Irina Artsimovitch

List of Publications by Year
in descending order

#	Article	IF	Citations
1	A nonâ€native Câ€terminal extension of the Î²â€™ subunit compromises RNA polymerase and Rho functions. Molecular Microbiology, 2022, , .	1.2	0
2	Positive supercoiling favors transcription elongation through lac repressor-mediated DNA loops. Nucleic Acids Research, 2022, 50, 2826-2835.	6.5	4
3	RfaH May Oppose Silencing by H-NS and YmoA Proteins during Transcription Elongation. Journal of Bacteriology, 2022, 204, e0059921.	1.0	6
4	High-throughput single-molecule experiments reveal heterogeneity, state switching, and three interconnected pause states in transcription. Cell Reports, 2022, 39, 110749.	2.9	18
5	Going Retro, Going Viral: Experiences and Lessons in Drug Discovery from COVID-19. Molecules, 2022, 27, 3815.	1.7	1
6	Allosteric couplings upon binding of RfaH to transcription elongation complexes. Nucleic Acids Research, 2022, 50, 6384-6397.	6.5	2
7	A Growing Gap between the RNAP and the Lead Ribosome. Trends in Microbiology, 2021, 29, 4-5.	3.5	4
8	Steps toward translocation-independent RNA polymerase inactivation by terminator ATPase Ï. Science, 2021, 371, .	6.0	78
9	A translational riboswitch coordinates nascent transcriptionâ€"translation coupling. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
10	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. MBio, 2021, 12, e0142321.	1.8	20
11	NMPylation and de-NMPylation of SARS-CoV-2 nsp9 by the NiRAN domain. Nucleic Acids Research, 2021, 49, 8822-8835.	6.5	30
12	Reductionism Ad Absurdum: The Misadventures of Structural Biology in the Time of Coronavirus. ACS Infectious Diseases, 2021, 7, 2948-2952.	1.8	1
13	Bacterial RNA synthesis: back to the limelight. Transcription, 2021, 12, 89-91.	1.7	0
14	Differential Local Stability Governs the Metamorphic Fold Switch of Bacterial Virulence Factor RfaH. Biophysical Journal, 2020, 118, 96-104.	0.2	22
15	Origins and Molecular Evolution of the NusG Paralog RfaH. MBio, 2020, 11, .	1.8	15
16	Benzyl and benzoyl benzoic acid inhibitors of bacterial RNA polymerase-sigma factor interaction. European Journal of Medicinal Chemistry, 2020, 208, 112671.	2.6	11
17	Discovery of Antibacterials That Inhibit Bacterial RNA Polymerase Interactions with Sigma Factors. Journal of Medicinal Chemistry, 2020, 63, 7695-7720.	2.9	18
18	NusG, an Ancient Yet Rapidly Evolving Transcription Factor. Frontiers in Microbiology, 2020, 11, 619618.	1.5	30

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19	The Î´ subunit and NTPase HelD institute a two-pronged mechanism for RNA polymerase recycling. Nature Communications, 2020, 11, 6418.	5.8	32
20	The dormancyâ€specific regulator, SutA, is intrinsically disordered and modulates transcription initiation in <i>Pseudomonas aeruginosa</i>. Molecular Microbiology, 2019, 112, 992-1009.	1.2	11
21	The Mechanisms of Substrate Selection, Catalysis, and Translocation by the Elongating RNA Polymerase. Journal of Molecular Biology, 2019, 431, 3975-4006.	2.0	56
22	Ancient Transcription Factors in the News. MBio, 2019, 10, .	1.8	23
23	Reversible fold-switching controls the functional cycle of the antitermination factor RfaH. Nature Communications, 2019, 10, 702.	5.8	50
24	RNA synthesis is a team effort. Nature Microbiology, 2019, 4, 1776-1777.	5.9	0
25	Uneven Braking Spins RNA Polymerase into a Pause. Molecular Cell, 2018, 69, 723-725.	4.5	4
26	Rebuilding the bridge between transcription and translation. Molecular Microbiology, 2018, 108, 467-472.	1.2	29
27	Locking the nontemplate DNA to control transcription. Molecular Microbiology, 2018, 109, 445-457.	1.2	16
28	Ligand Modulates Cross-Coupling between Riboswitch Folding and Transcriptional Pausing. Molecular Cell, 2018, 72, 541-552.e6.	4.5	48
29	Global DNA Compaction in Stationary-Phase Bacteria Does Not Affect Transcription. Cell, 2018, 174, 1188-1199.e14.	13.5	81
30	In silico discovery of small molecules that inhibit RfaH recruitment to RNA polymerase. Molecular Microbiology, 2018, 110, 128-142.	1.2	11
31	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. Molecular Cell, 2018, 71, 911-922.e4.	4.5	65
32	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. Cell, 2018, 173, 1650-1662.e14.	13.5	143
33	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. ELife, 2018, 7, .	2.8	45
34	A Screen for <i>rfaH</i> Suppressors Reveals a Key Role for a Connector Region of Termination Factor Rho. MBio, 2017, 8, .	1.8	23
35	Distributed biotinâ€“streptavidin transcription roadblocks for mapping cotranscriptional RNA folding. Nucleic Acids Research, 2017, 45, e109-e109.	6.5	38
36	Flipping states: a few key residues decide the winning conformation of the only universally conserved transcription factor. Nucleic Acids Research, 2017, 45, 8835-8843.	6.5	28

