

William C Nelson

List of Publications by Year in descending order

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100
papers

35,271
citations

22153

59
h-index

28297

105
g-index

118
all docs

118
docs citations

118
times ranked

31776
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of <i>Fusarium</i> sp. Strain DS 682, a Novel Fungal Isolate from the Grass Rhizosphere. Microbiology Resource Announcements, 2021, 10, .	0.6	7
2	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. MBio, 2021, 12, e0259521.	4.1	24
3	A <i>Histoplasma capsulatum</i> Lipid Metabolic Map Identifies Antifungal Targets. MBio, 2021, 12, e0297221.	4.1	6
4	Representing Organic Matter Thermodynamics in Biogeochemical Reactions via Substrate-Explicit Modeling. Frontiers in Microbiology, 2020, 11, 531756.	3.5	27
5	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. Microbiology Resource Announcements, 2020, 9, .	0.6	4
6	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn's Disease: A Randomized Diet Controlled Trial. Nutrients, 2020, 12, 3749.	4.1	62
7	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. MBio, 2020, 11, .	4.1	27
8	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. PLoS ONE, 2020, 15, e0228165.	2.5	12
9	Biases in genome reconstruction from metagenomic data. PeerJ, 2020, 8, e10119.	2.0	32
10	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
11	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
12	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
13	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
14	Metabolic effects of vitamin B12 on physiology, stress resistance, growth rate and biomass productivity of <i>Cyanobacterium stanieri</i> planktonic and biofilm cultures. Algal Research, 2019, 42, 101580.	4.6	2
15	Minimal Interspecies Interaction Adjustment (MIIA): Inference of Neighbor-Dependent Interactions in Microbial Communities. Frontiers in Microbiology, 2019, 10, 1264.	3.5	12
16	Phenotypic responses to interspecies competition and commensalism in a naturally-derived microbial co-culture. Scientific Reports, 2018, 8, 297.	3.3	32
17	Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. Nature Communications, 2018, 9, 585.	12.8	110
18	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . MBio, 2018, 9, .	4.1	86

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19	Draft Genome Sequence of Cyanobacterium sp. Strain HL-69, Isolated from a Benthic Microbial Mat from a Magnesium Sulfate-Dominated Hypersaline Lake. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
20	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.	8.0	60
21	<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.	1.7	25
22	Underlying mechanisms for syntrophic metabolism of essential enzyme cofactors in microbial communities. <i>ISME Journal</i> , 2017, 11, 1434-1446.	9.8	123
23	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.	10.0	79
24	Targeted quantification of functional enzyme dynamics in environmental samples for microbially mediated biogeochemical processes. <i>Environmental Microbiology Reports</i> , 2017, 9, 512-521.	2.4	16
25	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.	17.5	1,512
26	Geochemical and Microbial Community Attributes in Relation to Hyporheic Zone Geological Facies. <i>Scientific Reports</i> , 2017, 7, 12006.	3.3	40
27	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	23
28	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.	3.5	287
29	Groundwater-surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016, 7, 11237.	12.8	290
30	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. <i>Applied and Environmental Microbiology</i> , 2016, 82, 255-267.	3.1	41
31	The reduced genomes of <i>Parcubacteria</i> (OD1) contain signatures of a symbiotic lifestyle. <i>Frontiers in Microbiology</i> , 2015, 6, 713.	3.5	280
32	<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, 4251-4256.	7.1	45
33	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
34	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013, 4, 115.	3.5	53
35	Microbial secondary succession in soil microcosms of a desert oasis in the Cuatro Ciénegas Basin, Mexico. <i>PeerJ</i> , 2013, 1, e47.	2.0	50
36	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, 3958-3965.	3.1	39

