront of developing new and reliable ARMs for accurate diagnostic testing, surveillance, and research for many emerging and re-emerging infectious agents, helping laboratories stay ahead of the curve in the ever-evolving landscape of global health initiatives related to ID.⁵³⁻⁵⁵ For instance, in 2014, ATCC® launched the synthetic Dengue ARM panel (comprising all four serotypes), which has been instrumental in testing as this vector-borne disease has rapidly spread due to climate change. In 2016, we provided ARMs for the Zika outbreak, another critical vector-borne disease. At the beginning of 2020, ATCC® launched several synthetic ARMs in response to the COVID-19 pandemic in addition to providing native RNA and inactivated SARS-CoV-2 viral strains. Also in 2020, ATCC® launched the synthetic ARM for mpox, which was also highly needed and widely used by the community during the global outbreak in 2022 and onwards. The availability of such reliable reference materials is essential for scaling up surveillance efforts. Our offerings ensure that diagnostic laboratories can meet the demands of large-scale testing without compromising accuracy.

In diagnostics, the accuracy and reliability of positive controls are crucial for effective experimentation and analysis. Traditionally, researchers have relied on cultured microorganisms as controls. While live organisms are essential for assay development through validation, they have some drawbacks. RNA-based viruses, such as Influenza or SARS-CoV-2, evolve rapidly, leading to mutations affecting test results and complicating data interpretation. In addition, uncontrolled sequence variation poses a major problem in manufacturing and quality control (QC). Furthermore, the routine use of live biomaterials as reference materials poses a significant biosafety risk, potentially leading to laboratory-acquired infections.

Modern synthetic biology applications have revolutionized life sciences, offering fast, accurate, and inexpensive nucleic acid-based products. Besides live organisms and their native derivatives, ATCC® has supported the ID diagnostics community for over a decade with a wide array of synthetic nucleic acid-based ARMs for applications such as PCR or sequencing. The core of our ARMs comprises authenticated reliable synthetic technology, high-standard manufacturing and QC processes, and a preservation technology that enables a five-year-long shelf life, which sets these products apart from others in the market.

In addition to our traditional influenza strains, ATCC® now offers synthetic RNA standards for HPAI and additional seasonal influenza viruses that have become increasingly important (Table 1). The recent release of ten influenza synthetic RNA products and three drug-resistant virus strains (Tables 1 and 2)^{56,57} demonstrates ATCC®'s commitment to remaining a global partner in supporting ID surveillance, clinical diagnostics development, and implementation measures, as well as contributing to research in the field. These ARMs represent the most extensive set of synthetic influenza RNA products currently available and are a valued complement to our existing influenza resources including live influenza strains and their native genomic RNA derivatives, next-generation sequencing (NGS)/metagenomic standards, monoclonal antibodies, and antisera (Tables 3 and 4). The availability of these ARMs enables more accurate surveillance of influenza A and B strains, ensuring that diagnostic and surveillance tools remain up to date with evolving virus patterns.

Our synthetic RNA standards for HPAI include subtypes H5N1, H5N6, H7N7, H7N9, and H9N2, representing the most concerning and relevant influenza strains. For example, the H5N1 synthetic RNA product is based on a recent virus strain sequence belonging to the emerging clade 2.3.4.4b. Each of these ARMs consist of two transcripts with five segments, covering approximately 50% of the influenza genome. These segments are key diagnostic targets for nucleic acid-based tests and provide sufficient genomic context for assessing assay specificity. As of January 2025, these products are the most extensive set of synthetic avian influenza ARMs on the market, offering more genome content than other available products. As such, these ARMs provide crucial tools for calibrating diagnostic assays, ensuring the reliable detection and quantitation of avian influenza viruses in animal, human, and food samples.

Our synthetic RNA standards for human influenza virus are based on sequences from H1N1, H3N2, H1N1 2009 pandemic, and Influenza B virus strains used in developing and 510k clearance of several in vitro diagnostic (IVD) devices. Similar to the avian influenza ARMs, these products represent the most extensive set of synthetic human influenza ARMs on the market to date. These aspects underscore the due diligence of the product design team, ensuring that ATCC®'s products are highly relevant and valuable for ID diagnostics and surveillance purposes.