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37	RNA polymerase gate loop guides the nontemplate DNA strand in transcription complexes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14994-14999.	3.3	20
38	Maintenance of Transcription-Translation Coupling by Elongation Factor P. MBio, 2016, 7, .	1.8	24
39	Initial Events in Bacterial Transcription Initiation. Biomolecules, 2015, 5, 1035-1062.	1.8	157
40	pH Dependence of the Stress Regulator DksA. PLoS ONE, 2015, 10, e0120746.	1.1	22
41	Interdomain Contacts Control Native State Switching of RfaH on a Dual-Funneled Landscape. PLoS Computational Biology, 2015, 11, e1004379.	1.5	47
42	E. coli RNA Polymerase Determinants of Open Complex Lifetime and Structure. Journal of Molecular Biology, 2015, 427, 2435-2450.	2.0	45
43	Ubiquitous transcription factors display structural plasticity and diverse functions. BioEssays, 2015, 37, 324-334.	1.2	25
44	Creative Math of RNA Polymerase III Termination: Sense Plus Antisense Makes More Sense. Molecular Cell, 2015, 58, 974-976.	4.5	1
45	Regulation of Transcript Elongation. Annual Review of Microbiology, 2015, 69, 49-69.	2.9	64
46	Purification of Bacterial RNA Polymerase: Tools and Protocols. Methods in Molecular Biology, 2015, 1276, 13-29.	0.4	123
47	CBR antimicrobials alter coupling between the bridge helix and the Î² subunit in RNA polymerase. Nature Communications, 2014, 5, 3408.	5.8	34
48	Interplay between the trigger loop and the F loop during RNA polymerase catalysis. Nucleic Acids Research, 2014, 42, 544-552.	6.5	25
49	The tug of DNA repair. Nature, 2014, 505, 298-299.	13.7	15
50	Toward a General Mechanism for Transcription Initiation. Biophysical Journal, 2014, 106, 488a.	0.2	0
51	NusG-Spt5 Proteinsâ€"Universal Tools for Transcription Modification and Communication. Chemical Reviews, 2013, 113, 8604-8619.	23.0	54
52	An Insertion in the Catalytic Trigger Loop Gates the Secondary Channel of RNA Polymerase. Journal of Molecular Biology, 2013, 425, 82-93.	2.0	37
53	DksA2, a zincâ€independent structural analog of the transcription factor DksA. FEBS Letters, 2013, 587, 614-619.	1.3	33
54	A novel non-radioactive primaseâ€"pyrophosphatase activity assay and its application to the discovery of inhibitors of Mycobacterium tuberculosis primase DnaG. Nucleic Acids Research, 2013, 41, e56-e56.	6.5	49

