Owen White

List of Publications by Citations

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	Genome sequence of the human malaria parasite Plasmodium falciparum. *Nature*, **2002**, 419, 498-511	50.4	3336
114	Environmental genome shotgun sequencing of the Sargasso Sea. *Science*, **2004**, 304, 66-74	33.3	3231
113	The complete genome sequence of the gastric pathogen Helicobacter pylori. *Nature*, **1997**, 388, 539-47	50.4	3000
112	Improved microbial gene identification with GLIMMER. *Nucleic Acids Research*, **1999**, 27, 4636-41	20.1	1857
111	Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. *Nature*, **1997**, 390, 580-6	50.4	1729
110	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, 13950-5	11.5	1585
109	DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae. *Nature*, **2000**, 406, 477-83	50.4	1495
108	The genome of the African trypanosome Trypanosoma brucei. *Science*, **2005**, 309, 416-22	33.3	1323
107	Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima. *Nature*, **1999**, 399, 323-9	50.4	1260
106	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus. *Nature*, **1997**, 390, 364-70	50.4	1257
105	Automated eukaryotic gene structure annotation using EVidenceModeler and the Program to Assemble Spliced Alignments. *Genome Biology*, **2008**, 9, R7	18.3	1212
104	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. *Nature*, **2005**, 438, 1151-6	50.4	1114
103	Complete genome sequence of a virulent isolate of Streptococcus pneumoniae. *Science*, **2001**, 293, 498-506	33.3	1112
102	The genome sequence of Trypanosoma cruzi, etiologic agent of Chagas disease. *Science*, **2005**, 309, 409-15	33.3	1085
101	Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. *Science*, **2000**, 287, 1809-15	33.3	986
100	The minimum information about a genome sequence (MIGS) specification. *Nature Biotechnology*, **2008**, 26, 541-7	44.5	964
99	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. *Nucleic Acids Research*, **2003**, 31, 5654-66	20.1	939

98	Genome sequence of Aedes aegypti, a major arbovirus vector. *Science*, **2007**, 316, 1718-23	33.3	867
97	The genome of the blood fluke Schistosoma mansoni. *Nature*, **2009**, 460, 352-8	50.4	822
96	Complete genome sequence of Treponema pallidum, the syphilis spirochete. *Science*, **1998**, 281, 375-88	33.3	756
95	Global transposon mutagenesis and a minimal Mycoplasma genome. *Science*, **1999**, 286, 2165-9	33.3	749
94	Metabolic reconstruction for metagenomic data and its application to the human microbiome. *PLoS Computational Biology*, **2012**, 8, e1002358	5	730
93	The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 10181-6	11.5	695
92	The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria. *Nature*, **2003**, 423, 81-6	50.4	692
91	Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis. *Nature Biotechnology*, **2002**, 20, 1118-23	44.5	680
90	Comparative genomics of the neglected human malaria parasite Plasmodium vivax. *Nature*, **2008**, 455, 757-63	50.4	633
89	A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi. *Molecular Microbiology*, **2000**, 35, 490-516	4.1	625
88	Draft genome sequence of the sexually transmitted pathogen Trichomonas vaginalis. *Science*, **2007**, 315, 207-12	33.3	622
87	Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. *Nature*, **1999**, 402, 761-8	50.4	619
86	Comparative genomics of trypanosomatid parasitic protozoa. *Science*, **2005**, 309, 404-9	33.3	614
85	The TIGRFAMs database of protein families. *Nucleic Acids Research*, **2003**, 31, 371-3	20.1	602
84	Strains, functions and dynamics in the expanded Human Microbiome Project. *Nature*, **2017**, 550, 61-66	50.4	595
83	Alignment of whole genomes. *Nucleic Acids Research*, **1999**, 27, 2369-76	20.1	589
82	Big data: The future of biocuration. *Nature*, **2008**, 455, 47-50	50.4	527
81	Draft genome of the filarial nematode parasite Brugia malayi. *Science*, **2007**, 317, 1756-60	33.3	513

80	Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. *OMICS A Journal of Integrative Biology*, **2008**, 12, 137-41	3.8	491
79	The genome of M. acetivorans reveals extensive metabolic and physiological diversity. *Genome Research*, **2002**, 12, 532-42	9.7	487
78	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. *Nature Biotechnology*, **2011**, 29, 415-20	44.5	445
77	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, 2386-95	20.1	404
76	The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 13148-53	11.5	372
75	Splicing signals in Drosophila: intron size, information content, and consensus sequences. *Nucleic Acids Research*, **1992**, 20, 4255-62	20.1	371
74	Comparative genomics of emerging human ehrlichiosis agents. *PLoS Genetics*, **2006**, 2, e21	6	363
73	Sequencing of Culex quinquefasciatus establishes a platform for mosquito comparative genomics. *Science*, **2010**, 330, 86-8	33.3	352
72	Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. *Science*, **1998**, 282, 1126-32	33.3	350
71	The Comprehensive Microbial Resource. *Nucleic Acids Research*, **2001**, 29, 123-5	20.1	344
70	The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 9509-14	11.5	321
69	Structural flexibility in the Burkholderia mallei genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 14246-51	11.5	315
68	TIGRFAMs: a protein family resource for the functional identification of proteins. *Nucleic Acids Research*, **2001**, 29, 41-3	20.1	295
67	Genome sequence of Babesia bovis and comparative analysis of apicomplexan hemoprotozoa. *PLoS Pathogens*, **2007**, 3, 1401-13	7.6	279
66	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, 6488-98	3.5	270
65	The Human Microbiome Project: a community resource for the healthy human microbiome. *PLoS Biology*, **2012**, 10, e1001377	9.7	268
64	TIGR Assembler: A New Tool for Assembling Large Shotgun Sequencing Projects. *Genome Science & Technology*, **1995**, 1, 9-19		242
63	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. *Nature Biotechnology*, **2017**, 35, 1077-1086	44.5	240

