Term-seq reveals abundant ribo-regulation of antibiotic

Science 352, aad9822 DOI: 10.1126/science.aad9822

Citation Report

#	Article	IF	CITATIONS
1	(Meta-)genome mining for new ribo-regulators. Science, 2016, 352, 144-145.	6.0	3
2	Comparative transcriptomics across the prokaryotic tree of life. Nucleic Acids Research, 2016, 44, W46-W53.	6.5	35
3	The Expression of Antibiotic Resistance Methyltransferase Correlates with mRNA Stability Independently of Ribosome Stalling. Antimicrobial Agents and Chemotherapy, 2016, 60, 7178-7188.	1.4	28
4	Riboswitches: From living biosensors to novel targets of antibiotics. Gene, 2016, 592, 244-259.	1.0	71
5	Small Regulatory RNAs of Rickettsia conorii. Scientific Reports, 2016, 6, 36728.	1.6	36
6	Regulatory RNAs in Bacillus subtilis: a Gram-Positive Perspective on Bacterial RNA-Mediated Regulation of Gene Expression. Microbiology and Molecular Biology Reviews, 2016, 80, 1029-1057.	2.9	44
7	Widespread formation of alternative 3′ UTR isoforms via transcription termination in archaea. Nature Microbiology, 2016, 1, 16143.	5.9	58
8	How Widespread is Metabolite Sensing by Ribosome-Arresting Nascent Peptides?. Journal of Molecular Biology, 2016, 428, 2217-2227.	2.0	35
9	RNA- and protein-mediated control of Listeria monocytogenes virulence gene expression. RNA Biology, 2017, 14, 460-470.	1.5	54
10	Communication between viruses guides lysis–lysogeny decisions. Nature, 2017, 541, 488-493.	13.7	465
11	Identification of endoribonuclease specific cleavage positions reveals novel targets of RNase III in <i>Streptococcus pyogenes</i> . Nucleic Acids Research, 2017, 45, gkw1316.	6.5	18
12	Requirement of the RNA-binding protein SmpB during intracellular growth of Listeria monocytogenes. International Journal of Medical Microbiology, 2017, 307, 166-173.	1.5	8
13	New RNA-seq approaches for the study of bacterial pathogens. Current Opinion in Microbiology, 2017, 35, 78-87.	2.3	127
14	Elucidation of bacterial translation regulatory networks. Current Opinion in Systems Biology, 2017, 2, 84-90.	1.3	5
15	If it transcribes, we can sequence it: mining the complexities of host–pathogen–environment interactions using RNA-seq. Current Opinion in Microbiology, 2017, 36, 37-46.	2.3	38
16	N-terminomics identifies Prli42 as a membrane miniprotein conserved in Firmicutes and critical for stressosome activation in Listeria monocytogenes. Nature Microbiology, 2017, 2, 17005.	5.9	70
17	Environmental and genetic modulation of the phenotypic expression of antibiotic resistance. FEMS Microbiology Reviews, 2017, 41, 374-391.	3.9	112
18	Regulation of antibiotic-resistance by non-coding RNAs in bacteria. Current Opinion in Microbiology, 2017, 36, 111-117.	2.3	33

TATION REDO

#	ARTICLE	IF	CITATIONS
19	Deep sequencing approaches for the analysis of prokaryotic transcriptional boundaries and dynamics. Methods, 2017, 120, 76-84.	1.9	10
20	Neisseria genomics: current status and future perspectives. Pathogens and Disease, 2017, 75, .	0.8	23
21	How the study of <i>Listeria monocytogenes</i> has led to new concepts in biology. Future Microbiology, 2017, 12, 621-638.	1.0	45
22	Long-Range Interactions in Riboswitch Control of Gene Expression. Annual Review of Biophysics, 2017, 46, 455-481.	4.5	65
23	Listeriomics: an Interactive Web Platform for Systems Biology of <i>Listeria</i> . MSystems, 2017, 2, .	1.7	37
24	Activation of the <i>glmS</i> Ribozyme Confers Bacterial Growth Inhibition. ChemBioChem, 2017, 18, 435-440.	1.3	24
25	Modular arrangement of regulatory RNA elements. RNA Biology, 2017, 14, 287-292.	1.5	12
26	Small bacterial and phagic proteins: an updated view on a rapidly moving field. Current Opinion in Microbiology, 2017, 39, 81-88.	2.3	60
27	Chemical genomics reveals mechanistic hypotheses for uncharacterized bioactive molecules in bacteria. Current Opinion in Microbiology, 2017, 39, 42-47.	2.3	11
28	Regulation by 3′-Untranslated Regions. Annual Review of Genetics, 2017, 51, 171-194.	3.2	426
29	Regulating Bacterial Virulence with RNA. Annual Review of Microbiology, 2017, 71, 263-280.	2.9	67
30	Identification of c-di-GMP-Responsive Riboswitches. Methods in Molecular Biology, 2017, 1657, 377-402.	0.4	10
31	Ligand design for riboswitches, an emerging target class for novel antibiotics. Future Medicinal Chemistry, 2017, 9, 1649-1662.	1.1	16
32	RNAâ€mediated signal perception in pathogenic bacteria. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1429.	3.2	14
33	Detection of 224 candidate structured RNAs by comparative analysis of specific subsets of intergenic regions. Nucleic Acids Research, 2017, 45, 10811-10823.	6.5	116
34	Alternative transcriptional regulation in genome-reduced bacteria. Current Opinion in Microbiology, 2017, 39, 89-95.	2.3	18
35	A Bright Future for Antibiotics?. Annual Review of Biochemistry, 2017, 86, 567-583.	5.0	33
36	Computational prediction of regulatory, premature transcription termination in bacteria. Nucleic Acids Research, 2017, 45, 886-893.	6.5	30

