Vasili Hauryliuk

List of Publications by Year
in descending order

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77

papers

4,416

citations

126907

33

h-index

123424

61

g-index

99

all docs

99

docs citations

99

times ranked

4015

citing authors

#	Article	IF	Citations
1	Sal-type ABC-F proteins: intrinsic and common mediators of pleuromutilin resistance by target protection in staphylococci. Nucleic Acids Research, 2022, 50, 2128-2142.	14.5	16
2	A hyperpromiscuous antitoxin protein domain for the neutralization of diverse toxin domains. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	22
3	Structural basis for PoxtA-mediated resistance to phenicol and oxazolidinone antibiotics. Nature Communications, 2022, 13, 1860.	12.8	25
4	Clinically observed deletions in SARSâ€CoVâ€2 Nsp1 affect its stability and ability to inhibit translation. FEBS Letters, 2022, 596, 1203-1213.	2.8	3
5	Synthetic oxepanoprolinamide iboxamycin is active against <i>Listeria monocytogenes</i> despite the intrinsic resistance mediated by VgaL/Lmo0919 ABCF ATPase. JAC-Antimicrobial Resistance, 2022, 4, .	2.1	5
6	Expression of <i>Bacillus subtilis</i> ABCF antibiotic resistance factor VmlR is regulated by RNA polymerase pausing, transcription attenuation, translation attenuation and (p)ppGpp. Nucleic Acids Research, 2022, 50, 6174-6189.	14.5	15
7	Structural Basis for Bacterial Ribosome-Associated Quality Control by RqcH and RqcP. Molecular Cell, 2021, 81, 115-126.e7.	9.7	41
8	Structural basis of ABCF-mediated resistance to pleuromutilin, lincosamide, and streptogramin A antibiotics in Gram-positive pathogens. Nature Communications, 2021, 12, 3577.	12.8	40
9	RqcH and RqcP catalyze processive poly-alanine synthesis in a reconstituted ribosome-associated quality control system. Nucleic Acids Research, 2021, 49, 8355-8369.	14.5	11
10	<i>Photorhabdus</i> antibacterial Rhs polymorphic toxin inhibits translation through ADP-ribosylation of 23S ribosomal RNA. Nucleic Acids Research, 2021, 49, 8384-8395.	14.5	21
11	RelA-SpoT Homolog toxins pyrophosphorylate the CCA end of tRNA to inhibit protein synthesis. Molecular Cell, 2021, 81, 3160-3170.e9.	9.7	26
12	(p)ppGpp controls stringent factors by exploiting antagonistic allosteric coupling between catalytic domains. Molecular Cell, 2021, 81, 3310-3322.e6.	9.7	21
13	Nonhydrolysable Analogues of (p)ppGpp and (p)ppApp Alarmone Nucleotides as Novel Molecular Tools. ACS Chemical Biology, 2021, 16, 1680-1691.	3.4	2
14	Ribosome association primes the stringent factor Rel for tRNA-dependent locking in the A-site and activation of (p)ppGpp synthesis. Nucleic Acids Research, 2021, 49, 444-457.	14.5	29
15	<i>In Vitro</i>Studies of Persister Cells. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	42
16	Hfq-Assisted RsmA Regulation Is Central to Pseudomonas aeruginosa Biofilm Polysaccharide PEL Expression. Frontiers in Microbiology, 2020, 11, 482585.	3.5	10
17	A nucleotide-switch mechanism mediates opposing catalytic activities of Rel enzymes. Nature Chemical Biology, 2020, 16, 834-840.	8.0	39
18	A widespread toxinâˆ’antitoxin system exploiting growth control via alarmone signaling. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10500-10510.	7.1	81

