

# Owen White

## List of Publications by Year in Descending Order

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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.

115  
papers

50,376  
citations

75  
h-index

126  
g-index

126  
ext. papers

56,948  
ext. citations

21.9  
avg, IF

6.13  
L-index

#	Paper	IF	Citations
115	gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration. <i>Nature Methods</i> , <b>2021</b> , 18, 843-844	21.6	16
114	HMPDACC: a Human Microbiome Project Multi-omic data resource. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D734-D742	21.6	16
113	NeMO-AD, a new neuroscience multi-omic visualization and analysis platform for Alzheimer's disease research.. <i>Alzheimers and Dementia</i> , <b>2021</b> , 17 Suppl 3, e055686	1.2	
112	NeMO analytics-AD: The neuroscience multi-omic visualization and analysis platform, now extended to support Alzheimer's disease. <i>Alzheimers and Dementia</i> , <b>2020</b> , 16, e046097	1.2	
111	CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. <i>BMC Genomics</i> , <b>2017</b> , 18, 332	4.5	10
110	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1077-1086	44.5	240
109	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , <b>2017</b> , 550, 61-66	50.4	595
108	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 569	5.7	19
107	Toward a standard in structural genome annotation for prokaryotes. <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 45		12
106	The microbiome quality control project: baseline study design and future directions. <i>Genome Biology</i> , <b>2015</b> , 16, 276	18.3	140
105	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , <b>2014</b> , 2,	16.6	18
104	Advancing the microbiome research community. <i>Cell</i> , <b>2014</b> , 159, 227-30	56.2	50
103	MetaRef: a pan-genomic database for comparative and community microbial genomics. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D617-24	20.1	46
102	Genomic standards consortium projects. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 599-601		21
101	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , <b>2014</b> , 9, e99979	3.7	25
100	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , <b>2014</b> , 30, 3125-7	7.2	22
99	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001920	9.7	146

98	Standardized description of scientific evidence using the Evidence Ontology (ECO). <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014,	5	75
97	Genomic Standards Consortium Projects. <i>Standards in Genomic Sciences</i> , <b>2014</b> , 9, 599-601		23
96	CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. <i>Microbiome</i> , <b>2013</b> , 1, 6	16.6	40
95	The Human Microbiome Project: a community resource for the healthy human microbiome. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001377	9.7	268
94	Metabolic reconstruction for metagenomic data and its application to the human microbiome. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002358	5	730
93	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 438-47		6
92	Conceptualizing a Genomics Software Institute (GSI). <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 136-44		1
91	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 415-20	44.5	445
90	The IGS Standard Operating Procedure for Automated Prokaryotic Annotation. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 244-51		100
89	Solving the Problem: Genome Annotation Standards before the Data Deluge. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 5, 168-93		46
88	CloVR: a virtual machine for automated and portable sequence analysis from the desktop using cloud computing. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 356	3.6	220
87	The Genomic Standards Consortium. <i>PLoS Biology</i> , <b>2011</b> , 9, e1001088	9.7	143
86	Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. <i>PLoS ONE</i> , <b>2011</b> , 6, e26624	3.7	58
85	The comprehensive microbial resource. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D340-5	20.1	82
84	Ergatis: a web interface and scalable software system for bioinformatics workflows. <i>Bioinformatics</i> , <b>2010</b> , 26, 1488-92	7.2	73
83	Pathema: a clade-specific bioinformatics resource center for pathogen research. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D408-14	20.1	17
82	Meeting Report: BioSharing at ISMB 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 254-8		18
81	Meeting Report: Towards a Critical Assessment of Functional Annotation Experiment (CAFAE) for bacterial genome annotation. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 240-2		3

