

Supplementary Information

**Use of Quantitative Microbial Risk Assessment to Assess the Impact
of Drought and Seasonality on a De Facto Reuse System in Southern
Nevada, USA**

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Table of Contents

Table S1. Parameters for log ₁₀ -normal distributions of raw wastewater pathogen concentrations	3
Table S2. GC:IU ratios	4
Table S3. Percent contributions to Las Vegas Wash flow from each facility	5
Table S4. Las Vegas Wash travel times.....	6
Table S5. First order decay rate constants	6
Table S6. Uniform distributions of percent de facto reuse at drinking water treatment plants	7
Table S7. Dose-response parameters	8
Table S8. Daily log ₁₀ probability of infection and the percentile at which the probability of infection exceeds the daily risk threshold of 2.7×10^{-7}	11
 Figure S1. Schematics of the engineered treatment trains at the wastewater treatment plants	 5
Figure S2. Deterministic log reduction values (LRVs) illustrating decay/inactivation in the environmental buffers as a function of hypothetical travel time	6
Figure S3. Regression on Order Statistics determination of normal quantiles of censored recovery-corrected <i>Cryptosporidium</i> concentrations for the Las Vegas Wash	9
Figure S4. Histogram of travel times in Lake Mead from the Las Vegas Wash to the drinking water intake for lake elevations of (a) 297 m, (b) 312 m, and (c) 329 m.....	10
 References	 13

Table S1. Parameters for log₁₀-normal distributions of raw wastewater pathogen concentrations. All fittings were performed in this study from data reported by Crank et al. (2025).

Pathogen	μ	σ	Facility	Season	Unit
Adenovirus (molecular)	5.65	1.20	3	all	Log ₁₀ (gc/L)
Adenovirus (molecular)	7.12	0.96	2	all	Log ₁₀ (gc/L)
Adenovirus (molecular)	7.01	0.89	4	all	Log ₁₀ (gc/L)
Adenovirus (molecular)	6.84	1.07	1	all	Log ₁₀ (gc/L)
Enterovirus (molecular)	5.41	0.65	3	all	Log ₁₀ (gc/L)
Enterovirus (molecular)	5.92	1.29	2	all	Log ₁₀ (gc/L)
Enterovirus (molecular)	5.82	1.13	4	all	Log ₁₀ (gc/L)
Enterovirus (molecular)	5.76	1.41	1	all	Log ₁₀ (gc/L)
Norovirus (molecular)	6.50	2.13	1	all	Log ₁₀ (gc/L)
Norovirus (molecular)	6.10	2.27	1	fall	Log ₁₀ (gc/L)
Norovirus (molecular)	7.14	2.25	1	spring	Log ₁₀ (gc/L)
Norovirus (molecular)	5.66	2.29	1	summer	Log ₁₀ (gc/L)
Norovirus (molecular)	7.05	1.78	1	winter	Log ₁₀ (gc/L)
Norovirus (molecular)	6.97	1.64	2	all	Log ₁₀ (gc/L)
Norovirus (molecular)	6.98	1.58	2	fall	Log ₁₀ (gc/L)
Norovirus (molecular)	7.35	1.60	2	spring	Log ₁₀ (gc/L)
Norovirus (molecular)	5.92	2.06	2	summer	Log ₁₀ (gc/L)
Norovirus (molecular)	7.53	1.64	2	winter	Log ₁₀ (gc/L)
Norovirus (molecular)	6.46	1.02	3	all	Log ₁₀ (gc/L)
Norovirus (molecular)	6.30	1.32	3	fall	Log ₁₀ (gc/L)
Norovirus (molecular)	6.07	1.71	3	spring	Log ₁₀ (gc/L)
Norovirus (molecular)	6.19	0.90	3	summer	Log ₁₀ (gc/L)
Norovirus (molecular)	6.76	1.20	3	winter	Log ₁₀ (gc/L)
Norovirus (molecular)	6.91	1.43	4	all	Log ₁₀ (gc/L)
Norovirus (molecular)	6.78	1.71	4	fall	Log ₁₀ (gc/L)
Norovirus (molecular)	7.41	1.05	4	spring	Log ₁₀ (gc/L)
Norovirus (molecular)	5.86	1.60	4	summer	Log ₁₀ (gc/L)
Norovirus (molecular)	7.49	1.03	4	winter	Log ₁₀ (gc/L)
Adenovirus (culture)	3.84	0.95	1	all	Log ₁₀ (MPN/L)
Adenovirus (culture)	3.54	0.82	2	all	Log ₁₀ (MPN/L)
Adenovirus (culture)	3.44	0.55	3	all	Log ₁₀ (MPN/L)
Adenovirus (culture)	3.24	0.60	4	all	Log ₁₀ (MPN/L)
Enterovirus (culture)	4.08	0.45	1	all	Log ₁₀ (MPN/L)
Enterovirus (culture)	4.60	0.48	2	all	Log ₁₀ (MPN/L)

