

Yangbo Hu

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	A Feedback Regulatory Loop Containing McdR and WhiB2 Controls Cell Division and DNA Repair in Mycobacteria. <i>MBio</i> , 2022, 13, e0334321.	4.1	5
2	Roles of zinc-binding domain of bacterial RNA polymerase in transcription. <i>Trends in Biochemical Sciences</i> , 2022, 47, 710-724.	7.5	9
3	Mobile Plasmid Mediated Transition From Colistin-Sensitive to Resistant Phenotype in <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 619369.	3.5	3
4	Characterization of the binding motif for the T3SS master regulator LcrF in <i>Yersinia pseudotuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	2
5	Systematic Analysis of 42 <i>Autographa Californica</i> Multiple Nucleopolyhedrovirus Genes Identifies An Additional Six Genes Involved in the Production of Infectious Budded Virus. <i>Virologica Sinica</i> , 2021, 36, 762-773.	3.0	7
6	Inactivating SARS-CoV-2 by electrochemical oxidation. <i>Science Bulletin</i> , 2021, 66, 720-726.	9.0	18
7	Genome-scale analyses of transcriptional start sites in <i>Mycobacterium marinum</i> under normoxic and hypoxic conditions. <i>BMC Genomics</i> , 2021, 22, 235.	2.8	3
8	Label-Free Comparative Proteomics of Differentially Expressed <i>Mycobacterium tuberculosis</i> Protein in Rifampicin-Related Drug-Resistant Strains. <i>Pathogens</i> , 2021, 10, 607.	2.8	2
9	Structural visualization of transcription activated by a multidrug-sensing MerR family regulator. <i>Nature Communications</i> , 2021, 12, 2702.	12.8	25
10	Structural basis of copper-efflux-regulator-dependent transcription activation. <i>IScience</i> , 2021, 24, 102449.	4.1	16
11	LcrQ Coordinates with the YopD-LcrH Complex To Repress lcrF Expression and Control Type III Secretion by <i>Yersinia pseudotuberculosis</i> . <i>MBio</i> , 2021, 12, e0145721.	4.1	3
12	Structural basis for activation of Swi2/Snf2 ATPase RapA by RNA polymerase. <i>Nucleic Acids Research</i> , 2021, 49, 10707-10716.	14.5	5
13	CpxR regulates the Rcs phosphorelay system in controlling the Ysc-Yop type III secretion system in <i>Yersinia pseudotuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	10
14	Basal-Level Effects of (p)ppGpp in the Absence of Branched-Chain Amino Acids in <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	4
15	Structural basis of bacterial σ^{28} -mediated transcription reveals roles of the RNA polymerase zinc-binding domain. <i>EMBO Journal</i> , 2020, 39, e104389.	7.8	22
16	RbpA and σ^B association regulates polyphosphate levels to modulate mycobacterial isoniazid tolerance. <i>Molecular Microbiology</i> , 2018, 108, 627-640.	2.5	13
17	Association of σ^H with the C-Terminal Region of the β Subunit Is Essential for Assembly of RNA Polymerase in <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	5
18	PhoPR Positively Regulates <i>whiB3</i> Expression in Response to Low pH in Pathogenic Mycobacteria. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	20

