

Dmitry A Ravcheev

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.

36
papers

2,131
citations

23
h-index

36
g-index

36
ext. papers

3,025
ext. citations

6.5
avg, IF

4.92
L-index

#	Paper	IF	Citations
36	Systematic assessment of secondary bile acid metabolism in gut microbes reveals distinct metabolic capabilities in inflammatory bowel disease. <i>Microbiome</i> , 2019 , 7, 75	16.6	98
35	Comparative Genomic Analysis Reveals Novel Microcompartment-Associated Metabolic Pathways in the Human Gut Microbiome. <i>Frontiers in Genetics</i> , 2019 , 10, 636	4.5	16
34	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. <i>Nucleic Acids Research</i> , 2019 , 47, D614-D624	20.1	132
33	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. <i>Nature Biotechnology</i> , 2017 , 35, 81-89	44.5	368
32	Comparative Genomic Analysis of the Human Gut Microbiome Reveals a Broad Distribution of Metabolic Pathways for the Degradation of Host-Synthesized Mucin Glycans and Utilization of Mucin-Derived Monosaccharides. <i>Frontiers in Genetics</i> , 2017 , 8, 111	4.5	45
31	Genomic Analysis of the Human Gut Microbiome Suggests Novel Enzymes Involved in Quinone Biosynthesis. <i>Frontiers in Microbiology</i> , 2016 , 7, 128	5.7	35
30	Nitrogen Fixation and Molecular Oxygen: Comparative Genomic Reconstruction of Transcription Regulation in Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2016 , 7, 1343	5.7	45
29	Comparative genomics and evolution of transcriptional regulons in. <i>Microbial Genomics</i> , 2016 , 2, e000061	4.4	9
28	Systems biology of bacteria-host interactions 2016 , 113-137		1
27	Paracoccus denitrificans possesses two BioR homologs having a role in regulation of biotin metabolism. <i>MicrobiologyOpen</i> , 2015 , 4, 644-59	3.4	16
26	Two novel regulators of N-acetyl-galactosamine utilization pathway and distinct roles in bacterial infections. <i>MicrobiologyOpen</i> , 2015 , 4, 983-1000	3.4	17
25	Systematic genome assessment of B-vitamin biosynthesis suggests co-operation among gut microbes. <i>Frontiers in Genetics</i> , 2015 , 6, 148	4.5	313
24	Redox-responsive repressor Rex modulates alcohol production and oxidative stress tolerance in Clostridium acetobutylicum. <i>Journal of Bacteriology</i> , 2014 , 196, 3949-63	3.5	45
23	Comparative genomics and evolution of regulons of the LacI-family transcription factors. <i>Frontiers in Microbiology</i> , 2014 , 5, 294	5.7	48
22	Systematic genomic analysis reveals the complementary aerobic and anaerobic respiration capacities of the human gut microbiota. <i>Frontiers in Microbiology</i> , 2014 , 5, 674	5.7	25
21	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013 , 14, 94	4.5	27
20	Polysaccharides utilization in human gut bacterium Bacteroides thetaiotaomicron: comparative genomics reconstruction of metabolic and regulatory networks. <i>BMC Genomics</i> , 2013 , 14, 873	4.5	89

19	RegPrecise 3.0--a resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013 , 14, 745	4.5	229
18	Transcriptional regulation of the carbohydrate utilization network in <i>Thermotoga maritima</i> . <i>Frontiers in Microbiology</i> , 2013 , 4, 244	5.7	38
17	Temporal regulation of gene expression of the <i>Escherichia coli</i> bacteriophage phiEco32. <i>Journal of Molecular Biology</i> , 2012 , 416, 389-99	6.5	19
16	Regulation and evolution of malonate and propionate catabolism in proteobacteria. <i>Journal of Bacteriology</i> , 2012 , 194, 3234-40	3.5	29
15	Transcriptional regulation of central carbon and energy metabolism in bacteria by redox-responsive repressor Rex. <i>Journal of Bacteriology</i> , 2012 , 194, 1145-57	3.5	95
14	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011 , 12 Suppl 1, S3	4.5	44
13	Inference of the transcriptional regulatory network in <i>Staphylococcus aureus</i> by integration of experimental and genomics-based evidence. <i>Journal of Bacteriology</i> , 2011 , 193, 3228-40	3.5	32
12	Comparative genomic analysis of the hexuronate metabolism genes and their regulation in gamma-proteobacteria. <i>Journal of Bacteriology</i> , 2011 , 193, 3956-63	3.5	26
11	Comparative genomics of ethanolamine utilization. <i>Journal of Bacteriology</i> , 2009 , 191, 7157-64	3.5	76
10	Evolution of Regulatory Systems in Bacteria (Invited Keynote Talk). <i>Lecture Notes in Computer Science</i> , 2009 , 1-4	0.9	
9	Regulation of bacterial respiration: Comparison of microarray and comparative genomics data. <i>Molecular Biology</i> , 2007 , 41, 497-512	1.2	
8	Comparative genomic analysis of regulation of anaerobic respiration in ten genomes from three families of gamma-proteobacteria (Enterobacteriaceae, Pasteurellaceae, Vibrionaceae). <i>BMC Genomics</i> , 2007 , 8, 54	4.5	42
7	Regulation of Nitrate and Nitrite Respiration in E-Proteobacteria: A Comparative Genomics Study. <i>Molecular Biology</i> , 2005 , 39, 727-740	1.2	5
6	A Gibbs sampler for identification of symmetrically structured, spaced DNA motifs with improved estimation of the signal length. <i>Bioinformatics</i> , 2005 , 21, 2240-5	7.2	82
5	Visualization of individual DNA loops and a map of loop domains in the human dystrophin gene. <i>Nucleic Acids Research</i> , 2004 , 32, 2079-86	20.1	60
4	Purine Regulon of Gamma-Proteobacteria: A Detailed Description. <i>Russian Journal of Genetics</i> , 2002 , 38, 1015-1025	0.6	2
3	AGORA2: Large scale reconstruction of the microbiome highlights wide-spread drug-metabolising capacities		6
2	Personalized modeling of the human gut microbiome reveals distinct bile acid deconjugation and biotransformation potential in healthy and IBD individuals		11

- 1 The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease

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