#	ARTICLE	IF	CITATIONS
19	Target protection as a key antibiotic resistance mechanism. Nature Reviews Microbiology, 2020, 18, 637-648.	28.6	100
20	The C-Terminal RRM/ACT Domain Is Crucial for Fine-Tuning the Activation of â€˜Longâ€™ RelA-SpoT Homolog Enzymes by Ribosomal Complexes. Frontiers in Microbiology, 2020, 11, 277.	3.5	46
21	Intramolecular Interactions Dominate the Autoregulation of Escherichia coli Stringent Factor RelA. Frontiers in Microbiology, 2019, 10, 1966.	3.5	30
22	Analysis of nucleotide pools in bacteria using HPLC-MS in HILIC mode. Talanta, 2019, 205, 120161.	5.5	44
23	The Rel stringent factor from <i>Thermus thermophilus</i>: crystallization and X-ray analysis. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 561-569.	0.8	14
24	Reanalysis of Proteomics Results Fails To Detect MazF-Mediated Stress Proteins. MBio, 2019, 10, .	4.1	7
25	Ribosome profiling analysis of eEF3-depleted Saccharomyces cerevisiae. Scientific Reports, 2019, 9, 3037.	3.3	18
26	A role for the Saccharomyces cerevisiae ABCF protein New1 in translation termination/recycling. Nucleic Acids Research, 2019, 47, 8807-8820.	14.5	26
27	ABCF ATPases Involved in Protein Synthesis, Ribosome Assembly and Antibiotic Resistance: Structural and Functional Diversification across the Tree of Life. Journal of Molecular Biology, 2019, 431, 3568-3590.	4.2	90
28	The ribosomal A-site finger is crucial for binding and activation of the stringent factor RelA. Nucleic Acids Research, 2018, 46, 1973-1983.	14.5	53
29	Structural basis for (p)ppGpp synthesis by the Staphylococcus aureus small alarmone synthetase RelP. Journal of Biological Chemistry, 2018, 293, 3254-3264.	3.4	46
30	Antibiotic resistance ABCF proteins reset the peptidyl transferase centre of the ribosome to counter translational arrest. Nucleic Acids Research, 2018, 46, 3753-3763.	14.5	71
31	Elimination of Ribosome Inactivating Factors Improves the Efficiency of Bacillus subtilis and Saccharomyces cerevisiae Cell-Free Translation Systems. Frontiers in Microbiology, 2018, 9, 3041.	3.5	10
32	Reply to Holden and Errington, â€œType II Toxin-Antitoxin Systems and Persister Cellsâ€• MBio, 2018, 9, .	4.1	10
33	Structural basis for antibiotic resistance mediated by the <i>Bacillus subtilis</i> ABCF ATPase VmlR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8978-8983.	7.1	78
34	Reassessing the Role of Type II Toxin-Antitoxin Systems in Formation of Escherichia coli Type II Persister Cells. MBio, 2018, 9, .	4.1	174
35	Subinhibitory Concentrations of Bacteriostatic Antibiotics Induce <i>relA</i> -Dependent and <i>relA</i> -Independent Tolerance to Î²-Lactams. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	58
36	Molecular mutagenesis of ppGpp: turning a RelA activator into an inhibitor. Scientific Reports, 2017, 7, 41839.	3.3	21

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37	Negative allosteric regulation of <i>Enterococcus faecalis</i> small alarmone synthetase RelQ by single-stranded RNA. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3726-3731.	7.1	50
38	HPLC-based quantification of bacterial housekeeping nucleotides and alarmone messengers ppGpp and pppGpp. Scientific Reports, 2017, 7, 11022.	3.3	97
39	Small Alarmone Synthetases as novel bacterial RNA-binding proteins. RNA Biology, 2017, 14, 1695-1699.	3.1	17
40	The stringent factor RelA adopts an open conformation on the ribosome to stimulate ppGpp synthesis. Nucleic Acids Research, 2016, 44, 6471-6481.	14.5	129
41	Evaluation of the characteristics of leucyl-tRNA synthetase (LeuRS) inhibitor AN3365 in combination with different antibiotic classes. European Journal of Clinical Microbiology and Infectious Diseases, 2016, 35, 1857-1864.	2.9	9
42	Antibacterial activity of the nitrovinylfuran G1 (Furvina) and its conversion products. Scientific Reports, 2016, 6, 36844.	3.3	9
43	Cationic bactericidal peptide 1018 does not specifically target the stringent response alarmone (p)ppGpp. Scientific Reports, 2016, 6, 36549.	3.3	37
44	Aim-less translation: loss of Saccharomyces cerevisiae mitochondrial translation initiation factor mIF3/Aim23 leads to unbalanced protein synthesis. Scientific Reports, 2016, 6, 18749.	3.3	21
45	Composition of the outgrowth medium modulates wake-up kinetics and ampicillin sensitivity of stringent and relaxed Escherichia coli. Scientific Reports, 2016, 6, 22308.	3.3	18
46	Auxotrophy-based High Throughput Screening assay for the identification of Bacillus subtilis stringent response inhibitors. Scientific Reports, 2016, 6, 35824.	3.3	17
47	Persistersâ€"as elusive as ever. Applied Microbiology and Biotechnology, 2016, 100, 6545-6553.	3.6	87
48	Fusidic Acid Targets Elongation Factor G in Several Stages of Translocation on the Bacterial Ribosome. Journal of Biological Chemistry, 2015, 290, 3440-3454.	3.4	38
49	From (p)ppGpp to (pp)pGpp: Characterization of Regulatory Effects of pGpp Synthesized by the Small Alarmone Synthetase of Enterococcus faecalis. Journal of Bacteriology, 2015, 197, 2908-2919.	2.2	88
50	Recent functional insights into the role of (p)ppGpp in bacterial physiology. Nature Reviews Microbiology, 2015, 13, 298-309.	28.6	703
51	An evolutionary ratchet leading to loss of elongation factors in eukaryotes. BMC Evolutionary Biology, 2014, 14, 35.	3.2	6
52	Mitochondrial translation initiation machinery: Conservation andÂdiversification. Biochimie, 2014, 100, 132-140.	2.6	50
53	Protein biosynthesis in mitochondria. Biochemistry (Moscow), 2013, 78, 855-866.	1.5	13
54	Mechanism of tetracycline resistance by ribosomal protection protein Tet(O). Nature Communications, 2013, 4, 1477.	12.8	87

