

# Andreas H Farnleitner

## List of Publications by Year in descending order

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109  
papers

4,257  
citations

117571

34  
h-index

133188

59  
g-index

113  
all docs

113  
docs citations

113  
times ranked

4899  
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 805, 149877.	3.9	153
2	From Groundwater to Drinking Water – Microbiology of Karstic Water Resources. , 2022, , .		0
3	From Groundwater to Drinking Water – Current Approaches for Microbial Monitoring and Risk Assessment in Porous Aquifers. , 2022, , .		0
4	How dead is dead? Viable but non-culturable versus persister cells. <i>Environmental Microbiology Reports</i> , 2021, 13, 243-245.	1.0	12
5	Microbial faecal pollution of river water in a watershed of tropical Ethiopian highlands is driven by diffuse pollution sources. <i>Journal of Water and Health</i> , 2021, 19, 575-591.	1.1	6
6	Bacteriophages Are Good Estimators of Human Viruses Present in Water. <i>Frontiers in Microbiology</i> , 2021, 12, 619495.	1.5	19
7	Modelling the interplay of future changes and wastewater management measures on the microbiological river water quality considering safe drinking water production. <i>Science of the Total Environment</i> , 2021, 768, 144278.	3.9	22
8	Genetic Microbial Source Tracking Support QMRA Modeling for a Riverine Wetland Drinking Water Resource. <i>Frontiers in Microbiology</i> , 2021, 12, 668778.	1.5	7
9	Upscaling Transport of <i>Bacillus subtilis</i> Endospores and Coliphage phiX174 in Heterogeneous Porous Media from the Column to the Field Scale. <i>Environmental Science &amp; Technology</i> , 2021, 55, 11060-11069.	4.6	15
10	Detection of SARS-CoV-2 RNA in the Danube River in Serbia associated with the discharge of untreated wastewaters. <i>Science of the Total Environment</i> , 2021, 783, 146967.	3.9	29
11	Assessing biological stability in a porous groundwater aquifer of a riverbank filtration system: combining traditional cultivation-based and emerging cultivation-independent in situ and predictive methods. <i>Osterreichische Wasser- Und Abfallwirtschaft</i> , 2021, 73, 490-500.	0.3	0
12	Using hydrodynamic and hydraulic modelling to study microbiological water quality issues at a backwater area of the Danube to support decision-making. <i>Osterreichische Wasser- Und Abfallwirtschaft</i> , 2021, 73, 482-489.	0.3	1
13	Genetic microbial faecal source tracking: rising technology to support future water quality testing and safety management. <i>Osterreichische Wasser- Und Abfallwirtschaft</i> , 2021, 73, 468-481.	0.3	8
14	Vertebrate host phylogeny influences gut archaeal diversity. <i>Nature Microbiology</i> , 2021, 6, 1443-1454.	5.9	34
15	Identifying Inorganic Turbidity in Water Samples as Potential Loss Factor During Nucleic Acid Extraction: Implications for Molecular Fecal Pollution Diagnostics and Source Tracking. <i>Frontiers in Microbiology</i> , 2021, 12, 660566.	1.5	9
16	The intriguing new possibilities of the microbiological methodology and molecular diagnostics for water quality analysis. <i>Osterreichische Wasser- Und Abfallwirtschaft</i> , 2021, 73, 446.	0.3	0
17	Macroinvertebrate indices versus microbial fecal pollution characteristics for water quality monitoring reveals contrasting results for an Ethiopian river. <i>Ecological Indicators</i> , 2020, 108, 105733.	2.6	18
18	Improving the identification of the source of faecal pollution in water using a modelling approach: From multi-source to aged and diluted samples. <i>Water Research</i> , 2020, 171, 115392.	5.3	24