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19	RbpA relaxes promoter selectivity of <i>M. tuberculosis</i> RNA polymerase. <i>Nucleic Acids Research</i> , 2018, 46, 10106-10118.	14.5	14
20	RgsA, an RpoS-dependent sRNA, negatively regulates rpoS expression in <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2018, 164, 716-724.	1.8	13
21	Characterization of a Minimal Type of Promoter Containing the σ^{10} Element and a Guanine at the σ^{14} or σ^{13} Position in Mycobacteria. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	16
22	A pH-gated conformational switch regulates the phosphatase activity of bifunctional HisKA-family histidine kinases. <i>Nature Communications</i> , 2017, 8, 2104.	12.8	37
23	Mycobacterial WhiB6 Differentially Regulates ESX-1 and the Dos Regulon to Modulate Granuloma Formation and Virulence in Zebrafish. <i>Cell Reports</i> , 2016, 16, 2512-2524.	6.4	71
24	RpoS-dependent sRNA RgsA regulates Fis and AcpP in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2016, 102, 244-259.	2.5	29
25	σ^E -dependent activation of RbpA controls transcription of the <i>furA</i> operon in response to oxidative stress in mycobacteria. <i>Molecular Microbiology</i> , 2016, 102, 107-120.	2.5	15
26	Genome-wide characterization of monomeric transcriptional regulators in <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 889-897.	1.8	13
27	<i>RcsB</i> positively regulates the <i>Yersinia</i> <i>YscYop</i> type III secretion system by activating expression of the master transcriptional regulator <i>LcrF</i> . <i>Environmental Microbiology</i> , 2015, 17, 1219-1233.	3.8	19
28	LcrQ Blocks the Role of LcrF in Regulating the Ysc-Yop Type III Secretion Genes in <i>Yersinia pseudotuberculosis</i> . <i>PLoS ONE</i> , 2014, 9, e92243.	2.5	20
29	<i>Yersinia</i> <i>YscYop</i> type III secretion feedback inhibition is relieved through <i>YscV</i> -dependent recognition and secretion of <i>LcrQ</i> . <i>Molecular Microbiology</i> , 2014, 91, 494-507.	2.5	17
30	<i>Mycobacterium</i> RbpA cooperates with the stress-response σ^B subunit of RNA polymerase in promoter DNA unwinding. <i>Nucleic Acids Research</i> , 2014, 42, 10399-10408.	14.5	38
31	A <i>cis</i> -encoded sRNA controls the expression of <i>fabH2</i> in <i>Yersinia</i> . <i>FEBS Letters</i> , 2014, 588, 1961-1966.	2.8	6
32	<i>Mycobacterium tuberculosis</i> RbpA protein is a new type of transcriptional activator that stabilizes the σ^A -containing RNA polymerase holoenzyme. <i>Nucleic Acids Research</i> , 2012, 40, 6547-6557.	14.5	60
33	Ribosomal Binding Site Switching: An Effective Strategy for High-Throughput Cloning Constructions. <i>PLoS ONE</i> , 2012, 7, e50142.	2.5	3
34	Small non-coding RNA SraG regulates the operon YPK_1206-1205 in <i>Yersinia pseudotuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2012, 331, 37-43.	1.8	16
35	Cra negatively regulates acid survival in <i>Yersinia pseudotuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2011, 317, 190-195.	1.8	4
36	Characterization of an aspartate-dependent acid survival system in <i>Yersinia pseudotuberculosis</i> . <i>FEBS Letters</i> , 2010, 584, 2311-2314.	2.8	33

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37	Duckweed (<i>Lemna minor</i>) as a Model Plant System for the Study of Human Microbial Pathogenesis. PLoS ONE, 2010, 5, e13527.	2.5	32
38	OmpR positively regulates urease expression to enhance acid survival of <i>Yersinia pseudotuberculosis</i> . Microbiology (United Kingdom), 2009, 155, 2522-2531.	1.8	66
39	Positive regulation of flhDC expression by OmpR in <i>Yersinia pseudotuberculosis</i> . Microbiology (United Kingdom), 2009, 155, 3622-3631.	1.8	21
40	Functional characterization of FlgM in the regulation of flagellar synthesis and motility in <i>Yersinia pseudotuberculosis</i> . Microbiology (United Kingdom), 2009, 155, 1890-1900.	1.8	20
41	Effects of quorum sensing autoinducer degradation gene on virulence and biofilm formation of <i>Pseudomonas aeruginosa</i> . Science in China Series C: Life Sciences, 2007, 50, 385-391.	1.3	29
42	The flhDC gene affects motility and biofilm formation in <i>Yersinia pseudotuberculosis</i> . Science in China Series C: Life Sciences, 2007, 50, 814-821.	1.3	11