

William C Nelson

List of Publications by Year in Descending Order

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Version: 2024-04-19

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

103
papers

28,796
citations

56
h-index

118
g-index

118
ext. papers

32,913
ext. citations

13.6
avg, IF

5.61
L-index

#	Paper	IF	Citations
103	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. <i>MBio</i> , 2021 , e0259521	7.8	1
102	A <i>Histoplasma capsulatum</i> Lipid Metabolic Map Identifies Antifungal Targets. <i>MBio</i> , 2021 , e0297221	7.8	1
101	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. <i>Nutrients</i> , 2020 , 12,	6.7	24
100	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. <i>MBio</i> , 2020 , 11,	7.8	13
99	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. <i>PLoS ONE</i> , 2020 , 15, e0228165	3.7	7
98	Biases in genome reconstruction from metagenomic data. <i>PeerJ</i> , 2020 , 8, e10119	3.1	9
97	Representing Organic Matter Thermodynamics in Biogeochemical Reactions via Substrate-Explicit Modeling. <i>Frontiers in Microbiology</i> , 2020 , 11, 531756	5.7	6
96	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
95	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome 2020 , 15, e0228165		
94	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome 2020 , 15, e0228165		
93	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome 2020 , 15, e0228165		
92	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome 2020 , 15, e0228165		
91	Minimal Interspecies Interaction Adjustment (MIIA): Inference of Neighbor-Dependent Interactions in Microbial Communities. <i>Frontiers in Microbiology</i> , 2019 , 10, 1264	5.7	8
90	Metabolic effects of vitamin B12 on physiology, stress resistance, growth rate and biomass productivity of <i>Cyanobacterium stanieri</i> planktonic and biofilm cultures. <i>Algal Research</i> , 2019 , 42, 101580		
89	Phenotypic responses to interspecies competition and commensalism in a naturally-derived microbial co-culture. <i>Scientific Reports</i> , 2018 , 8, 297	4.9	12
88	Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018 , 9, 585	17.4	56
87	Metabolic Network Modeling for Computer-Aided Design of Microbial Interactions 2018 , 793-801		5

86	Multi Omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone. <i>Science of the Total Environment</i> , 2018 , 642, 742-753	10.2	29
85	<i>Salinivirga fredricksonii</i> gen. nov., sp. nov., a heterotrophic halophile isolated from a photosynthetic mat, a member of a novel lineage (<i>Salinarimonadaceae</i> fam. nov.) within the order Rhizobiales, and reclassification of the genus <i>Salinarimonas</i> Liu et al. 2010 into <i>Salinarimonadaceae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 1591-1598	2.2	8
84	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . <i>MBio</i> , 2018 , 9,	7.8	39
83	Draft Genome Sequence of sp. Strain HL-69, Isolated from a Benthic Microbial Mat from a Magnesium Sulfate-Dominated Hypersaline Lake. <i>Genome Announcements</i> , 2018 , 6,		5
82	Underlying mechanisms for syntrophic metabolism of essential enzyme cofactors in microbial communities. <i>ISME Journal</i> , 2017 , 11, 1434-1446	11.9	47
81	Effect of Water Chemistry and Hydrodynamics on Nitrogen Transformation Activity and Microbial Community Functional Potential in Hyporheic Zone Sediment Columns. <i>Environmental Science & Technology</i> , 2017 , 51, 4877-4886	10.3	48
80	Targeted quantification of functional enzyme dynamics in environmental samples for microbially mediated biogeochemical processes. <i>Environmental Microbiology Reports</i> , 2017 , 9, 512-521	3.7	12
79	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
78	Geochemical and Microbial Community Attributes in Relation to Hyporheic Zone Geological Facies. <i>Scientific Reports</i> , 2017 , 7, 12006	4.9	19
77	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	14
76	Predicting Species-Resolved Macronutrient Acquisition during Succession in a Model Phototrophic Biofilm Using an Integrated Omics Approach. <i>Frontiers in Microbiology</i> , 2017 , 8, 1020	5.7	83
75	Groundwater-surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016 , 7, 11237	17.4	171
74	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 255-67	4.8	34
73	<i>Trichodesmium</i> genome maintains abundant, widespread noncoding DNA in situ, despite oligotrophic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 4251-6	11.5	31
72	The reduced genomes of <i>Parcubacteria</i> (OD1) contain signatures of a symbiotic lifestyle. <i>Frontiers in Microbiology</i> , 2015 , 6, 713	5.7	176
71	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. <i>Genome Announcements</i> , 2014 , 2,		12
70	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013 , 4, 115	5.7	40
69	Microbial secondary succession in soil microcosms of a desert oasis in the Cuatro Ciénegas Basin, Mexico. <i>PeerJ</i> , 2013 , 1, e47	3.1	26

