

# 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	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	27.8	2,475
2	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
3	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
4	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009, 462, 1056-1060.	27.8	924
5	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
6	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	17.5	634
7	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. <i>Nucleic Acids Research</i> , 2005, 33, 6083-6089.	14.5	570
8	Experimental factors affecting PCR-based estimates of microbial species richness and evenness. <i>ISME Journal</i> , 2010, 4, 642-647.	9.8	523
9	Evolutionary conservation of sequence and secondary structures in CRISPR repeats. <i>Genome Biology</i> , 2007, 8, R61.	9.6	382
10	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	6.6	361
11	The net of life: Reconstructing the microbial phylogenetic network. <i>Genome Research</i> , 2005, 15, 954-959.	5.5	211
12	The Balance of Driving Forces During Genome Evolution in Prokaryotes. <i>Genome Research</i> , 2003, 13, 1589-1594.	5.5	173
13	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
14	A bacterial metapopulation adapts locally to phage predation despite global dispersal. <i>Genome Research</i> , 2008, 18, 293-297.	5.5	135
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	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	14.5	113
17	Classification schemes for protein structure and function. <i>Nature Reviews Genetics</i> , 2003, 4, 508-519.	16.3	101
18	An experimental metagenome data management and analysis system. <i>Bioinformatics</i> , 2006, 22, e359-e367.	4.1	81

#	ARTICLE	IF	CITATIONS
19	Metatranscriptomic array analysis of <i>Candidatus</i> Accumulibacter phosphatis <sup>TM</sup> -enriched enhanced biological phosphorus removal sludge. Environmental Microbiology, 2010, 12, 1205-1217.	3.8	73
20	Measuring genome conservation across taxa: divided strains and united kingdoms. Nucleic Acids Research, 2005, 33, 616-621.	14.5	69
21	Functional Evolution of the Yeast Protein Interaction Network. Molecular Biology and Evolution, 2004, 21, 1171-1176.	8.9	66
22	Genome Analysis of the Anaerobic Thermohalophilic Bacterium Halothermothrix orenii. PLoS ONE, 2009, 4, e4192.	2.5	58
23	Myriads of protein families, and still counting. Genome Biology, 2003, 4, 401.	9.6	55
24	Effects of OTU Clustering and PCR Artifacts on Microbial Diversity Estimates. Microbial Ecology, 2013, 65, 709-719.	2.8	47
25	GeneTRACE-reconstruction of gene content of ancestral species. Bioinformatics, 2003, 19, 1412-1416.	4.1	46
26	Complete GENome Tracking (COGENT): a flexible data environment for computational genomics. Bioinformatics, 2003, 19, 1451-1452.	4.1	40
27	A system of two polymerases--a model for the origin of life. , 2000, 30, 459-466.		36
28	Genome coverage, literally speaking. EMBO Reports, 2005, 6, 397-399.	4.5	34
29	Beyond 100 genomes. Genome Biology, 2003, 4, 402.	9.6	23
30	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	4.1	22
31	MagicMatch--cross-referencing sequence identifiers across databases. Bioinformatics, 2005, 21, 3429-3430.	4.1	21
32	Clustering the annotation space of proteins. BMC Bioinformatics, 2005, 6, 24.	2.6	16
33	Denoising inferred functional association networks obtained by gene fusion analysis. BMC Genomics, 2007, 8, 460.	2.8	16
34	The properties of protein family space depend on experimental design. Bioinformatics, 2005, 21, 2618-2622.	4.1	10