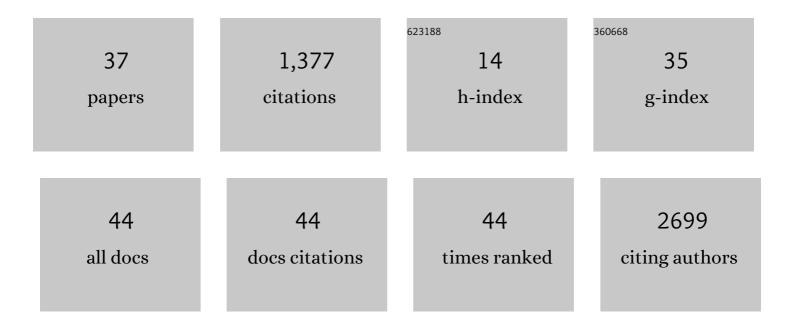
Vladislav V Babenko

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Deep Functional Profiling of Wild Animal Microbiomes Reveals Probiotic Bacillus pumilus Strains with a Common Biosynthetic Fingerprint. International Journal of Molecular Sciences, 2022, 23, 1168.	1.8	5
2	Spontaneous DNA Synapsis by Forming Noncanonical Intermolecular Structures. Polymers, 2022, 14, 2118.	2.0	4
3	Effect of Temperature on Biobeneficiation of Bulk Copper-Nickel Concentrate with Thermoacidophilic Microbial Communities. Metals, 2021, 11, 1969.	1.0	5
4	The Hirudo Medicinalis Microbiome Is a Source of New Antimicrobial Peptides. International Journal of Molecular Sciences, 2020, 21, 7141.	1.8	12
5	The ecogenomics of dsDNA bacteriophages in feces of stabled and feral horses. Computational and Structural Biotechnology Journal, 2020, 18, 3457-3467.	1.9	14
6	Novel Bradykinin-Potentiating Peptides and Three-Finger Toxins from Viper Venom: Combined NGS Venom Gland Transcriptomics and Quantitative Venom Proteomics of the Azemiops feae Viper. Biomedicines, 2020, 8, 249.	1.4	15
7	Draft genome sequences of Hirudo medicinalis and salivary transcriptome of three closely related medicinal leeches. BMC Genomics, 2020, 21, 331.	1.2	21
8	A Simple Method for Extraction of the Horse Feces Virome DNA, Suitable for Oxford Nanopore Sequencing. Microbiology, 2020, 89, 246-249.	0.5	4
9	Genome Sequences of a Green-Colored Chlorobium phaeovibrioides Strain Containing Two Plasmids and a Closely Related Plasmid-Free Brown-Colored Strain. Microbiology Resource Announcements, 2020, 9, .	0.3	2
10	Shifts in the Human Gut Microbiota Structure Caused by Quadruple Helicobacter pylori Eradication Therapy. Frontiers in Microbiology, 2019, 10, 1902.	1.5	39
11	Medicinal leech antimicrobial peptides lacking toxicity represent a promising alternative strategy to combat antibiotic-resistant pathogens. European Journal of Medicinal Chemistry, 2019, 180, 143-153.	2.6	17
12	Two novel transcriptional reporter systems for monitoring Helicobacter pylori stress responses. Plasmid, 2019, 106, 102442.	0.4	0
13	Sulfobacillus thermotolerans: new insights into resistance and metabolic capacities of acidophilic chemolithotrophs. Scientific Reports, 2019, 9, 15069.	1.6	25
14	Seasonal Variations in the Structure of an Anoxygenic Phototrophic Bacterial Community from the Meromictic Lake Trekhtsvetnoe (Kandalaksha Bay, White Sea). Microbiology, 2019, 88, 100-114.	0.5	14
15	Proteomic dataset: Profiling of cultivated Echerichia coli isolates from Crohn's disease patients and healthy individuals. Data in Brief, 2019, 23, 103734.	0.5	1
16	Structure and gene cluster of the O antigen of Escherichia coli F17, a candidate for a new O-serogroup. International Journal of Biological Macromolecules, 2019, 124, 389-395.	3.6	10
17	Escherichia coli bacteriophage Gostya9, representing a new species within the genus T5virus. Archives of Virology, 2019, 164, 879-884.	0.9	11
18	Discovery of novel antimicrobial peptides: A transcriptomic study of the sea anemone <i>Cnidopus japonicus</i> . Journal of Bioinformatics and Computational Biology, 2018, 16, 1840006.	0.3	13