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55	Evolutionary and genetic analyses of mitochondrial translation initiation factors identify the missing mitochondrial IF3 in S. cerevisiae. Nucleic Acids Research, 2012, 40, 6122-6134.	14.5	41
56	GTPases IF2 and EF-G bind GDP and the SRL RNA in a mutually exclusive manner. Scientific Reports, 2012, 2, 843.	3.3	11
57	Positive allosteric feedback regulation of the stringent response enzyme RelA by its product. EMBO Reports, 2012, 13, 835-839.	4.5	95
58	The RelA/SpoT Homolog (RSH) Superfamily: Distribution and Functional Evolution of ppGpp Synthetases and Hydrolases across the Tree of Life. PLoS ONE, 2011, 6, e23479.	2.5	418
59	An ancient family of SelB elongation factor-like proteins with a broad but disjunct distribution across archaea. BMC Evolutionary Biology, 2011, 11, 22.	3.2	12
60	Single-molecule investigations of the stringent response machinery in living bacterial cells. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E365-73.	7.1	254
61	Single molecule tracking fluorescence microscopy in mitochondria reveals highly dynamic but confined movement of Tom40. Scientific Reports, 2011, 1, 195.	3.3	31
62	Structure of the Dom34â€“Hbs1 complex and implications for no-go decay. Nature Structural and Molecular Biology, 2010, 17, 1233-1240.	8.2	98
63	GTP-dependent structural rearrangement of the eRF1:eRF3 complex and eRF3 sequence motifs essential for PABP binding. Nucleic Acids Research, 2010, 38, 548-558.	14.5	30
64	Single Molecule Tracking Inside Individual Living Bacterial Cells. Biophysical Journal, 2010, 98, 587a.	0.5	0
65	Thermodynamic Characterization of ppGpp Binding to EF-G or IF2 and of Initiator tRNA Binding to Free IF2 in the Presence of GDP, GTP, or ppGpp. Journal of Molecular Biology, 2010, 402, 838-846.	4.2	76
66	Does the ribosome have initiation and elongation modes of translation?. Molecular Microbiology, 2009, 72, 1310-1315.	2.5	9
67	Thermodynamics of GTP and GDP Binding to Bacterial Initiation Factor 2 Suggests Two Types of Structural Transitions. Journal of Molecular Biology, 2009, 394, 621-626.	4.2	23
68	The bacterial toxin RelE induces specific mRNA cleavage in the A site of the eukaryote ribosome. Rna, 2008, 14, 233-239.	3.5	35
69	Evolution of nonstop, no-go and nonsense-mediated mRNA decay and their termination factor-derived components. BMC Evolutionary Biology, 2008, 8, 290.	3.2	91
70	Cofactor Dependent Conformational Switching of GTPases. Biophysical Journal, 2008, 95, 1704-1715.	0.5	33
71	The pretranslocation ribosome is targeted by GTP-bound EF-G in partially activated form. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15678-15683.	7.1	36
72	Evolution of translational machinery: Could translation termination come into being before elongation?. Journal of Theoretical Biology, 2007, 248, 574-578.	1.7	0

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73	Class-1Ârelease factor eRF1 promotes GTP binding byÂclass-2Ârelease factor eRF3. Biochimie, 2006, 88, 747-757.	2.6	54
74	Two-Step Selection of mRNAs in Initiation of Protein Synthesis. Molecular Cell, 2006, 22, 155-156.	9.7	7
75	GTPases of the prokaryotic translation apparatus. Molecular Biology, 2006, 40, 688-701.	1.3	12
76	Guanine-nucleotide exchange on ribosome-bound elongation factor G initiates the translocation of tRNAs. Journal of Biology, 2005, 4, 9.	2.7	56
77	Splitting of the Posttermination Ribosome into Subunits by the Concerted Action of RRF and EF-G. Molecular Cell, 2005, 18, 675-686.	9.7	132