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37	Novel Miniature Transposable Elements in Thermophilic <i>Synechococcus</i> Strains and Their Impact on an Environmental Population. <i>Journal of Bacteriology</i> , 2012, 194, 3636-3642.	2.2	8
38	Metagenomic analysis of a complex marine planktonic thaumarchaeal community from the Gulf of Maine. <i>Environmental Microbiology</i> , 2012, 14, 254-267.	3.8	56
39	<i>Mariprofundus ferrooxydans</i> PV-1 the First Genome of a Marine Fe(II) Oxidizing Zetaproteobacterium. <i>PLoS ONE</i> , 2011, 6, e25386.	2.5	132
40	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, 5458-5466.	3.1	23
41	Genomic Potential of <i>Marinobacter aquaeolei</i> , a Biogeochemical "Opportunitroph" <i>Applied and Environmental Microbiology</i> , 2011, 77, 2763-2771.	3.1	120
42	Prospects for the study of evolution in the deep biosphere. <i>Frontiers in Microbiology</i> , 2011, 2, 285.	3.5	52
43	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, 212-213.	2.8	13
44	Comparative Genome Analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : Insights into Their Environmental Niche. <i>Microbial Ecology</i> , 2010, 60, 721-729.	2.8	293
45	Genome Degradation in <i>Brucella ovis</i> Corresponds with Narrowing of Its Host Range and Tissue Tropism. <i>PLoS ONE</i> , 2009, 4, e5519.	2.5	110
46	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	3.1	804
47	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.	2.5	154
48	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, 987-993.	3.1	14
49	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-D264.	14.5	266
50	<i>Candidatus</i> <i>Chloracidobacterium thermophilum</i> : An Aerobic Phototrophic Acidobacterium. <i>Science</i> , 2007, 317, 523-526.	12.6	384
51	Genome sequence and identification of candidate vaccine antigens from the animal pathogen <i>Dichelobacter nodosus</i> . <i>Nature Biotechnology</i> , 2007, 25, 569-575.	17.5	66
52	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006, 16, 1031-1040.	5.5	281
53	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, 1528-1533.	7.1	998
54	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, 13555-13559.	7.1	230

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55	Comparative Genomics of Emerging Human Ehrlichiosis Agents. PLoS Genetics, 2006, 2, e21.	3.5	423
56	Life in Hot Carbon Monoxide: The Complete Genome Sequence of Carboxydothemus hydrogenoformans Z-2901. PLoS Genetics, 2005, 1, e65.	3.5	226
57	Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5. Nature Biotechnology, 2005, 23, 873-878.	17.5	615
58	Whole-Genome Sequence Analysis of Pseudomonas syringae pv. phaseolicola 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. Journal of Bacteriology, 2005, 187, 6488-6498.	2.2	301
59	The psychrophilic lifestyle as revealed by the genome sequence of Colwellia psychrerythraea 34H through genomic and proteomic analyses. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10913-10918.	7.1	529
60	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . Science, 2005, 307, 105-108.	12.6	402
61	Novel Molecular Features of the Fibrolytic Intestinal Bacterium Fibrobacter intestinalis Not Shared with Fibrobacter succinogenes as Determined by Suppressive Subtractive Hybridization. Journal of Bacteriology, 2005, 187, 3739-3751.	2.2	63
62	Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: Implications for the microbial "pan-genome". Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13950-13955.	7.1	2,161
63	Serendipitous discovery of Wolbachia genomes in multiple Drosophila species. Genome Biology, 2005, 6, R23.	9.6	126
64	Life in Hot Carbon Monoxide: the Complete Genome Sequence of Carboxydothemus hydrogenoformans Z-2901. PLoS Genetics, 2005, preprint, e65.	3.5	1
65	Phylogenomics of the Reproductive Parasite Wolbachia pipientis wMel: A Streamlined Genome Overrun by Mobile Genetic Elements. PLoS Biology, 2004, 2, e69.	5.6	713
66	Genomic Insights into Methanotrophy: The Complete Genome Sequence of Methylococcus capsulatus (Bath). PLoS Biology, 2004, 2, e303.	5.6	275
67	The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough. Nature Biotechnology, 2004, 22, 554-559.	17.5	559
68	Genome sequence of Silicibacter pomeroyi reveals adaptations to the marine environment. Nature, 2004, 432, 910-913.	27.8	415
69	The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1. Nucleic Acids Research, 2004, 32, 977-988.	14.5	273
70	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species. Nucleic Acids Research, 2004, 32, 2386-2395.	14.5	460
71	Environmental Genome Shotgun Sequencing of the Sargasso Sea. Science, 2004, 304, 66-74.	12.6	3,776
72	Structural flexibility in the <i>Burkholderia mallei</i> genome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14246-14251.	7.1	366