Pathogen	μ	σ	Facility	Season	Unit
Enterovirus (culture)	3.99	0.87	3	all	Log ₁₀ (MPN/L)
Enterovirus (culture)	4.02	0.44	4	all	Log ₁₀ (MPN/L)
<i>Cryptosporidium</i>	2.21	0.42	1	all	Log ₁₀ (oocysts/L)
<i>Cryptosporidium</i>	2.29	0.42	2	all	Log ₁₀ (oocysts/L)
<i>Cryptosporidium</i>	2.22	0.44	3	all	Log ₁₀ (oocysts/L)
<i>Cryptosporidium</i>	1.92	0.56	4	all	Log ₁₀ (oocysts/L)
<i>Giardia</i>	3.81	0.11	1	all	Log ₁₀ (cysts/L)
<i>Giardia</i>	3.90	0.12	2	all	Log ₁₀ (cysts/L)
<i>Giardia</i>	4.01	0.27	3	all	Log ₁₀ (cysts/L)
<i>Giardia</i>	3.58	0.14	4	all	Log ₁₀ (cysts/L)

Table S2. GC:IU ratios.

Pathogen	Log ₁₀ -Normal Distribution		Log ₁₀ -Uniform Distribution		Citation
	μ	σ	Minimum	Maximum	
Enterovirus	2.45	0.84	NA	NA	Crank et al. (2025)
Adenovirus	3.67	1.12	NA	NA	Crank et al. (2025)
Norovirus (GI & GII) ^a	-0.87	0.47	0	2.30	Donia et al. (2010); Gerrity et al. (2023)

^a The norovirus dose-response relationship was developed based on gene copies (GC) in the inoculum, with an unknown GC:IU ratio. When extrapolating to wastewater, a GC:IU ratio of 1:1 assumes that the GC:IU ratio within the challenge inoculum from the dose-response study is equal to that of influent wastewater. However, a recent human intestinal enteroid (HIE) cell culture study suggests that GC:IU ratios within inoculums and wastewater may be uncorrelated (Carmona-Vicente et al., 2024), potentially justifying an additional GC:IU adjustment to account for inactivation that occurs within a sewer collection system.