80	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 225-31		7
79	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 357-60		2
78	Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 232-4		3
77	Sequencing of <i>Culex quinquefasciatus</i> establishes a platform for mosquito comparative genomics. <i>Science</i> , <b>2010</b> , 330, 86-8	33.3	352
76	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , <b>2009</b> , 460, 352-8	50.4	822
75	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , <b>2008</b> , 455, 757-63	50.4	633
74	Big data: The future of biocuration. <i>Nature</i> , <b>2008</b> , 455, 47-50	50.4	527
73	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 541-7	44.5	964
72	Automated eukaryotic gene structure annotation using EvidenceModeler and the Program to Assemble Spliced Alignments. <i>Genome Biology</i> , <b>2008</b> , 9, R7	18.3	1212
71	Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. <i>OMICS A Journal of Integrative Biology</i> , <b>2008</b> , 12, 137-41	3.8	491
70	Toward a standards-compliant genomic and metagenomic publication record. <i>OMICS A Journal of Integrative Biology</i> , <b>2008</b> , 12, 157-60	3.8	31
69	Genome sequence of <i>Aedes aegypti</i> , a major arbovirus vector. <i>Science</i> , <b>2007</b> , 316, 1718-23	33.3	867
68	Genome sequence of <i>Babesia bovis</i> and comparative analysis of apicomplexan hemoprotozoa. <i>PLoS Pathogens</i> , <b>2007</b> , 3, 1401-13	7.6	279
67	TIGRFAMs and Genome Properties: tools for the assignment of molecular function and biological process in prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D260-4	20.1	225
66	National Institute of Allergy and Infectious Diseases bioinformatics resource centers: new assets for pathogen informatics. <i>Infection and Immunity</i> , <b>2007</b> , 75, 3212-9	3.7	45
65	Draft genome sequence of the sexually transmitted pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , <b>2007</b> , 315, 207-12	33.3	622
64	Draft genome of the filarial nematode parasite <i>Brugia malayi</i> . <i>Science</i> , <b>2007</b> , 317, 1756-60	33.3	513
63	Comparative genomics of emerging human ehrlichiosis agents. <i>PLoS Genetics</i> , <b>2006</b> , 2, e21	6	363

62	Analysis of the transcriptome of the protozoan <i>Theileria parva</i> using MPSS reveals that the majority of genes are transcriptionally active in the schizont stage. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 5503-11	20.1	45
61	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> , <b>2005</b> , 102, 13950-5	11.5	1585
60	The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , <b>2005</b> , 309, 409-15	33.3	1085
59	Comparative genomics of trypanosomatid parasitic protozoa. <i>Science</i> , <b>2005</b> , 309, 404-9	33.3	614
58	The genome of the African trypanosome <i>Trypanosoma brucei</i> . <i>Science</i> , <b>2005</b> , 309, 416-22	33.3	1323
57	Genome Properties: a system for the investigation of prokaryotic genetic content for microbiology, genome annotation and comparative genomics. <i>Bioinformatics</i> , <b>2005</b> , 21, 293-306	7.2	68
56	Complete reannotation of the <i>Arabidopsis</i> genome: methods, tools, protocols and the final release. <i>BMC Biology</i> , <b>2005</b> , 3, 7	7.3	118
55	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . <i>Nature</i> , <b>2005</b> , 438, 1151-6	50.4	1114
54	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , <b>2005</b> , 15, 1284-91	9.7	66
53	Whole-genome sequence analysis of <i>Pseudomonas syringae</i> pv. phaseolicola 1448A reveals divergence among pathovars in genes involved in virulence and transposition. <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 6488-98	3.5	270
52	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , <b>2004</b> , 134, 183-91	1.9	83
51	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> , <b>2004</b> , 32, 2386-95	20.1	404
50	Environmental genome shotgun sequencing of the Sargasso Sea. <i>Science</i> , <b>2004</b> , 304, 66-74	33.3	3231
49	Structural flexibility in the <i>Burkholderia mallei</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 14246-51	11.5	315
48	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , <b>2003</b> , 423, 81-6	50.4	692
47	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> , <b>2003</b> , 100, 10181-6	11.5	695
46	The TIGRFAMs database of protein families. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 371-3	20.1	602
45	The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 4856-63	20.1	48