68	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. <i>Environmental Microbiology</i> , 2012 , 14, 254-67	5.2	52
67	Comparative analysis of eukaryotic marine microbial assemblages from 18S rRNA gene and gene transcript clone libraries by using different methods of extraction. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 3958-65	4.8	30
66	Novel miniature transposable elements in thermophilic <i>Synechococcus</i> strains and their impact on an environmental population. <i>Journal of Bacteriology</i> , 2012 , 194, 3636-42	3.5	5
65	Prospects for the study of evolution in the deep biosphere. <i>Frontiers in Microbiology</i> , 2011 , 2, 285	5.7	28
64	Mariprofundus ferrooxydans PV-1 the first genome of a marine Fe(II) oxidizing Zetaproteobacterium. <i>PLoS ONE</i> , 2011 , 6, e25386	3.7	112
63	Analysis of insertion sequences in thermophilic cyanobacteria: exploring the mechanisms of establishing, maintaining, and withstanding high insertion sequence abundance. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 5458-66	4.8	19
62	Genomic potential of <i>Marinobacter aquaeolei</i> , a biogeochemical "opportunitroph". <i>Applied and Environmental Microbiology</i> , 2011 , 77, 2763-71	4.8	85
61	The FibRumBa database: a resource for biologists with interests in gastrointestinal microbial ecology, plant biomass degradation, and anaerobic microbiology. <i>Microbial Ecology</i> , 2010 , 59, 212-3	4.4	12
60	Comparative genome analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : insights into their environmental niche. <i>Microbial Ecology</i> , 2010 , 60, 721-9	4.4	192
59	Genome degradation in <i>Brucella ovis</i> corresponds with narrowing of its host range and tissue tropism. <i>PLoS ONE</i> , 2009 , 4, e5519	3.7	84
58	Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2046-56	4.8	590
57	Germ warfare in a microbial mat community: CRISPRs provide insights into the co-evolution of host and viral genomes. <i>PLoS ONE</i> , 2009 , 4, e4169	3.7	127
56	Genomic differences between <i>Fibrobacter succinogenes</i> S85 and <i>Fibrobacter intestinalis</i> DR7, identified by suppression subtractive hybridization. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 987-93	4.8	10
55	Genome sequence and identification of candidate vaccine antigens from the animal pathogen <i>Dichelobacter nodosus</i> . <i>Nature Biotechnology</i> , 2007 , 25, 569-75	44.5	58
54	TIGRFAMs and Genome Properties: tools for the assignment of molecular function and biological process in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2007 , 35, D260-4	20.1	225
53	Candidatus <i>Chloracidobacterium thermophilum</i> : an aerobic phototrophic Acidobacterium. <i>Science</i> , 2007 , 317, 523-6	33.3	305
52	Genome sequence of <i>Synechococcus</i> CC9311: Insights into adaptation to a coastal environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13555-9	11.5	200
51	Comparative genomics of emerging human ehrlichiosis agents. <i>PLoS Genetics</i> , 2006 , 2, e21	6	363

50	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006 , 16, 1031-40	9.7	250
49	Identification of a conserved bacterial protein secretion system in <i>Vibrio cholerae</i> using the <i>Dictyostelium</i> host model system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 1528-33	11.5	810
48	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : implications for the microbial "pan-genome". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13950-5	11.5	1585
47	Serendipitous discovery of <i>Wolbachia</i> genomes in multiple <i>Drosophila</i> species. <i>Genome Biology</i> , 2005 , 6, R23	18.3	108
46	Life in hot carbon monoxide: the complete genome sequence of <i>Carboxydothemus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005 , 1, e65	6	184
45	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005 , 23, 873-8	44.5	522
44	Whole-genome sequence analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A reveals divergence among pathovars in genes involved in virulence and transposition. <i>Journal of Bacteriology</i> , 2005 , 187, 6488-98	3.5	270
43	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 10913-8	11.5	430
42	Genome sequence of the PCE-dechlorinating bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005 , 307, 105-8	33.3	363
41	Novel molecular features of the fibrolytic intestinal bacterium <i>Fibrobacter intestinalis</i> not shared with <i>Fibrobacter succinogenes</i> as determined by suppressive subtractive hybridization. <i>Journal of Bacteriology</i> , 2005 , 187, 3739-51	3.5	43
40	Life in Hot Carbon Monoxide: the Complete Genome Sequence of <i>Carboxydothemus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005 , preprint, e65	6	1
39	Phylogenomics of the reproductive parasite <i>Wolbachia pipientis</i> wMel: a streamlined genome overrun by mobile genetic elements. <i>PLoS Biology</i> , 2004 , 2, E69	9.7	613
38	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
37	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004 , 22, 554-9	44.5	477
36	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004 , 432, 910-3	50.4	345
35	The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004 , 32, 977-88	20.1	253
34	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004 , 32, 2386-95	20.1	404
33	Environmental genome shotgun sequencing of the Sargasso Sea. <i>Science</i> , 2004 , 304, 66-74	33.3	3231