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19	Complete Genome Sequence of Bacteriophage St11Ph5, Which Infects Uropathogenic Escherichia coli Strain up11. Genome Announcements, 2018, 6, .	0.8	9
20	O-Antigens of Escherichia coli Strains O81 and HS3-104 Are Structurally and Genetically Related, Except O-Antigen Glucosylation in E. coli HS3-104. Biochemistry (Moscow), 2018, 83, 534-541.	0.7	7
21	Sharp water column stratification with an extremely dense microbial population in a small meromictic lake, Trekhtzvetnoe. Environmental Microbiology, 2018, 20, 3784-3797.	1.8	30
22	Data on gut metagenomes of the patients with Helicobacter pylori infection before and after the antibiotic therapy. Data in Brief, 2017, 11, 68-71.	0.5	14
23	Microfluidic droplet platform for ultrahigh-throughput single-cell screening of biodiversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2550-2555.	3.3	182
24	Analysis of Gut Microbiota in Patients with Parkinson's Disease. Bulletin of Experimental Biology and Medicine, 2017, 162, 734-737.	0.3	378
25	Genetic Environment of the bla KPC-2 Gene in a Klebsiella pneumoniae Isolate That May Have Been Imported to Russia from Southeast Asia. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	8
26	Data on genome analysis of Mycoplasma gallisepticum during intracellular infection. Data in Brief, 2017, 10, 264-268.	0.5	0
27	Identification of unusual peptides with new Cys frameworks in the venom of the cold-water sea anemone Cnidopus japonicus. Scientific Reports, 2017, 7, 14534.	1.6	10
28	Genome analysis of E. coli isolated from Crohn's disease patients. BMC Genomics, 2017, 18, 544.	1.2	37
29	Phase Transition of the Bacterium upon Invasion of a Host Cell as a Mechanism of Adaptation: a Mycoplasma gallisepticum Model. Scientific Reports, 2016, 6, 35959.	1.6	31
30	Draft mitochondrial genomes of Hirudo medicinalis and Hirudo verbana (Annelida, Hirudinea) Mitochondrial DNA Part B: Resources, 2016, 1, 254-256.	0.2	9
31	Primary screening of candidate RNA biomarkers for diagnostics of prostate cancer. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2016, 10, 180-183.	0.2	Ο
32	Gut microbiota and diet in patients with different glucose tolerance. Endocrine Connections, 2016, 5, 1-9.	0.8	148
33	Complete Genome Sequence of an Enterotoxigenic Bacteroides fragilis Clinical Isolate. Genome Announcements, 2015, 3, .	0.8	17
34	Isolation of single Chlamydia-infected cells using laser microdissection. Journal of Microbiological Methods, 2015, 109, 123-128.	0.7	8
35	Structure of the capsular polysaccharide of Acinetobacter baumannii 1053 having the KL91 capsule biosynthesis gene locus. Carbohydrate Research, 2015, 404, 79-82.	1.1	21
36	Human gut microbiota community structures in urban and rural populations in Russia. Nature Communications, 2013, 4, 2469.	5.8	233

#	Article	IF	CITATIONS
37	Isolation and sequencing of three RB49-like bacteriophages infecting O antigen-producing E. coli strains. F1000Research, 0, 10, 1113.	0.8	2