		CITATION REPORT		
#	Article		IF	CITATIONS
37	RNA Regulators: Formidable Modulators of Yersinia Virulence. Trends in Microbiology,	2017, 25, 19-34.	3.5	12
38	Direct modulation of T-box riboswitch-controlled transcription by protein synthesis inh Nucleic Acids Research, 2017, 45, 10242-10258.	ibitors.	6.5	21
39	<i>In vivo</i> expression technology and 5′ end mapping of the <i>Borrelia burgdorferi</i> transcriptome identify novel RNAs expressed during mammalian infection Acids Research, 2017, 45, 775-792.	on. Nucleic	6.5	81
40	The Complex Relationship between Virulence and Antibiotic Resistance. Genes, 2017, 8	8, 39.	1.0	183
41	Roles of Regulatory RNAs for Antibiotic Resistance in Bacteria and Their Potential Value Targets. Frontiers in Microbiology, 2017, 8, 803.	e as Novel Drug	1.5	114
42	RNA-Seq-Based Transcript Structure Analysis with TrBorderExt. Methods in Molecular E 1751, 89-99.	Biology, 2018,	0.4	2
43	Antibiotic Stimulation of a Bacillus subtilis Migratory Response. MSphere, 2018, 3, .		1.3	35
44	High-resolution RNA 3â€2-ends mapping of bacterial Rho-dependent transcripts. Nucle 2018, 46, 6797-6805.	ic Acids Research,	6.5	88
45	Regulatory RNA in Mycobacterium tuberculosis, back to basics. Pathogens and Disease	2, 2018, 76, .	0.8	33
46	Cell-wall synthesis and ribosome maturation are co-regulated by an RNA switch in Myc tuberculosis. Nucleic Acids Research, 2018, 46, 5837-5849.	obacterium	6.5	19
47	Design and optimization of genetically encoded biosensors for high-throughput screer chemicals. Current Opinion in Biotechnology, 2018, 54, 18-25.	iing of	3.3	72
48	Bacterial RNA Biology on a Genome Scale. Molecular Cell, 2018, 70, 785-799.		4.5	201
49	Systematic discovery of antiphage defense systems in the microbial pangenome. Scier	ıce, 2018, 359, .	6.0	776
50	Identification and functional characterization of bacterial small non-coding RNAs and t review. Gene Reports, 2018, 10, 167-176.	heir target: A	0.4	11
51	Evolutionary Convergence of Pathway-Specific Enzyme Expression Stoichiometry. Cell, 749-761.e38.	2018, 173,	13.5	150
52	Genome-wide identification of natural RNA aptamers in prokaryotes and eukaryotes. N Communications, 2018, 9, 1289.	ature	5.8	37
53	rRNA Mimicry in RNA Regulation of Gene Expression. Microbiology Spectrum, 2018, 6,		1.2	17
54	Achieving a Predictive Understanding of Antimicrobial Stress Physiology through Syste Trends in Microbiology, 2018, 26, 296-312.	ms Biology.	3.5	14

