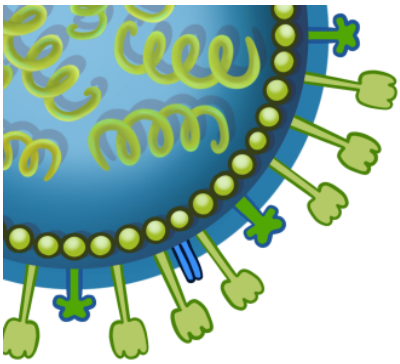
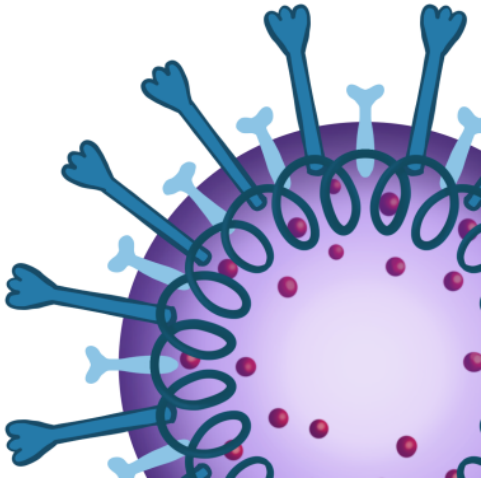


Wastewater-Based Infectious Disease Surveillance in Switzerland

July 2024 - October 2025: Final Report

Final: April 2026



eawag
aquatic research

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Background

Wastewater monitoring for communicable diseases continues at Eawag since its origins in February 2020 as a joint research project with EPFL during the Covid-19 pandemic. In February 2021, the Swiss Federal Office of Public Health provided funding for the work to explore its utility to inform public health responses. In July 2023, the program expanded to also track Influenza A virus, Influenza B virus, and Respiratory Syncytial Virus alongside SARS-CoV-2. Today, Eawag is responsible for surveillance at ten wastewater treatment plants (WWTPs) across Switzerland, collecting the wastewater of approximately 22% of the Swiss population.

The scope of this report is on quantifying target respiratory pathogens in raw wastewater after gross solids removal. This is only one type of public health data currently derived from wastewater in Switzerland. The program contributes directly to the genomic surveillance of SARS-CoV-2[1], Influenza A virus[2], and RSV[3] by providing the extracted nucleic acids from six of the monitored sites to our partners at the Functional Genomics Center Zurich (FGCZ), ETH Zurich (ETHZ), and NEXUS, which sequence and analyze samples to determine lineages and track mutations. Other projects include DroMedAario[4], which monitors pharmaceuticals, illicit drugs, and other substances; and estimating the effective reproduction number for SARS-CoV-2, Influenza A and B viruses, and Respiratory Syncytial Virus[5]. Monitoring of antibiotic resistance was concluded after the initial pilot.[6]

The monitoring program represents the collaborative efforts of a large network of stakeholders, including the staff at the WWTPs who collect, store and ship samples every week; staff at Eawag who process samples and analyze results; staff at EPFL, ETHZ, FGCZ; and NEXUS who support data collection, storage, analysis, and interpretation; and staff at the Federal Office of Public Health who interpret and disseminate results. We also acknowledge the large network of cantonal and private laboratories and their staff who have supported the program in the past through sample processing and analysis.

This publication is the final report for the project “Abwassermonitoring für übertragbare Krankheiten” (Contract number 142006655); funded by the Federal Office of Public

[1] CovSpectrum wastewater data available at: https://cov-spectrum.org/stories/wastewater-in-switzerland; (Accessed 28 Oct 2025)
[2] GenSpectrum Influenza A virus in wastewater data available at: https://genspectrum.org/swiss-wastewater/flu; (Accessed 8 Nov 2026)
[3] GenSpectrum RSV in wastewater data available at: https://genspectrum.org/swiss-wastewater/rsv; (Accessed 8 Nov 2025).
[4] DroMedAario project available at: https://www.dromedario.ch/ (Accessed 28 Oct 2025)
[5] Effective Reproduction Number estimates available at https://wise.ethz.ch (Accessed 28 Oct 2025).

Health).[6] The report template is based on, repeats information from, and extends data from:

> *Wastewater-Based Infectious Disease Surveillance in Switzerland Update: July 2023 - April 2024, Version 3 (13 September 2024), Final*[7]

The Wastewater Monitoring Lab at Eawag holds an establishment license issued by Swissmedic with validity from 24 July 2024 through 23 July 2029. The lab is also supported by the Swiss National Science Foundation, through the Sinergia funding scheme, which provides a research grant to a consortium of researchers at ETHZ, EPFL, and Eawag to advance the field of wastewater-based surveillance scientifically. The funding supports novel research to improve characterization and understanding of wastewater as a resource for infectious disease epidemiology. The recent integration of Influenza A virus and RSV sequencing into routine monitoring is a prescient example in which research funding motivates innovation that is then adopted by stakeholders. A full list of publications from the reporting period is included at the end of the report.

[6] https://www.aramis.admin.ch/Grunddaten/?ProjectID=54487(Accessed 1 Apr 2026)
[7] https://www.aramis.admin.ch/Texte/?ProjectID=53837 (Accessed 28 Oct 2025)

Sampling Sites

For the reporting period, we processed wastewater from ten WWTPs across Switzerland serving approximately 2.0 million people, or 22% of the total Swiss population (Table 1, Figure 1).

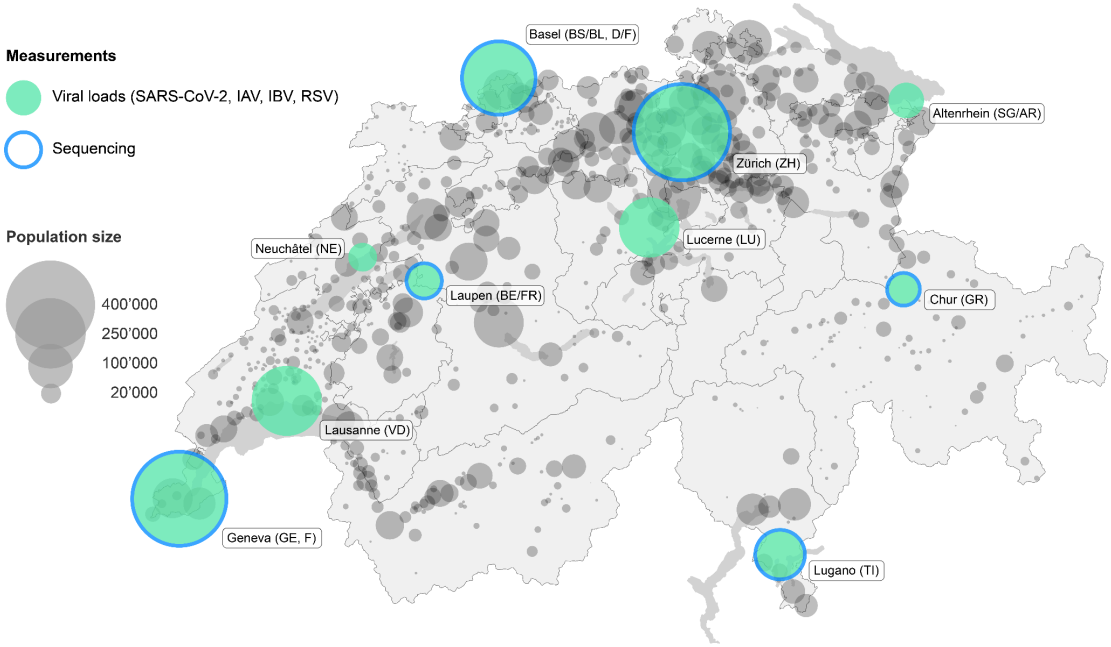


Figure 1: Map of the locations of all central WWTPs in Switzerland (grey circles), with the locations of ten WWTPs providing samples for quantifying viral loads of respiratory viruses highlighted in color (green). At six of the ten sites, noted by a blue outline, a subset of samples are sent for sequencing to determine SARS-CoV-2 variants throughout the year. In the winter season, Influenza A virus and RSV are also sequenced.

Table 1: Names, locations, and estimated populations served by the WWTPs enrolled in the monitoring of respiratory pathogens. WWTPs that are also monitored for variants and chemicals are noted in the additional columns (x=over the entire monitoring period, o=only since January 2025).

