Elizabeth M H Wellington

List of Publications by Year
in descending order

47 papers	2,990 citations	236833 25 h-index	214721 47 g-index
53 all docs	53 docs citations	53 times ranked	4362 citing authors

#	Article	IF	Citations
1	Biosynthetic potential of uncultured Antarctic soil bacteria revealed through long-read metagenomic sequencing. ISME Journal, 2022, 16, 101-111.	4.4	40
2	2â€Aminoethylphosphonate utilization in <i>Pseudomonas putida</i>â€‰<scp>BIRD</scp>â€1 is controlled by multiple master regulators. Environmental Microbiology, 2022, 24, 1902-1917.	1.8	4
3	Stimulation of Distinct Rhizosphere Bacteria Drives Phosphorus and Nitrogen Mineralization in Oilseed Rape under Field Conditions. MSystems, 2022, 7, .	1.7	7
4	Niche-adaptation in plant-associated <i>Bacteroidetes</i> favours specialisation in organic phosphorus mineralisation. ISME Journal, 2021, 15, 1040-1055.	4.4	74
5	Manipulating the Microbiome: An Alternative Treatment for Bile Acid Diarrhoea. Microbiology Research, 2021, 12, 335-353.	0.8	1
6	Transporter characterisation reveals aminoethylphosphonate mineralisation as a key step in the marine phosphorus redox cycle. Nature Communications, 2021, 12, 4554.	5.8	21
7	Impact of sulfamethoxazole on a riverine microbiome. Water Research, 2021, 201, 117382.	5.3	19
8	Mechanisms Involved in the Active Secretion of CTX-M-15 Î^{2}-Lactamase by Pathogenic Escherichia coli ST131. Antimicrobial Agents and Chemotherapy, 2021, 65, e0066321.	1.4	7
9	Exploring how microbiome signatures change across inflammatory bowel disease conditions and disease locations. Scientific Reports, 2021, 11, 18699.	1.6	9
10	Microbial imbalance in inflammatory bowel disease patients at different taxonomic levels. Gut Pathogens, 2020, 12, 1.	1.6	230
11	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. Microbiome, 2020, 8, 2.	4.9	80
12	Genomic analysis reveals high virulence and antibiotic resistance amongst phage susceptible Acinetobacter baumannii. Scientific Reports, 2020, 10, 16154.	1.6	18
13	Investigating Bacteriophages Targeting the Opportunistic Pathogen Acinetobacter baumannii. Antibiotics, 2020, 9, 200.	1.5	26
14	Microbiological and molecular insights on rare Actinobacteria harboring bioactive prospective. Bulletin of the National Research Centre, 2020, 44, .	0.7	38
15	Evaluation of a Fecal Shedding Test To Detect Badger Social Groups Infected with Mycobacterium bovis. Journal of Clinical Microbiology, 2020, 59, .	1.8	4
16	Microbial community drivers of PK/NRP gene diversity in selected global soils. Microbiome, 2019, 7, 78.	4.9	30
17	A novel sulfonamide resistance mechanism by two-component flavin-dependent monooxygenase system in sulfonamide-degrading actinobacteria. Environment International, 2019, 127, 206-215.	4.8	53
18	The widespread dissemination of integrons throughout bacterial communities in a riverine system. ISME Journal, 2018, 12, 681-691.	4.4	103