#	Article	IF	CITATIONS
55	Bacterial Adaptation to Antibiotics through Regulatory RNAs. Antimicrobial Agents and Chemotherapy, 2018, 62, .	1.4	61
56	Surface modification of valve metals using plasma electrolytic oxidation for antibacterial applications: A review. Journal of Biomedical Materials Research - Part A, 2018, 106, 590-605.	2.1	74
57	Metabolic-flux dependent regulation of microbial physiology. Current Opinion in Microbiology, 2018, 42, 71-78.	2.3	56
58	RNA-based dynamic genetic controllers: development strategies and applications. Current Opinion in Biotechnology, 2018, 53, 1-11.	3.3	37
59	Regulatory genes coordinating antibioticâ€induced changes in promoter activity and early transcriptional termination of the mycobacterial intrinsic resistance gene <i>whiB7</i> . Molecular Microbiology, 2018, 107, 402-415.	1.2	34
60	HflXr, a homolog of a ribosome-splitting factor, mediates antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13359-13364.	3.3	41
61	The Transcriptional landscape of Streptococcus pneumoniae TIGR4 reveals a complex operon architecture and abundant riboregulation critical for growth and virulence. PLoS Pathogens, 2018, 14, e1007461.	2.1	37
62	Noncoding RNAs in Archaea: Genome-Wide Identification and Functional Classification. Methods in Enzymology, 2018, 612, 413-442.	0.4	7
63	Superior cellular activities of azido- over amino-functionalized ligands for engineered preQ ₁ riboswitches in <i>E.coli</i> . RNA Biology, 2018, 15, 1376-1383.	1.5	11
64	SMRT-Cappable-seq reveals complex operon variants in bacteria. Nature Communications, 2018, 9, 3676.	5.8	80
65			
	Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487.	3.2	11
66	Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, .	3.2 3.3	11 60
66 67	Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, . Transcriptomic study on persistence and survival of Listeria monocytogenes following lethal treatment with nisin. Journal of Global Antimicrobial Resistance, 2018, 15, 25-31.	3.2 3.3 0.9	11 60 26
66 67 68	Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, . Transcriptomic study on persistence and survival of Listeria monocytogenes following lethal treatment with nisin. Journal of Global Antimicrobial Resistance, 2018, 15, 25-31. rRNA Mimicry in RNA Regulation of Gene Expression. , 2018, , 101-116.	3.2 3.3 0.9	11 60 26 0
66676869	 Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, . Transcriptomic study on persistence and survival of Listeria monocytogenes following lethal treatment with nisin. Journal of Clobal Antimicrobial Resistance, 2018, 15, 25-31. rRNA Mimicry in RNA Regulation of Gene Expression. , 2018, , 101-116. Type I Toxin-Antitoxin Systems: Regulating Toxin Expression via Shine-Dalgarno Sequence Sequestration and Small RNA Binding. , 2018, , 171-190. 	3.2 3.3 0.9	11 60 26 0 5
 66 67 68 69 70 	Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, . Transcriptomic study on persistence and survival of Listeria monocytogenes following lethal treatment with nisin. Journal of Global Antimicrobial Resistance, 2018, 15, 25-31. rRNA Mimicry in RNA Regulation of Gene Expression. , 2018, , 101-116. Type I Toxin-Antitoxin Systems: Regulating Toxin Expression via Shine-Dalgarno Sequence Sequestration and Small RNA Binding. , 2018, , 171-190. Regulatory RNAs in Virulence and Host-Microbe Interactions. , 2018, , 305-337.	3.2 3.3 0.9	11 60 26 0 5
 66 67 68 69 70 71 	 Unique Archaeal Small RNAs. Annual Review of Genetics, 2018, 52, 465-487. ANNOgesic: a Swiss army knife for the RNA-seq based annotation of bacterial/archaeal genomes. GigaScience, 2018, 7, . Transcriptomic study on persistence and survival of Listeria monocytogenes following lethal treatment with nisin. Journal of Global Antimicrobial Resistance, 2018, 15, 25-31. rRNA Mimicry in RNA Regulation of Gene Expression., 2018, , 101-116. Type I Toxin-Antitoxin Systems: Regulating Toxin Expression via Shine-Dalgarno Sequence Sequestration and Small RNA Binding., 2018, , 171-190. Regulatory RNAs in Virulence and Host-Microbe Interactions., 2018, , 305-337. Bacterial regulatory RNAs: complexity, function, and putative drug targeting. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 335-355. 	3.2 3.3 0.9 2.3	 11 60 26 0 5 4 9