32	Structural flexibility in the <i>Burkholderia mallei</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 14246-51	11.5	315
31	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2003 , 5, 630-630	5.2	8
30	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5455-60	11.5	428
29	Role of mobile DNA in the evolution of vancomycin-resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003 , 299, 2071-4	33.3	725
28	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003 , 423, 81-6	50.4	692
27	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10181-6	11.5	695
26	Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. <i>Journal of Bacteriology</i> , 2003 , 185, 5220-33	3.5	194
25	Genome sequence of <i>Chlamydomonas reinhardtii</i> (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , 2003 , 31, 2134-47	20.1	233
24	Complete genome sequence of the oral pathogenic bacterium <i>Porphyromonas gingivalis</i> strain W83. <i>Journal of Bacteriology</i> , 2003 , 185, 5591-601	3.5	321
23	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , 2003 , 302, 1967-9	33.3	573
22	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2002 , 4, 799-808	5.2	1069
21	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002 , 415, 630-3	50.4	333
20	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002 , 20, 1118-23	44.5	680
19	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13148-53	11.5	372
18	Whole-genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains. <i>Journal of Bacteriology</i> , 2002 , 184, 5479-90	3.5	569
17	The complete genome sequence of <i>Chlorobium tepidum</i> TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9509-14	11.5	321
16	Complete genome sequence of <i>Caulobacter crescentus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 4136-41	11.5	436
15	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001 , 293, 498-506	50.6	1112

14	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000 , 406, 477-83	50.4	1495
13	Genome sequences of <i>Chlamydia trachomatis</i> MoPn and <i>Chlamydia pneumoniae</i> AR39. <i>Nucleic Acids Research</i> , 2000 , 28, 1397-406	20.1	610
12	Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58. <i>Science</i> , 2000 , 287, 1809-15	33.3	986
11	Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , 1999 , 399, 323-9	50.4	1260
10	Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999 , 286, 1571-3	33.3	760
9	The F plasmid <i>traY</i> gene product binds DNA as a monomer or a dimer: structural and functional implications. <i>Molecular Microbiology</i> , 1996 , 20, 1179-87	4.1	14
8	The <i>traY</i> Gene Product and Integration Host Factor Stimulate <i>Escherichia coli</i> DNA Helicase I-catalyzed Nicking at the F Plasmid <i>oriT</i> . <i>Journal of Biological Chemistry</i> , 1995 , 270, 28374-28380	5.4	70
7	Stepwise Assembly of a Relaxosome at the F Plasmid Origin of Transfer. <i>Journal of Biological Chemistry</i> , 1995 , 270, 28381-28386	5.4	58
6	The <i>traY</i> gene product and integration host factor stimulate <i>Escherichia coli</i> DNA helicase I-catalyzed nicking at the F plasmid <i>oriT</i> . <i>Journal of Biological Chemistry</i> , 1995 , 270, 28374-80	5.4	39
5	Characterization of the <i>Escherichia coli</i> F Factor <i>traY</i> gene product and its binding sites. <i>Journal of Bacteriology</i> , 1993 , 175, 2221-8	3.5	39
4	Characterization of the reaction product of the <i>oriT</i> nicking reaction catalyzed by <i>Escherichia coli</i> DNA helicase I. <i>Journal of Bacteriology</i> , 1993 , 175, 2599-606	3.5	55
3	Representing Organic Matter Thermodynamics in Biogeochemical Reactions via Substrate-Explicit Modeling		3
2	Multi Omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone		2
1	Identification of novel protein lysine acetyltransferases in <i>Escherichia coli</i>		1