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19	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , 2020, 5, .	1.7	47
20	Evaluation of groundwater bacterial community composition to inform waterborne pathogen vulnerability assessments. <i>Science of the Total Environment</i> , 2020, 743, 140472.	3.9	10
21	Elucidating fecal pollution patterns in alluvial water resources by linking standard fecal indicator bacteria to river connectivity and genetic microbial source tracking. <i>Water Research</i> , 2020, 184, 116132.	5.3	19
22	Automated online monitoring of fecal pollution in water by enzymatic methods. <i>Current Opinion in Environmental Science and Health</i> , 2020, 16, 82-91.	2.1	9
23	Phenotypic and Genotypic Antimicrobial Resistance Traits of <i>Vibrio cholerae</i> Non-O1/Non-O139 Isolated From a Large Austrian Lake Frequently Associated With Cases of Human Infection. <i>Frontiers in Microbiology</i> , 2019, 10, 2600.	1.5	27
24	Simple lysis of bacterial cells for DNA-based diagnostics using hydrophilic ionic liquids. <i>Scientific Reports</i> , 2019, 9, 13994.	1.6	31
25	Detection of a microbial source tracking marker by isothermal helicase-dependent amplification and a nucleic acid lateral-flow strip test. <i>Scientific Reports</i> , 2019, 9, 393.	1.6	27
26	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. <i>Nature Communications</i> , 2019, 10, 2200.	5.8	317
27	Event-transport of beta-d-glucuronidase in an agricultural headwater stream: Assessment of seasonal patterns by on-line enzymatic activity measurements and environmental isotopes. <i>Science of the Total Environment</i> , 2019, 662, 236-245.	3.9	7
28	Spring Water of an Alpine Karst Aquifer Is Dominated by a Taxonomically Stable but Discharge-Responsive Bacterial Community. <i>Frontiers in Microbiology</i> , 2019, 10, 28.	1.5	23
29	Microbiological Water Quality of Rivers in Montenegro. <i>Handbook of Environmental Chemistry</i> , 2019, , 135-155.	0.2	2
30	Spatiotemporal resolved sampling for the interpretation of micropollutant removal during riverbank filtration. <i>Science of the Total Environment</i> , 2019, 649, 212-223.	3.9	30
31	Challenges and perspectives in the application of isothermal DNA amplification methods for food and water analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 1695-1702.	1.9	45
32	Spatial patterns of enzymatic activity in large water bodies: Ship-borne measurements of beta-D-glucuronidase activity as a rapid indicator of microbial water quality. <i>Science of the Total Environment</i> , 2019, 651, 1742-1752.	3.9	10
33	Opening the black box of spring water microbiology from alpine karst aquifers to support proactive drinking water resource management. <i>Wiley Interdisciplinary Reviews: Water</i> , 2018, 5, e1282.	2.8	28
34	Spatiotemporal Dynamics of <i>Vibrio cholerae</i> in Turbid Alkaline Lakes as Determined by Quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	23
35	Spatiotemporal analysis of bacterial biomass and activity to understand surface and groundwater interactions in a highly dynamic riverbank filtration system. <i>Science of the Total Environment</i> , 2018, 627, 450-461.	3.9	36
36	Global Distribution of Human-Associated Fecal Genetic Markers in Reference Samples from Six Continents. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5076-5084.	4.6	73

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37	Integrated Strategy to Guide Health-Related Microbial Quality Management at Alpine Karstic Drinking Water Resources. <i>Advances in Karst Science</i> , 2018, , 185-192.	0.3	3
38	Antibiotic Resistance of <i>Acinetobacter</i> spp. Isolates from the River Danube: Susceptibility Stays High. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 52.	1.2	29
39	Hotspots and main drivers of fecal pollution in Neusiedler See, a large shallow lake in Central Europe. <i>Environmental Science and Pollution Research</i> , 2018, 25, 28884-28898.	2.7	18
40	Poikilothermic Animals as a Previously Unrecognized Source of Fecal Indicator Bacteria in a Backwater Ecosystem of a Large River. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	17
41	The microbiological water quality of Vienna's River Danube section and its associated water bodies. <i>Osterreichische Wasser- Und Abfallwirtschaft</i> , 2017, 69, 76-88.	0.3	2
42	A loop-mediated isothermal amplification (LAMP) assay for the rapid detection of <i>Enterococcus</i> spp. in water. <i>Water Research</i> , 2017, 122, 62-69.	5.3	60
43	A Complementary Isothermal Amplification Method to the U.S. EPA Quantitative Polymerase Chain Reaction Approach for the Detection of <i>Enterococci</i> in Environmental Waters. <i>Environmental Science &amp; Technology</i> , 2017, 51, 7028-7035.	4.6	12
44	Development and evaluation of a self-cleaning custom-built auto sampler controlled by a low-cost RaspberryPi microcomputer for online enzymatic activity measurements. <i>Talanta</i> , 2017, 162, 390-397.	2.9	8
45	High genetic diversity of <i>Vibrio cholerae</i> in the European lake Neusiedler See is associated with intensive recombination in the reed habitat and the long-distance transfer of strains. <i>Environmental Microbiology</i> , 2017, 19, 328-344.	1.8	41
46	Does Pumping Volume Affect the Concentration of Micropollutants in Groundwater Samples?. <i>Ground Water Monitoring and Remediation</i> , 2017, 37, 82-88.	0.6	7
47	Antibiotic Resistance Patterns of <i>Pseudomonas</i> spp. Isolated from the River Danube. <i>Frontiers in Microbiology</i> , 2016, 7, 586.	1.5	72
48	QMRAcatch: Human-associated Fecal Pollution and Infection Risk Modeling for a River/Floodplain Environment. <i>Journal of Environmental Quality</i> , 2016, 45, 1205-1214.	1.0	24
49	Determination of the sources of nitrate and the microbiological sources of pollution in the Sava River Basin. <i>Science of the Total Environment</i> , 2016, 573, 1460-1471.	3.9	56
50	Real-time monitoring of beta-d-glucuronidase activity in sediment laden streams: A comparison of prototypes. <i>Water Research</i> , 2016, 101, 252-261.	5.3	25
51	Occurrence of human-associated <i>Bacteroidetes</i> genetic source tracking markers in raw and treated wastewater of municipal and domestic origin and comparison to standard and alternative indicators of faecal pollution. <i>Water Research</i> , 2016, 90, 265-276.	5.3	59
52	A rapid genomic DNA extraction method and its combination with helicase dependent amplification for the detection of genetically modified maize. <i>Analytical Methods</i> , 2016, 8, 136-141.	1.3	13
53	Evaluation of Genotoxic Pressure along the Sava River. <i>PLoS ONE</i> , 2016, 11, e0162450.	1.1	25
54	<i>Enterobacteriaceae</i> Isolated from the River Danube: Antibiotic Resistances, with a Focus on the Presence of ESBL and Carbapenemases. <i>PLoS ONE</i> , 2016, 11, e0165820.	1.1	77