#	Article	IF	CITATIONS
73	Type I Toxin-Antitoxin Systems: Regulating Toxin Expression via Shine-Dalgarno Sequence Sequestration and Small RNA Binding. Microbiology Spectrum, 2018, 6, .	1.2	47
74	The Infection Process of Yersinia ruckeri: Reviewing the Pieces of the Jigsaw Puzzle. Frontiers in Cellular and Infection Microbiology, 2018, 8, 218.	1.8	20
75	Z-scheme 2D/3D g-C3N4@ZnO with enhanced photocatalytic activity for cephalexin oxidation under solar light. Chemical Engineering Journal, 2018, 352, 412-422.	6.6	192
76	The evolving interface between synthetic biology and functional metagenomics. Nature Chemical Biology, 2018, 14, 752-759.	3.9	44
77	Regulatory RNAs in Virulence and Host-Microbe Interactions. Microbiology Spectrum, 2018, 6, .	1.2	34
78	Extensive reshaping of bacterial operons by programmed mRNA decay. PLoS Genetics, 2018, 14, e1007354.	1.5	60
79	Multidrug efflux pumps: structure, function and regulation. Nature Reviews Microbiology, 2018, 16, 523-539.	13.6	580
80	Codon usage of highly expressed genes affects proteome-wide translation efficiency. Proceedings of the United States of America, 2018, 115, E4940-E4949.	3.3	177
81	Full-length RNA profiling reveals pervasive bidirectional transcription terminators in bacteria. Nature Microbiology, 2019, 4, 1907-1918.	5.9	87
82	Riboswitches: choosing the best platform. Biochemical Society Transactions, 2019, 47, 1091-1099.	1.6	10
83	Key Concepts and Challenges in Archaeal Transcription. Journal of Molecular Biology, 2019, 431, 4184-4201.	2.0	35
84	The Transcription Unit Architecture of Streptomyces lividans TK24. Frontiers in Microbiology, 2019, 10, 2074.	1.5	25
85	Determination of the Gene Regulatory Network of a Genome-Reduced Bacterium Highlights Alternative Regulation Independent of Transcription Factors. Cell Systems, 2019, 9, 143-158.e13.	2.9	36
86	Tools and systems for evolutionary engineering of biomolecules and microorganisms. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1313-1326.	1.4	12
87	Widespread Utilization of Peptide Communication in Phages Infecting Soil and Pathogenic Bacteria. Cell Host and Microbe, 2019, 25, 746-755.e5.	5.1	77
88	Noncoding RNA. Microbiology Spectrum, 2019, 7, .	1.2	34
89	Physiological roles of antisense RNAs in prokaryotes. Biochimie, 2019, 164, 3-16.	1.3	19
90	Exploring bacterial resistome and resistance dessemination: an approach of whole genome sequencing. Future Medicinal Chemistry, 2019, 11, 247-260.	1.1	4

	ChAnon		
#	Article	IF	CITATIONS
91	Wiring cell growth to product formation. Current Opinion in Biotechnology, 2019, 59, 85-92.	3.3	13
92	Integron-Derived Aminoglycoside-Sensing Riboswitches Control Aminoglycoside Acetyltransferase Resistance Gene Expression. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	11
93	It's all about the T: transcription termination in archaea. Biochemical Society Transactions, 2019, 47, 461-468.	1.6	23
94	Synthetic Regulatory Tools to Engineer Microbial Cell Factories for Chemical Production. , 2019, , 115-141.		0
95	Rapid generation of sequence-diverse terminator libraries and their parameterization using quantitative Term-Seq. Synthetic Biology, 2019, 4, ysz026.	1.2	11
96	Noncoding RNA. , 2019, , 562-573.		0
97	NusG-Dependent RNA Polymerase Pausing and Tylosin-Dependent Ribosome Stalling Are Required for Tylosin Resistance by Inducing 23S rRNA Methylation in Bacillus subtilis. MBio, 2019, 10, .	1.8	18
98	A <i>rhll</i> 5′ UTR-Derived sRNA Regulates RhlR-Dependent Quorum Sensing in Pseudomonas aeruginosa. MBio, 2019, 10, .	1.8	40
99	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105.	3.6	52
100	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.	2.0	90
101	Kinetics coming into focus: single-molecule microscopy of riboswitch dynamics. RNA Biology, 2019, 16, 1077-1085.	1.5	25
102	Post-transcriptional control of virulence gene expression in Staphylococcus aureus. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 734-741.	0.9	7
103	Dynamics of transcription–translation coordination tune bacterial indole signaling. Nature Chemical Biology, 2020, 16, 440-449.	3.9	19
104	Early termination of the Shiga toxin transcript generates a regulatory small RNA. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25055-25065.	3.3	16
105	Single-Nucleotide RNA Maps for the Two Major Nosocomial Pathogens Enterococcus faecalis and Enterococcus faecium. Frontiers in Cellular and Infection Microbiology, 2020, 10, 600325.	1.8	16
106	Genome-Scale Transcription-Translation Mapping Reveals Features of Zymomonas mobilis Transcription Units and Promoters. MSystems, 2020, 5, .	1.7	19
107	System-level understanding of gene expression and regulation for engineering secondary metabolite production in <i>Streptomyces</i> . Journal of Industrial Microbiology and Biotechnology, 2020, 47, 739-752.	1.4	10
108	Interplay between Regulatory RNAs and Signal Transduction Systems during Bacterial Infection. Genes, 2020, 11, 1209.	1.0	5