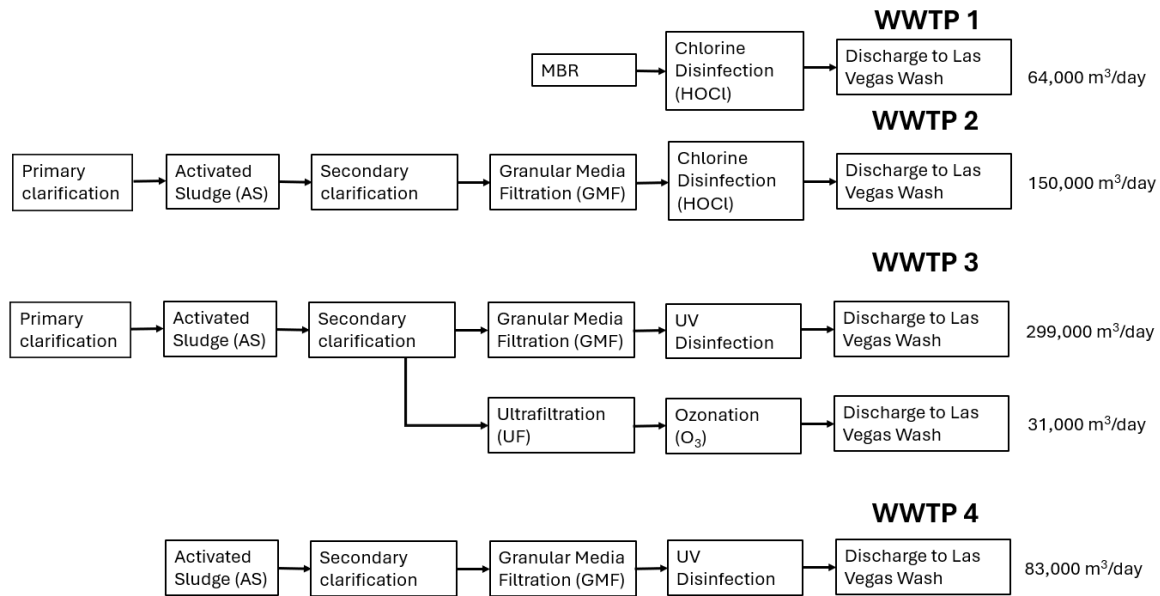


Figure S1. Schematics of the engineered treatment trains at the wastewater treatment plants (WWTPs).

Table S3. Percent contributions to Las Vegas Wash (LVW) flow from each wastewater treatment plant (WWTP). The percent contributions were converted to pathogen log reduction values (LRVs) to account for dilution by the other WWTP discharges and the base flow of LVW.

Discharge	Flow Rate (m ³ /day)	Percent Contribution	Dilution LRV
WWTP 1	64,000 ^a	9%	1.06
WWTP 2	150,000 ^a	21%	0.69
WWTP 3	360,000 ^a	49%	0.31
WWTP 4	83,000 ^a	11%	0.94
Subtotal	657,000	90%^b	--
LVW Base Flow	73,000	10%	--
Total	730,000	100%	--

^aThompson et al. (2024)

^bTreated wastewater effluent was assumed to comprise 90% of the total flow in LVW (Gerrity et al., 2022)

Table S4. Las Vegas Wash travel times determined from rhodamine tracer study data (Blasius et al., 2016).

WWTP	Time (hours)
1	15.48
2	13.48
3	11.98
4	7.48

Table S5. First order decay rate constants (d^{-1}). All pathogens had $\log_{10}$ -normal fits for base e k values.

Pathogen	Base e k (d^{-1})		Citation	N	Method
	$\log_{10} \mu$	$\log_{10} \sigma$			
Enterovirus	-0.07	0.57	Boehm et al. (2019)	250	Cell culture
Adenovirus	-0.44	0.97	Boehm et al. (2019); this study	20	Cell culture
Norovirus (GI & GII)	-0.87	0.47	Boehm et al. (2019); this study	5	Cell culture ^a
<i>Giardia</i>	-1.36	0.96	Boehm et al. (2018)	14	Microscopy
<i>Cryptosporidium</i>	-1.38	0.86	Boehm et al. (2018); this study	15	Microscopy