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73	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2003, 5, 630-630.	3.8	10
74	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, 5455-5460.	7.1	506
75	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	12.6	849
76	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003, 423, 81-86.	27.8	760
77	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10181-10186.	7.1	785
78	Complete Genome Sequence of the Broad-Host-Range Vibriophage KVP40: Comparative Genomics of a T4-Related Bacteriophage. <i>Journal of Bacteriology</i> , 2003, 185, 5220-5233.	2.2	214
79	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, 2134-2147.	14.5	266
80	Complete Genome Sequence of the Oral Pathogenic Bacterium <i>Porphyromonas gingivalis</i> Strain W83. <i>Journal of Bacteriology</i> , 2003, 185, 5591-5601.	2.2	362
81	Genome of <i>Geobacter sulfurreducens</i> : Metal Reduction in Subsurface Environments. <i>Science</i> , 2003, 302, 1967-1969.	12.6	648
82	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, 13148-13153.	7.1	422
83	Whole-Genome Comparison of <i>Mycobacterium tuberculosis</i> Clinical and Laboratory Strains. <i>Journal of Bacteriology</i> , 2002, 184, 5479-5490.	2.2	645
84	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, 9509-9514.	7.1	362
85	Complete genome sequence and comparative analysis of the metabolically versatile <i>Pseudomonas putida</i> KT2440. <i>Environmental Microbiology</i> , 2002, 4, 799-808.	3.8	1,218
86	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002, 415, 630-633.	27.8	380
87	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	17.5	771
88	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	12.6	1,281
89	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, 4136-4141.	7.1	489
90	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	27.8	1,723

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91	Genome sequences of <i>Chlamydia trachomatis</i> MoPn and <i>Chlamydia pneumoniae</i> AR39. <i>Nucleic Acids Research</i> , 2000, 28, 1397-1406.	14.5	696
92	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	12.6	1,083
93	Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , 1999, 399, 323-329.	27.8	1,397
94	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
95	The F plasmid traY gene product binds DNA as a monomer or a dimer: structural and functional implications. <i>Molecular Microbiology</i> , 1996, 20, 1179-1187.	2.5	15
96	The traY Gene Product and Integration Host Factor Stimulate <i>Escherichia coli</i> DNA Helicase I-catalyzed Nicking at the F Plasmid oriT. <i>Journal of Biological Chemistry</i> , 1995, 270, 28374-28380.	3.4	77
97	Stepwise Assembly of a Relaxosome at the F Plasmid Origin of Transfer. <i>Journal of Biological Chemistry</i> , 1995, 270, 28381-28386.	3.4	64
98	The traY gene product and integration host factor stimulate <i>Escherichia coli</i> DNA helicase I-catalyzed nicking at the F plasmid oriT. <i>Journal of Biological Chemistry</i> , 1995, 270, 28374-80.	3.4	44
99	Characterization of the <i>Escherichia coli</i> F factor traY gene product and its binding sites. <i>Journal of Bacteriology</i> , 1993, 175, 2221-2228.	2.2	42
100	Characterization of the reaction product of the oriT nicking reaction catalyzed by <i>Escherichia coli</i> DNA helicase I. <i>Journal of Bacteriology</i> , 1993, 175, 2599-2606.	2.2	60