		CITATION REP	PORT	
#	Article		IF	CITATIONS
109	Functionally uncoupled transcription–translation in Bacillus subtilis. Nature, 2020, 585, 124-128	3.	13.7	109
110	The conserved ribonuclease aCPSF1 triggers genome-wide transcription termination of Archaea vi 3′-end cleavage mode. Nucleic Acids Research, 2020, 48, 9589-9605.	аа	6.5	31
111	Ribosome-Mediated Attenuation of <i>vga</i> (A) Expression Is Shaped by the Antibiotic Resistant Specificity of Vga(A) Protein Variants. Antimicrobial Agents and Chemotherapy, 2020, 64, .	ce	1.4	17
112	Bacterial Retrons Function In Anti-Phage Defense. Cell, 2020, 183, 1551-1561.e12.		13.5	208
113	The Sponge RNAs of bacteria – How to find them and their role in regulating the post-transcript network. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194565.	ional	0.9	34
114	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. MBio, 2020, 11, .		1.8	10
115	Advances in bacterial transcriptome understanding: From overlapping transcription to the exclude concept. Molecular Microbiology, 2020, 113, 593-602.	'n	1.2	24
116	An RNA biology perspective on speciesâ€specific programmable RNA antibiotics. Molecular Microb 2020, 113, 550-559.	viology,	1.2	30
117	Prevalence of small base-pairing RNAs derived from diverse genomic loci. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194524.		0.9	66
118	Structure-seq2 probing of RNA structure upon amino acid starvation reveals both known and nove RNA switches in <i>Bacillus subtilis</i> . Rna, 2020, 26, 1431-1447.	21	1.6	15
119	Target protection as a key antibiotic resistance mechanism. Nature Reviews Microbiology, 2020, 1 637-648.	8,	13.6	100
120	MetaRibo-Seq measures translation in microbiomes. Nature Communications, 2020, 11, 3268.		5.8	30
121	Differential evolution in 3â€2UTRs leads to specific gene expression in Staphylococcus. Nucleic Ac Research, 2020, 48, 2544-2563.	ids	6.5	19
122	Navigation through the twists and turns of RNA sequencing technologies: Application to bacterial regulatory RNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 1945	06.	0.9	11
123	FttA is a CPSF73 homologue that terminates transcription in Archaea. Nature Microbiology, 2020, 545-553.	5,	5.9	23
124	Identification of RNA 3´ ends and termination sites in <i>Haloferax volcanii</i> . RNA Biology, 202 663-676.	0, 17,	1.5	16
125	STATR: A simple analysis pipeline of Ribo-Seq in bacteria. Journal of Microbiology, 2020, 58, 217-2	26.	1.3	9
126	Efficient Photocatalytic Degradation and Adsorption of Tetracycline over Type-II Heterojunctions Consisting of ZnO Nanorods and K-Doped Exfoliated g-C ₃ N ₄ Nanoshee Industrial & Engineering Chemistry Research, 2020, 59, 2860-2873.	ːs	1.8	69

