

# 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	Environmental Genome Shotgun Sequencing of the Sargasso Sea. <i>Science</i> , 2004, 304, 66-74.	12.6	3,776
2	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, 13950-13955.	7.1	2,161
3	DNA sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . <i>Nature</i> , 2000, 406, 477-483.	27.8	1,723
4	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
5	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
6	Complete Genome Sequence of a Virulent Isolate of <i>Streptococcus pneumoniae</i> . <i>Science</i> , 2001, 293, 498-506.	12.6	1,281
7	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
8	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	12.6	1,083
9	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
10	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
11	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	12.6	849
12	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
13	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
14	Genome sequence of the dissimilatory metal ion-reducing bacterium <i>Shewanella oneidensis</i> . <i>Nature Biotechnology</i> , 2002, 20, 1118-1123.	17.5	771
15	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
16	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.	5.6	713
17	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
18	Genome of <i>Geobacter sulfurreducens</i> : Metal Reduction in Subsurface Environments. <i>Science</i> , 2003, 302, 1967-1969.	12.6	648

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19	Whole-Genome Comparison of <i>Mycobacterium tuberculosis</i> Clinical and Laboratory Strains. <i>Journal of Bacteriology</i> , 2002, 184, 5479-5490.	2.2	645
20	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	17.5	615
21	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	17.5	559
22	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, 10913-10918.	7.1	529
23	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
24	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
25	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, 2386-2395.	14.5	460
26	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	3.5	423
27	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
28	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	27.8	415
29	Genome Sequence of the PCE-Dechlorinating Bacterium <i>Dehalococcoides ethenogenes</i> . <i>Science</i> , 2005, 307, 105-108.	12.6	402
30	<i>Candidatus</i> <i>Chloracidobacterium thermophilum</i> : An Aerobic Phototrophic Acidobacterium. <i>Science</i> , 2007, 317, 523-526.	12.6	384
31	Unsuspected diversity among marine aerobic anoxygenic phototrophs. <i>Nature</i> , 2002, 415, 630-633.	27.8	380
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, 14246-14251.	7.1	366
33	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
34	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
35	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, 6488-6498.	2.2	301
36	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

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37	Groundwater–surface water mixing shifts ecological assembly processes and stimulates organic carbon turnover. <i>Nature Communications</i> , 2016, 7, 11237.	12.8	290
38	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
39	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
40	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
41	Genomic Insights into Methanotrophy: The Complete Genome Sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004, 2, e303.	5.6	275
42	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, 977-988.	14.5	273
43	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
44	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
45	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
46	Life in Hot Carbon Monoxide: The Complete Genome Sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005, 1, e65.	3.5	226
47	Complete Genome Sequence of the Broad-Host-Range <i>Vibriophage</i> KVP40: Comparative Genomics of a T4-Related Bacteriophage. <i>Journal of Bacteriology</i> , 2003, 185, 5220-5233.	2.2	214
48	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
49	<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
50	Serendipitous discovery of <i>Wolbachia</i> genomes in multiple <i>Drosophila</i> species. <i>Genome Biology</i> , 2005, 6, R23.	9.6	126
51	Underlying mechanisms for syntrophic metabolism of essential enzyme cofactors in microbial communities. <i>ISME Journal</i> , 2017, 11, 1434-1446.	9.8	123
52	Genomic Potential of <i>Marinobacter aquaeolei</i> , a Biogeochemical –Opportunotroph–. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2763-2771.	3.1	120
53	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
54	Influences of organic carbon speciation on hyporheic corridor biogeochemistry and microbial ecology. <i>Nature Communications</i> , 2018, 9, 585.	12.8	110

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55	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	4.1	86
56	Effect of Water Chemistry and Hydrodynamics on Nitrogen Transformation Activity and Microbial Community Functional Potential in Hyporheic Zone Sediment Columns. <i>Environmental Science &amp; Technology</i> , 2017, 51, 4877-4886.	10.0	79
57	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
58	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
59	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
60	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, 3739-3751.	2.2	63
61	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, 3749.	4.1	62
62	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
63	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
64	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
65	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013, 4, 115.	3.5	53
66	Prospects for the study of evolution in the deep biosphere. <i>Frontiers in Microbiology</i> , 2011, 2, 285.	3.5	52
67	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
68	<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
69	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
70	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
71	Identification and Resolution of Microdiversity through Metagenomic Sequencing of Parallel Consortia. <i>Applied and Environmental Microbiology</i> , 2016, 82, 255-267.	3.1	41
72	Geochemical and Microbial Community Attributes in Relation to Hyporheic Zone Geological Facies. <i>Scientific Reports</i> , 2017, 7, 12006.	3.3	40

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73	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
74	Phenotypic responses to interspecies competition and commensalism in a naturally-derived microbial co-culture. <i>Scientific Reports</i> , 2018, 8, 297.	3.3	32
75	Biases in genome reconstruction from metagenomic data. <i>PeerJ</i> , 2020, 8, e10119.	2.0	32
76	Representing Organic Matter Thermodynamics in Biogeochemical Reactions via Substrate-Explicit Modeling. <i>Frontiers in Microbiology</i> , 2020, 11, 531756.	3.5	27
77	Deconstructing the Soil Microbiome into Reduced-Complexity Functional Modules. <i>MBio</i> , 2020, 11, .	4.1	27
78	<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
79	DNA Viral Diversity, Abundance, and Functional Potential Vary across Grassland Soils with a Range of Historical Moisture Regimes. <i>MBio</i> , 2021, 12, e0259521.	4.1	24
80	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
81	Organismal and spatial partitioning of energy and macronutrient transformations within a hypersaline mat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	23
82	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. <i>Genome Announcements</i> , 2014, 2, .	0.8	20
83	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
84	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
85	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
86	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
87	Minimal Interspecies Interaction Adjustment (MIIA): Inference of Neighbor-Dependent Interactions in Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1264.	3.5	12
88	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. <i>PLoS ONE</i> , 2020, 15, e0228165.	2.5	12
89	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
90	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

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91	Draft Genome Sequence of Cyanobacterium sp. Strain HL-69, Isolated from a Benthic Microbial Mat from a Magnesium Sulfate-Dominated Hypersaline Lake. Genome Announcements, 2018, 6, .	0.8	7
92	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
93	A <i>Histoplasma capsulatum</i> Lipid Metabolic Map Identifies Antifungal Targets. MBio, 2021, 12, e0297221.	4.1	6
94	Terabase Metagenome Sequencing of Grassland Soil Microbiomes. Microbiology Resource Announcements, 2020, 9, .	0.6	4
95	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
96	Life in Hot Carbon Monoxide: the Complete Genome Sequence of Carboxydotherrmus hydrogenoformans Z-2901. PLoS Genetics, 2005, preprint, e65.	3.5	1
97	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
98	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
99	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0
100	Distinct temporal diversity profiles for nitrogen cycling genes in a hyporheic microbiome. , 2020, 15, e0228165.		0