Kanton	**WWTP Name**	**City/Region**	**Est. Pop.**	**Variants**	**Chemicals**
ZH	ARA Werdhölzli	Zürich	471000	x	x
GE	STEP Aïre	Genève	451000	x	x
BS	ARA Basel /ProRheno	Basel	273000	x	x
VD	STEP Vidy	Lausanne	248000		x
LU	ARA Buholz	Luzern	184000		o
TI	IDA CDA Lugano	Lugano	124000	x	x
GR	ARA Chur	Chur	55000	x	x
BE/FR	ARA Sensetal	Laupen BE	62000	x	o
NE	STEP Neuchâtel	Neuchâtel	41000		x
SG/AR	ARA Altenrhein	Altenrhein	64000		o

Methods

From July 2024 until October 2025, 2,565 wastewater samples were processed for respiratory virus pathogens from ten WWTP (see Sampling Sites) over 65 processing weeks. The total number of processed wastewater samples highlights the effectiveness of the program logistics, as it is equivalent to over 3.9 samples per week per WWTP. Samples were shipped cooled weekly for 50 weeks per year from the WWTP to Eawag (Dübendorf). A processing break occurs two weeks in the summer for laboratory maintenance and organization. To quantify loads of respiratory pathogens, samples were typically processed within 24 hours of receipt. Samples that failed quality control were re-analyzed within 48 hours of receipt, or were excluded if that was not possible. The methods described below are the same as described in previous reports, highlighting that our methods remain consistent, an important consideration for maintaining historic comparison.

Wastewater sample processing and nucleic acid extraction.

Wastewater influent (24-hour composite) samples were routinely collected by WWTP personnel, stored at 4°C and transported on ice within one week to our laboratory at Eawag, Swiss Federal Institute of Aquatic Science and Technology in Dübendorf. Throughout the study, we aimed to process four samples per treatment plant per week. Nucleic acids were extracted from 45 ml of wastewater using a modified version of the Wizard Enviro Total Nucleic Acid Kit (Promega Corporation, USA), as previously described (Nadeau et al. 2024; Pitton et al. 2025). Nucleic acids were eluted in 80 µl RNAse-free water and then purified using the OneStep PCR Inhibitor Removal Kit (Zymo Research, USA). Extracts were analyzed using dPCR immediately following their preparation on the same day, and additional aliquots were stored at -80°C.

Digital PCR assays and PCR inhibition.

All dPCR assays were developed on the Naica® system 6-color Crystal Digital PCR Prism-6 (Stilla Technologies, France). For this reporting period, we relied on a six-plex digital PCR assay, referred to as RESPV6, which measures the presence of SARS-CoV-2, Influenza A virus, Influenza B virus, and Respiratory Syncytial Virus (Pitton et al. 2025). The RESPV6 assay was prepared using a total 27 µl pre-reaction volume, which consisted of 21.6 µl of mastermix (qScript XLT One-Step RT-qPCR ToughMix, QuantaBio) and 5.4 µl of template until March 31st. From April 1, pre-reaction volume was increased to 27.5 µl consisting of 22 µl mastermix and 5.5 µl template. The reaction volume (25 µl) was loaded into Sapphire chips (Stilla Technologies). Chips were loaded into a Geode (Stilla Technologies) which partitions the mastermix into droplets (12 min at 40°C) before thermocycling using the following conditions: reverse transcription (50°C for 1 h), enzyme

activation (95°C for 5 min), and 40 cycles of denaturation (95°C for 30 s) and annealing/extension (57.5°C for 1 min).

PCR inhibition in the RESPV6 assay was evaluated for a subset of samples, as previously described (Huisman et al. 2022; Pitton et al. 2025; Nadeau et al. 2024). When inhibition was detected above our specified threshold of 40% or more inhibition, samples from the corresponding wastewater treatment plant were processed again on digital PCR with increased dilution. In this way, inhibition measurements were used for quality control, to ensure measurements were not impacted substantially by inhibitory substances.

RNA extraction efficiency quality control.

To determine the efficiency of RNA extraction, a known amount of viral control (Murine Hepatitis Virus strain MHV-A59, or MHV) was spiked into 45 ml of wastewater prior to processing. Measurement of MHV RNA simultaneous to the other respiratory pathogens in six-plex dPCR assay allowed estimation of recovery efficiency by dividing the measured concentration by the estimated spiked concentration and expressing the result as a percentage. Recovery efficiency was used to monitor consistency in lab processing, but was not used to adjust viral concentration measurements.

Positive and negative controls.

Positive controls used in dPCR assays were prepared by combining nucleic acid templates to achieve approximately 100 gene copies per µl reaction for each target. Synthetic viral RNA (SARS-CoV-2 RNA reference material; EURM-019, Joint Research Center) was used for SARS-CoV-2, whereas gBlocks (Integrated DNA Technologies, USA) were used for Influenza A and B viruses, and RSV. Positive material for MHV was obtained by extraction.

Negative controls included one bottle control per week, which consists of a sampling bottle that is shipped to one of the WWTPs and filled on site with tap water prior to return shipping. The bottle is returned with the samples, and then processed alongside the samples from that treatment plant. Additionally, every day in which extractions were performed, we included a full processing control (FPC), in which tap water from our lab was processed alongside the samples. Finally, every thermocycler included one no template control (NTC) alongside up to five samples each processed in duplicates. The bottle and full process controls consistently had 2 or fewer positive fluorescent droplets, consistent with our definition of a non-detect, with the exception of one bottle control and two full process controls in the study period. When the NTC had 3 or more positive fluorescent droplets, all samples in that thermocycler were measured a second time. When the bottle or full process controls were contaminated, we first re-ran the dPCR

assays. If contamination was detectable, sample extractions were repeated or the samples were excluded from further analysis.

Data and statistical analysis.

All dPCR data were analyzed using the Crystal Miner Software version 4.0.10.3 (Stilla Technologies), which provides RNA quantities expressed as gene copies per microliter of reaction (gc/µl of reaction). Wastewater samples were defined as positive when the concentration was above the limit of detection (LoD), which was set to a threshold of at least three positive partitions per well, corresponding to approximately 5 gc/reaction. Values were transformed to gene copies per liter of wastewater (gc/Lww). Viral RNA concentrations were then converted to total daily loads per treatment plant by multiplying by total daily wastewater flow. A per person viral RNA load (expressed as gc/person-day) was calculated by dividing the total daily load by the average population in the wastewater treatment plant catchment area.

Statistical analyses

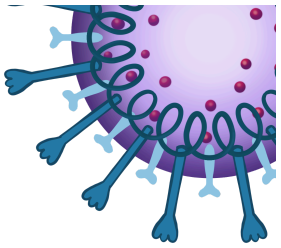
All analyses were conducted using R (v4.4.0) and R Studio (v2025.9.1.401).

Comparison with clinical data from Sentinella.

The Swiss Federal Office of Public Health (FOPH) collects clinical data about respiratory viruses mainly through two surveillance systems: the mandatory reporting system and a primary care sentinel reporting system (Sentinella). In this report, as in the previous report, we refer only to data collected via Sentinella[8], which is a voluntary reporting system involving around 160 to 180 family physicians and pediatricians and provides data on consultations for acute respiratory infections (ARI) or for influenza-like illnesses (ILI) including virological testing for the four pathogens we currently target. Data is presented as it is publicly available[9], aggregated to the total number of cases reported per week across all of Switzerland.

[8] https://www.idd.bag.admin.ch/survey-systems/overview
[9] https://www.idd.bag.admin.ch/survey-systems/sentinella

Results: SARS-CoV-2



Overview

SARS-CoV-2 is the causative agent of Covid-19. We monitor two targets for SARS-CoV-2, the N1 and N2 gene regions. These gene targets are widely used in clinical diagnostics and wastewater monitoring. The decision to use two targets was driven by mutations in the N1 gene region, causing concern that counts in wastewater may be underestimated due to reduced amplification efficiency (Lesbon et al. 2021).

Throughout the monitoring period, we detected SARS-CoV-2 in almost all of our samples across all sites (99.7% of the samples). From this finding, we assume SARS-CoV-2 circulates throughout Switzerland the entire year. This high detectability is distinct from the detectability of the other three viruses we quantify, which follow seasonal patterns with peak detection rates in the winter, and less frequent in the late spring, summer, and early fall. In contrast, SARS-CoV-2 appears to transmit throughout the year, with intermittent peaks not strongly linked to seasons, but instead typically occurring with new variant introductions. The samples processed at Eawag are also sequenced to determine the presence and relative abundance of circulating SARS-CoV-2 variants. This work is conducted by the group of Niko Beerenwinkel (ETHZ), FGCZ, and NEXUS (ETHZ). Results are reported on covSpectrum[10].

As in previous years, the SARS-CoV-2 signal in wastewater in 2024-25 was more than one order of magnitude higher than loads for the other respiratory pathogens. The reasons for the higher magnitude remain unclear, but may be driven by a combination of higher viral loads in people during infections (leading to higher viral counts in wastewater per infected person), more pronounced fecal shedding, longer duration of shedding, and higher infection prevalence rates (a higher number of people infected). Pathogen-specific fate and transport processes or laboratory recovery efficiency may also influence differences in loads.

National Trend

The dynamics of SARS-CoV-2 for the reporting period were different from the dynamics in the previous year (Figure 2). Viral loads were moderately high throughout the summer 2024 (Figure 2, blue line), which contrasts to summer 2023 in which viral loads remained very low (Figure 2, black line). From the wastewater sequencing data, we attribute the moderate summer SARS-CoV-2 circulation to the introduction and circulation of

[10] https://cov-spectrum.org/stories/wastewater-in-switzerland (Accessed June 28, 2024)

SARS-CoV-2 KP.2 and then KP.3 variants.[11] In the fall from October through December 2024, we observed a notable and extended increase in viral loads in this reporting period, which we attribute to the introduction of the SARS-CoV-2 XEC variant. Comparing the peak to the previous year, we observed that the timing of the peak in fall 2024 was similar to the timing in 2023, though the viral loads were substantially higher in 2023.