^aMurine norovirus

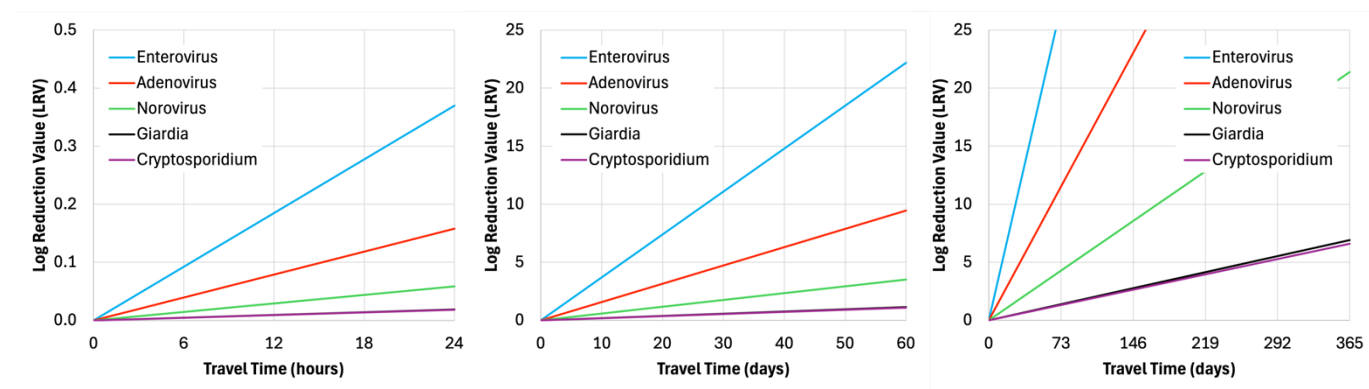


Figure S2. Deterministic log reduction values (LRVs) illustrating decay/inactivation in the environmental buffers as a function of hypothetical travel time: (left) one day, (middle) two months, (right) one year. LRVs were calculated using the mean first order decay rate constants in Table S5. The LRV relationships shown here are only for illustrative purposes; actual simulated LRVs incorporated stochastic first order decay rate constants and Lake Mead travel times. LRVs associated with decay/inactivation were not capped at any value.

Table S6. Uniform distributions of percent de facto reuse (DFR) at the drinking water treatment plants (DWTPs), as reported by van der Nagel et al. (2025). Fall = September, October, November; winter = December, January, February; spring = March, April, May; and summer = June, July, August.

Lake Level (m)	Season	Minimum % DFR	Maximum % DFR
329	all	1.9	5.4
312	all	2.8	6.9
297	all	2.6	5.3
329	fall	4.3	5.4
312	fall	4.4	5.4
297	fall	3.5	3.6
329	winter	3.4	3.6
312	winter	3.0	3.6
297	winter	2.6	3.3
329	spring	1.9	2.4
312	spring	2.8	3.2
297	spring	4.1	4.7
329	summer	3.5	4.8
312	summer	5.3	6.9
297	summer	4.5	5.3

Table S7. Dose-response parameters.

Pathogen	Model	Parameters	Citation
Enterovirus	Beta-Poisson	$\alpha = 0.253$; $\beta = 0.426$	Ward et al. (1986)
Adenovirus	Exact Beta-Poisson	$\alpha = 5.11$; $\beta = 2.8$	Teunis et al. (2016)
Norovirus (GI & GII)	Hypergeometric ${}_1F_1$	$\alpha = 0.04$; $\beta = 0.055$	Teunis et al. (2008) ^a
<i>Giardia</i>	Exponential	$r = 0.0199$	Regli et al. (1991); Teunis et al. (1997)
<i>Cryptosporidium</i>	Beta-Poisson	$\alpha = 0.116$; $\beta = 0.121$	Messner and Berger (2016)