As a premier biological materials resource and standards development organization, ATCC® ensures that the materials used in research and diagnostics meet high standards of quality and reliability, maintaining consistency and accuracy in influenza research and other ID

surveillance. Our current portfolio of molecular standards comprises over 230 native genomic and over 70 synthetic nucleic acid ARMs, comprehensively covering various ID diseases (respiratory, vectorborne, enteric, sexually transmitted, urinary, agricultural, etc.). Each of these products are fully validated via sequencing and quantified by Droplet Digital PCR (ddPCR; Bio-Rad Laboratories, Inc.) to ensure the highest level of authenticity and precision. Our native nucleic acid-based products derive from fully authenticated original live cultures from our biorepository, and the genome sequences of these products can be accessed via the ATCC® Genome Portal.⁵⁸ Our synthetic ARMs are manufactured under ISO 13485 guidance and do not contain any viable material, cannot replicate, are available in fixed concentrations, and can be safely used under BSL-1 settings. Overall, these high-quality products provide an extensive array of reliable reference materials for ensuring the accuracy of diagnostic tests for ID surveillance.

4. Preparing for Future Influenza Threats

ATCC®'s role in providing influenza reference materials goes beyond current strains. The organization is also preparing to extend the offerings to include the next generation of influenza viruses, which could pose serious public health threats. Our goal is to continuously support cutting-edge research, provide reliable ARMs crucial to diagnostic and surveillance systems, and ensure that diagnostic tools remain up to date with evolving virus patterns, allowing for rapid response time.

5. Conclusion

The increasing health and economic risks posed by human and avian influenza strains underscore the necessity of robust surveillance systems. Accurate detection of influenza viruses is crucial for improving outbreak preparedness and response, thereby mitigating their impact on public health and the economy. Continuous surveillance, reliable diagnostic testing, and control measures are essential for managing these risks.

Investing in surveillance infrastructure, fostering global collaboration, and utilizing diagnostic tools that leverage reliable and highly authenticated ARMs are vital steps toward this goal. Organizations like ATCC® play a pivotal role in advancing diagnostic testing and surveillance, providing industry standard products and solutions that enhance research and public health responses to influenza and other IDs. With over a century of championing reproducibility and standards, ATCC® continues to support life sciences research and public health initiatives, ensuring the development of safe, effective drugs and accurate diagnostic tools.

Table 1: ATCC® synthetic RNA for influenza^{a,b}

| ATCC® Item | Sequence of Origin | Type | Serotype | Isolation source of the original virus |
|------------|--------------------------------------|---------------------|------------------------|--|
| VR-3436SD™ | A/white-tailed eagle/Japan/OU-1/2022 | A | H5N1 | Avian |
| VR-3437SD™ | A/Shanghai/4664T/2013 | A | H7N9 | Avian |
| VR-3438SD™ | A/chicken/Wenzhou/334b/2013 | A | H7N7 | Avian |
| VR-3439SD™ | A/goose/Guangdong/GS018/2015 | A | H5N6 | Avian |
| VR-3440SD™ | A/ostrich/Yunnan/438/2014 | A | H9N2 | Avian |
| VR-3386SD™ | A/Brisbane/59/07 | A | H1N1 | Human |
| VR-3388SD™ | A/Netherlands/2629/2009 | A | H1N1pdm09 ^c | Human |
| VR-3387SD™ | A/Hiroshima/52/2005 | A | H3N2 | Human |
| VR-3384SD™ | B/Malaysia/2506/2004 | B, Victoria lineage | | Human |
| VR-3385SD™ | B/Brisbane/60/2008 | B, Victoria lineage | | Human |

^a The synthetic RNA preparation includes two constructs (transcripts). One construct consists of the complete sequences from segments 4 and 5 encoding the HA and NP genes, respectively. The other construct includes complete sequences from segment 6 (encoding the NA gene), segment 7 (encoding M1 and M2 genes), and segment 8 (encoding NS1 and NEP/NS1 genes). In all constructs based on HPAI viruses, the section of the hemagglutinin gene encoding the polybasic cleavage site in the protein has been removed. Altogether the constructs cover 50% of the influenza genome. The product content is verified via sequencing, and the concentration of the transcripts is measured via ddPCR (Bio-Rad Laboratories, Inc). All synthetic products are manufactured under ISO 13485 guidance and can be handled in BSL-1 settings.

^b All ATCC® synthetic products are stored in a proprietary nucleic acid buffer, enabling a five-year-long shelf life.

^c 2009 pandemic isolate.

