

# Ilya S Korotetskiy

## List of Publications by Year in descending order

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24  
papers

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citations

1477746

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citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequences of Gram-Positive Opportunistic Pathogens Isolated from Hospitals in Almaty, Kazakhstan. <i>Microbiology Resource Announcements</i> , 2022, , e0009322.	0.3	2
2	Comparison of Transcriptional Responses and Metabolic Alterations in Three Multidrug-Resistant Model Microorganisms, <i>Staphylococcus aureus</i> ATCC BAA-39, <i>Escherichia coli</i> ATCC BAA-196, and <i>Acinetobacter baumannii</i> ATCC BAA-1790, on Exposure to Iodine-Containing Nano-micelle Drug FS-1. <i>MSystems</i> , 2021, 6, .	1.7	2
3	Coding-Complete Genome Sequence of Swine Influenza Virus Isolate A/Swine/Karaganda/04/2020 (H1N1) from Kazakhstan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0078621.	0.3	2
4	Complete Genome Sequences of Gram-Negative Opportunistic Pathogens Isolated in Hospitals in Almaty, Kazakhstan. <i>Microbiology Resource Announcements</i> , 2021, 10, e0097421.	0.3	5
5	Transcriptomics and methylomics study on the effect of iodine-containing drug FS-1 on ATCC BAA-196. <i>Future Microbiology</i> , 2021, 16, 1063-1085.	1.0	0
6	The Effect of Iodine-Containing Nano-Micelles, FS-1, on Antibiotic Resistance, Gene Expression and Epigenetic Modifications in the Genome of Multidrug Resistant MRSA Strain <i>Staphylococcus aureus</i> ATCC BAA-39. <i>Frontiers in Microbiology</i> , 2020, 11, 581660.	1.5	9
7	Complete Genome Sequence of Collection Strain <i>Acinetobacter baumannii</i> ATCC BAA-1790, Used as a Model To Study the Antibiotic Resistance Reversion Induced by Iodine-Containing Complexes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	6
8	GENE EXPRESSION PROFILING OF MULTI-DRUG RESISTANT E. COLI AFTER EXPOSURE BY NANOMOLECULAR IODINE-CONTAINING COMPLEX. <i>News of the National Academy of Sciences of the Republic of Kazakhstan Series of Biological and Medical</i> , 2020, 4, 10-18.	0.0	4
9	Assembly of Complete Genome Sequences of Negative-Control and Experimental Strain Variants of <i>Staphylococcus aureus</i> ATCC BAA-39 Selected under the Effect of the Drug FS-1, Which Induces Antibiotic Resistance Reversion. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	7
10	Complete Genome Sequence of a Multidrug-Resistant Strain, <i>Escherichia coli</i> ATCC BAA-196, as a Model for Studying Induced Antibiotic Resistance Reversion. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
11	ISOLATION AND CHARACTERIZATION ISOLATES OF NOSOCOMIAL INFECTIONS. <i>The Bulletin</i> , 2019, 5, 199-209.	0.0	6
12	NEW SEMIORGANIC IODINE COMPLEX, ITS STRUCTURE AND BIOLOGICAL ACTIVITY. <i>Series Chemistry and Technology</i> , 2019, 1, 70-77.	0.1	0
13	Clade-Specific Distribution of Antibiotic Resistance Mutations in the Population of <i>Mycobacterium tuberculosis</i> - Prospects for Drug Resistance Reversion. , 2018, , .		5
14	Genomic Insight into Mechanisms of Reversion of Antibiotic Resistance in Multidrug Resistant <i>Mycobacterium tuberculosis</i> Induced by a Nanomolecular Iodine-Containing Complex FS-1. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 151.	1.8	26
15	Constraints of Drug Resistance in <i>Mycobacterium tuberculosis</i> - Prospects for Pharmacological Reversion of Susceptibility to Antibiotics. <i>The Open Conference Proceedings Journal</i> , 2017, 8, 33-43.	0.6	3
16	The Effect of Antibiotic-Resistant and Sensitive <i>Escherichia coli</i> on the Production of Pro-Inflammatory Cytokine Response by Human Peripheral Blood Mononuclear Cells. <i>Journal of Clinical &amp; Cellular Immunology</i> , 2017, 8, .	1.5	3
17	STUDY ON ANTIVIRAL ACTIVITY OF COORDINATION COMPOUND BASED ON MOLECULAR IODINE AGAINST INFLUENZA A VIRUS. , 2017, , .		0
18	Genetic Changes in Influenza a Virus Genes Responsible for Formation of Drug Resistance Phenotype. <i>Journal of Human Virology &amp; Retrovirology</i> , 2016, 3, .	0.1	1

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19	Role of the horizontal gene exchange in evolution of pathogenic Mycobacteria. BMC Evolutionary Biology, 2015, 15, S2.	3.2	23
20	Complete Genome Sequence of Multidrug-Resistant Clinical Isolate Mycobacterium tuberculosis 187.0, Used To Study the Effect of Drug Susceptibility Reversion by the New Medicinal Drug FS-1. Genome Announcements, 2015, 3, .	0.8	5
21	Characterization of pigeon paramyxoviruses (Newcastle disease virus) isolated in Kazakhstan in 2005. Virologica Sinica, 2012, 27, 93-99.	1.2	11
22	Impact Genetic Characterization of H5N1 Avian Influenza Virus Isolated from Dead Mute Swan (Cygnus Tj ETQq0 0,0 rgBT /Overlock 10	0.6	0
23	Newcastle disease outbreaks in Kazakhstan and Kyrgyzstan during 1998, 2000, 2001, 2003, 2004, and 2005 were caused by viruses of the genotypes VIIb and VIId. Virus Genes, 2009, 39, 94-101.	0.7	47
24	Molecular Characterization of Virulent Newcastle Disease Virus Isolates from Chickens during the 1998 NDV Outbreak in Kazakhstan. Virus Genes, 2005, 31, 13-20.	0.7	17