Starting in January 2025, we observed a sharp reduction in SARS-CoV-2 viral loads, which persisted through the spring and early summer. Although viral loads were dramatically reduced, viral RNA remained detectable throughout the season. Viral loads showed a moderate peak in June, coincident with the introduction of the XFG variant, before receding again in June. While the late spring increase in SARS-CoV-2 we observed in 2025 aligned with 2024, the subsequent decrease did not. In 2024, viral loads increased in the late spring and remained high throughout the summer. Starting in August 2025, viral loads increased again, while variant XFG remained the primary circulating variant. SARS-CoV-2 loads peaked in early October, before beginning a slow descent.

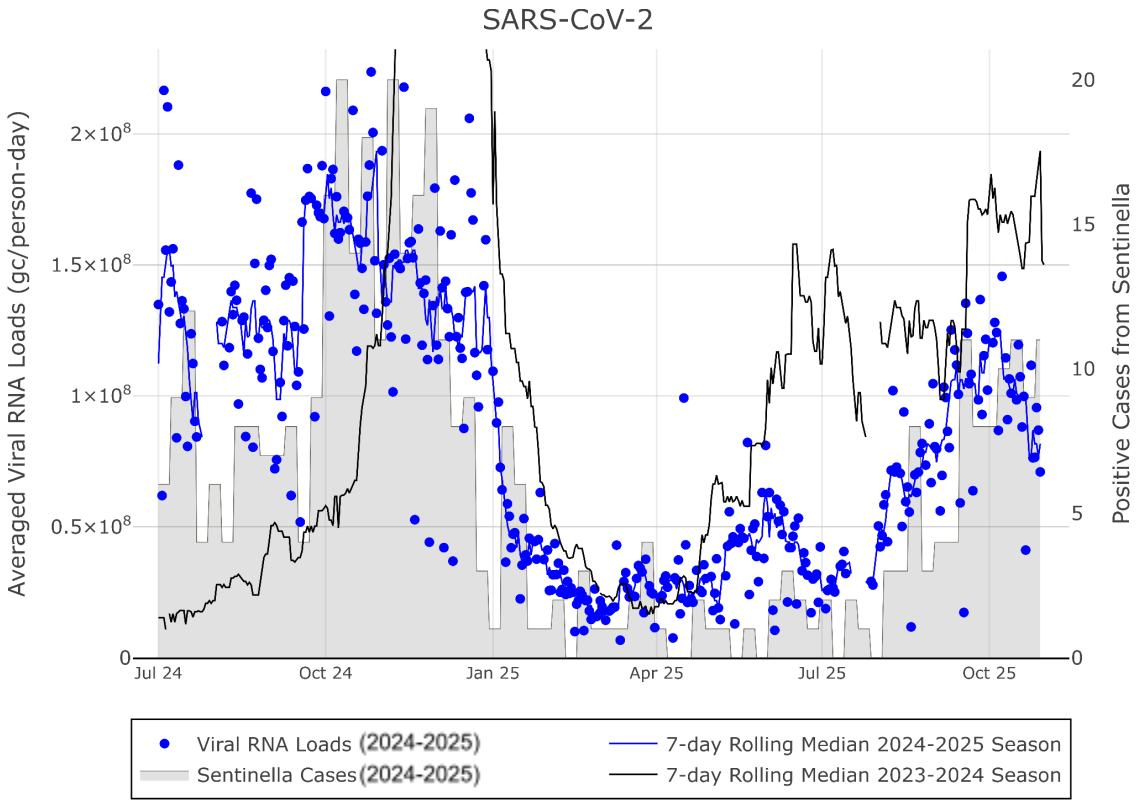


Figure 2: The national trend for SARS-CoV-2 viral load, which is the population weighted mean of all ten WWTPs. SARS-CoV-2 viral RNA load measurements (genome copies per person per day) are plotted as blue dots, while a 7-day rolling median is reported as a blue line on the left y-axis. The previous season (2023-2024) 7-day rolling median is reported as a black line to provide

[11] https://wise.ethz.ch/?page=viruses/variants

historic comparison in magnitude and trends. Sentinella cases, aggregated to the calendar week, are plotted as gray shaded boxplots with the number of cases on the right y-axis.

Alignment with Clinical Data

As in past years, viral loads aligned well with clinical data obtained through Sentinella network. Positive tests for SARS-CoV-2 reported through Sentinella were significantly correlated with both SARS-CoV-2 N1 (Spearman's $\rho = 0.76$, $p < 0.001$) and N2 (Spearman's $\rho = 0.75$, $p < 0.001$) targets. The correlation coefficients are lower than in the previous year, which we attribute to deviations between viral loads and clinical cases from July 2024 through January 2025. In the summer 2024, national viral loads were higher than would be expected based on the historic relationship with Sentinella cases; and in the fall 2024, national viral loads were lower than would be expected. We attribute this deviation to differences in regional trends. In many locations (i.e., Altenrhein, Chur, and Lugano), viral load dynamics aligned more closely with the observed dynamics from the Sentinella cases, with low summer circulation followed by higher rates of fall circulation. In other locations, particularly in some of the larger cities (i.e., Geneva, Lausanne, and Zurich), we did not observe this trend, and due to their population size, these cities had a disproportionate impact on our national trend data (see Regional Trends).

Regional Trends

The observed national trend was largely consistent with regional trends (Figure 3-4), however the dynamics of the wastewater in the summer and fall of 2024 revealed site-specific differences. Viral loads in some locations, including Geneva, Lausanne and Zurich, were consistently elevated and did not further increase in mid-September 2024, whereas at other sites (i.e., Altenrhein, Chur, and Lugano) we observed lower viral loads during the summer followed by a more dramatic rise in mid-September (Figure 3-4). The national trend, which shows a slight elevation of viral loads in mid-September compared to the summer viral loads, averages the effects of the two distinct dynamics.

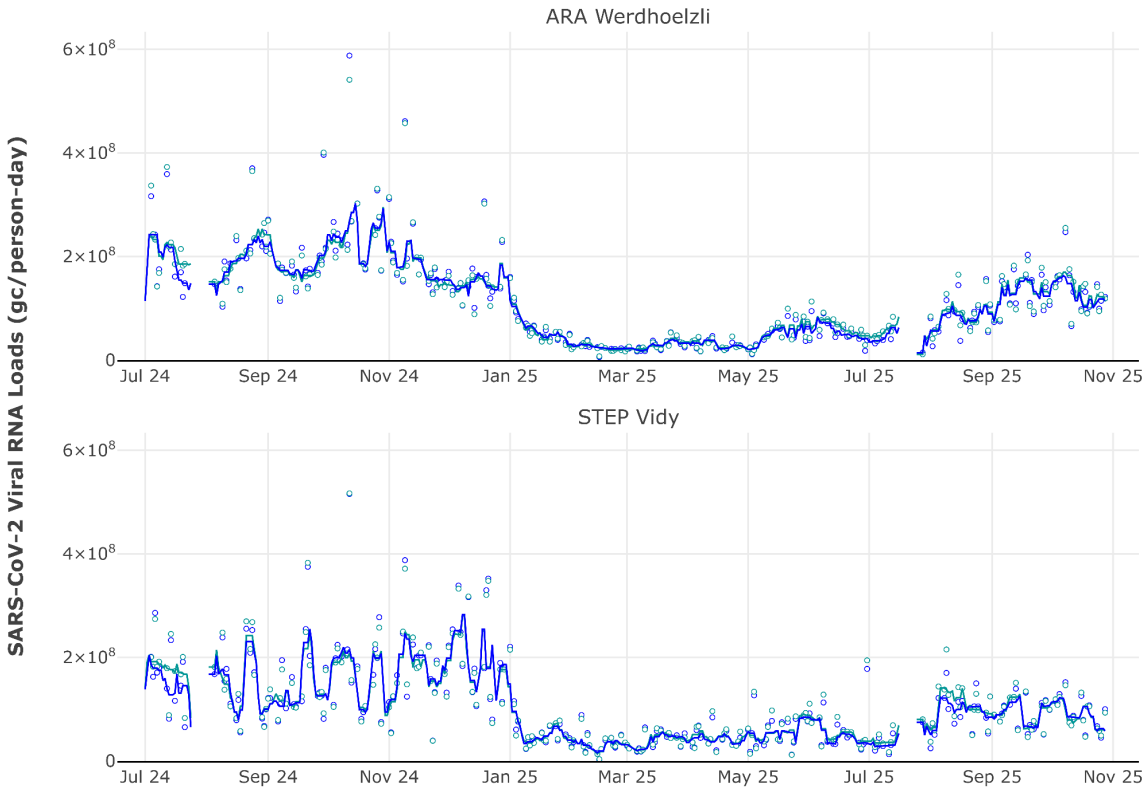


Figure 3: SARS-CoV-2 loads (genome copies per person-day) for ARA Werdhölzli (Zurich) and STEP Vidy (Lausanne) over the reporting period. Sample loads (open circles) and 7-day rolling median (linesare presented for two SARS-CoV-2 targets N1 (dark blue) and N2 (light blue).