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55	Bacterial diversity along a 2600 km river continuum. <i>Environmental Microbiology</i> , 2015, 17, 4994-5007.	1.8	265
56	Attachment and Detachment Behavior of Human Adenovirus and Surrogates in Fine Granular Limestone Aquifer Material. <i>Journal of Environmental Quality</i> , 2015, 44, 1392-1401.	1.0	21
57	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. <i>Water Science and Technology</i> , 2015, 72, 1962-1972.	1.2	53
58	QMRAcatch: Microbial Quality Simulation of Water Resources including Infection Risk Assessment. <i>Journal of Environmental Quality</i> , 2015, 44, 1491-1502.	1.0	44
59	Dynamics of <i>Vibrio cholerae</i> abundance in Austrian saline lakes, assessed with quantitative solid-phase cytometry. <i>Environmental Microbiology</i> , 2015, 17, 4366-4378.	1.8	19
60	Loop-Mediated Isothermal Amplification (LAMP) for the Detection of Horse Meat in Meat and Processed Meat Products. <i>Food Analytical Methods</i> , 2015, 8, 1576-1581.	1.3	35
61	A Novel Triplex Quantitative PCR Strategy for Quantification of Toxigenic and Nontoxigenic <i>Vibrio cholerae</i> in Aquatic Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3077-3085.	1.4	19
62	Preliminary Toxicological Evaluation of the River Danube Using in Vitro Bioassays. <i>Water (Switzerland)</i> , 2015, 7, 1959-1968.	1.2	9
63	Automated Sampling Procedures Supported by High Persistence of Bacterial Fecal Indicators and Bacteroidetes Genetic Microbial Source Tracking Markers in Municipal Wastewater during Short-Term Storage at 5°C. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5134-5143.	1.4	18
64	The development of a multiplex real-time PCR to quantify <i>Fusarium</i> DNA of trichothecene and fumonisin producing strains in maize. <i>Analytical Methods</i> , 2015, 7, 1358-1365.	1.3	14
65	Response to Letter to the Editor regarding "Detection of the 35S promoter in transgenic maize via various isothermal amplification techniques: a practical approach". <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 8061-8062.	1.9	2
66	Microbiological Water Quality of the Danube River: Status Quo and Future Perspectives. <i>Handbook of Environmental Chemistry</i> , 2014, , 439-468.	0.2	6
67	Enumerating Microorganism Surrogates for Groundwater Transport Studies Using Solid-Phase Cytometry. <i>Water, Air, and Soil Pollution</i> , 2014, 225, 1827.	1.1	6
68	Detection of the food allergen celery via loop-mediated isothermal amplification technique. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 6827-6833.	1.9	18
69	Detection of the 35S promoter in transgenic maize via various isothermal amplification techniques: a practical approach. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 6835-6842.	1.9	25
70	<i>Enterococcus</i> and <i>Escherichia coli</i> fecal source apportionment with microbial source tracking genetic markers "Is it feasible?". <i>Water Research</i> , 2013, 47, 6849-6861.	5.3	39
71	Comparison of PCR and quantitative real-time PCR methods for the characterization of ruminant and cattle fecal pollution sources. <i>Water Research</i> , 2013, 47, 6921-6928.	5.3	45
72	Performance of human fecal anaerobe-associated PCR-based assays in a multi-laboratory method evaluation study. <i>Water Research</i> , 2013, 47, 6897-6908.	5.3	117