#	Article	IF	CITATIONS
127	Expression of ribosomal protection protein RppA is regulated by a ribosomeâ€dependent riboâ€regulator and two mistranslation products. Environmental Microbiology, 2021, 23, 696-712.	1.8	9
128	Prokaryotic viperins produce diverse antiviral molecules. Nature, 2021, 589, 120-124.	13.7	172
129	Networks of Resistance: Small RNA Control of Antibiotic Resistance. Trends in Genetics, 2021, 37, 35-45.	2.9	26
130	Regulatory roles of Escherichia coli 5' UTR and ORF-internal RNAs detected by 3' end mapping. ELife, 2021, 10, .	2.8	60
131	Grad-seq identifies KhpB as a global RNA-binding protein in <i>Clostridioides difficile</i> that regulates toxin production. MicroLife, 2021, 2, .	1.0	25
133	High-pressure processing-induced transcriptome response during recovery of Listeria monocytogenes. BMC Genomics, 2021, 22, 117.	1.2	18
134	BSGatlas: a unified Bacillus subtilis genome and transcriptome annotation atlas with enhanced information access. Microbial Genomics, 2021, 7, .	1.0	12
135	Cross-species RNA-seq for deciphering host–microbe interactions. Nature Reviews Genetics, 2021, 22, 361-378.	7.7	52
136	Attenuator LRR – a regulatory tool for modulating gene expression in Gramâ€positive bacteria. Microbial Biotechnology, 2021, 14, 2538-2551.	2.0	3
137	RNA-Mediated Control in Listeria monocytogenes: Insights Into Regulatory Mechanisms and Roles in Metabolism and Virulence. Frontiers in Microbiology, 2021, 12, 622829.	1.5	7
138	Genome-scale analyses of transcriptional start sites in Mycobacterium marinum under normoxic and hypoxic conditions. BMC Genomics, 2021, 22, 235.	1.2	3
139	Retrospective Use of Whole-Genome Sequencing Expands the Multicountry Outbreak Cluster of Listeria monocytogenes ST1247. International Journal of Genomics, 2021, 2021, 1-5.	0.8	6
141	NusG is an intrinsic transcription termination factor that stimulates motility and coordinates gene expression with NusA. ELife, 2021, 10, .	2.8	27
142	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium Synechocystis sp. PCC 7338. Frontiers in Microbiology, 2021, 12, 667450.	1.5	6
143	Comprehensive discovery of novel structured noncoding RNAs in 26 bacterial genomes. RNA Biology, 2021, 18, 2417-2432.	1.5	13
144	A novel computational framework for genome-scale alternative transcription units prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	0
146	Advanced strategies and tools to facilitate and streamline microbial adaptive laboratory evolution. Trends in Biotechnology, 2022, 40, 38-59.	4.9	49
148	Elucidating the Regulatory Elements for Transcription Termination and Posttranscriptional Processing in the Streptomyces clavuligerus Genome. MSystems, 2021, 6, .	1.7	6

#	ARTICLE	IF	CITATIONS
149	Structural basis of ABCF-mediated resistance to pleuromutilin, lincosamide, and streptogramin A antibiotics in Gram-positive pathogens. Nature Communications, 2021, 12, 3577.	5.8	40
150	Quantitative mapping of mRNA 3' ends in Pseudomonas aeruginosa reveals a pervasive role for premature 3' end formation in response to azithromycin. PLoS Genetics, 2021, 17, e1009634.	1.5	7
151	Simultaneous ribosome profiling of hundreds of microbes from the human microbiome. Nature Protocols, 2021, 16, 4676-4691.	5.5	7
152	Diversity and Versatility in Small RNA-Mediated Regulation in Bacterial Pathogens. Frontiers in Microbiology, 2021, 12, 719977.	1.5	23
153	Identifying Small Open Reading Frames in Prokaryotes with Ribosome Profiling. Journal of Bacteriology, 2022, 204, JB0029421.	1.0	26
154	Specific and Global RNA Regulators in Pseudomonas aeruginosa. International Journal of Molecular Sciences, 2021, 22, 8632.	1.8	17
155	Quantitative Control for Stoichiometric Protein Synthesis. Annual Review of Microbiology, 2021, 75, 243-267.	2.9	14
156	Beyond Self-Resistance: ABCF ATPase LmrC Is a Signal-Transducing Component of an Antibiotic-Driven Signaling Cascade Accelerating the Onset of Lincomycin Biosynthesis. MBio, 2021, 12, e0173121.	1.8	23
158	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. PLoS Genetics, 2021, 17, e1009821.	1.5	16
159	High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. Scientific Reports, 2021, 11, 18319.	1.6	6
160	Facile synthesis of visible-light-induced mesoporous Ag2O/Fe2(MoO4)3 photocatalysts for degradation of tetracycline. Optical Materials, 2021, 121, 111505.	1.7	9
161	Systems and synthetic biology to elucidate secondary metabolite biosynthetic gene clusters encoded in <i>Streptomyces</i> genomes. Natural Product Reports, 2021, 38, 1330-1361.	5.2	35
162	Bacterial 3′UTRs: A Useful Resource in Post-transcriptional Regulation. Frontiers in Molecular Biosciences, 2020, 7, 617633.	1.6	21
163	Listeria monocytogenes: towards a complete picture of its physiology and pathogenesis. Nature Reviews Microbiology, 2018, 16, 32-46.	13.6	584
164	Genome-scale determination of 5´ and 3´ boundaries of RNA transcripts in Streptomyces genomes. Scientific Data, 2020, 7, 436.	2.4	6
176	Evidence for a cytoplasmic pool of ribosome-free mRNAs encoding inner membrane proteins in Escherichia coli. PLoS ONE, 2017, 12, e0183862.	1.1	12
177	Discovery of numerous novel small genes in the intergenic regions of the Escherichia coli O157:H7 Sakai genome. PLoS ONE, 2017, 12, e0184119.	1.1	38
178	Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . Life Science Alliance, 2020, 3, e202000847.	1.3	11