^a Norovirus dose-response model

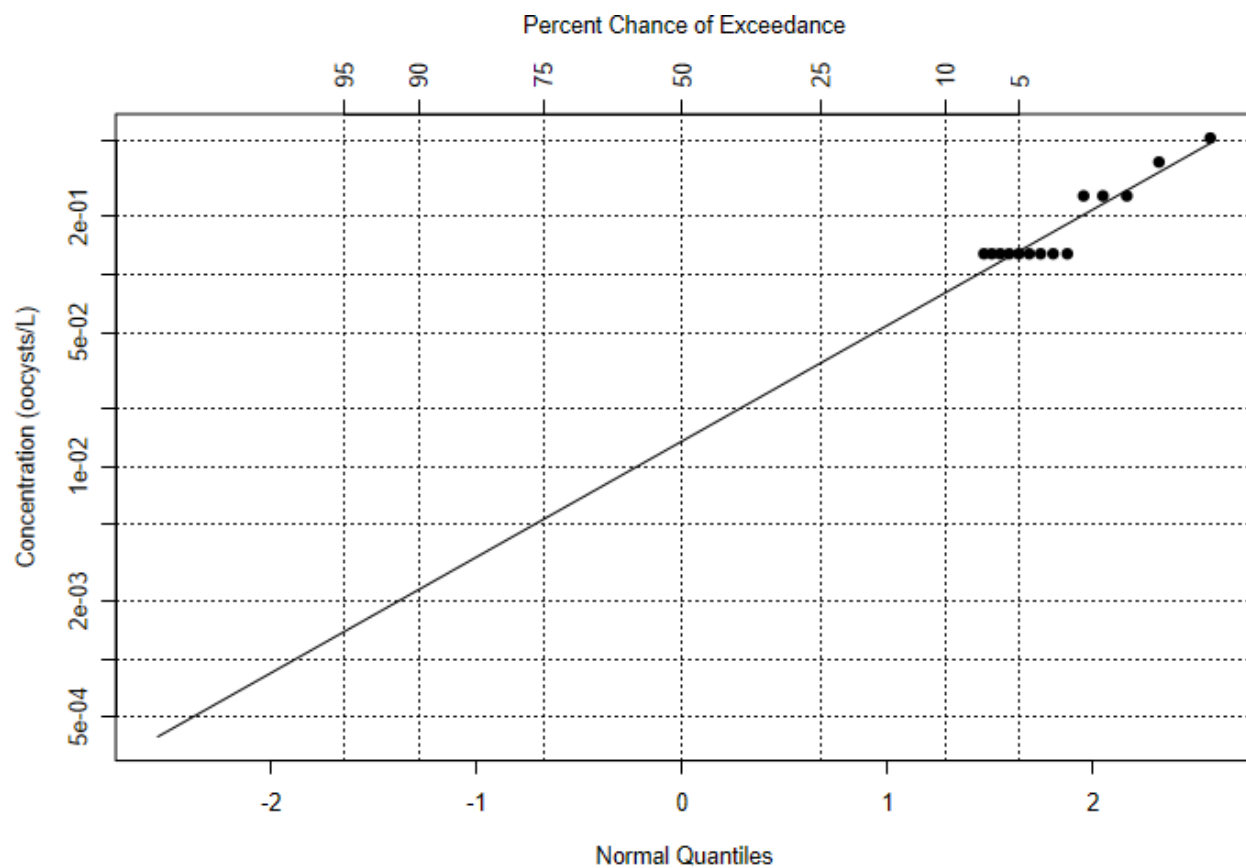


Figure S3. Regression on Order Statistics (ROS) determination of normal quantiles of censored recovery-corrected *Cryptosporidium* concentrations in the Las Vegas Wash.

