

# Vinayak Kapatral

## List of Publications by Year in descending order

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papers

4,392

citations

257450

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434195

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docs citations

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times ranked

5592

citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional Profiling the 150 kb Linear Megaplasmid of <i>Borrelia turicatae</i> Suggests a Role in Vector Colonization and Initiating Mammalian Infection. PLoS ONE, 2016, 11, e0147707.	2.5	20
2	Genome Sequence and Comparative Pathogenic Determinants of Multidrug Resistant Uropathogenic <i>Escherichia coli</i> O25b:H4, A Clinical Isolate from Saudi Arabia. Journal of Pure and Applied Microbiology, 2016, 10, .	0.9	1
3	Metabolic Network Analysis-Based Identification of Antimicrobial Drug Target in Pathogenic Bacteria. , 2015, , 385-399.		0
4	The genome of <i>Shigella dysenteriae</i> strain Sd1617 comparison to representative strains in evaluating pathogenesis. FEMS Microbiology Letters, 2015, 362, .	1.8	10
5	Draft Genome Sequence of a New Homofermentative, Lactic Acid-Producing <i>Enterococcus faecalis</i> Isolate, CBRD01. Genome Announcements, 2014, 2, .	0.8	3
6	Complete Genome Sequence of <i>Flavobacterium psychrophilum</i> Strain CSF259-93, Used To Select Rainbow Trout for Increased Genetic Resistance against Bacterial Cold Water Disease. Genome Announcements, 2014, 2, .	0.8	34
7	Metabolic Network Analysis-Based Identification of Antimicrobial Drug Targets in Category A Bioterrorism Agents. PLoS ONE, 2014, 9, e85195.	2.5	16
8	The Genetic Basis of Laboratory Adaptation in <i>&lt; i&gt;Caulobacter crescentus&lt;/i&gt;</i> . Journal of Bacteriology, 2010, 192, 3678-3688.	2.2	166
9	Blueprint for antimicrobial hit discovery targeting metabolic networks. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1082-1087.	7.1	98
10	Comparative Genome-Scale Metabolic Reconstruction and Flux Balance Analysis of Multiple <i>&lt; i&gt;Staphylococcus aureus&lt;/i&gt;</i> Genomes Identify Novel Antimicrobial Drug Targets. Journal of Bacteriology, 2009, 191, 4015-4024.	2.2	148
11	Comparative genome analysis of <i>Bacillus cereus</i> group genomes with <i>Bacillus subtilis</i> . FEMS Microbiology Letters, 2005, 250, 175-184.	1.8	73
12	The Wolbachia Genome of <i>Brugia malayi</i> : Endosymbiont Evolution within a Human Pathogenic Nematode. PLoS Biology, 2005, 3, e121.	5.6	529
13	Gene array analysis of <i>Yersinia enterocolitica</i> FlhD and FlhC: regulation of enzymes affecting synthesis and degradation of carbamoylphosphate. Microbiology (United Kingdom), 2004, 150, 2289-2300.	1.8	45
14	Characterization of a Recombinant <i>Yersinia enterocolitica</i> Lipoprotein; Implications for its Role in Autoimmune Response against Thyrotropin Receptor. Autoimmunity, 2004, 37, 515-520.	2.6	12
15	Genome sequence of <i>Bacillus cereus</i> and comparative analysis with <i>Bacillus anthracis</i> . Nature, 2003, 423, 87-91.	27.8	740
16	Experimental Determination and System Level Analysis of Essential Genes in <i>Escherichia coli</i> MG1655. Journal of Bacteriology, 2003, 185, 5673-5684.	2.2	678
17	Genome Analysis of <i>&lt; i&gt;F. nucleatum sub spp vincentii&lt;/i&gt;</i> and Its Comparison With the Genome of <i>&lt; i&gt;F. nucleatum&lt;/i&gt;</i> ATCC 25586. Genome Research, 2003, 13, 1180-1189.	5.5	72
18	The ERGOTM genome analysis and discovery system. Nucleic Acids Research, 2003, 31, 164-171.	14.5	207

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19	Whole-genome comparative analysis of three phytopathogenic <i>Xylella fastidiosa</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12403-12408.	7.1	94
20	Draft Sequencing and Comparative Genomics of <i>Xylella fastidiosa</i> Strains Reveal Novel Biological Insights. <i>Genome Research</i> , 2002, 12, 1556-1563.	5.5	70
21	The genome sequence of the facultative intracellular pathogen <i>Brucella melitensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 443-448.	7.1	513
22	Genome Sequence and Analysis of the Oral Bacterium <i>Fusobacterium nucleatum</i> Strain ATCC 25586. <i>Journal of Bacteriology</i> , 2002, 184, 2005-2018.	2.2	311
23	The genome of <i>Brucella melitensis</i> . <i>Veterinary Microbiology</i> , 2002, 90, 587-592.	1.9	48
24	The Rhodobacter capsulatus genome. <i>Photosynthesis Research</i> , 2001, 70, 43-52.	2.9	35
25	Succinyl Coenzyme A Synthetase of <i>Pseudomonas aeruginosa</i> with a Broad Specificity for Nucleoside Triphosphate (NTP) Synthesis Modulates Specificity for NTP Synthesis by the 12-Kilodalton Form of Nucleoside Diphosphate Kinase. <i>Journal of Bacteriology</i> , 2000, 182, 1333-1339.	2.2	29
26	Secretion of ATP-utilizing enzymes, nucleoside diphosphate kinase and ATPase, by <i>Mycobacterium bovis</i> Molecular Microbiology, 1999, 31, 1333-1343.	2.5	77
27	P2Z-Independent and P2Z Receptor-Mediated Macrophage Killing by <i>Pseudomonas aeruginosa</i> Isolated from Cystic Fibrosis Patients. <i>Infection and Immunity</i> , 1999, 67, 5231-5242.	2.2	46
28	Characterization of a Hankâ€™s Type Serine/Threonine Kinase and Serine/Threonine Phosphoprotein Phosphatase in <i>Pseudomonas aeruginosa</i>. <i>Journal of Bacteriology</i> , 1999, 181, 6615-6622.	2.2	48
29	Cellular function of elastase in <i>Pseudomonas aeruginosa</i> : role in the cleavage of nucleoside diphosphate kinase and in alginate synthesis. <i>Molecular Microbiology</i> , 1998, 30, 933-941.	2.5	93
30	Mammalian heterotrimeric Gâ€proteinâ€like proteins in mycobacteria: implications for cell signalling and survival in eukaryotic host cells. <i>Molecular Microbiology</i> , 1997, 26, 607-618.	2.5	13
31	Temperatureâ€dependent regulation of <i>Yersinia enterocolitica</i> Class III flagellar genes. <i>Molecular Microbiology</i> , 1996, 19, 1061-1071.	2.5	97
32	Co-ordinate, temperature-sensitive regulation of the three <i>Yersinia enterocolitica</i> flagellin genes. <i>Molecular Microbiology</i> , 1995, 17, 49-56.	2.5	66