

# Dmitry A Ravcheev

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6432065/publications.pdf>

Version: 2024-02-01

32  
papers

3,443  
citations

279487

23  
h-index

454577

30  
g-index

36  
all docs

36  
docs citations

36  
times ranked

5283  
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. <i>Nature Biotechnology</i> , 2017, 35, 81-89.	9.4	629
2	Systematic genome assessment of B-vitamin biosynthesis suggests co-operation among gut microbes. <i>Frontiers in Genetics</i> , 2015, 6, 148.	1.1	565
3	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	1.2	408
4	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. <i>Nucleic Acids Research</i> , 2019, 47, D614-D624.	6.5	257
5	Systematic assessment of secondary bile acid metabolism in gut microbes reveals distinct metabolic capabilities in inflammatory bowel disease. <i>Microbiome</i> , 2019, 7, 75.	4.9	215
6	Polysaccharides utilization in human gut bacterium <i>Bacteroides thetaiotaomicron</i> : comparative genomics reconstruction of metabolic and regulatory networks. <i>BMC Genomics</i> , 2013, 14, 873.	1.2	122
7	Transcriptional Regulation of Central Carbon and Energy Metabolism in Bacteria by Redox-Responsive Repressor Rex. <i>Journal of Bacteriology</i> , 2012, 194, 1145-1157.	1.0	120
8	Comparative Genomics of Ethanolamine Utilization. <i>Journal of Bacteriology</i> , 2009, 191, 7157-7164.	1.0	113
9	A Gibbs sampler for identification of symmetrically structured, spaced DNA motifs with improved estimation of the signal length. <i>Bioinformatics</i> , 2005, 21, 2240-2245.	1.8	95
10	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.	1.1	79
11	Comparative genomics and evolution of regulons of the LacI-family transcription factors. <i>Frontiers in Microbiology</i> , 2014, 5, 294.	1.5	76
12	Nitrogen Fixation and Molecular Oxygen: Comparative Genomic Reconstruction of Transcription Regulation in Alphaproteobacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 1343.	1.5	66
13	Visualization of individual DNA loops and a map of loop domains in the human dystrophin gene. <i>Nucleic Acids Research</i> , 2004, 32, 2079-2086.	6.5	62
14	Redox-Responsive Repressor Rex Modulates Alcohol Production and Oxidative Stress Tolerance in <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2014, 196, 3949-3963.	1.0	60
15	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	1.2	59
16	Genomic Analysis of the Human Gut Microbiome Suggests Novel Enzymes Involved in Quinone Biosynthesis. <i>Frontiers in Microbiology</i> , 2016, 7, 128.	1.5	56
17	Comparative genomic analysis of regulation of anaerobic respiration in ten genomes from three families of gamma-proteobacteria ( <i>Enterobacteriaceae</i> , <i>Pasteurellaceae</i> , <i>Vibrionaceae</i> ). <i>BMC Genomics</i> , 2007, 8, 54.	1.2	48
18	Transcriptional regulation of the carbohydrate utilization network in <i>Thermotoga maritima</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 244.	1.5	48

#	ARTICLE	IF	CITATIONS
19	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, 3228-3240.	1.0	45
20	Systematic genomic analysis reveals the complementary aerobic and anaerobic respiration capacities of the human gut microbiota. <i>Frontiers in Microbiology</i> , 2014, 5, 674.	1.5	45
21	Regulation and Evolution of Malonate and Propionate Catabolism in Proteobacteria. <i>Journal of Bacteriology</i> , 2012, 194, 3234-3240.	1.0	42
22	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013, 14, 94.	1.2	38
23	Comparative Genomic Analysis of the Hexuronate Metabolism Genes and Their Regulation in Gammaproteobacteria. <i>Journal of Bacteriology</i> , 2011, 193, 3956-3963.	1.0	34
24	Two novel regulators of <i>N</i> -acetylglucosamine utilization pathway and distinct roles in bacterial infections. <i>MicrobiologyOpen</i> , 2015, 4, 983-1000.	1.2	22
25	Comparative Genomic Analysis Reveals Novel Microcompartment-Associated Metabolic Pathways in the Human Gut Microbiome. <i>Frontiers in Genetics</i> , 2019, 10, 636.	1.1	22
26	Temporal Regulation of Gene Expression of the <i>Escherichia coli</i> Bacteriophage phiEco32. <i>Journal of Molecular Biology</i> , 2012, 416, 389-399.	2.0	21
27	<i>Paracoccus denitrificans</i> possesses two BioR homologs having a role in regulation of biotin metabolism. <i>MicrobiologyOpen</i> , 2015, 4, 644-659.	1.2	18
28	Comparative genomics and evolution of transcriptional regulons in Proteobacteria. <i>Microbial Genomics</i> , 2016, 2, e000061.	1.0	18
29	Purine Regulon of Gamma-Proteobacteria: A Detailed Description. <i>Russian Journal of Genetics</i> , 2002, 38, 1015-1025.	0.2	9
30	Regulation of Nitrate and Nitrite Respiration in $\hat{1}^3$ -Proteobacteria: A Comparative Genomics Study. <i>Molecular Biology</i> , 2005, 39, 727-740.	0.4	6
31	Regulation of bacterial respiration: Comparison of microarray and comparative genomics data. <i>Molecular Biology</i> , 2007, 41, 497-512.	0.4	0
32	Evolution of Regulatory Systems in Bacteria (Invited Keynote Talk). <i>Lecture Notes in Computer Science</i> , 2009, , 1-4.	1.0	0