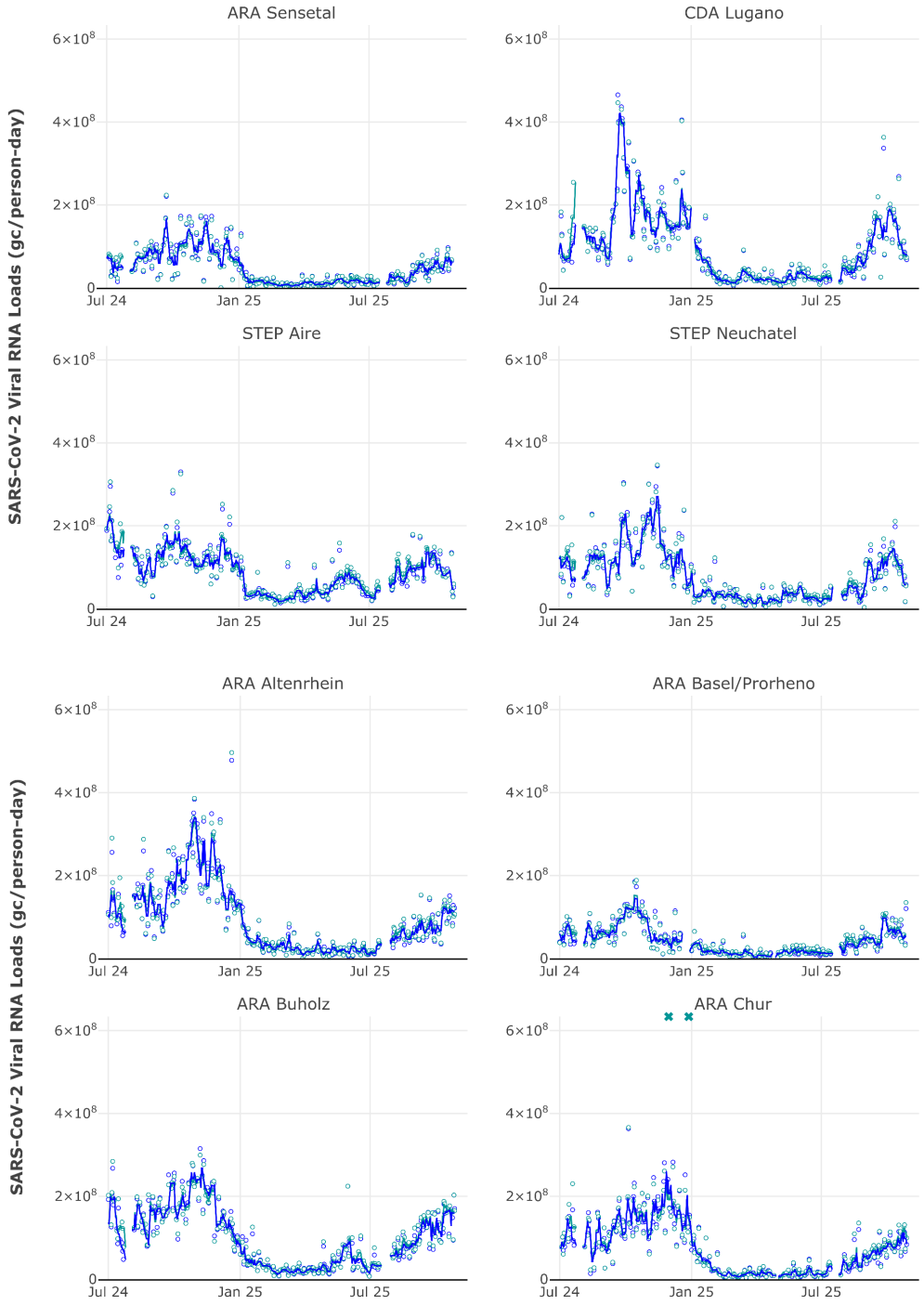
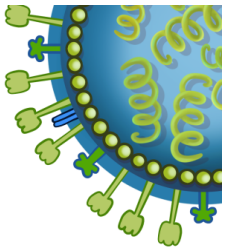


Figure 4: SARS-CoV-2 loads for ARA Sensetal, CDA Lugano, STEP Aïre, and STEP Neuchatel Altenrhein, ARA Basel, ARA Buholz in Emmen, ARA Chur, ARA Region Bern, and ARA Schwyz over the reporting period. Sample loads (open circles) and 7-day rolling median (lines) are presented for two SARS-CoV-2 targets N1 (dark blue) and N2 (light blue) monitored throughout the study period.

Results for Influenza A, Influenza B, and Respiratory Syncytial Virus



Overview

Seasonal flu (influenza) is caused by the Influenza A and Influenza B viruses.[12] Influenza viruses are included within the set of infectious diseases requiring notification in Switzerland.[13] Respiratory Syncytial Virus is also a respiratory virus[14], but notification is not required in Switzerland.

During the monitoring period, all three viruses were regularly detected in wastewater across all ten sites. Influenza A was detected in 35% of the 2,565 samples processed, Influenza B was detected in 40%, and Respiratory Syncytial Virus was also detected in 39%. The lower frequency of detection of these pathogens relative to SARS-CoV-2 is attributable to the seasonality of transmission, which stands in distinct contrast to the persistent transmission of SARS-CoV-2 throughout the year. Throughout much of the spring, summer, and fall, we detected these pathogens only intermittently at or near the limit of detection.

Influenza A virus, Influenza B virus, and RSV were also present in wastewater at substantially lower viral loads as compared to SARS-CoV-2, which is similar to historic observations (Figure 3-8). This may be attributable to a combination of potential factors, including: 1) lower prevalence rates in the community (fewer people infected), 2) lower shedding loads (fewer viruses shed into wastewater per infected person), 3) shorter durations of shedding (infected people shed into wastewater for shorter periods) relative to SARS-CoV-2, and 4) differential stability of the viral RNA in the wastewater stream (i.e., SARS-CoV-2 RNA is more stable than the other viruses tested).

Influenza A Virus National Trend

Influenza A viral loads followed a clear seasonal pattern, as in the previous year (Figure 5). In the national trend data, we observed viral loads increase, remaining consistently above the limit of detection in late November 2024, before increasing at a faster pace and reaching a higher total viral load than in the previous year. Viral loads remained elevated

[12] For more information, please see website maintained by FOPH at https://www.bag.admin.ch/de/saisonale-grippe-influenza (Accessed 11 Nov 2025)

[13] For more information, please see website maintained by FOPH at: https://www.idd.bag.admin.ch/survey-systems/oblig (Accessed 11 Nov 2025).

[14] For more information, please see website maintained by FOPH at https://www.bag.admin.ch/de/respiratorisches-synzytial-virus-rsv (Accessed 11 Nov 2025).

through late January before starting a slow decline before reaching baseline in mid April 2025. The more rapid ascent, higher overall loads, and delayed decline suggests the seasonal epidemic of Influenza A virus exceeded the 2023/2024 season.

