Dmitry G Alexeev

List of Publications by Citations

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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.

63 papers	1,907 citations	26 h-index	42 g-index
69 ext. papers	2,419 ext. citations	5.4 avg, IF	4.23 L-index

#	Paper	IF	Citations
63	Human gut microbiota community structures in urban and rural populations in Russia. *Nature Communications*, **2013**, 4, 2469	17.4	174
62	Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease. *Microbiome*, **2017**, 5, 141	16.6	158
61	Gut microbiota and diet in patients with different glucose tolerance. *Endocrine Connections*, **2016**, 5, 1-9	3.5	96
60	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. *Nature Communications*, **2018**, 9, 2427	17.4	95
59	Association between the gut microbiota and diet: Fetal life, early childhood, and further life. *Nutrition*, **2016**, 32, 620-7	4.8	88
58	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. *Nature Communications*, **2014**, 5, 4784	17.4	85
57	Proteome-metabolome profiling of ovarian cancer ascites reveals novel components involved in intercellular communication. *Molecular and Cellular Proteomics*, **2014**, 13, 3558-71	7.6	76
56	No Evidence of a Common DNA Variant Profile Specific to World Class Endurance Athletes. *PLoS ONE*, **2016**, 11, e0147330	3.7	74
55	Microbiome Responses to an Uncontrolled Short-Term Diet Intervention in the Frame of the Citizen Science Project. *Nutrients*, **2018**, 10,	6.7	63
54	Genome-wide association study identifies three novel genetic markers associated with elite endurance performance. *Biology of Sport*, **2015**, 32, 3-9	4.3	49
53	Complete genome and proteome of Acholeplasma laidlawii. *Journal of Bacteriology*, **2011**, 193, 4943-53	3.5	49
52	Chromosome 18 transcriptome profiling and targeted proteome mapping in depleted plasma, liver tissue and HepG2 cells. *Journal of Proteome Research*, **2013**, 12, 123-34	5.6	46
51	Gut Microbiota in Patients with Different Metabolic Statuses: Moscow Study. *Microorganisms*, **2018**, 6,	4.9	38
50	Dissection of affinity captured LINE-1 macromolecular complexes. *ELife*, **2018**, 7,	8.9	38
49	Human Gut Microbiome Response Induced by Fermented Dairy Product Intake in Healthy Volunteers. *Nutrients*, **2019**, 11,	6.7	37
48	Comparative genomic analysis of Mycobacterium tuberculosis drug resistant strains from Russia. *PLoS ONE*, **2013**, 8, e56577	3.7	37
47	Assessment of k-mer spectrum applicability for metagenomic dissimilarity analysis. *BMC Bioinformatics*, **2016**, 17, 38	3.6	36

46	Application of Spiroplasma melliferum proteogenomic profiling for the discovery of virulence factors and pathogenicity mechanisms in host-associated spiroplasmas. *Journal of Proteome Research*, **2012**, 11, 224-36	5.6	34
45	Chromosome 18 transcriptoproteome of liver tissue and HepG2 cells and targeted proteome mapping in depleted plasma: update 2013. *Journal of Proteome Research*, **2014**, 13, 183-90	5.6	33
44	Transcriptome analysis reveals novel regulatory mechanisms in a genome-reduced bacterium. *Nucleic Acids Research*, **2014**, 42, 13254-68	20.1	33
43	Agent Based Modeling of Human Gut Microbiome Interactions and Perturbations. *PLoS ONE*, **2016**, 11, e0148386	3.7	33
42	Specific pools of endogenous peptides are present in gametophore, protonema, and protoplast cells of the moss Physcomitrella patens. *BMC Plant Biology*, **2015**, 15, 87	5.3	31
41	AGTR2 gene polymorphism is associated with muscle fibre composition, athletic status and aerobic performance. *Experimental Physiology*, **2014**, 99, 1042-52	2.4	28
40	RNA-Seq gene expression profiling of HepG2 cells: the influence of experimental factors and comparison with liver tissue. *BMC Genomics*, **2014**, 15, 1108	4.5	28
39	MetaFast: fast reference-free graph-based comparison of shotgun metagenomic data. *Bioinformatics*, **2016**, 32, 2760-7	7.2	27
38	DNA repair in Mycoplasma gallisepticum. *BMC Genomics*, **2013**, 14, 726	4.5	27
37	Rural and urban microbiota: To be or not to be?. *Gut Microbes*, **2014**, 5, 351-6	8.8	26
36	Core proteome of the minimal cell: comparative proteomics of three mollicute species. *PLoS ONE*, **2011**, 6, e21964	3.7	25
35	ResistoMap-online visualization of human gut microbiota antibiotic resistome. *Bioinformatics*, **2017**, 33, 2205-2206	7.2	21
34	Novel fusion transcripts in bladder cancer identified by RNA-seq. *Cancer Letters*, **2016**, 374, 224-8	9.9	21
33	Abundance profiling of specific gene groups using precomputed gut metagenomes yields novel biological hypotheses. *PLoS ONE*, **2017**, 12, e0176154	3.7	20
32	SOD2 gene polymorphism and muscle damage markers in elite athletes. *Free Radical Research*, **2014**, 48, 948-55	4	18
31	Functional divergence of Helicobacter pylori related to early gastric cancer. *Journal of Proteome Research*, **2010**, 9, 254-67	5.6	18
30	Methods for The Metagenomic Data Visualization and Analysis. *Current Issues in Molecular Biology*, **2017**, 24, 37-58	2.9	18
29	Knomics-Biota - a system for exploratory analysis of human gut microbiota data. *BioData Mining*, **2018**, 11, 25	4.3	18