44	Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 5220-33	3.5	194
43	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 5654-66	20.1	939
42	Sequence of Plasmodium falciparum chromosomes 2, 10, 11 and 14. <i>Nature</i> , <b>2002</b> , 419, 531-4	50.4	146
41	Genome sequence of the human malaria parasite Plasmodium falciparum. <i>Nature</i> , <b>2002</b> , 419, 498-511	50.4	3336
40	Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis. <i>Nature Biotechnology</i> , <b>2002</b> , 20, 1118-23	44.5	680
39	The Brucella suis 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> , <b>2002</b> , 99, 13148-53	11.5	372
38	The genome of M. acetivorans reveals extensive metabolic and physiological diversity. <i>Genome Research</i> , <b>2002</b> , 12, 532-42	9.7	487
37	The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 9509-14	11.5	321
36	Full-length messenger RNA sequences greatly improve genome annotation. <i>Genome Biology</i> , <b>2002</b> , 3, RESEARCH0029	18.3	127
35	Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , <b>2001</b> , 4, 105-10	9.9	62
34	Prediction of operons in microbial genomes. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 1216-21	20.1	211
33	The Comprehensive Microbial Resource. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 123-5	20.1	344
32	TIGRFAMs: a protein family resource for the functional identification of proteins. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 41-3	20.1	295
31	Complete genome sequence of a virulent isolate of Streptococcus pneumoniae. <i>Science</i> , <b>2001</b> , 293, 498-506	39.6	1112
30	Microbial genes in the human genome: lateral transfer or gene loss?. <i>Science</i> , <b>2001</b> , 292, 1903-6	33.3	232
29	Comparison of Sensory Profile scores of young children with and without autism spectrum disorders. <i>American Journal of Occupational Therapy</i> , <b>2001</b> , 55, 416-23	0.4	174
28	A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi. <i>Molecular Microbiology</i> , <b>2000</b> , 35, 490-516	4.1	625
27	DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae. <i>Nature</i> , <b>2000</b> , 406, 477-83	30.4	1495

26	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>2000</b> , 408, 816-20	50.4	183
25	Prediction of transcription terminators in bacterial genomes. <i>Journal of Molecular Biology</i> , <b>2000</b> , 301, 27-33	6.5	207
24	Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58. <i>Science</i> , <b>2000</b> , 287, 1809-15	33.3	986
23	Evidence for symmetric chromosomal inversions around the replication origin in bacteria. <i>Genome Biology</i> , <b>2000</b> , 1, RESEARCH0011	18.3	234
22	Children with burn injuries: purposeful activity versus rote exercise. <i>American Journal of Occupational Therapy</i> , <b>2000</b> , 54, 381-90	0.4	15
21	Alignment of whole genomes. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 2369-76	20.1	589
20	Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of <i>Thermotoga maritima</i> . <i>Nature</i> , <b>1999</b> , 399, 323-9	50.4	1260
19	Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , <b>1999</b> , 402, 761-8	50.4	619
18	Whole-genome shotgun optical mapping of <i>Deinococcus radiodurans</i> . <i>Science</i> , <b>1999</b> , 285, 1558-62	33.3	166
17	Global transposon mutagenesis and a minimal <i>Mycoplasma</i> genome. <i>Science</i> , <b>1999</b> , 286, 2165-9	33.3	749
16	Short repeats and IS elements in the extremely radiation-resistant bacterium <i>Deinococcus radiodurans</i> and comparison to other bacterial species. <i>Research in Microbiology</i> , <b>1999</b> , 150, 711-24	4	20
15	Improved microbial gene identification with GLIMMER. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 4636-41	20.1	1857
14	Findings emerging from complete microbial genome sequences. <i>Current Opinion in Microbiology</i> , <b>1998</b> , 1, 562-6	7.9	21
13	Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete. <i>Science</i> , <b>1998</b> , 281, 375-88	33.3	756
12	Chromosome 2 sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Science</i> , <b>1998</b> , 282, 1126-32	33.3	350
11	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , <b>1997</b> , 390, 364-70	50.4	1257
10	Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> . <i>Nature</i> , <b>1997</b> , 390, 580-6	50.4	1729
9	The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , <b>1997</b> , 388, 539-47	50.4	3000

8	TDB: new databases for biological discovery. <i>Methods in Enzymology</i> , <b>1996</b> , 266, 27-40	1.7	37
7	Response : Methanococcus Genome. <i>Science</i> , <b>1996</b> , 274, 902-903	33.3	
6	Response : Methanococcus Genome. <i>Science</i> , <b>1996</b> , 274, 902-903	33.3	
5	TIGR Assembler: A New Tool for Assembling Large Shotgun Sequencing Projects. <i>Genome Science &amp; Technology</i> , <b>1995</b> , 1, 9-19		242
4	Reply to [Predicting the total number of human genes. <i>Nature Genetics</i> , <b>1994</b> , 8, 114-114	36.3	5
3	A quality control algorithm for DNA sequencing projects. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 3829-38	20.1	29
2	Splicing signals in Drosophila: intron size, information content, and consensus sequences. <i>Nucleic Acids Research</i> , <b>1992</b> , 20, 4255-62	20.1	371
1	Information contents and dinucleotide compositions of plant intron sequences vary with evolutionary origin. <i>Plant Molecular Biology</i> , <b>1992</b> , 19, 1057-64	4.6	38