Table 2: ATCC® antiviral drug-resistant influenza virus strains^a

| ATCC® Item | Designation | Serotype | Antiviral Drug Resistance and Corresponding Mutation Profile |
|------------|-----------------------|-------------------------|---|
| VR-1987™ | A/Washington/10/2008 | H1N1 | Amantadine, rimantadine, M2: S31N ⁵⁶ |
| VR-1988™ | A/Washington/29/2009 | H1N1 pdm09 ^b | Amantadine, rimantadine, M2: S31N; Oseltamivir, NA: H275Y ⁵⁶ |
| VR-3441™ | A/Connecticut/11/2023 | H1N1 pdm09 ^c | Oseltamivir, NA-I223V and NA-S247N ⁵⁷ |

^a As of January 2025. The ATCC® catalog is regularly enriched with new items.

^b 2009 pandemic isolate.

^c Genetically similar to 2009 pandemic isolates.

Table 3: ATCC® influenza-related products^a

| Organism | Type | Lineage | Serotype | Temporal Distribution | Geographic Distribution | No. of Cultured Items | No. of Genomic RNA Items | No. of Antisera & Antibodies | Application |
|-------------------|--------------|---------|-------------------------|-----------------------|--|-----------------------|--------------------------|---|---|
| Influenza viruses | A | | H1N1 | 1934-2022 | US, UK, Malaya | 22 | 11 | 8 ^f | <ul style="list-style-type: none"> • Basic research • Analytical assay development and validation • Analytical reference material • Diagnostics and surveillance • Antiviral discovery |
| | | | H1N1 pdm09 ^b | 2009 | US | 5 | 3 | | |
| | | | H3N2 | 1968-2022 | US, Japan, China, NZ, Australia, Switzerland | 20 | 9 | | |
| | | | H3N8 | | | 1 | | 1 ^g | |
| | | | H5N1 | | | | | 8 ^f | |
| | | | H5N2 | | US | 1 | | | |
| | | | N7N7 | | | | | 1 ^h | |
| | | H9N2 | | | | | 1 ^h | | |
| | | H9N7 | | US | 1 | | | | |
| | | B | Victoria | | 1975-2015 | US | 2 | 1 | |
| | Yamagata | | | 1940-2012 | US | 6 | 5 | | |
| | Unclassified | | | 1945-2021 | US, Russia, Taiwan | 19 | 6 | | |
| Cell Lines | | | | | | 3 ^{c,d,e} | | <ul style="list-style-type: none"> • Basic research • Vaccine manufacturing | |

^a As of January 2025. The ATCC® catalog is regularly enriched with new items.

^b 2009 pandemic isolate.

^c 293-STAT1 BAX KO cell line (ATCC® CRL-1573-VHG™).

^d MDCK (NBL-2) cells (ATCC® CCL-34-VHG™).

^e *Spodoptera frugiperda* (Sf9 cell line, ATCC® CRL-1711™)

^f 8 serotype-specific monoclonal antibodies.

^g 1 Influenza A antisera.

^h 1 serotype-specific monoclonal antibody.

Table 4: Viral NGS Standards that mimic mixed metagenomic samples.

| ATCC® Item | Product Name | Product Description and Content | Utility |
|------------|-------------------------|---|---|
| MSA-1008™ | Virome Nucleic Acid Mix | <p>This product comprises an even mixture of nucleic acids prepared from fully sequenced, characterized, and authenticated viral strains selected based on genomic size, DNA/RNA genome, envelope/non-envelope, and other special features.</p> <p>Components:</p> <ul style="list-style-type: none"> • Human adenovirus 40 (ATCC® VR-931DQ™) • Human herpesvirus 5 (ATCC® VR-538DQ™) • Human respiratory syncytial virus (ATCC® VR-1540DQ™) • Influenza B virus B/Florida/4/2006 (ATCC® VR-1804DQ™) • Reovirus 3 (ATCC® VR-824DQ™) • Zika virus (ATCC® VR-1838DQ™) | <ul style="list-style-type: none"> • Basic research • Analytical assay development and validation • Analytical reference materials |
| MSA-2008™ | Virome Virus Mix | <p>This product comprises an even mixture of fully sequenced, characterized, and authenticated viral strains selected based on genomic size, DNA/RNA genome, envelope/non-envelope, and other special features.</p> <p>Components:</p> <ul style="list-style-type: none"> - Human adenovirus 40 (ATCC® VR-931™) - Human herpesvirus 5 (ATCC® VR-538™) - Human respiratory syncytial virus (ATCC® VR-1540™) - Influenza B virus B/Florida/4/2006 (ATCC® VR-1804™) - Reovirus 3 (ATCC® VR-824™) - Zika virus (ATCC® VR-1838™) | <ul style="list-style-type: none"> • Diagnostics and surveillance • Microbiome/metagenomic analysis • Bioinformatics |


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