28	New method for peptide desorption from abundant blood proteins for plasma/serum peptidome analyses by mass spectrometry. *Journal of Proteomics*, **2011**, 74, 595-606	3.9	17
27	Proteome analysis of the Mycobacterium tuberculosis Beijing B0/W148 cluster. *Scientific Reports*, **2016**, 6, 28985	4.9	16
26	Genome analysis of E. coli isolated from Crohnıs disease patients. *BMC Genomics*, **2017**, 18, 544	4.5	15
25	Unusual large-scale chromosomal rearrangements in Mycobacterium tuberculosis Beijing B0/W148 cluster isolates. *PLoS ONE*, **2014**, 9, e84971	3.7	15
24	Genetic diversity of Escherichia coli in gut microbiota of patients with Crohnıs disease discovered using metagenomic and genomic analyses. *BMC Genomics*, **2018**, 19, 968	4.5	14
23	Comprehensive analysis of the venom gland transcriptome of the spider Dolomedes fimbriatus. *Scientific Data*, **2014**, 1, 140023	8.2	13
22	Guidelines to Statistical Analysis of Microbial Composition Data Inferred from Metagenomic Sequencing. *Current Issues in Molecular Biology*, **2017**, 24, 17-36	2.9	12
21	AGTR2 and sprint/power performance: a case-control replication study for rs11091046 polymorphism in two ethnicities. *Biology of Sport*, **2018**, 35, 105-109	4.3	10
20	Respiratory Pathways Reconstructed by Multi-Omics Analysis in , Residing in a Deep Thermal Aquifer of the West-Siberian Megabasin. *Frontiers in Microbiology*, **2017**, 8, 1228	5.7	9
19	Modified nucleotides m(2)G966/m(5)C967 of Escherichia coli 16S rRNA are required for attenuation of tryptophan operon. *Scientific Reports*, **2013**, 3, 3236	4.9	9
18	Variation in Copy Number of Ty3/Gypsy Centromeric Retrotransposons in the Genomes of Thinopyrum intermedium and Its Diploid Progenitors. *PLoS ONE*, **2016**, 11, e0154241	3.7	9
17	Prioritization of causal genes for coronary artery disease based on cumulative evidence from experimental and in silico studies. *Scientific Reports*, **2020**, 10, 10486	4.9	8
16	Co-occurrence patterns of bacteria within microbiome of Moscow subway. *Computational and Structural Biotechnology Journal*, **2020**, 18, 314-322	6.8	8
15	Draft Genome of the Nitrogen-Fixing Bacterium Pseudomonas stutzeri Strain KOS6 Isolated from Industrial Hydrocarbon Sludge. *Genome Announcements*, **2013**, 1,		8
14	Proteome analysis of chloroplasts from the moss Physcomitrella patens (Hedw.) B.S.G. *Biochemistry (Moscow)*, **2010**, 75, 1470-83	2.9	8
13	Development of qPCR platform with probes for quantifying prevalent and biomedically relevant human gut microbial taxa. *Molecular and Cellular Probes*, **2020**, 52, 101570	3.3	6
12	Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis. *Data in Brief*, **2017**, 11, 98-102	1.2	5
11	Gut microbiota and vascular biomarkers in patients without clinical cardiovascular diseases. *Artery Research*, **2017**, 18, 41	2.2	5

10	Purification and characterisation of recombinant Bacteroides fragilis toxin-2. *Biochimie*, **2013**, 95, 2123-31	4.6	4
9	MALINA: a web service for visual analytics of human gut microbiota whole-genome metagenomic reads. *Source Code for Biology and Medicine*, **2012**, 7, 13	1.9	3
8	Temporal dynamics of probiotic Lacticaseibacillus casei and rhamnosus abundance in a fermented dairy product evaluated using a combination of cultivation-dependent and -independent methods. *LWT - Food Science and Technology*, **2021**, 148, 111750	5.4	3
7	Large scale analysis of amino acid substitutions in bacterial proteomics. *BMC Bioinformatics*, **2016**, 17, 450	3.6	2
6	Serum proteome profiling for diagnostics of ovarian cancer using ClinProt magnetic technique and MALDI-TOF mass spectrometry. *Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry*, **2008**, 2, 335-342	0.4	2
5	Bacterial rose garden for metagenomic SNP-based phylogeny visualization. *BioData Mining*, **2015**, 8, 10	4.3	1
4	ResistoMap – online visualization of human gut microbiota antibiotic resistome		1
3	Gut microbiome signature of Viliuisk encephalomyelitis in Yakuts includes an increase in microbes linked to lean body mass and eating behaviour. *Orphanet Journal of Rare Diseases*, **2020**, 15, 327	4.2	1
2	Yogurt fortified with vitamins and probiotics impacts the frequency of upper respiratory tract infections but not gut microbiome: A multicenter double-blind placebo controlled randomized study. *Journal of Functional Foods*, **2021**, 83, 104572	5.1	0
1	Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with the alcohol dependence syndrome. *Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry*, **2016**, 10, 184-190	0.4	