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73	Performance Characteristics of qPCR Assays Targeting Human- and Ruminant-Associated <i>Bacteroidetes</i> for Microbial Source Tracking across Sixteen Countries on Six Continents. <i>Environmental Science &amp; Technology</i> , 2013, 47, 8548-8556.	4.6	111
74	<i>Clostridium perfringens</i> Is Not Suitable for the Indication of Fecal Pollution from Ruminant Wildlife but Is Associated with Excreta from Nonherbivorous Animals and Human Sewage. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5089-5092.	1.4	40
75	Dynamics of natural prokaryotes, viruses, and heterotrophic nanoflagellates in alpine karstic groundwater. <i>MicrobiologyOpen</i> , 2013, 2, 633-643.	1.2	22
76	Holy springs and holy water: underestimated sources of illness?. <i>Journal of Water and Health</i> , 2012, 10, 349-357.	1.1	15
77	Sanitary inspection of wells using risk-of-contamination scoring indicates a high predictive ability for bacterial faecal pollution in the peri-urban tropical lowlands of Dar es Salaam, Tanzania. <i>Journal of Water and Health</i> , 2012, 10, 236-243.	1.1	29
78	Rapid and Sensitive Quantification of <i>Vibrio cholerae</i> and <i>Vibrio mimicus</i> Cells in Water Samples by Use of Catalyzed Reporter Deposition Fluorescence In Situ Hybridization Combined with Solid-Phase Cytometry. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7369-7375.	1.4	29
79	High abundance of genetic <i>Bacteroidetes</i> markers for total fecal pollution in pristine alpine soils suggests lack in specificity for feces. <i>Journal of Microbiological Methods</i> , 2012, 88, 433-435.	0.7	28
80	Hypothesis-Driven Approach for the Identification of Fecal Pollution Sources in Water Resources. <i>Environmental Science &amp; Technology</i> , 2011, 45, 4038-4045.	4.6	57
81	Development of the Bacterial Compartment Along the Danube River: a Continuum Despite Local Influences. <i>Microbial Ecology</i> , 2011, 61, 955-967.	1.4	24
82	Applicability of solid-phase cytometry and epifluorescence microscopy for rapid assessment of the microbiological quality of dialysis water. <i>Nephrology Dialysis Transplantation</i> , 2011, 26, 3640-3645.	0.4	17
83	Agricultural and Rural Watersheds. , 2011, , 399-431.		9
84	Library-Independent Bacterial Source Tracking Methods. , 2011, , 61-112.		25
85	Comment on "Non-permanent shallow halocline in a fractured carbonate aquifer, southern Italy" by E. Petrella, G. Naclerio, A. Falasca, A. Bucci, P. Capuano, V. De Felice and F. Celico [J. Hydrol. 373 (2009) 267-272]. <i>Journal of Hydrology</i> , 2010, 391, 387-388.	2.3	1
86	<i>Escherichia coli</i> and enterococci are sensitive and reliable indicators for human, livestock and wildlife faecal pollution in alpine mountainous water resources. <i>Journal of Applied Microbiology</i> , 2010, 109, no-no.	1.4	64
87	Sorbitol-fermenting <i>Bifidobacteria</i> are indicators of very recent human faecal pollution in streams and groundwater habitats in urban tropical lowlands. <i>Journal of Water and Health</i> , 2010, 8, 466-478.	1.1	14
88	A pilot study on anthropogenic faecal pollution impact in Bahir Dar Gulf of Lake Tana, Northern Ethiopia. <i>Ecohydrology and Hydrobiology</i> , 2010, 10, 271-279.	1.0	15
89	Use of faecal pollution indicators to estimate pathogen die off conditions in source separated faeces in Kathmandu Valley, Nepal. <i>Journal of Water and Health</i> , 2009, 7, 97-107.	1.1	12
90	Heterotrophic prokaryotic production in ultraoligotrophic alpine karst aquifers and ecological implications. <i>FEMS Microbiology Ecology</i> , 2009, 68, 287-299.	1.3	55

