

Victor Kunin

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

10,692
citations

201674

27
h-index

395702

33
g-index

34
all docs

34
docs citations

34
times ranked

13807
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of OTU Clustering and PCR Artifacts on Microbial Diversity Estimates. <i>Microbial Ecology</i> , 2013, 65, 709-719.	2.8	47
2	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	27.8	2,475
3	Experimental factors affecting PCR-based estimates of microbial species richness and evenness. <i>ISME Journal</i> , 2010, 4, 642-647.	9.8	523
4	Wrinkles in the rare biosphere: pyrosequencing errors can lead to artificial inflation of diversity estimates. <i>Environmental Microbiology</i> , 2010, 12, 118-123.	3.8	1,138
5	Metatranscriptomic array analysis of <i>Candidatus</i> <i>Accumulibacter phosphatis</i> ™-enriched enhanced biological phosphorus removal sludge. <i>Environmental Microbiology</i> , 2010, 12, 1205-1217.	3.8	73
6	Genome Analysis of the Anaerobic Thermohalophilic Bacterium <i>Halothermothrix orenii</i> . <i>PLoS ONE</i> , 2009, 4, e4192.	2.5	58
7	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	27.8	924
8	CRISPR – a widespread system that provides acquired resistance against phages in bacteria and archaea. <i>Nature Reviews Microbiology</i> , 2008, 6, 181-186.	28.6	789
9	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008, 4, 198.	7.2	139
10	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	6.6	361
11	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	5.5	135
12	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. <i>Genome Biology</i> , 2007, 8, R61.	9.6	382
13	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
14	Denoising inferred functional association networks obtained by gene fusion analysis. <i>BMC Genomics</i> , 2007, 8, 460.	2.8	16
15	A minimal estimate for the gene content of the last universal common ancestor – exobiology from a terrestrial perspective. <i>Research in Microbiology</i> , 2006, 157, 57-68.	2.1	130
16	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	17.5	634
17	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006, 22, e359-e367.	4.1	81
18	Genome coverage, literally speaking. <i>EMBO Reports</i> , 2005, 6, 397-399.	4.5	34

#	ARTICLE	IF	CITATIONS
19	Clustering the annotation space of proteins. BMC Bioinformatics, 2005, 6, 24.	2.6	16
20	Measuring genome conservation across taxa: divided strains and united kingdoms. Nucleic Acids Research, 2005, 33, 616-621.	14.5	69
21	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Research, 2005, 33, 6083-6089.	14.5	570
22	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	4.1	22
23	The properties of protein family space depend on experimental design. Bioinformatics, 2005, 21, 2618-2622.	4.1	10
24	MagicMatch--cross-referencing sequence identifiers across databases. Bioinformatics, 2005, 21, 3429-3430.	4.1	21
25	The net of life: Reconstructing the microbial phylogenetic network. Genome Research, 2005, 15, 954-959.	5.5	211
26	Functional Evolution of the Yeast Protein Interaction Network. Molecular Biology and Evolution, 2004, 21, 1171-1176.	8.9	66
27	Classification schemes for protein structure and function. Nature Reviews Genetics, 2003, 4, 508-519.	16.3	101
28	Beyond 100 genomes. Genome Biology, 2003, 4, 402.	9.6	23
29	Myriads of protein families, and still counting. Genome Biology, 2003, 4, 401.	9.6	55
30	GeneTRACE-reconstruction of gene content of ancestral species. Bioinformatics, 2003, 19, 1412-1416.	4.1	46
31	COmplete GENome Tracking (COGENT): a flexible data environment for computational genomics. Bioinformatics, 2003, 19, 1451-1452.	4.1	40
32	Protein families and TRIBES in genome sequence space. Nucleic Acids Research, 2003, 31, 4632-4638.	14.5	113
33	The Balance of Driving Forces During Genome Evolution in Prokaryotes. Genome Research, 2003, 13, 1589-1594.	5.5	173
34	A system of two polymerases--a model for the origin of life. , 2000, 30, 459-466.		36