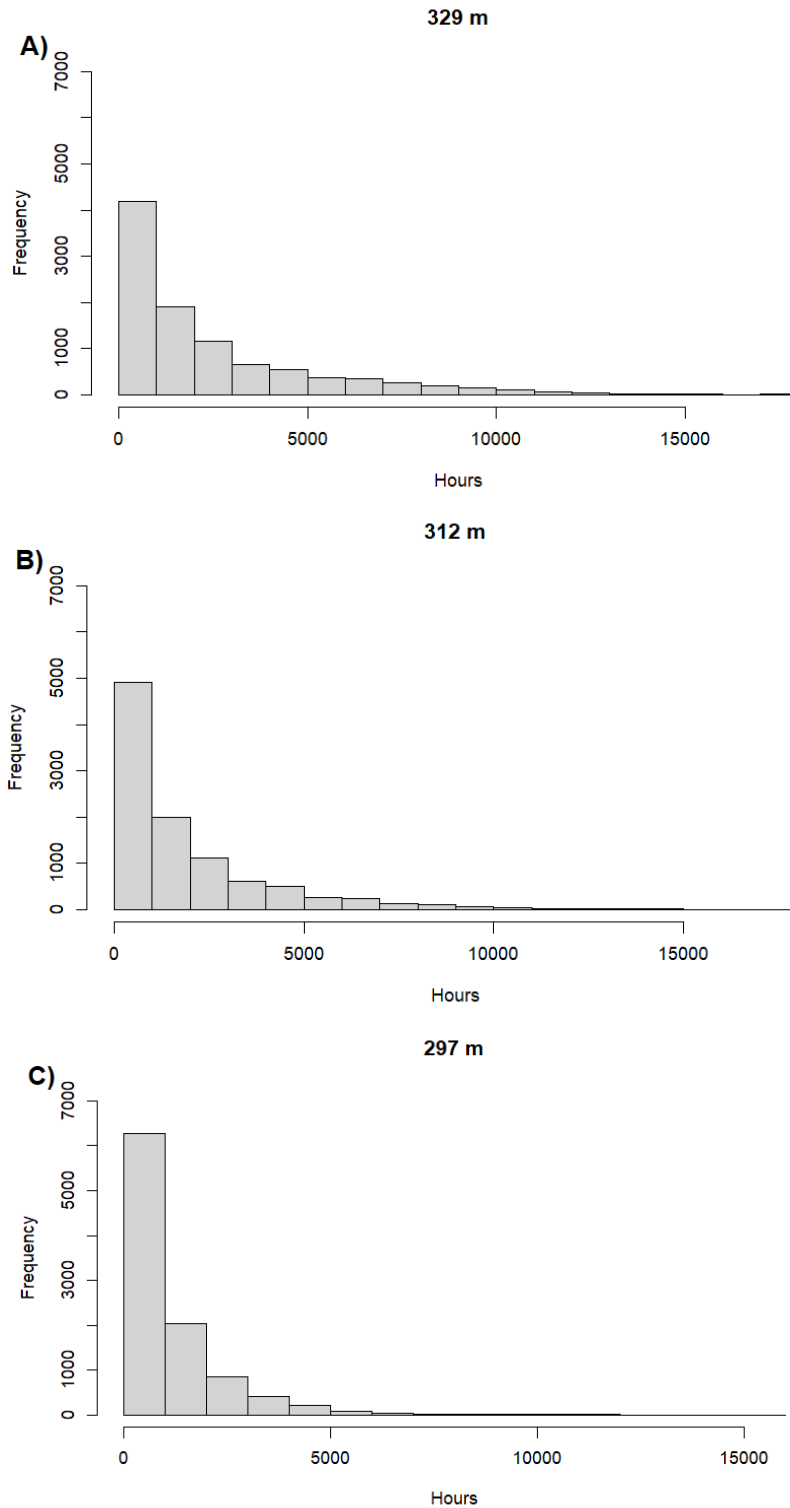


Figure S4. Histogram of travel times in Lake Mead from the Las Vegas Wash discharge point to the drinking water intake for lake elevations of (a) 329 m, (b) 312 m, and (c) 297 m.

Table S8. Daily log₁₀ probabilities of infection and the percentile at which the probability of infection exceeds the daily risk threshold of 2.7×10^{-7} (or -6.57 log₁₀). Values are shown for individual pathogens at various lake levels (m) and with/without ozone treatment at the drinking water treatment plants.