ARTICLE IF CITATIONS Bacterial fumarase and L-malic acid are evolutionary ancient components of the DNA damage response. 179 13 2.8 ELife, 2017, 6, . Gene autoregulation by 3' UTR-derived bacterial small RNAs. ELife, 2020, 9, . 2.8 181 Prioritizing bona fide bacterial small RNAs with machine learning classifiers. PeerJ, 2019, 7, e6304. 0.9 9 Riboregulation in bacteria: From general principles to novel mechanisms of the <i>trp</i> attenuator and its <scp>sRNA</scp> and peptide products. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1696. uORFâ€mediated riboregulation controls transcription of <i>whiB7/wblC</i> antibiotic resistance gene. 183 1.2 12 Molecular Microbiology, 2022, 117, 179-192. A Global Characterisation of the Archaeal Transcription Machinery. Nucleic Acids and Molecular 184 0.2 Biology, 2017, , 1-26. Reconstruction of the Regulatory Network in a Minimal Bacterium Reveals Extensive 186 0.4 0 Non-Transcription Factor Dependent Regulation. SSRN Electronic Journal, 0, , . The T-Box Riboswitch: tRNA as an Effector to Modulate Gene Regulation., 0,, 89-100. 188 Siblings or doppelgA#gers? Deciphering the evolution of structured cis-regulatory RNAs beyond 197 1.6 3 homology. Biochemical Society Transactions, 2020, 48, 1941-1951. Direct RNA Sequencing Unfolds the Complex Transcriptome of Vibrio parahaemolyticus. MSystems, 1.7 2021, 6, e0099621. RiboReport - benchmarking tools for ribosome profiling-based identification of open reading frames in 202 3.2 15 bacteria. Briefings in Bioinformatics, 2022, 23, Massively parallel characterization of engineered transcript isoforms using direct RNA sequencing. 5.8 Nature Communications, 2022, 13, 434 Construction of a Z-scheme g-C₃N₄/NBGO/BiVO₄ heterostructure with visible-light driven photocatalytic degradation of tetracycline: efficiency, reaction pathway and 204 2.1 26 mechanism. Čatalysis Science and Technology, 2022, 12, 1339-1358. Genome-scale analysis of genetic regulatory elements in Streptomyces avermitilis MA-4680 using 1.2 transcript boundary information. BMC Genomics, 2022, 23, 68. Synthetic 3â€²-UTR valves for optimal metabolic flux control in <i>Escherichia coli</i>. Nucleic Acids 207 6.5 3 Research, 2022, 50, 4171-4186. Analysis of mRNA Decay Intermediates in Bacillus subtilis 3′ Exoribonuclease and RNA Helicase Mutant 208 1.8 Strains. MBio, 2022, 13, e0040022. An overview of gene regulation in bacteria by small RNAs derived from mRNA 3â€² ends. FEMS 209 3.9 37 Microbiology Reviews, 2022, 46, . Development of highly characterized genetic bioparts for efficient gene expression in CO2-fixing Eubacterium limosum. Metabolic Engineering, 2022, 72, 215-226.

