

Ilya Borovok

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	<i>Listeria monocytogenes</i> TcyKLMN Cystine/Cysteine Transporter Facilitates Glutathione Synthesis and Virulence Gene Expression. MBio, 2022, 13, e0044822.	4.1	6
2	A dual-function phage regulator controls the response of cohabiting phage elements via regulation of the bacterial SOS response. Cell Reports, 2022, 39, 110723.	6.4	10
3	A Metzincin and TIMP-Like Protein Pair of a Phage Origin Sensitize <i>Listeria monocytogenes</i> to Phage Lysins and Other Cell Wall Targeting Agents. Microorganisms, 2021, 9, 1323.	3.6	1
4	Renewable fatty acid ester production in <i>Clostridium</i> . Nature Communications, 2021, 12, 4368.	12.8	24
5	A GC-Rich Prophage-Like Genomic Region of <i>Mycoplasma bovirhinis</i> HAZ141_2 Carries a Gene Cluster Encoding Resistance to Kanamycin and Neomycin. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	7
6	The aadE*-sat4-aphA-3 Gene Cluster of <i>Mycoplasma bovirhinis</i> HAZ141_2 Undergoes Genomic Rearrangements Influencing the Primary Promoter Sequence. Antibiotics, 2021, 10, 1335.	3.7	1
7	Active Lysogeny in <i>Listeria Monocytogenes</i> Is a Bacteria-Phage Adaptive Response in the Mammalian Environment. Cell Reports, 2020, 32, 107956.	6.4	31
8	RRNPP-type quorum-sensing systems regulate solvent formation, sporulation and cell motility in <i>Clostridium saccharoperbutylacetonicum</i> . Biotechnology for Biofuels, 2020, 13, 84.	6.2	12
9	Genomics-based epidemiology of bovine <i>Mycoplasma bovis</i> strains in Israel. BMC Genomics, 2020, 21, 70.	2.8	22
10	Distinctive ligand-binding specificities of tandem PA14 biomass-sensory elements from <i>Clostridium thermocellum</i> and <i>Clostridium clariflavum</i> . Proteins: Structure, Function and Bioinformatics, 2019, 87, 917-930.	2.6	8
11	Faecal Proteases from Pouchitis Patients Activate Protease Activating Receptor-2 to Disrupt the Epithelial Barrier. Journal of Crohn's and Colitis, 2019, 13, 1558-1568.	1.3	8
12	Coordination of cohabiting phage elements supports bacteria-phage cooperation. Nature Communications, 2019, 10, 5288.	12.8	35
13	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. ELife, 2018, 7, .	6.0	40
14	Controlled branched-chain amino acids auxotrophy in <i>Listeria monocytogenes</i> allows isoleucine to serve as a host signal and virulence effector. PLoS Genetics, 2018, 14, e1007283.	3.5	25
15	Revisiting the Regulation of the Primary Scaffoldin Gene in <i>Clostridium thermocellum</i> . Applied and Environmental Microbiology, 2017, 83, .	3.1	10
16	Complexity of the <i>Ruminococcus flavefaciens</i> FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. Scientific Reports, 2017, 7, 42355.	3.3	31
17	Temperate bacteriophages as regulators of host behavior. Current Opinion in Microbiology, 2017, 38, 81-87.	5.1	94
18	How does cellulosome composition influence deconstruction of lignocellulosic substrates in <i>Clostridium</i> (<i>Ruminiclostridium</i>) <i>thermocellum</i> DSM 1313?. Biotechnology for Biofuels, 2017, 10, 222.	6.2	47