Ozone Included							
Lake Level	Pathogen	Mean	Median	95 th	99 th	Max	Exceedance Percentile
297	NoV (molecular, GC:IU corrected)	-8.83	-12.68	-9.42	-8.40	-4.91	0.999817
312	NoV (molecular, GC:IU corrected)	-8.74	-13.39	-9.56	-8.42	-4.80	0.999726
329	NoV (molecular, GC:IU corrected)	-9.57	-14.16	-9.79	-8.65	-6.21	0.999817
297	AdV (molecular, GC:IU corrected)	-12.69	-19.74	-13.26	-11.82	-9.37	1.000000
312	AdV (molecular, GC:IU corrected)	-12.74	-21.70	-13.40	-11.96	-9.11	1.000000
329	AdV (molecular, GC:IU corrected)	-12.95	-23.69	-13.62	-12.06	-9.64	1.000000
297	AdV (culture)	-13.77	-18.93	-13.27	-12.48	-10.94	1.000000
312	AdV (culture)	-13.81	-20.95	-13.35	-12.53	-11.15	1.000000
329	AdV (culture)	-13.96	-23.06	-13.54	-12.72	-11.15	1.000000
297	EnV (molecular, GC:IU corrected)	-11.36	-25.12	-13.77	-12.40	-7.33	1.000000
312	EnV (molecular, GC:IU corrected)	-13.14	-30.86	-14.01	-12.54	-9.61	1.000000
329	EnV (molecular, GC:IU corrected)	-11.75	-35.04	-14.32	-12.84	-7.72	1.000000
297	EnV (culture)	-12.97	-24.37	-13.06	-11.86	-9.92	1.000000
312	EnV (culture)	-13.03	-29.99	-13.37	-12.00	-9.88	1.000000
329	EnV (culture)	-13.29	-34.18	-13.60	-12.21	-10.40	1.000000
297	<i>Cryptosporidium</i>	-7.01	-7.42	-6.41	-6.11	-5.61	0.908219
312	<i>Cryptosporidium</i>	-6.99	-7.57	-6.36	-6.04	-5.52	0.896256
329	<i>Cryptosporidium</i>	-7.15	-7.88	-6.52	-6.16	-5.63	0.940365
297	<i>Giardia</i>	-16.48	-16.72	-15.99	-15.87	-15.72	1.000000
312	<i>Giardia</i>	-16.46	-16.91	-15.91	-15.79	-15.59	1.000000
329	<i>Giardia</i>	-16.61	-17.19	-16.03	-15.90	-15.69	1.000000
Ozone Omitted							
Lake Level	Pathogen	Mean	Median	95 th	99 th	Max	Exceedance Percentile
297	NoV (molecular, GC:IU corrected)	-3.47	-6.68	-3.42	-2.40	-0.30	0.515434
312	NoV (molecular, GC:IU corrected)	-3.43	-7.39	-3.56	-2.42	-0.29	0.593151
329	NoV (molecular, GC:IU corrected)	-3.65	-8.16	-3.79	-2.65	-0.47	0.652877
297	AdV (molecular, GC:IU corrected)	-6.69	-13.74	-7.26	-5.82	-3.37	0.976438
312	AdV (molecular, GC:IU corrected)	-6.74	-15.70	-7.40	-5.96	-3.11	0.977808
329	AdV (molecular, GC:IU corrected)	-6.95	-17.69	-7.62	-6.06	-3.64	0.981370
297	AdV (culture)	-7.77	-12.93	-7.27	-6.48	-4.94	0.988402
312	AdV (culture)	-7.81	-14.95	-7.35	-6.53	-5.15	0.988767
329	AdV (culture)	-7.96	-17.06	-7.54	-6.72	-5.15	0.992329
297	EnV (molecular, GC:IU corrected)	-5.41	-19.12	-7.77	-6.40	-1.37	0.986575
312	EnV (molecular, GC:IU corrected)	-7.14	-24.86	-8.01	-6.54	-3.61	0.989772
329	EnV (molecular, GC:IU corrected)	-5.77	-29.04	-8.32	-6.84	-1.74	0.992785

Ozone Omitted							
Lake Level	Pathogen	Mean	Median	95 th	99 th	Max	Exceedance Percentile
297	EnV (culture)	-6.97	-18.37	-7.06	-5.86	-3.92	0.972968
312	EnV (culture)	-7.03	-23.99	-7.37	-6.00	-3.88	0.978539
329	EnV (culture)	-7.29	-28.18	-7.60	-6.21	-4.40	0.983562
297	<i>Cryptosporidium</i>	-6.54	-6.95	-5.94	-5.64	-5.14	0.678995
312	<i>Cryptosporidium</i>	-6.52	-7.10	-5.89	-5.57	-5.05	0.687032
329	<i>Cryptosporidium</i>	-6.68	-7.41	-6.05	-5.69	-5.16	0.763288
297	<i>Giardia</i>	-10.71	-10.95	-10.22	-10.10	-9.95	1.000000
312	<i>Giardia</i>	-10.69	-11.14	-10.14	-10.02	-9.82	1.000000
329	<i>Giardia</i>	-10.84	-11.42	-10.26	-10.13	-9.92	1.000000