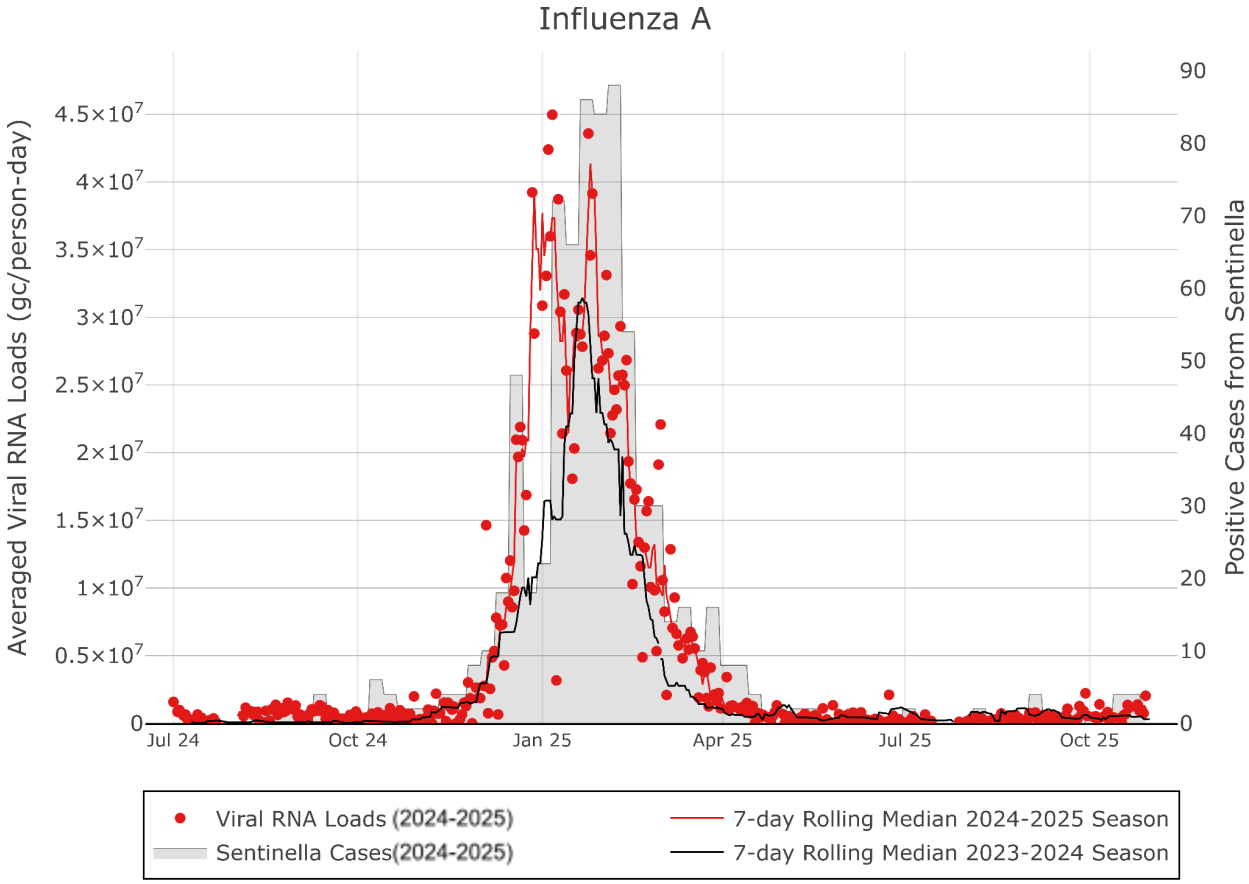


Figure 5: The national trend for Influenza A viral load, which is the population weighted mean of all ten WWTPs. Influenza A viral RNA load measurements (genome copies per person per day) are plotted as red dots, while a 7-day rolling median is reported as a red line on the left y-axis. The previous season (2023-2024) 7-day rolling median is reported as a black line to provide historic comparison in magnitude and trends. Sentinella cases, aggregated to the calendar week, are plotted as gray shaded boxplots with the number of cases on the right y-axis.

Influenza B Virus National Trend

Influenza B viral loads followed a clear seasonal pattern, which was distinct from the previous year in which there was no clear outbreak (Figure 6). The rise in Influenza B virus was coincident to the rise of Influenza A virus in late November, but had a slower ascent, peaking in late January through mid-February before returning to low viral loads at our baseline in early May. In 2023-2024, we did not observe a clear viral load peak suggestive of a typical seasonal epidemic; rather Influenza B viral loads hovered above the baseline value throughout the fall,

winter, and spring, which was consistent with other surveillance systems[15]. As with the other respiratory viruses, we intermittently detected Influenza B virus outside of the peak in viral load. Notably, short term viral load increases were observed in August and again in mid-September.

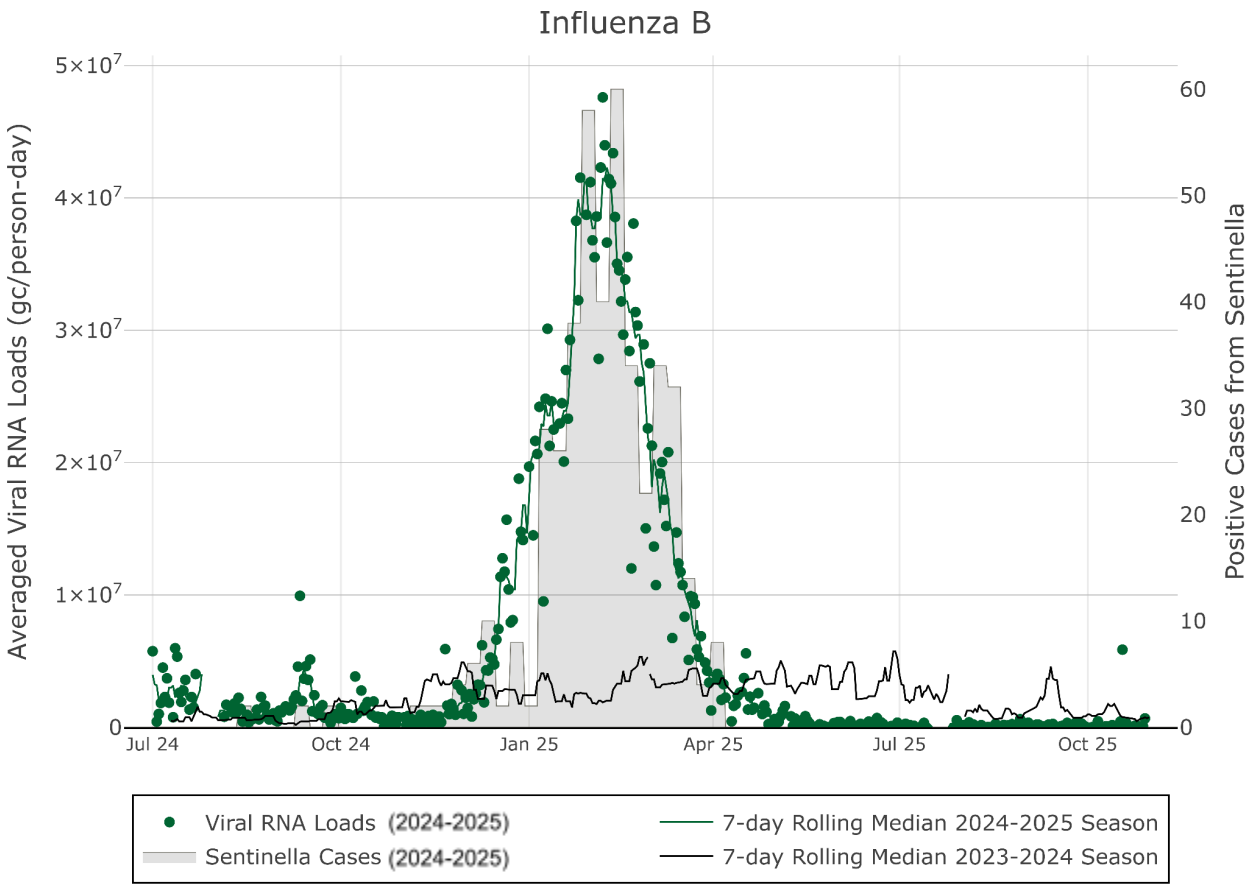


Figure 6: The national trend for Influenza B viral load, which is the population weighted mean of all ten WWTPs. Influenza B viral RNA load measurements (genome copies per person per day) are plotted as green dots, while a 7-day rolling median is reported as a green line on the left y-axis. The previous season (2023-2024) 7-day rolling median is reported as a black line to provide historic comparison in magnitude and trends. Sentinella cases, aggregated to the calendar week, are plotted as gray shaded boxplots with the number of cases on the right y-axis.

RSV National Trend

RSV national viral loads also followed a clear seasonal pattern, in line with previous years (Figure 7). The rise in RSV was observable already in early October, but viral loads remained low before starting a slow ascent throughout November to peak in late December. RSV viral loads historically increase before Influenza viral loads; a pattern we also observed in this reporting period. In the national trend data, a second peak in viral loads is observed in late January. This dynamic is a consequence of the national trend representing an aggregate of

[15] https://www.hug.ch/sites/interhug/files/structures/laboratoire_de_virologie/CNRI/nrci_report.2023-2024.pdf (Accessed 7 April 2026)

regional data from multiple distinct sites, which each experienced distinct seasonal epidemic timings (see Regional Trends). In comparison to the previous year, the viral loads during this reporting period were characterized by a later rise, a substantially higher peak, and a much later descent, suggesting the seasonal epidemic of RSV exceeded the previous year's.