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19	Pan-Cellulosomics of Mesophilic Clostridia: Variations on a Theme. <i>Microorganisms</i> , 2017, 5, 74.	3.6	17
20	Application of Long Sequence Reads To Improve Genomes for <i>Clostridium thermocellum</i> AD2, <i>Clostridium thermocellum</i> LQRI, and <i>Pelosinus fermentans</i> R7. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
21	High Prevalence of Diverse Insertion Sequences within the rRNA Operons of <i>Mycoplasma bovis</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 6386-6394.	3.1	3
22	An Extended Cyclic Di-GMP Network in the Predatory Bacterium <i>Bdellovibrio bacteriovorus</i> . <i>Journal of Bacteriology</i> , 2016, 198, 127-137.	2.2	25
23	Decoding Biomass-Sensing Regulons of <i>Clostridium thermocellum</i> Alternative Sigma-I Factors in a Heterologous <i>Bacillus subtilis</i> Host System. <i>PLoS ONE</i> , 2016, 11, e0146316.	2.5	31
24	Near-Complete Genome Sequence of the Cellulolytic Bacterium <i>Bacteroides</i> (<i>Bacteroides</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 Td (<i>Bacteroides</i>)	0.8	12
25	The metabolic regulator <i>CodY</i> links <i>L</i> <i>isteria monocytogenes</i> metabolism to virulence by directly activating the virulence regulatory gene <i>prfA</i> . <i>Molecular Microbiology</i> , 2015, 95, 624-644.	2.5	81
26	Standalone cohesin as a molecular shuttle in cellulosome assembly. <i>FEBS Letters</i> , 2015, 589, 1569-1576.	2.8	14
27	Functional phylotyping approach for assessing intraspecific diversity of <i>Ruminococcus albus</i> within the rumen microbiome. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-10.	1.8	12
28	Ruminococcal cellulosome systems from rumen to human. <i>Environmental Microbiology</i> , 2015, 17, 3407-3426.	3.8	104
29	A new perspective on lysogeny: prophages as active regulatory switches of bacteria. <i>Nature Reviews Microbiology</i> , 2015, 13, 641-650.	28.6	357
30	Three cellulosomal xylanase genes in <i>Clostridium thermocellum</i> are regulated by both vegetative SigA (<i>I</i> ^A) and alternative SigI6 (<i>I</i> ^{I6}) factors. <i>FEBS Letters</i> , 2015, 589, 3133-3140.	2.8	19
31	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. <i>PLoS ONE</i> , 2014, 9, e99221.	2.5	73
32	Structural characterization of a novel autonomous cohesin from <i>Ruminococcus flavefaciens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 450-456.	0.8	3
33	Fine-structural variance of family 3 carbohydrate-binding modules as extracellular biomass-sensing components of <i>Clostridium thermocellum</i> anti- <i>I</i> ^I factors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 522-534.	2.5	26
34	Cellulosomics of the cellulolytic thermophile <i>Clostridium clariflavum</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 100.	6.2	53
35	Structure and regulation of the cellulose degradome in <i>Clostridium cellulolyticum</i> . <i>Biotechnology for Biofuels</i> , 2013, 6, 73.	6.2	49
36	Integrative Genomic Analysis Identifies Isoleucine and CodY as Regulators of <i>Listeria monocytogenes</i> Virulence. <i>PLoS Genetics</i> , 2012, 8, e1002887.	3.5	108

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37	Prophage Excision Activates <i>Listeria</i> Competence Genes that Promote Phagosomal Escape and Virulence. <i>Cell</i> , 2012, 150, 792-802.	28.9	199
38	Genome-wide analysis of <i>Acetivibrio cellulolyticus</i> provides a blueprint of an elaborate cellulosome system. <i>BMC Genomics</i> , 2012, 13, 210.	2.8	54
39	Genetic makeup of the <i>Corynebacterium glutamicum</i> LexA regulon deduced from comparative transcriptomics and in vitro DNA band shift assays. <i>Microbiology (United Kingdom)</i> , 2009, 155, 1459-1477.	1.8	41
40	Coenzyme B12 Controls Transcription of the <i>Streptomyces</i> Class Ia Ribonucleotide Reductase <i>nrdABS</i> Operon via a Riboswitch Mechanism. <i>Journal of Bacteriology</i> , 2006, 188, 2512-2520.	2.2	48
41	The <i>Streptomyces</i> NrdR Transcriptional Regulator Is a Zn Ribbon/ATP Cone Protein That Binds to the Promoter Regions of Class Ia and Class II Ribonucleotide Reductase Operons. <i>Journal of Bacteriology</i> , 2006, 188, 7635-7644.	2.2	47
42	Alternative oxygen-dependent and oxygen-independent ribonucleotide reductases in <i>Streptomyces</i> : cross-regulation and physiological role in response to oxygen limitation. <i>Molecular Microbiology</i> , 2004, 54, 1022-1035.	2.5	42
43	<i>Streptomyces</i> spp. contain class Ia and class II ribonucleotide reductases: expression analysis of the genes in vegetative growth The GenBank/EMBL/DDBJ accession numbers for the sequences determined in this paper are AJ224870, AJ276618, AJ277778, AJ295338 and AJ295339.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 391-404.	1.8	28
44	Analysis of Transcription of the <i>Staphylococcus aureus</i> Aerobic Class Ib and Anaerobic Class III Ribonucleotide Reductase Genes in Response to Oxygen. <i>Journal of Bacteriology</i> , 2001, 183, 7260-7272.	2.2	96
45	Recent advances in the structure and function of isopenicillin N synthase. <i>Antonie Van Leeuwenhoek</i> , 1999, 75, 33-39.	1.7	16
46	The glutamine ligand in the ferrous iron active site of isopenicillin N synthase of <i>Streptomyces jumonjinensis</i> is not essential for catalysis. <i>FEBS Letters</i> , 1997, 405, 172-174.	2.8	31