References

- Blasius, B., Kirsch, J., Danner, A., 2016. Las Vegas Wash Time-of-Travel Study. Science and Technology Program Final Report, Reclamation Managing Water in the West. United States Bureau of Reclamation.
- Boehm, A.B., Graham, K.E., Jennings, W.C., 2018. Can we swim yet? Systematic review, meta-analysis, and risk assessment of aging sewage in surface waters. *Environ. Sci. Technol.* 52, 9634–9645. <https://doi.org/10.1021/acs.est.8b01948>
- Boehm, A.B., Silverman, A.I., Schriewer, A., Goodwin, K., 2019. Systematic review and meta-analysis of decay rates of waterborne mammalian viruses and coliphages in surface waters. *Water Res.* 164, 114898. <https://doi.org/10.1016/j.watres.2019.114898>
- Carmona-Vicente, N., Pandiscia, A., Santiso-Bellón, C., Perez-Cataluña, A., Rodríguez-Díaz, J., Costantini, V.P., Buesa, J., Vinjé, J., Sánchez, G., Randazzo, W., 2024. Human intestinal enteroids platform to assess the infectivity of gastroenteritis viruses in wastewater. *Water Res.* 255, 121481. <https://doi.org/10.1016/j.watres.2024.121481>
- Crank, K., Papp, K., Barber, C., Chung, K., Clements, E., Frehner, W., Hannoun, D., Lane, T., Morrison, C., Mull, B., Oh, E., Wang, P., Gerrity, D., 2025. Pathogen and indicator trends in southern Nevada wastewater during and after the COVID-19 pandemic. *Environ. Sci. Water Res. Technol.* <https://doi.org/10.1039/d4ew00620h>
- Donia, D., Bonanni, E., Diaco, L., Divizia, M., 2010. Statistical correlation between enterovirus genome copy numbers and infectious viral particles in wastewater samples. *Letters Appl. Microbiol.* 50, 237–240. <https://doi.org/10.1111/j.1472-765X.2009.02775.x>
- Gerrity, D., Crank, K., Steinle-Darling, E., Pecson, B.M., 2023. Establishing pathogen log reduction value targets for direct potable reuse in the United States. *AWWA Water Science* 5, e1353. <https://doi.org/10.1002/aws2.1353>
- Gerrity, D., Papp, K., Dickenson, E., Ejada, M., Marti, E., Quinones, O., Sarria, M., Thompson, K., Trenholm, R.A., 2022. Characterizing the chemical and microbial fingerprint of unsheltered homelessness in an urban watershed. *Sci. Tot. Environ.* 840, 156714. <https://doi.org/10.1016/j.scitotenv.2022.156714>
- Messner, M.J., Berger, P., 2016. *Cryptosporidium* infection risk: Results of new dose-response modeling. *Risk Analysis* 36, 1969–1982. <https://doi.org/10.1111/risa.12541>

- Regli, S., Rose, J.B., Haas, C.N., Gerba, C.P., 1991. Modeling the risk from *Giardia* and viruses in drinking water. *Journal AWWA* 83, 76–84. <https://doi.org/10.1002/j.1551-8833.1991.tb07252.x>
- Teunis, P., Schijven, J., Rutjes, S., 2016. A generalized dose-response relationship for adenovirus infection and illness by exposure pathway. *Epidemiol. Infect.* 144, 3461–3473. <https://doi.org/10.1017/S0950268816001862>
- Teunis, P.F.M., Medema, G.J., Kruidenier, L., Havelaar, A.H., 1997. Assessment of the risk of infection by *Cryptosporidium* or *Giardia* in drinking water from a surface water source. *Water Res.* 31, 1333–1346. [https://doi.org/10.1016/S0043-1354\(96\)00387-9](https://doi.org/10.1016/S0043-1354(96)00387-9)
- Teunis, P.F.M., Moe, C.L., Liu, P., E. Miller, S., Lindesmith, L., Baric, R.S., Le Pendu, J., Calderon, R.L., 2008. Norwalk virus: How infectious is it? *J. Med. Virol.* 80, 1468–1476. <https://doi.org/10.1002/jmv.21237>
- Thompson, K.A., Ray, H., Gerrity, D., Quiñones, O., Dano, E., Prieur, J., Vanderford, B., Steinle-Darling, E., Dickenson, E.R.V., 2024. Sources of per- and polyfluoroalkyl substances in an arid, urban, wastewater-dominated watershed. *Sci. Tot. Environ.* 940, 173361. <https://doi.org/10.1016/j.scitotenv.2024.173361>
- van der Nagel, C., Clements, E., Wilkerson, C., Hannoun, D., Tietjen, T., Impact of drought on de facto reuse and water quality: Insights from hydrodynamic modeling versus machine learning. *Environ. Model. Softw.* 193, 106649. <https://doi.org/10.1016/j.envsoft.2025.106649>
- Ward, R.L., Bernstein, D.I., Young, E.C., Sherwood, J.R., Knowlton, D.R., Schiff, G.M., 1986. Human rotavirus studies in volunteers: Determination of infectious dose and serological response to infection. *J. Infect. Dis.* 154, 871–880. <https://doi.org/10.1093/infdis/154.5.871>