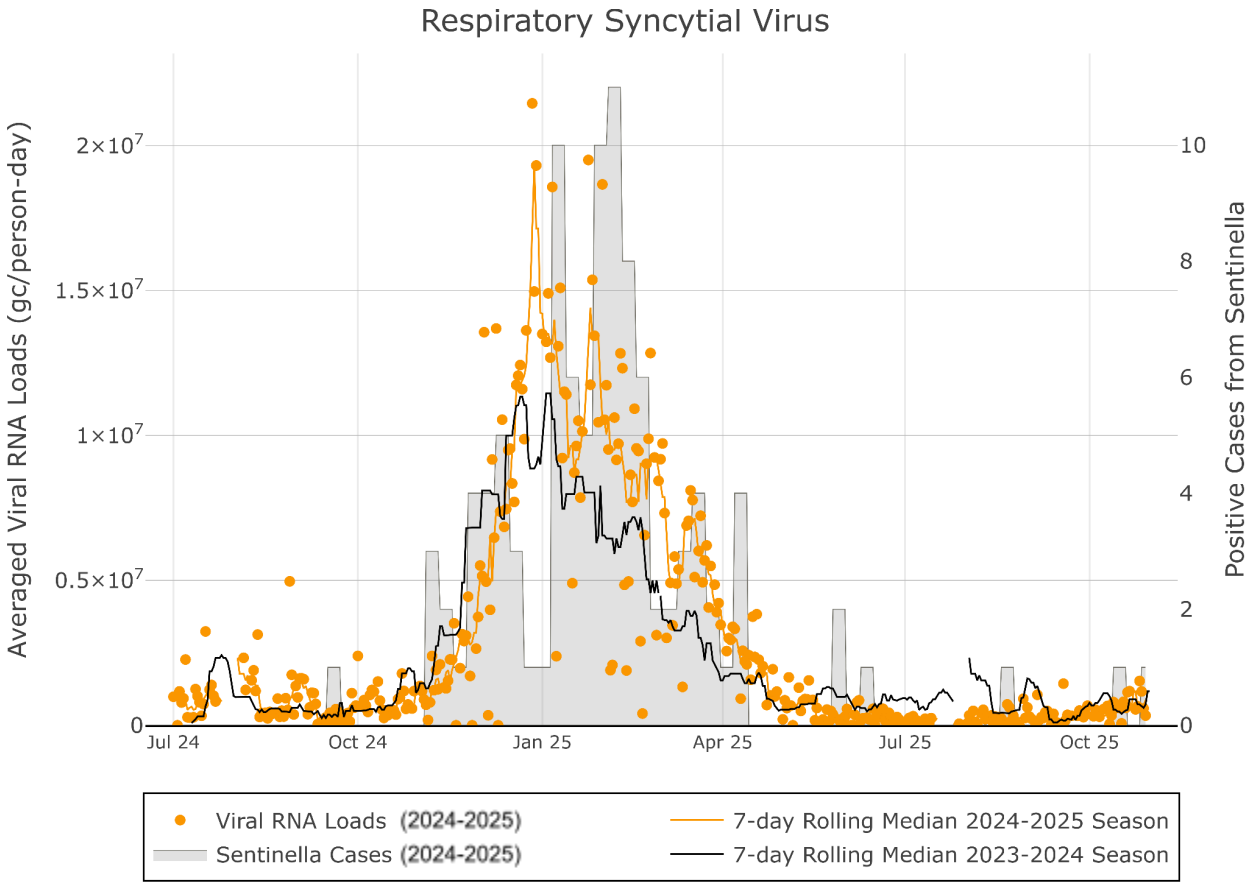


Figure 7: The national trend for RSV viral load, which is the population weighted mean of all ten WWTPs. RSV viral RNA load measurements (genome copies per person per day) are plotted as orange dots, while a 7-day rolling median is reported as an orange line on the left y-axis. The previous season (2023-2024) 7-day rolling median is reported as a black line to provide historic comparison in magnitude and trends. Sentinella cases, aggregated to the calendar week, are plotted as gray shaded boxplots with the number of cases on the right y-axis.

Alignment with Clinical Data

The national trend of viral loads in wastewater or all three pathogens were well aligned with clinically reported positive tests within the Sentinella network. Influenza A virus (Spearman's $\rho = 0.75$, $p < 0.001$), Influenza B virus (Spearman's $\rho = 0.74$, $p < 0.001$), and RSV (Spearman's $\rho = 0.63$, $p < 0.001$) correlation coefficients were all moderate-to-high. Deviations were observed for all three pathogens particularly in late December when Sentinella reported cases declined while viral loads remained high, which is likely a consequence of reduced clinical case testing or reporting during holidays.

Regional Trends

Regional differences in the timing, duration, and magnitude of Influenza A virus, Influenza B virus, and RSV were observed in the reporting period (Figure 8-9). Amongst the most notable regional trends, we noted that Influenza A viral loads in Western Switzerland (STEP Aïre, STEP Vidy, STEP Neuchatel, and ARA Sensatal) were higher than Influenza B viral loads, whereas at other sites in Switzerland (i.e., ARA Werdhölzli, ARA Basel/Prorhen, ARA Buholz) Influenza B viral loads were higher. Generally, across all sites, Influenza viral loads were higher than RSV.

At most sites we sampled, Influenza A viral load peaks were rapid, and were therefore timed ahead of Influenza B viral load peaks. Notably different dynamics were observed at ARA Basel/Prorheno, ARA Chur, and ARA Werdhölzli in which increases in Influenza A viral loads were more gradual, and as a consequence were coincident to the peak of B. Taken together, our results reaffirm regional differences in respiratory dynamics in Switzerland.

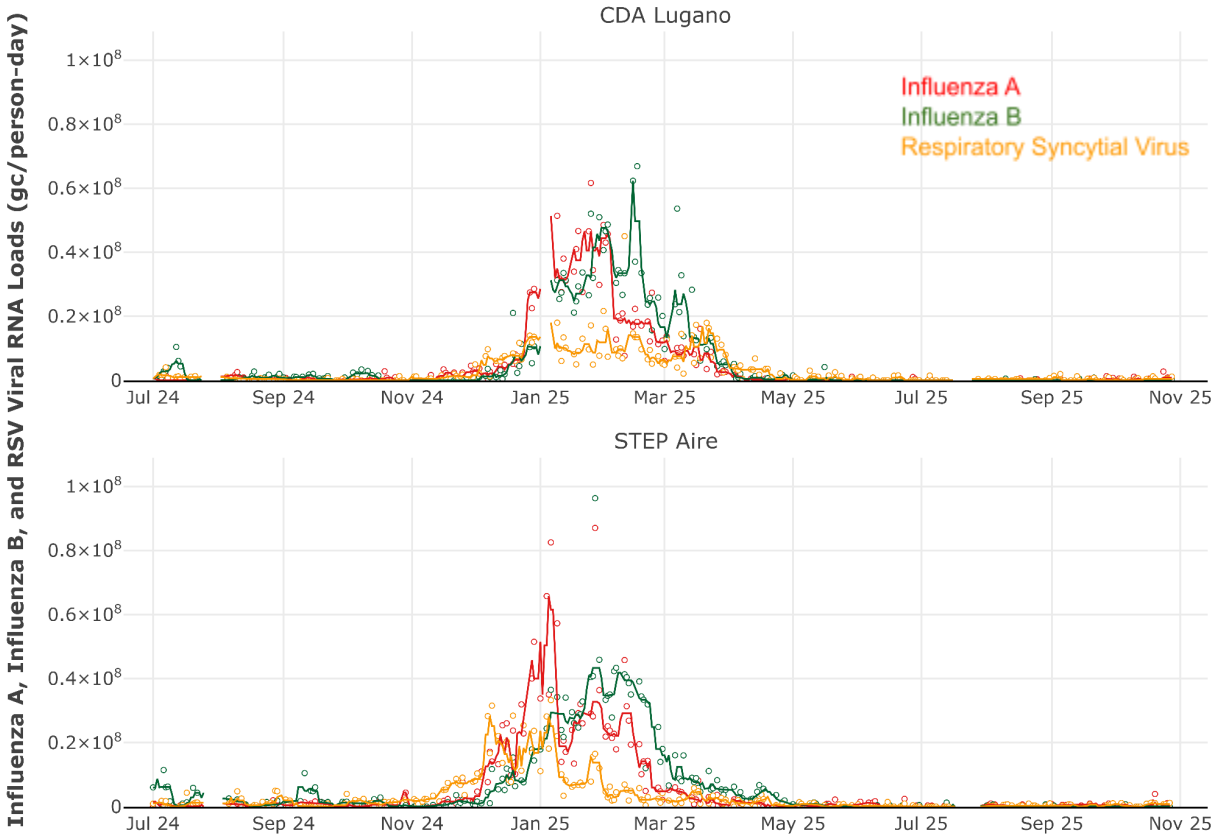


Figure 8: Influenza A virus (red), Influenza B virus (green), and Respiratory Syncytial Virus (yellow) viral loads for CDA Lugano and STEP Aïre over the reporting period. Sample loads (open circles) and 7-day rolling median (lines) are presented.

