

Gary J Olsen

List of Publications by Year in descending order

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56
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30,063
citations

109311

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161844

54
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58
all docs

58
docs citations

58
times ranked

26007
citing authors

#	ARTICLE	IF	CITATIONS
1	The RAST Server: Rapid Annotations using Subsystems Technology. BMC Genomics, 2008, 9, 75.	2.8	9,977
2	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Research, 2014, 42, D206-D214.	14.5	3,832
3	RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. Scientific Reports, 2015, 5, 8365.	3.3	2,080
4	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus. Nature, 1997, 390, 364-370.	27.8	1,460
5	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. Nucleic Acids Research, 2017, 45, D535-D542.	14.5	1,445
6	Critical Evaluation of Two Primers Commonly Used for Amplification of Bacterial 16S rRNA Genes. Applied and Environmental Microbiology, 2008, 74, 2461-2470.	3.1	1,318
7	The Ribosomal Database project. Nucleic Acids Research, 1994, 22, 3485-3487.	14.5	1,250
8	The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Nature, 1998, 392, 353-358.	27.8	1,120
9	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	17.5	955
10	Genomic Minimalism in the Early Diverging Intestinal Parasite <i>Giardia lamblia</i> . Science, 2007, 317, 1921-1926.	12.6	725
11	The Analysis of Natural Microbial Populations by Ribosomal RNA Sequences. Advances in Microbial Ecology, 1986, , 1-55.	0.1	659
12	Ribosomal RNA: a key to phylogeny.. FASEB Journal, 1993, 7, 113-123.	0.5	621
13	The ribosomal database project. Nucleic Acids Research, 1993, 21, 3021-3023.	14.5	598
14	Aminoacyl-tRNA Synthetases, the Genetic Code, and the Evolutionary Process. Microbiology and Molecular Biology Reviews, 2000, 64, 202-236.	6.6	597
15	fastDNAmI: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. Bioinformatics, 1994, 10, 41-48.	4.1	582
16	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612.	14.5	552
17	Archaeal Genomics: An Overview. Cell, 1997, 89, 991-994.	28.9	235
18	Nucleotide sequence of the Dictyostelium discoideum small-subunit ribosomal ribonucleic acid inferred from the gene sequence: evolutionary implications. Biochemistry, 1983, 22, 5858-5868.	2.5	197

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19	SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. PLoS ONE, 2012, 7, e48053.	2.5	169
20	Heterogeneity of Vaginal Microbial Communities within Individuals. Journal of Clinical Microbiology, 2009, 47, 1181-1189.	3.9	156
21	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	3.5	153
22	[53] Phylogenetic analysis using ribosomal RNA. Methods in Enzymology, 1988, 164, 793-812.	1.0	152
23	A reconstruction of the metabolism of Methanococcus jannaschii from sequence data. Gene, 1997, 197, GC11-GC26.	2.2	106
24	PATRIC as a unique resource for studying antimicrobial resistance. Briefings in Bioinformatics, 2019, 20, 1094-1102.	6.5	93
25	Evolution of Eukaryotic Transcription: Insights From the Genome of Giardia lamblia. Genome Research, 2004, 14, 1537-1547.	5.5	87
26	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. Nucleic Acids Research, 2007, 35, D347-D353.	14.5	87
27	The essential genome of the crenarchaeal model Sulfolobus islandicus. Nature Communications, 2018, 9, 4908.	12.8	83
28	Lessons from an Archaeal genome: what are we learning from Methanococcus jannaschii?. Trends in Genetics, 1996, 12, 377-379.	6.7	60
29	Shotgun Proteomics of Methanococcus jannaschii and Insights into Methanogenesis. Journal of Proteome Research, 2004, 3, 538-548.	3.7	60
30	Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry?. Trends in Genetics, 1999, 15, 298-299.	6.7	57
31	Nucleotide sequence of Dictyostelium discoideum 5.8S ribosomal RNA: evolutionary and secondary structural implications. Biochemistry, 1982, 21, 2335-2343.	2.5	44
32	Secondary structure of the Dictyostelium discoideum small subunit ribosomal RNA. Nucleic Acids Research, 1983, 11, 8037-8049.	14.5	41
33	Archaea, Archaea, every where. Nature, 1994, 371, 657-658.	27.8	41
34	Modal Codon Usage: Assessing the Typical Codon Usage of a Genome. Molecular Biology and Evolution, 2010, 27, 800-810.	8.9	41
35	Enzymic and chemical structure mapping of mouse 28S ribosomal RNA-contacts in 5.8S ribosomal RNA. Biochemistry, 1982, 21, 2320-2329.	2.5	40
36	Genomes of the class Erysipelotrichia clarify the firmicute origin of the class Mollicutes. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2727-2741.	1.7	40

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37	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. PLoS ONE, 2015, 10, e0126883.	2.5	39
38	Similarity of genes horizontally acquired by <i>Escherichia coli</i> and <i>Salmonella enterica</i> is evidence of a supraspecies pangenome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20154-20159.	7.1	38
39	Protein-coding gene promoters in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . Nucleic Acids Research, 2009, 37, 3588-3601.	14.5	28
40	Differences between the normal vaginal bacterial community of baboons and that of humans. American Journal of Primatology, 2011, 73, 119-126.	1.7	27
41	A brief note concerning archaeobacterial phylogeny. Canadian Journal of Microbiology, 1989, 35, 119-123.	1.7	24
42	The <i>repABC</i> Plasmids with Quorum-Regulated Transfer Systems in Members of the Rhizobiales Divide into Two Structurally and Separately Evolving Groups. Genome Biology and Evolution, 2015, 7, 3337-3357.	2.5	24
43	Characterizing the Native Codon Usages of a Genome: An Axis Projection Approach. Molecular Biology and Evolution, 2011, 28, 211-221.	8.9	23
44	Archaeal RecA homologues: different response to DNA-damaging agents in mesophilic and thermophilic Archaea. Extremophiles, 2001, 5, 265-275.	2.3	21
45	Are arguments against archaeobacteria valid?. Nature, 1986, 320, 401-402.	27.8	18
46	Variation among the masses. Nature, 1990, 345, 20-20.	27.8	18
47	Structural modifications of <i>Methanococcus jannaschii</i> flagellin proteins revealed by proteome analysis. Proteomics, 2001, 1, 1033-1042.	2.2	18
48	The history of life. Nature Genetics, 2001, 28, 197-198.	21.4	16
49	Quorum-Dependent Mannopine-Inducible Conjugative Transfer of an <i>Agrobacterium</i> Opine-Catabolic Plasmid. Journal of Bacteriology, 2014, 196, 1031-1044.	2.2	15
50	Similar subunit architecture of archaeal and eukaryal RNA polymerases. FEMS Microbiology Letters, 2001, 195, 85-90.	1.8	14
51	Messenger RNA processing in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . Rna, 2009, 15, 1909-1916.	3.5	12
52	What's eating the free lunch?. Nature, 1999, 400, 403-405.	27.8	6
53	In search of genome annotation consistency: solid gene clusters and how to use them. 3 Biotech, 2014, 4, 331-335.	2.2	5
54	A whole-genome approach to identifying protein binding sites: promoters in <i>Methanocaldococcus</i> (<i>Methanococcus</i>) <i>jannaschii</i> . Nucleic Acids Research, 2008, 36, 6948-6958.	14.5	4

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55	<i>Response</i> : Methanococcus Genome. Science, 1996, 274, 902-903.	12.6	0
56	<i>Response</i> : Methanococcus Genome. Science, 1996, 274, 902-903.	12.6	0