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19	Editorial: The Search for Biological Active Agent(s) From Actinobacteria. Frontiers in Microbiology, 2018, 9, 824.	1.5	43
20	Allocyclinones, hyperchlorinated angucyclinones from Actinoallomurus. Journal of Antibiotics, 2017, 70, 73-78.	1.0	11
21	The â€˜knownâ€™ genetic potential for microbial communities to degrade organic phosphorus is reduced in lowâ€pH soils. MicrobiologyOpen, 2017, 6, e00474.	1.2	34
22	Bioprospecting Soil Metagenomes for Antibiotics. Topics in Biodiversity and Conservation, 2017, , 113-136.	0.3	2
23	Identification of extracellular glycerophosphodiesterases in Pseudomonas and their role in soil organic phosphorus remineralisation. Scientific Reports, 2017, 7, 2179.	1.6	30
24	Expanding the Repertoire of Carbapenem-Hydrolyzing Metallo-ÃŸ-Lactamases by Functional Metagenomic Analysis of Soil Microbiota. Frontiers in Microbiology, 2016, 7, 1985.	1.5	18
25	Comparative genomic, proteomic and exoproteomic analyses of three <i>Pseudomonas</i> strains reveals novel insights into the phosphorus scavenging capabilities of soil bacteria. Environmental Microbiology, 2016, 18, 3535-3549.	1.8	95
26	Long-term antibiotic exposure in soil is associated with changes in microbial community structure and prevalence of class 1 integrons. FEMS Microbiology Ecology, 2016, 92, fiw159.	1.3	46
27	Trace levels of sewage effluent are sufficient to increase class 1 integron prevalence in freshwater biofilms without changing the core community. Water Research, 2016, 106, 163-170.	5.3	37
28	Structural and Biochemical Characterization of Rm3, a Subclass B3 Metallo-Î²-Lactamase Identified from a Functional Metagenomic Study. Antimicrobial Agents and Chemotherapy, 2016, 60, 5828-5840.	1.4	22
29	Survival of the ovine footrot pathogen Dichelobacter nodosus in different soils. Anaerobe, 2016, 38, 81-87.	1.0	16
30	The Soil Microbiota Harbors a Diversity of Carbapenem-Hydrolyzing Î²-Lactamases of Potential Clinical Relevance. Antimicrobial Agents and Chemotherapy, 2016, 60, 151-160.	1.4	54
31	Designing and Implementing an Assay for the Detection of Rare and Divergent NRPS and PKS Clones in European, Antarctic and Cuban Soils. PLoS ONE, 2015, 10, e0138327.	1.1	36
32	First study of pathogen load and localisation of ovine footrot using fluorescence in situ hybridisation (FISH). Veterinary Microbiology, 2015, 176, 321-327.	0.8	24
33	Mining for Nonribosomal Peptide Synthetase and Polyketide Synthase Genes Revealed a High Level of Diversity in the Sphagnum Bog Metagenome. Applied and Environmental Microbiology, 2015, 81, 5064-5072.	1.4	29
34	Validated predictive modelling of the environmental resistome. ISME Journal, 2015, 9, 1467-1476.	4.4	117
35	The role of the environment in transmission of Dichelobacter nodosus between ewes and their lambs. Veterinary Microbiology, 2015, 179, 53-59.	0.8	16
36	Screening for Genes Coding for Putative Antitumor Compounds, Antimicrobial and Enzymatic Activities from Haloalkalitolerant and Haloalkaliphilic Bacteria Strains of Algerian Sahara Soils. BioMed Research International, 2014, 2014, 1-11.	0.9	5

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37	Exploring the functional soil-microbe interface and exoenzymes through soil metaexoproteomics. ISME Journal, 2014, 8, 2148-2150.	4.4	39
38	A longitudinal study of the role of Dichelobacter nodosus and Fusobacterium necrophorum load in initiation and severity of footrot in sheep. Preventive Veterinary Medicine, 2014, 115, 48-55.	0.7	76
39	Dynamics and impact of footrot and climate on hoof horn length in 50 ewes from one farm over a period of 10 months. Veterinary Journal, 2014, 201, 295-301.	0.6	30
40	Multiple locus VNTR analysis highlights that geographical clustering and distribution of Dichelobacter nodosus, the causal agent of footrot in sheep, correlates with inter-country movements. Infection, Genetics and Evolution, 2014, 22, 273-279.	1.0	11
41	The role of the natural environment in the emergence of antibiotic resistance in Gram-negative bacteria. Lancet Infectious Diseases, The, 2013, 13, 155-165.	4.6	839
42	Impacts of anthropogenic activity on the ecology of class 1 integrons and integron-associated genes in the environment. ISME Journal, 2011, 5, 1253-1261.	4.4	377
43	Ovine pedomics: the first study of the ovine foot 16S rRNA-based microbiome. ISME Journal, 2011, 5, 1426-1437.	4.4	46
44	Detection and diversity of a putative novel heterogeneous polymorphic proline-glycine repeat (Pgr) protein in the footrot pathogen Dichelobacter nodosus. Veterinary Microbiology, 2011, 147, 358-366.	0.8	13
45	Antibiotic Resistance in the Environment, with Particular Reference to MRSA. Advances in Applied Microbiology, 2008, 63, 249-280.	1.3	31
46	Molecular Detection of Mycobacterium bovis and Mycobacterium bovis BCG (Pasteur) in Soil. Applied and Environmental Microbiology, 2005, 71, 1946-1952.	1.4	92
47	In Situ Monitoring of Streptothricin Production by Streptomyces rochei F20 in Soil and Rhizosphere. Applied and Environmental Microbiology, 2004, 70, 5222-5228.	1.4	31