

Guy Plunkett Iii

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

39
papers

14,395
citations

29
h-index

39
g-index

39
ext. papers

15,584
ext. citations

13
avg, IF

4.95
L-index

#	Paper	IF	Citations
39	The Enterobacterium Trabulsiella odontotermitis Presents Novel Adaptations Related to Its Association with Fungus-Growing Termites. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 6577-88	4.8	13
38	Genome of Enterobacteriophage Lula/phi80 and insights into its ability to spread in the laboratory environment. <i>Journal of Bacteriology</i> , 2012 , 194, 6802-17	3.5	15
37	Genome sequence of the plant-pathogenic bacterium Dickeya dadantii 3937. <i>Journal of Bacteriology</i> , 2011 , 193, 2076-7	3.5	78
36	Text-mining of PubMed abstracts by natural language processing to create a public knowledge base on molecular mechanisms of bacterial enteropathogens. <i>BMC Bioinformatics</i> , 2009 , 10, 177	3.6	14
35	The complete genome sequence of Escherichia coli DH10B: insights into the biology of a laboratory workhorse. <i>Journal of Bacteriology</i> , 2008 , 190, 2597-606	3.5	248
34	Enteropathogen Resource Integration Center (ERIC): bioinformatics support for research on biodefense-relevant enterobacteria. <i>Nucleic Acids Research</i> , 2008 , 36, D519-23	20.1	12
33	Escherichia coli K1-specific bacteriophage CUS-3 distribution and function in phase-variable capsular polysialic acid O acetylation. <i>Journal of Bacteriology</i> , 2007 , 189, 6447-56	3.5	26
32	A new asset for pathogen informatics--the Enteropathogen Resource Integration Center (ERIC), an NIAID Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Disease. <i>Advances in Experimental Medicine and Biology</i> , 2007 , 603, 28-42	3.6	7
31	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. <i>Nucleic Acids Research</i> , 2006 , 34, D41-5	20.1	54
30	Identification and characterization of Escherichia coli RS218-derived islands in the pathogenesis of E. coli meningitis. <i>Journal of Infectious Diseases</i> , 2006 , 194, 358-64	7	34
29	Escherichia coli K-12: a cooperatively developed annotation snapshot--2005. <i>Nucleic Acids Research</i> , 2006 , 34, 1-9	20.1	525
28	Emergent properties of reduced-genome Escherichia coli. <i>Science</i> , 2006 , 312, 1044-6	33.3	542
27	Genome of bacteriophage P1. <i>Journal of Bacteriology</i> , 2004 , 186, 7032-68	3.5	183
26	Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T. <i>Infection and Immunity</i> , 2003 , 71, 2775-86	3.7	349
25	ASAP, a systematic annotation package for community analysis of genomes. <i>Nucleic Acids Research</i> , 2003 , 31, 147-51	20.1	132
24	Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18. <i>Journal of Bacteriology</i> , 2003 , 185, 2330-7	3.5	291
23	Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 17020-4	11.5	1175

22	Genome sequence of <i>Yersinia pestis</i> KIM. <i>Journal of Bacteriology</i> , 2002 , 184, 4601-11	3.5	474
21	Engineering a reduced <i>Escherichia coli</i> genome. <i>Genome Research</i> , 2002 , 12, 640-7	9.7	214
20	Genome sequence of enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Nature</i> , 2001 , 409, 529-33	50.4	1671
19	erratum Genome sequence of enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Nature</i> , 2001 , 410, 240-240	50.4	13
18	Shotgun optical maps of the whole <i>Escherichia coli</i> O157:H7 genome. <i>Genome Research</i> , 2001 , 11, 1584-93	9.7	69
17	Sequence of Shiga toxin 2 phage 933W from <i>Escherichia coli</i> O157:H7: Shiga toxin as a phage late-gene product. <i>Journal of Bacteriology</i> , 1999 , 181, 1767-78	3.5	310
16	Subdivision of the <i>Escherichia coli</i> K-12 genome for sequencing: manipulation and DNA sequence of transposable elements introducing unique restriction sites. <i>Gene</i> , 1998 , 223, 47-54	3.8	26
15	The complete DNA sequence and analysis of the large virulence plasmid of <i>Escherichia coli</i> O157:H7. <i>Nucleic Acids Research</i> , 1998 , 26, 4196-204	20.1	267
14	The complete genome sequence of <i>Escherichia coli</i> K-12. <i>Science</i> , 1997 , 277, 1453-62	33.3	6157
13	Novel phosphotransferase-encoding genes revealed by analysis of the <i>Escherichia coli</i> genome: a chimeric gene encoding an Enzyme I homologue that possesses a putative sensory transduction domain. <i>Gene</i> , 1996 , 181, 103-8	3.8	66
12	Analysis of the <i>Escherichia coli</i> genome VI: DNA sequence of the region from 92.8 through 100 minutes. <i>Nucleic Acids Research</i> , 1995 , 23, 2105-19	20.1	141
11	A new family of peptidyl-prolyl isomerases. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 12-4	10.3	83
10	Analysis of the <i>Escherichia coli</i> genome. V. DNA sequence of the region from 76.0 to 81.5 minutes. <i>Nucleic Acids Research</i> , 1994 , 22, 2576-86	20.1	217
9	DNA sequence and analysis of 136 kilobases of the <i>Escherichia coli</i> genome: organizational symmetry around the origin of replication. <i>Genomics</i> , 1993 , 16, 551-61	4.3	197
8	Sequence analysis of four new heat-shock genes constituting the hslTS/ibpAB and hslVU operons in <i>Escherichia coli</i> . <i>Gene</i> , 1993 , 134, 1-6	3.8	145
7	Genome sequencing on both strands: the Janus strategy. <i>Nucleic Acids Research</i> , 1993 , 21, 3385-90	20.1	31
6	Analysis of the <i>Escherichia coli</i> genome. III. DNA sequence of the region from 87.2 to 89.2 minutes. <i>Nucleic Acids Research</i> , 1993 , 21, 3391-8	20.1	157
5	Analysis of the <i>Escherichia coli</i> genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes. <i>Nucleic Acids Research</i> , 1993 , 21, 5408-17	20.1	153

4	Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes. <i>Science</i> , 1992 , 257, 771-8	33.3	250
3	Retroregulation of the bacteriophage lambda int gene: limited secondary degradation of the RNase III-processed transcript. <i>Journal of Bacteriology</i> , 1989 , 171, 588-92	3.5	23
2	Characterization of bacteriophage T4 and D RNA, a low-molecular-weight RNA of unknown function. <i>Archives of Biochemistry and Biophysics</i> , 1981 , 210, 298-306	4.1	2
1	DNA sequence of the transfer RNA region of bacteriophage T4: implications for transfer RNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1981 , 78, 889-92	11.5	31