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List of articles citing

**Habitat-Lite: a GSC case study based on free text terms for environmental metadata**

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#	Paper	IF	Citations
35	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , <b>2008</b> , 11, 442-6	7.9	337
34	Discovering functional novelty in metagenomes: examples from light-mediated processes. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 32-41	3.5	50
33	Issues in learning an ontology from text. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 5, S1	3.6	11
32	COMPARATIVE ANALYSIS OF AEROBIC AND ANAEROBIC PROKARYOTES TO IDENTIFY CORRELATION BETWEEN OXYGEN REQUIREMENT AND GENE-GENE FUNCTIONAL ASSOCIATION PATTERNS. <b>2009</b> ,		1
31	Extending Standards for Genomics and Metagenomics Data: A Research Coordination Network for the Genomic Standards Consortium (RCN4GSC). <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 87-90		7
30	Meeting report for SIGS1: First Conference of the Standards in Genomic Sciences eJournal. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 72-6		0
29	Meeting Report from the Genomic Standards Consortium (GSC) Workshops 6 and 7. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 68-71		11
28	The Earth Microbiome Project: Meeting report of the "1 EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 249-53		146
27	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 235-9		6
26	Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 225-31		7
25	EnvMine: a text-mining system for the automatic extraction of contextual information. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 294	3.6	14
24	Megx.net: integrated database resource for marine ecological genomics. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D391-5	20.1	33
23	The Genomes On Line Database (GOLD) in 2009: status of genomic and metagenomic projects and their associated metadata. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D346-54	20.1	331
22	Association analysis of the general environmental conditions and prokaryotesSgene distributions in various functional groups. <i>Genomics</i> , <b>2010</b> , 96, 27-38	4.3	9
21	The Enduring Legacy of Small Subunit rRNA in Microbiology. <b>2011</b> , 123-128		1
20	Competitive and cooperative metabolic interactions in bacterial communities. <i>Nature Communications</i> , <b>2011</b> , 2, 589	17.4	308
19	Automatic extraction of microorganisms and their habitats from free text using text mining workflows. <i>Journal of Integrative Bioinformatics</i> , <b>2011</b> , 8, 176-186	3.8	5

18	Enriching public descriptions of marine phages using the Genomic Standards Consortium MIGS standard. <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 271-85		2
17	Bacterial community comparisons by taxonomy-supervised analysis independent of sequence alignment and clustering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 14637-42	11.5	66
16	Report of the 13(th) Genomic Standards Consortium Meeting, Shenzhen, China, March 4-7, 2012. <i>Standards in Genomic Sciences</i> , <b>2012</b> , 6, 276-86		1
15	Current opportunities and challenges in microbial metagenome analysis--a bioinformatic perspective. <i>Briefings in Bioinformatics</i> , <b>2012</b> , 13, 728-42	13.4	143
14	Substrate-controlled succession of marine bacterioplankton populations induced by a phytoplankton bloom. <i>Science</i> , <b>2012</b> , 336, 608-11	33.3	846
13	BioNLP Shared Task--The Bacteria Track. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 11, S3	3.6	18
12	Alignment-free genome tree inference by learning group-specific distance metrics. <i>Genome Biology and Evolution</i> , <b>2013</b> , 5, 1470-84	3.9	13
11	Common and pathogen-specific virulence factors are different in function and structure. <i>Virulence</i> , <b>2013</b> , 4, 473-82	4.7	28
10	The environment ontology: contextualising biological and biomedical entities. <i>Journal of Biomedical Semantics</i> , <b>2013</b> , 4, 43	2.2	165
9	Does habitat variability really promote metabolic network modularity?. <i>PLoS ONE</i> , <b>2013</b> , 8, e61348	3.7	13
8	Advancing the microbiome research community. <i>Cell</i> , <b>2014</b> , 159, 227-30	56.2	50
7	Climatic seasonality may affect ecological network structure: food webs and mutualistic networks. <i>BioSystems</i> , <b>2014</b> , 121, 29-37	1.9	17
6	ENVIRONMENTS and EOL: identification of Environment Ontology terms in text and the annotation of the Encyclopedia of Life. <i>Bioinformatics</i> , <b>2015</b> , 31, 1872-4	7.2	14
5	Accelerating the Digitization of Biodiversity Research Specimens through Online Public Participation. <i>BioScience</i> , <b>2015</b> , 65, 383-396	5.7	45
4	MetaHCR: a web-enabled metagenome data management system for hydrocarbon resources. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2018</b> , 2018, 1-10	5	0
3	Habitat-associated phylogenetic community patterns of microbial ammonia oxidizers. <i>PLoS ONE</i> , <b>2012</b> , 7, e47330	3.7	43
2	Encyclopedia of Metagenomics. <b>2013</b> , 1-6		
1	Towards Structuring Unstructured GenBank Metadata for Enhancing Comparative Biological Studies. <i>AMIA Summits on Translational Science Proceedings</i> , <b>2011</b> , 2011, 6-10	1.1	4