#	Article	IF	CITATIONS
211	Different Regulatory Modes of <i>Synechocystis</i> sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. MSystems, 2021, 6, e0094321.	1.7	7
212	aCPSF1 cooperates with terminator U-tract to dictate archaeal transcription termination efficacy. ELife, 2021, 10, .	2.8	12
213	Challenges in defining the functional, nonâ€coding, expressed genome of members of the <i>Mycobacterium tuberculosis</i> complex. Molecular Microbiology, 2022, 117, 20-31.	1.2	7
214	Ubiquitous mRNA decay fragments in <i>E. coli</i> redefine the functional transcriptome. Nucleic Acids Research, 2022, 50, 5029-5046.	6.5	15
234	Lineage-specific insertions in T-box riboswitches modulate antibiotic binding and action. Nucleic Acids Research, 2022, , .	6.5	2
236	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, .	0.9	5
238	RNase III-CLASH of multi-drug resistant Staphylococcus aureus reveals a regulatory mRNA 3′UTR required for intermediate vancomycin resistance. Nature Communications, 2022, 13, .	5.8	15
239	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.	6.5	15
240	Inverse folding based pre-training for the reliable identification of intrinsic transcription terminators. PLoS Computational Biology, 2022, 18, e1010240.	1.5	1
241	Retrospective Investigation of the Whole Genome of the Hypovirulent Listeria monocytogenes Strain of ST201, CC69, Lineage III, Isolated from a Piglet with Fatal Neurolisteriosis. Microorganisms, 2022, 10, 1442.	1.6	1
242	Bacteria deplete deoxynucleotides to defend against bacteriophage infection. Nature Microbiology, 2022, 7, 1200-1209.	5.9	58
243	Na+ riboswitches regulate genes for diverse physiological processes in bacteria. Nature Chemical Biology, 2022, 18, 878-885.	3.9	13
244	Gene rppA co-regulated by LRR, SigA, and CcpA mediates antibiotic resistance in Bacillus thuringiensis. Applied Microbiology and Biotechnology, 2022, 106, 5687-5699.	1.7	0
246	Profiling of bacterial transcriptome from ultraâ€low input with <scp>MiniBac</scp> â€seq. Environmental Microbiology, 0, , .	1.8	3
248	The expression of aminoglycoside resistance genes in integron cassettes is not controlled by riboswitches. Nucleic Acids Research, 2022, 50, 8566-8579.	6.5	4
249	Factor-stimulated intrinsic termination: getting by with a little help from some friends. Transcription, 2022, 13, 96-108.	1.7	4
250	Transcription-Translation Coupling in Bacteria. Annual Review of Genetics, 2022, 56, 187-205.	3.2	15
251	Transcriptional regulation and drug resistance in Mycobacterium tuberculosis. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	9

	CHAIL	IN REPORT	
#	Article	IF	Citations
252	Discovering riboswitches: the past and the future. Trends in Biochemical Sciences, 2023, 48, 119-141.	3.7	62
253	Comprehensive transcription terminator atlas for Bacillus subtilis. Nature Microbiology, 2022, 7, 1918-1931.	5.9	13
254	Structural basis for HflXr-mediated antibiotic resistance in <i>Listeria monocytogenes</i> . Nucleic Acids Research, 2022, 50, 11285-11300.	6.5	9
255	The transcriptomic landscape of Magnetospirillum gryphiswaldense during magnetosome biomineralization. BMC Genomics, 2022, 23, .	1.2	2
256	Genetic and metabolic engineering of Methanococcus spp. Current Research in Biotechnology, 2023, 5, 100115.	1.9	2
258	An RNA sponge controls quorum sensing dynamics and biofilm formation in Vibrio cholerae. Nature Communications, 2022, 13, .	5.8	19
260	Identification and characterization of RNA binding sites for (p)ppGpp using RNA-DRaCALA. Nucleic Acids Research, 2023, 51, 852-869.	6.5	1
261	Small regulatory RNAs in microbial pathogenesis and biofilm formation: An emerging role as potential drug targets. , 2023, , 373-394.		0
263	Premature termination of transcription is shaped by Rho and translated uORFS in Mycobacterium tuberculosis. IScience, 2023, 26, 106465.	1.9	7
264	Cryo-EM structure of the RADAR supramolecular anti-phage defense complex. Cell, 2023, 186, 987-998.e15.	13.5	28
265	Genome-encoded ABCF factors implicated in intrinsic antibiotic resistance in Gram-positive bacteria: VmlR2, Ard1 and CplR. Nucleic Acids Research, 2023, 51, 4536-4554.	6.5	9
267	Using a whole genome coâ€expression network to inform the functional characterisation of predicted genomic elements from <i>Mycobacterium tuberculosis</i> transcriptomic data. Molecular Microbiology, 2023, 119, 381-400.	1.2	1
269	Sourcing Phage-Encoded Terminators Using ONT-cappable-seq for SynBio Applications in <i>Pseudomonas</i> . ACS Synthetic Biology, 2023, 12, 1415-1423.	1.9	3
281	Genome-Scale Analysis of the Structure and Function of RNA Pathways and Networks in Pseudomonas aeruginosa. Methods in Molecular Biology, 2024, , 183-195.	0.4	0
292	Obtaining Detailed Phage Transcriptomes Using ONT-Cappable-Seq. Methods in Molecular Biology, 2024, , 207-235.	0.4	0