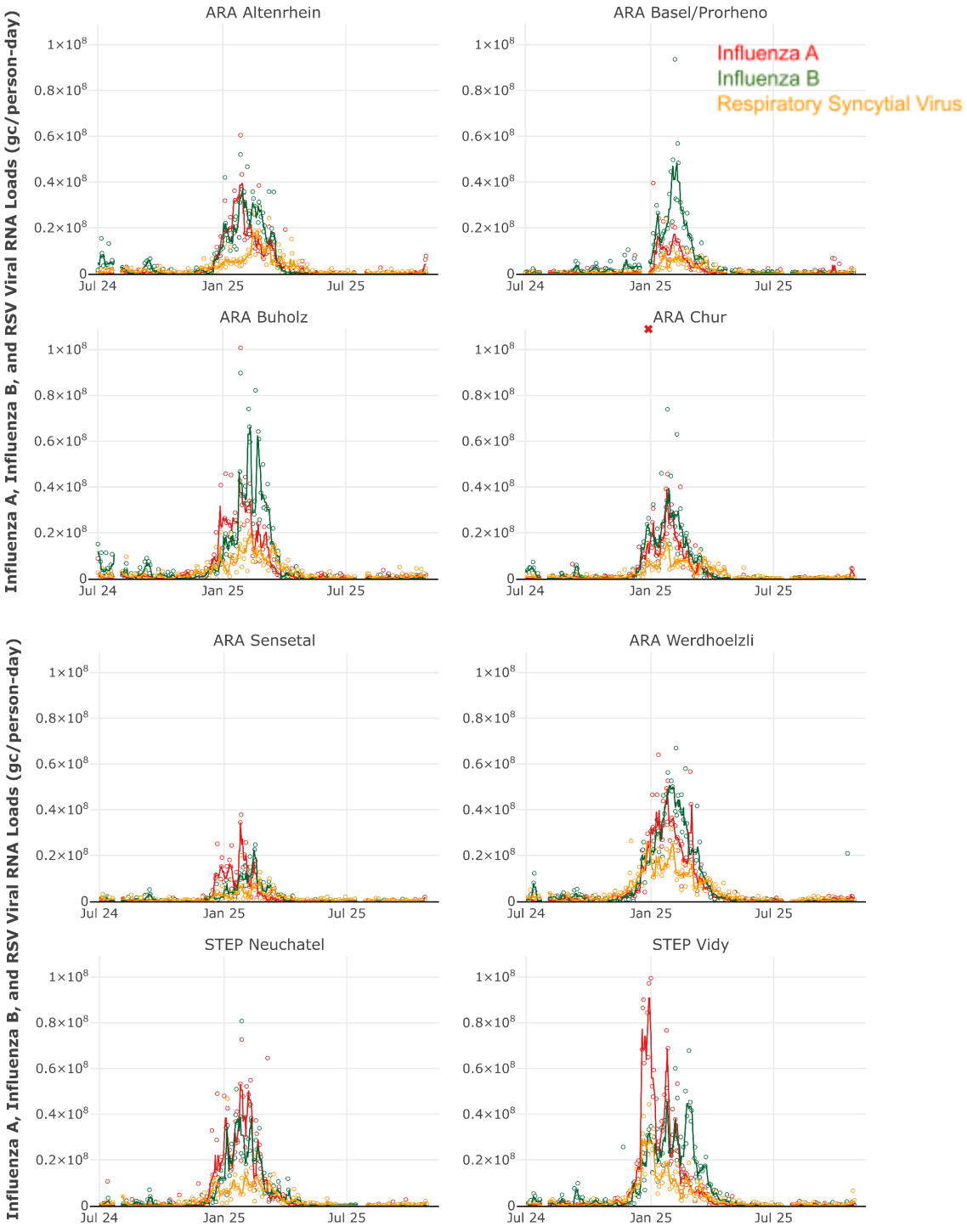


Figure 9: Influenza A virus (red), Influenza B virus (green), and Respiratory Syncytial Virus (yellow) viral loads for ARA Altenrhein, ARA Basel/ProRheno, ARA Buholz in Emmen, ARA Chur, ARA Sensetal, ARA Werdhölzli, STEP Neuchatel, and STEP Vidy in Lausanne over the reporting period. Sample loads (open circles) and 7-day rolling median (lines) are presented.

Conclusions and Outlook

Wastewater-based surveillance of respiratory viruses over the study period continues to provide insights into disease dynamics in the Swiss population. The results support clinical surveillance by providing a geographically-resolved and consistent method for tracking seasonal epidemics. Our methods for wastewater-based surveillance in Switzerland have remained largely unchanged, therefore, peak loads in a given year can be meaningfully compared to previously observed peak loads since October 2020. Although marked by uncertainty of the potential for differential shedding from distinct viral variants to shift relationships, wastewater nevertheless provides some insight into the relative magnitude of seasonal epidemics.

The period covered by this report (July 2024 - October 2025) was characterized by a high rate of successful data collection. Our laboratory processed 2,565 out of a planned 2600 (98.6%) samples over the 65 sampling weeks. The high rate of success demonstrates the commitment of the WWTP operators to consistently collect and ship samples. Causes for the missing data include issues arising in the collection (autosampler failure) or shipment of samples (delay and consequently deterioration of samples at room/ambient temperature). Sometimes, samples fail internal laboratory quality control. For example, contamination of samples with internal controls at unexpected concentrations, which are consequently excluded. Flexibility in the laboratory can often compensate for such issues. Missing samples can be replaced with samples collected from different days. Similarly, most samples that fail quality control can be re-processed, re-analyzed, or replaced with other samples. The laboratory's rapid quality control assessment and agility contributes to the high sample completion rate.

The laboratory also continued to support innovation in wastewater monitoring (see Publications). Prominent examples published in the last year include:

- Documenting the development, validation, and application in Switzerland of our digital PCR six-plex assay targeting viral respiratory pathogens (Pitton et al. 2025).
- Expanding assays in the laboratory to include poliovirus, measles, mumps, and rubella.[16]
- Reporting the application of the developed measles assay to retrospective detection during the outbreak in Vaud in 2024 (Gan et al. 2025).
- Demonstrating that epidemiological indicators derived from wastewater, including variant growth rate and effective reproduction number, are robust to changes in the pathogen shedding profiles (Dreifuss et al. 2025). This work reaffirms the value in wastewater-based monitoring during periods of shifting pathogen variants.

[16] See Publications/Results at: https://www.aramis.admin.ch/Texte/?ProjectID=53837 (Accessed 13 Nov 2025)

- Documenting development, validation, and its application in Switzerland of Influenza A virus sequencing from wastewater using tiling amplicons to characterize lineages and clinically relevant mutations (John et al. 2025).
- Demonstrating that longitudinal tracking of pharmaceuticals relevant to respiratory infections can track symptom burdens and attribute burdens to circulating viral infections (Baumgartner et al. 2025).

Swiss wastewater data is widely available, and has been integrated into multiple databases. Viral loads are reported directly by the Federal Office of Public Health (FOPH) through the Infectious Diseases Dashboard.[17] Data is also reported through the WISE dashboard, a project specific dashboard that visualizes laboratory data maintained through the associated WISE database.[18] Swiss data is also featured as part of The European Wastewater Surveillance Dashboard,[19] in which 77% of the wastewater data incorporated in the database is from Switzerland (see Measurements by Country).

The future of the program remains promising. Current efforts in the laboratory are devoted to maintaining state-of-the-art methodological approaches for detection and quantification of nucleic acids, while ensuring historic comparability of generated data. The laboratory is also committed to maintaining a high level of quality management, and continues to support and expand its quality management system, including the supporting laboratory information management systems. Expansion of the laboratories capabilities is also an area of ongoing investment, as we seek to expand the analytes beyond the suite of pathogens we report in this document. A prominent example is the expected expansion of routine surveillance to include RSV subtyping data, providing a data source on the relative abundance of circulating RSV subtypes throughout Switzerland for the upcoming 2025/26 season.

In addition to the laboratory-based surveillance and associated viral loads of respiratory pathogens included in this report, the Wastewater Monitoring Laboratory supports additional wastewater-based surveillance activities. Examples of additional innovation already implemented includes estimating the effective reproduction number (Re)[17] of the respiratory pathogens (Nadeau et al. 2024; Huisman et al. 2022), tracking SARS-CoV-2 variants[20] through sequencing extracts from wastewater (Jahn et al. 2022), and monitoring for pharmaceuticals, opioids, and other medications[21].

[17] https://www.idd.bag.admin.ch/ (accessed 13 Nov 2025)
[18] The WISE dashboard: https://wise.ethz.ch/ (accessed 13 Nov 2025)
[19] https://arcgis.jrc.ec.europa.eu/portal/apps/dashboards/e296cdf0c0d042e6b60b07a351f2dc5c (accessed 13 Nov 2025)
[20] SARS-CoV-2 variants are available at https://cov-spectrum.org/stories/wastewater-in-switzerland (accessed 13 Nov 2025)
[21] DroMedAario project website and associated data is available at https://www.dromedario.ch/ (accessed 28 June 2024)

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Contributors

The work was made possible through the extensive contributions of a large and interdisciplinary team. Specific acknowledgement goes out to members of the Wastewater Monitoring Laboratory at Eawag responsible for managing logistics, data collection and analysis, visualization and reporting. Members during the period of reporting are: Lara Achermann, Andrea Aquize, Lea Caduff, Jolinda de Korne, Noemi Fehr, Charlie Gan, Nadine Hürlimann, Timothy R. Julian, Rachel McLeod, Christoph Ort, Melissa Pitton, Patrick Schmidhalter, Linda Schneider, Ida Werner, Anna Wettlauffer, Nadja Widrig, Damla Uyan, Kerstin Vogler, and Daniela Yordanova.

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Members of the Swiss National Science Foundation *Sinergia*-funded WISE: Wastewater-based Infectious Surveillance[22] consortium provided guidance throughout the monitoring period. WISE is led by Prof. Dr. Tanja Stadler (ETHZ), with co-applicants Prof. Dr. Niko Beerenwinkel (ETHZ), Dr. Christoph Ort (Eawag), Timothy R. Julian (Eawag), and project partner Tamar Kohn (EPFL).

