List of Publications by Year in descending order

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DAVAN FIELD

#	Article	IF	CITATIONS
1	The effect of anthropogenic arsenic contamination on the earthworm microbiome. Environmental Microbiology, 2015, 17, 1884-1896.	3.8	118
2	Desktop as a Service Supporting Environmental 'omics. , 2015, , .		0
3	Satellite remote sensing data can be used to model marine microbial metabolite turnover. ISME Journal, 2015, 9, 166-179.	9.8	17
4	Catchment-scale biogeography of riverine bacterioplankton. ISME Journal, 2015, 9, 516-526.	9.8	202
5	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
6	EBI metagenomics—a new resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2014, 42, D600-D606.	14.5	127
7	The hospital microbiome project: meeting report for the UK science and innovation network UK-USA workshop â€`beating the superbugs: hospital microbiome studies for tackling antimicrobial resistance', October 14th 2013. Standards in Genomic Sciences, 2014, 9, .	1.5	6
8	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	26
9	Report of the 14th Genomic Standards Consortium Meeting, Oxford, UK, September 17-21, 2012 Standards in Genomic Sciences, 2014, 9, 1236-1250.	1.5	1
10	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	29
11	A decadal view of biodiversity informatics: challenges and priorities. BMC Ecology, 2013, 13, 16.	3.0	110
12	Genomics in marine monitoring: New opportunities for assessing marine health status. Marine Pollution Bulletin, 2013, 74, 19-31.	5.0	196
13	Evidence for a persistent microbial seed bank throughout the global ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4651-4655.	7.1	200
14	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	21.4	362
15	Investigation-Study-Assay, a toolkit for standardizing data capture and sharing. , 2012, , 173-188.		1
16	The Metadata Coverage Index (MCI): A standardized metric for quantifying database metadata richness. Standards in Genomic Sciences, 2012, 6, 444-453.	1.5	8
17	Conceptualizing a Genomics Software Institute (GSI). Standards in Genomic Sciences, 2012, 6, 136-144.	1.5	1
18	Report of the 13th Genomic Standards Consortium Meeting, Shenzhen, China, March 4–7, 2012 Standards in Genomic Sciences, 2012, 6, 276-286.	1.5	3

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19	RCN4CSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta)Genomics, March 2011. Standards in Genomic Sciences, 2012, 7, 159-165.	1.5	5
20	Cloud BioLinux: pre-configured and on-demand bioinformatics computing for the genomics community. BMC Bioinformatics, 2012, 13, 42.	2.6	136
21	Bio-Linux as a tool for bioinformatics training. , 2012, , .		1
22	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
23	A call for an international network of genomic observatories (GOs). GigaScience, 2012, 1, 5.	6.4	25
24	A genomic network to monitor Earth. Nature, 2012, 481, 145-145.	27.8	24
25	Defining seasonal marine microbial community dynamics. ISME Journal, 2012, 6, 298-308.	9.8	928
26	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	17.5	250
27	Predicting bacterial community assemblages using an artificial neural network approach. Nature Methods, 2012, 9, 621-625.	19.0	159
28	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. Methods in Molecular Biology, 2011, 719, 31-69.	0.9	73
29	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
30	A Call for Papers for the second special issue of SIGS from the Genomic Standards Consortium. Standards in Genomic Sciences, 2011, 4, 111-112.	1.5	0
31	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. Standards in Genomic Sciences, 2011, 5, 243-247.	1.5	18
32	Enriching public descriptions of marine phages using the Genomic Standards Consortium MIGS standard. Standards in Genomic Sciences, 2011, 4, 271-285.	1.5	4
33	Data shopping in an open marketplace: Introducing the Ontogrator web application for marking up data using ontologies and browsing using facets. Standards in Genomic Sciences, 2011, 4, 286-292.	1.5	4
34	The genomic standards consortium: bringing standards to life for microbial ecology. ISME Journal, 2011, 5, 1565-1567.	9.8	59
35	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. Microbial Informatics and Experimentation, 2011, 1, 4.	7.6	93
36	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30

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37	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
38	The Genomic Standards Consortium. PLoS Biology, 2011, 9, e1001088.	5.6	180
39	Metagenomes and metatranscriptomes from the L4 long-term coastal monitoring station in the Western English Channel. Standards in Genomic Sciences, 2010, 3, 183-193.	1.5	28
40	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. Standards in Genomic Sciences, 2010, 3, 243-248.	1.5	228
41	The first special issue of Standards in Genomic Sciences from the Genomic Standards Consortium. Standards in Genomic Sciences, 2010, 3, 214-215.	1.5	0
42	The Earth Microbiome Project: Meeting report of the "1st EMP meeting on sample selection and acquisition―at Argonne National Laboratory October 6th 2010 Standards in Genomic Sciences, 2010, 3, 249-253.	1.5	176
43	Meeting Report: BioSharing at ISMB 2010. Standards in Genomic Sciences, 2010, 3, 254-258.	1.5	19
44	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. Standards in Genomic Sciences, 2010, 3, 235-239.	1.5	7
45	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 9. Standards in Genomic Sciences, 2010, 3, 216-224.	1.5	3
46	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. Standards in Genomic Sciences, 2010, 3, 225-231.	1.5	8
47	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations― (MIBBI) workshop. Standards in Genomic Sciences, 2010, 3, 259-266.	1.5	32
48	Meeting Report: "Metagenomics, Metadata and Meta-analysis―(M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, 2010, 2, 357-360.	1.5	2
49	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 8. Standards in Genomic Sciences, 2010, 3, 93-96.	1.5	1
50	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. ISME Journal, 2010, 4, 1236-1242.	9.8	43
51	Day-length is central to maintaining consistent seasonal diversity in marine bacterioplankton. Nature Precedings, 2010, , .	0.1	8
52	ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. Bioinformatics, 2010, 26, 2354-2356.	4.1	247
53	The Taxonomic and Functional Diversity of Microbes at a Temperate Coastal Site: A â€~Multi-Omic' Study of Seasonal and Diel Temporal Variation. PLoS ONE, 2010, 5, e15545.	2.5	219
54	The seasonal structure of microbial communities in the Western English Channel. Environmental Microbiology, 2009, 11, 3132-3139.	3.8	384