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91	Microbiological water quality along the Danube River: Integrating data from two whole-river surveys and a transnational monitoring network. <i>Water Research</i> , 2009, 43, 3673-3684.	5.3	79
92	Quantitative microbial faecal source tracking with sampling guided by hydrological catchment dynamics. <i>Environmental Microbiology</i> , 2008, 10, 2598-2608.	1.8	99
93	Rapid Growth of Planktonic <i>Vibrio cholerae</i> Non-O1/Non-O139 Strains in a Large Alkaline Lake in Austria: Dependence on Temperature and Dissolved Organic Carbon Quality. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2004-2015.	1.4	69
94	Longitudinal Changes in the Bacterial Community Composition of the Danube River: a Whole-River Approach. <i>Applied and Environmental Microbiology</i> , 2007, 73, 421-431.	1.4	110
95	A quantitative real-time PCR assay for the highly sensitive and specific detection of human faecal influence in spring water from a large alpine catchment area. <i>Letters in Applied Microbiology</i> , 2007, 44, 351-356.	1.0	114
96	Primers containing universal bases reduce multiple amoA gene specific DGGE band patterns when analysing the diversity of beta-ammonia oxidizers in the environment. <i>Journal of Microbiological Methods</i> , 2006, 66, 147-155.	0.7	77
97	Quantitative PCR Method for Sensitive Detection of Ruminant Fecal Pollution in Freshwater and Evaluation of This Method in Alpine Karstic Regions. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5610-5614.	1.4	163
98	Contrasting occurrence of <i>Chromobacterium violaceum</i> in tropical drinking water springs of Uganda. <i>Journal of Water and Health</i> , 2005, 3, 229-238.	1.1	15
99	Bacterial dynamics in spring water of alpine karst aquifers indicates the presence of stable autochthonous microbial endokarst communities. <i>Environmental Microbiology</i> , 2005, 7, 1248-1259.	1.8	126
100	Discrimination Efficacy of Fecal Pollution Detection in Different Aquatic Habitats of a High-Altitude Tropical Country, Using Presumptive Coliforms, <i>Escherichia coli</i> , and <i>Clostridium perfringens</i> Spores. <i>Applied and Environmental Microbiology</i> , 2005, 71, 65-71.	1.4	62
101	Prevalence of botulinum neurotoxin C1 and its corresponding gene in environmental samples from low and high risk avian botulism areas. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2005, 22, 185-95.	0.9	8
102	Integral Strategy for Evaluation of Fecal Indicator Performance in Bird-Influenced Saline Inland Waters. <i>Applied and Environmental Microbiology</i> , 2004, 70, 7396-7403.	1.4	41
103	Eubacterial 16S-rDNA amplicon profiling: a rapid technique for comparison and differentiation of heterotrophic plate count communities from drinking water. <i>International Journal of Food Microbiology</i> , 2004, 92, 333-345.	2.1	21
104	Specific detection of <i>Fusarium langsethiae</i> and related species by DGGE and ARMS-PCR of a $\beta$ -tubulin (tub1) gene fragment. <i>International Journal of Food Microbiology</i> , 2004, 95, 333-339.	2.1	20
105	Quantification of <i>Fusarium graminearum</i> in infected wheat by species specific real-time PCR applying a TaqMan Probe. <i>Journal of Microbiological Methods</i> , 2004, 59, 141-146.	0.7	81
106	The Choice of Standardisation Reveals a Significant Influence on the Dynamics of Bacterial Abundance in Newly Deposited River Sediments. <i>International Review of Hydrobiology</i> , 2003, 88, 284-289.	0.5	3
107	Application of single-strand conformation polymorphism and denaturing gradient gel electrophoresis for fla sequence typing of <i>Campylobacter jejuni</i> . <i>Journal of Microbiological Methods</i> , 2003, 52, 305-313.	0.7	16
108	Simultaneous Detection and Differentiation of <i>Escherichia coli</i> Populations from Environmental Freshwaters by Means of Sequence Variations in a Fragment of the $\beta$ -d-Glucuronidase Gene. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1340-1346.	1.4	63

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109	Determination of Escherichia coli Contamination with Chromocult Coliform Agar Showed a High Level of Discrimination Efficiency for Differing Fecal Pollution Levels in Tropical Waters of Kampala, Uganda. Applied and Environmental Microbiology, 2000, 66, 864-868.	1.4	90