The report was prepared by Patrick Schmidhalter, Christoph Ort, and Timothy R. Julian. Images of viruses and *E. coli* are artistic interpretations created by Paola Galinova. For further information or clarification about the contents of the report, please contact covid.abwasser@eawag.ch.

[22] https://data.snf.ch/grants/grant/205933

Data Availability

Data on respiratory pathogens is submitted regularly to the Federal Office of Public Health, which maintains the Infectious Disease Dashboard at https://www.idd.bag.admin.ch/ (accessed 05 Nov 2025).

The WISE consortium maintains an independent database and associated dashboard with respiratory pathogen data available at: https://wisedb.ethz.ch/api/docs/ (accessed 18 Nov 2025) and https://wise.ethz.ch/ (accessed 05 Nov 2025). Sequencing data for SARS-CoV-2 is available at https://cov-spectrum.org/stories/wastewater-in-switzerland (accessed 05 Nov 2025) and for Influenza A virus and RSV at: https://genspectrum.org/swiss-wastewater (accessed 05 Nov 2025).

Publications

The WML contributes to scientific communication through publication of reports and peer-reviewed manuscripts. The following table includes published outputs within the reporting period. A full list of outputs, including previously published work and pre-prints currently in review, is available at: https://wise.ethz.ch/?page=about/publications (Accessed 6 Nov 2025).

Gan C, Pitton M, Caduff L, Julian TR. 2025. Evaluating viral inactivation in the liquid waste stream from a viral total nucleic acid extraction kit for safe disposal. *Biosafety and Health.* 7(5): 275-280 *We demonstrated that the liquid waste produced by our nucleic acid extraction protocol inactivates surrogate MS2 sufficiently to justify disposal as chemical solvent waste without additional biological decontamination.*	
John A, Kang S, Furhmann L, Topolsky I, Kent C, Quick J, Stadler T, Julian TR, Beerenwinkel N. 2025. Characterizing influenza A virus lineages and clinically relevant mutations through high-coverage wastewater sequencing. *Water Research.* 287(Part B): 124453. *We established and applied a tiled amplicon approach for sequencing HA, NA, and M segments of Influenza A H1N1 and H3N2 from wastewater, which is now a part of the routine genomic surveillance program.*	
Dreifuss D, Huisman JS, Rusch JC, Caduff L, Ganesanandamoorthy P, Devaux AJ, Gan C, Stadler T, Kohn T, Ort C, Beerenwinkel N, and Julian TR. 2025. Estimated transmission dynamics of SARS-CoV-2 variants from wastewater are unbiased and robust to differential shedding. *Nature Communications.* 16:7456. *We demonstrated that the introduction of new SARS-CoV-2 variants with distinct shedding profiles, which decouple the relationship between viral load and clinical cases, will nevertheless have minimal impacts on derived epidemiological indicators on selective advantage and effective reproduction numbers.*	
Huisman JS, Torri S, Wynn HK, Gan C, Woellmy IK, Huber M, Julian TR, Kohn T. 2025. Transmission dynamics of norovirus GII and enterovirus in Switzerland during the Covid-19 pandemic (2021-2022) as evidenced in wastewater. *Epidemics*. 52:100851. *We quantified norovirus GII and enterovirus viral loads in wastewater from December 2020 through October 2022 in Zurich wastewater and established a method to estimate the effective reproduction number to*	

track transmission dynamics. Through this, we found non-pharmaceutical interventions for Covid-19 reduced transmission of norovirus GII and enterovirus.	
Pitton M, McLeod RE, Caduff L, Dauletova A, de Korne-Elenbaas J, Gan C, Hablützel C, Holschneider A, Kang S, Loustalot G, Schmidhalter P, Schneider L, Wettlauffer A, Yordanova D, Julian TR, Ort C. 2025. A six-plex digital PCR assay for monitoring respiratory viruses in wastewater. *Nature Water.* 3:1174-1186. *We report on the development and implementation of our digital PCR assay for monitoring of respiratory viruses in wastewater, and we demonstrate alignment of wastewater viral loads with clinically-reported cases in Switzerland.*	
Gan C, Pitton M, de Korne-Elenbaas J, Cobuccio L, Cassini A, Ort C, Julian TR. 2025. Retrospective wastewater tracking of measles outbreak in western Switzerland in winter 2024. *Environmental Science and Technology Letters.* 12(6): 689-694. *We developed and applied a digital PCR assay for the detection of measles virus in wastewater that is capable of differentiating between wild type and vaccine strains. Applying the assay to wastewater extracts we had previously processed from Lausanne revealed that peak measles viral loads coincided with the primary measles outbreak as reported by clinical cases. The work highlights tracking measles in wastewater in Switzerland is a potential surveillance opportunity.*	
Baumgartner S, Salvisberg M, Schmidhalter P, Julian TR, Ort C, Singer H. 2025. Insights into respiratory illness at the population level through parallel analysis of pharmaceutical and viral markers in wastewater. 2025. *Nature Water.* 3:580-589. *We developed and applied methods for the longitudinal analyses of 15 pharmaceuticals in Swiss wastewater at locations coincident to the surveillance of SARS-CoV-2, RSV, IAV, IBV. Analyses highlighted strong correlations of pharmaceuticals associated with symptom relief (dextromethorphan, pheniramine, clarithromycin, acetaminophen, and codeine) with viral loads. Analyses also revealed periods where pharmaceutical use is high without corresponding viral loads, suggesting circulation of pathogens not currently surveilled through wastewater.*	
Conforti S, Pruden A, Acosta N, Anderson C, Buergmann H, Calabria De Araujo J, Cristobal JR, Drigo B, Ellison C, Franzis Z, Frigon D, Gaenzle M, Vierheilig J, Julian TR, Klümper U, Ma L, Mangat C, Nadimpalli M, Nakashita M, Osena G, Rathinavelu S, Reid-Smith R, Saldana M, Schmitt H, Li S, Singer AC, Tran TT, Yanac K, Ybazeta G, Harnisz M. 2025. Strengthening policy relevance of wastewater-based surveillance for	

antimicrobial resistance. *Environmental Science and Technology.* 59(5):2339-2343. *The Viewpoint was developed and discussed within the scope of a collaborative workshop of international scientific experts on how wastewater-based surveillance can be used to strengthen antimicrobial resistance policy.*	
De Korne-Elenbaas J, Caduff L, Lison A, McLeod R, Pitton M, Gan C, Julian TR. 2025. Design, validation, and implementation of multiplex digital PCR assays for simultaneous quantification of multiple targets. *Letters of Applied Microbiology.* 78(1): ovae137. *The publication establishes and details our workflow for designing, validating and implementing multiplex digital PCR assays. The work is a primary resource for our laboratory as we seek to extend targets for wastewater-based surveillance.*	

Recommended Citation

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Version 1 was submitted for internal review on 13 November 2025.
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Version 3 was submitted as the final version on 07 April 2026.

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Baumgartner, Stephan, Michelle Salvisberg, Patrick Schmidhalter, Timothy R. Julian, Christoph Ort, and Heinz Singer. 2025. "Insights into Respiratory Illness at the Population Level through Parallel Analysis of Pharmaceutical and Viral Markers in Wastewater." *Nature Water* 3 (5): 580–589.

Dreifuss, David, Jana S. Huisman, Johannes C. Rusch, et al. 2025. "Estimated Transmission Dynamics of SARS-CoV-2 Variants from Wastewater Are Unbiased and Robust to Differential Shedding." *Nature Communications* 16 (1): 7456.

Gan, Charles, Melissa Pitton, Jolinda de Korne-Elenbaas, et al. 2025. "Retrospective Wastewater Tracking of Measles Outbreak in Western Switzerland in Winter 2024." *Environmental Science & Technology Letters* 12 (6): 689–694.

Huisman, Jana S., Jérémie Scire, Lea Caduff, et al. 2022. "Wastewater-Based Estimation of the Effective Reproductive Number of SARS-CoV-2." *Environmental Health Perspectives* 130 (5): 57011.

Jahn, Katharina, David Dreifuss, Ivan Topolsky, et al. 2022. "Early Detection and Surveillance of SARS-CoV-2 Genomic Variants in Wastewater Using COJAC." *Nature Microbiology* 7 (8): 1151–1160.

Lesbon, Jéssika Cristina Chagas, Mirele Daiana Poleti, Elisângela Chicaroni de Mattos Oliveira, et al. 2021. "Nucleocapsid (N) Gene Mutations of SARS-CoV-2 Can Affect Real-Time RT-PCR Diagnostic and Impact False-Negative Results." *Viruses* 13 (12). https://doi.org/10.3390/v13122474.

Nadeau, Sarah, Alexander J. Devaux, Claudia Bagutti, et al. 2024. "Influenza Transmission Dynamics Quantified from RNA in Wastewater in Switzerland." *Swiss Medical Weekly* 154 (January): 3503.

Pitton, Melissa, Rachel E. McLeod, Lea Caduff, et al. 2025. "A Six-Plex Digital PCR Assay for Monitoring Respiratory Viruses in Wastewater." *Nature Water* 3 (10): 1174–1186.