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55	Potential for phosphonoacetate utilization by marine bacteria in temperate coastal waters. Environmental Microbiology, 2009, 11, 111-125.	3.8	55
56	'Omics Data Sharing. Science, 2009, 326, 234-236.	12.6	136
57	Extending Standards for Genomics and Metagenomics Data: A Research Coordination Network for the Genomic Standards Consortium (RCN4GSC). Standards in Genomic Sciences, 2009, 1, 85-90.	1.5	13
58	Meeting Report: Metagenomics, Metadata and Meta-analysis; (M3) Special Interest Group at ISMB 2009. Standards in Genomic Sciences, 2009, 1, 278-282.	1.5	4
59	Meeting Report from the Genomic Standards Consortium (GSC) Workshops 6 and 7. Standards in Genomic Sciences, 2009, 1, 68-71.	1.5	13
60	Standards for Functional Genomics. , 2009, , 293-329.		0
61	Towards interoperable reporting standards for omics data: hopes and hurdles. Summit on Translational Bioinformatics, 2009, 2009, 112-5.	0.7	1
62	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
63	Working together to put molecules on the map. Nature, 2008, 453, 978-978.	27.8	12
64	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	17.5	1,069
65	Habitat-Lite: A GSC Case Study Based on Free Text Terms for Environmental Metadata. OMICS A Journal of Integrative Biology, 2008, 12, 129-136.	2.0	39
66	Toward an Online Repository of Standard Operating Procedures (SOPs) for (Meta)genomic Annotation. OMICS A Journal of Integrative Biology, 2008, 12, 137-141.	2.0	598
67	Defining Linkages between the GSC and NSF's LTER Program: How the Ecological Metadata Language (EML) Relates to GCDML and Other Outcomes. OMICS A Journal of Integrative Biology, 2008, 12, 151-156.	2.0	6
68	A Standard MIGS/MIMS Compliant XML Schema: Toward the Development of the Genomic Contextual Data Markup Language (GCDML). OMICS A Journal of Integrative Biology, 2008, 12, 115-121.	2.0	59
69	Laying the Foundation for a Genomic Rosetta Stone: Creating Information Hubs through the Use of Consensus Identifiers. OMICS A Journal of Integrative Biology, 2008, 12, 123-127.	2.0	12
70	Toward a Standards-Compliant Genomic and Metagenomic Publication Record. OMICS A Journal of Integrative Biology, 2008, 12, 157-160.	2.0	33
71	Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. PLoS ONE, 2008, 3, e3042.	2.5	321
72	eGenomics: Cataloguing Our Complete Genome Collection III. Comparative and Functional Genomics, 2007, 1-7.	2.0	4

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73	Handlebar: a flexible, web-based inventory manager for handling barcoded samples. BioTechniques, 2007, 42, 300-302.	1.8	8
74	The Positive Role of the Ecological Community in the Genomic Revolution. Microbial Ecology, 2007, 53, 507-511.	2.8	5
75	Standard reporting requirements for biological samples in metabolomics experiments: environmental context. Metabolomics, 2007, 3, 203-210.	3.0	93
76	Large-Scale Comparative Genomic Ranking of Taxonomically Restricted Genes (TRGs) in Bacterial and Archaeal Genomes. PLoS ONE, 2007, 2, e324.	2.5	28
77	Concept of Sample in OMICS Technology. OMICS A Journal of Integrative Biology, 2006, 10, 127-137.	2.0	44
78	Standard Annotation of Environmental OMICS Data: Application to the Transcriptomics Domain. OMICS A Journal of Integrative Biology, 2006, 10, 172-178.	2.0	21
79	A Special Issue on Data Standards. OMICS A Journal of Integrative Biology, 2006, 10, 84-93.	2.0	46
80	Open software for biologists: from famine to feast. Nature Biotechnology, 2006, 24, 801-803.	17.5	185
81	Development of FuGO: An Ontology for Functional Genomics Investigations. OMICS A Journal of Integrative Biology, 2006, 10, 199-204.	2.0	56
82	Ecological perspectives on the sequenced genome collection. Ecology Letters, 2005, 8, 1334-1345.	6.4	28
83	eGenomics: Genomes and the Environment. Comparative and Functional Genomics, 2005, 6, 357-362.	2.0	7
84	Bioinformatics and Data Management Support for Environmental Genomics. PLoS Biology, 2005, 3, e297.	5.6	18
85	Cataloguing our current genome collection. Microbiology (United Kingdom), 2005, 151, 1016-1019.	1.8	17
86	Notes on designing a partial genomic database: The PfSBW25 Encyclopaedia, a sequence database for Pseudomonas fluorescens SBW25. Microbiology (United Kingdom), 2001, 147, 247-249.	1.8	8
87	The simple sequence contingency loci of Haemophilus influenzae and Neisseria meningitidis. Journal of Clinical Investigation, 2001, 107, 657-666.	8.2	137
88	The length of a tetranucleotide repeat tract in Haemophilus influenzae determines the phase variation rate of a gene with homology to type III DNA methyltransferases. Molecular Microbiology, 2000, 35, 211-222.	2.5	164
89	The generation of diversity by Haemophilus influenzae: Response. Trends in Microbiology, 2000, 8, 435-436.	7.7	6