44	The comprehensive microbial resource. *Nucleic Acids Research*, **2010**, 38, D340-5	20.1	82
43	Standardized description of scientific evidence using the Evidence Ontology (ECO). *Database: the Journal of Biological Databases and Curation*, **2014**, 2014,	5	75
42	Ergatis: a web interface and scalable software system for bioinformatics workflows. *Bioinformatics*, **2010**, 26, 1488-92	7.2	73
41	Genome Properties: a system for the investigation of prokaryotic genetic content for microbiology, genome annotation and comparative genomics. *Bioinformatics*, **2005**, 21, 293-306	7.2	68
40	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. *Genome Research*, **2005**, 15, 1284-91	9.7	66
39	Sequence and analysis of the Arabidopsis genome. *Current Opinion in Plant Biology*, **2001**, 4, 105-10	9.9	62
38	Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. *PLoS ONE*, **2011**, 6, e26624	3.7	58
37	Advancing the microbiome research community. *Cell*, **2014**, 159, 227-30	56.2	50
36	The sequence and analysis of Trypanosoma brucei chromosome II. *Nucleic Acids Research*, **2003**, 31, 4856-63	20.1	48
35	MetaRef: a pan-genomic database for comparative and community microbial genomics. *Nucleic Acids Research*, **2014**, 42, D617-24	20.1	46
34	Solving the Problem: Genome Annotation Standards before the Data Deluge. *Standards in Genomic Sciences*, **2011**, 5, 168-93		46
33	National Institute of Allergy and Infectious Diseases bioinformatics resource centers: new assets for pathogen informatics. *Infection and Immunity*, **2007**, 75, 3212-9	3.7	45
32	Analysis of the transcriptome of the protozoan Theileria parva using MPSS reveals that the majority of genes are transcriptionally active in the schizont stage. *Nucleic Acids Research*, **2005**, 33, 5503-11	20.1	45
31	CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. *Microbiome*, **2013**, 1, 6	16.6	40
30	Information contents and dinucleotide compositions of plant intron sequences vary with evolutionary origin. *Plant Molecular Biology*, **1992**, 19, 1057-64	4.6	38
29	TDB: new databases for biological discovery. *Methods in Enzymology*, **1996**, 266, 27-40	1.7	37
28	Toward a standards-compliant genomic and metagenomic publication record. *OMICS A Journal of Integrative Biology*, **2008**, 12, 157-60	3.8	31
27	A quality control algorithm for DNA sequencing projects. *Nucleic Acids Research*, **1993**, 21, 3829-38	20.1	29

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26	Standardized metadata for human pathogen/vector genomic sequences. *PLoS ONE*, **2014**, 9, e99979	3.7	25
25	Genomic Standards Consortium Projects. *Standards in Genomic Sciences*, **2014**, 9, 599-601		23
24	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. *Bioinformatics*, **2014**, 30, 3125-7	7.2	22
23	Genomic standards consortium projects. *Standards in Genomic Sciences*, **2014**, 9, 599-601		21
22	Findings emerging from complete microbial genome sequences. *Current Opinion in Microbiology*, **1998**, 1, 562-6	7.9	21
21	Short repeats and IS elements in the extremely radiation-resistant bacterium Deinococcus radiodurans and comparison to other bacterial species. *Research in Microbiology*, **1999**, 150, 711-24	4	20
20	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. *Frontiers in Microbiology*, **2015**, 6, 569	5.7	19
19	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. *Microbiome*, **2014**, 2,	16.6	18
18	Meeting Report: BioSharing at ISMB 2010. *Standards in Genomic Sciences*, **2010**, 3, 254-8		18
17	Pathema: a clade-specific bioinformatics resource center for pathogen research. *Nucleic Acids Research*, **2010**, 38, D408-14	20.1	17
16	gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration. *Nature Methods*, **2021**, 18, 843-844	21.6	16
15	Children with burn injuries: purposeful activity versus rote exercise. *American Journal of Occupational Therapy*, **2000**, 54, 381-90	0.4	15
14	Toward a standard in structural genome annotation for prokaryotes. *Standards in Genomic Sciences*, **2015**, 10, 45		12
13	CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. *BMC Genomics*, **2017**, 18, 332	4.5	10
12	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. *Standards in Genomic Sciences*, **2010**, 3, 225-31		7
11	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. *Standards in Genomic Sciences*, **2012**, 6, 438-47		6
10	Reply to Predicting the total number of human genes. *Nature Genetics*, **1994**, 8, 114-114	36.3	5
9	HMPDACC: a Human Microbiome Project Multi-omic data resource. *Nucleic Acids Research*, **2021**, 49, D734-D742	20.1	5

8	Meeting Report: Towards a Critical Assessment of Functional Annotation Experiment (CAFAE) for bacterial genome annotation. *Standards in Genomic Sciences*, **2010**, 3, 240-2	3
7	Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010. *Standards in Genomic Sciences*, **2010**, 3, 232-4	3
6	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. *Standards in Genomic Sciences*, **2010**, 2, 357-60	2
5	Conceptualizing a Genomics Software Institute (GSI). *Standards in Genomic Sciences*, **2012**, 6, 136-44	1
4	NeMO analytics-AD: The neuroscience multi-omic visualization and analysis platform, now extended to support Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, e046097	1.2
3	Response : Methanococcus Genome. *Science*, **1996**, 274, 902-903	33.3
2	Response : Methanococcus Genome. *Science*, **1996**, 274, 902-903	33.3
1	NeMO-AD, a new neuroscience multi-omic visualization and analysis platform for Alzheimer's disease research.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e055686	1.2