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55	Interdomain contacts control folding of transcription factor RfaH. Nucleic Acids Research, 2013, 41, 10077-10085.	6.5	37
56	Response to Klyuyev and Vassylyev: On the mechanism of tagetitoxin inhibition of transcription. Transcription, 2012, 3, 51-55.	1.7	3
57	Transformer proteins. Cell Cycle, 2012, 11, 4289-4290.	1.3	25
58	Nucleotide excision repair (NER) machinery recruitment by the transcription-repair coupling factor involves unmasking of a conserved intramolecular interface. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3353-3358.	3.3	42
59	Fidaxomicin Is an Inhibitor of the Initiation of Bacterial RNA Synthesis. Clinical Infectious Diseases, 2012, 55, S127-S131.	2.9	85
60	Transcription initiation factor DksA has diverse effects on RNA chain elongation. Nucleic Acids Research, 2012, 40, 3392-3402.	6.5	47
61	Transformation. RNA Biology, 2012, 9, 1418-1423.	1.5	11
62	An Î± Helix to Î² Barrel Domain Switch Transforms the Transcription Factor RfaH into a Translation Factor. Cell, 2012, 150, 291-303.	13.5	201
63	Interplay of DNA repair with transcription: from structures to mechanisms. Trends in Biochemical Sciences, 2012, 37, 543-552.	3.7	12
64	E. Coli RNA Polymerase: A Molecular DNA Opening Machine. Biophysical Journal, 2012, 102, 286a.	0.2	0
65	Transcriptional pausing coordinates folding of the aptamer domain and the expression platform of a riboswitch. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3323-3328.	3.3	93
66	Termination and antitermination: RNA polymerase runs a stop sign. Nature Reviews Microbiology, 2011, 9, 319-329.	13.6	175
67	The Î² Subunit Gate Loop Is Required for RNA Polymerase Modification by RfaH and NusG. Molecular Cell, 2011, 43, 253-262.	4.5	96
68	Role of a Zn-independent DksA in Zn homeostasis and stringent response. Molecular Microbiology, 2011, 79, 700-715.	1.2	68
69	Tagetitoxin Inhibits RNA Polymerase through Trapping of the Trigger Loop. Journal of Biological Chemistry, 2011, 286, 40395-40400.	1.6	31
70	Functional regions of the Nâ€terminal domain of the antiterminator RfaH. Molecular Microbiology, 2010, 76, 286-301.	1.2	63
71	A processive riboantiterminator seeks a switch to make biofilms. Molecular Microbiology, 2010, 76, 535-539.	1.2	4
72	Functional analysis of Thermus thermophilus transcription factor NusG. Nucleic Acids Research, 2010, 38, 7432-7445.	6.5	44

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73	Multiple roles of the RNA polymerase Î²â€² SW2 region in transcription initiation, promoter escape, and RNA elongation. Nucleic Acids Research, 2010, 38, 5784-5796.	6.5	25
74	Modulation of RNA polymerase activity through the trigger loop folding. Transcription, 2010, 1, 89-94.	1.7	9
75	The Î² Subunit Gate Loop Mediates Antitermination Modification of RNA Polymerase. FASEB Journal, 2010, 24, .	0.2	0
76	Allosteric control of catalysis by the F loop of RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18942-18947.	3.3	41
77	Functional specialization of transcription elongation factors. EMBO Journal, 2009, 28, 112-122.	3.5	114
78	Transcription inactivation through local refolding of the RNA polymerase structure. Nature, 2009, 457, 332-335.	13.7	131
79	Mechanism of chromatin remodeling and recovery during passage of RNA polymerase II. Nature Structural and Molecular Biology, 2009, 16, 1272-1278.	3.6	162
80	In vitro approaches to analysis of transcription termination. Methods, 2009, 47, 37-43.	1.9	42
81	Post-initiation control by the initiation factor sigma. Molecular Microbiology, 2008, 68, 1-3.	1.2	13
82	The elongation factor RfaH and the initiation factor Ïƒ bind to the same site on the transcription elongation complex. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 865-870.	3.3	60
83	Allosteric control of the RNA polymerase by the elongation factor RfaH. Nucleic Acids Research, 2007, 35, 5694-5705.	6.5	68
84	Structural Basis for Converting a General Transcription Factor into an Operon-Specific Virulence Regulator. Molecular Cell, 2007, 26, 117-129.	4.5	191
85	The carboxyâ€terminal coiledâ€coil of the RNA polymerase Î²â€²â€subunit is the main binding site for Gre factors. EMBO Reports, 2007, 8, 1038-1043.	2.0	53
86	Merging the RNA and DNA worlds. Nature Structural and Molecular Biology, 2007, 14, 1122-1123.	3.6	3
87	Structural basis for substrate loading in bacterial RNA polymerase. Nature, 2007, 448, 163-168.	13.7	333
88	Structural basis for transcription elongation by bacterial RNA polymerase. Nature, 2007, 448, 157-162.	13.7	380
89	Is It Easy to Stop RNA Polymerase?. Cell Cycle, 2006, 5, 399-404.	1.3	22
90	Regulation through the RNA Polymerase Secondary Channel. Journal of Biological Chemistry, 2006, 281, 1309-1312.	1.6	39

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91	Structural basis for transcription inhibition by tagetitoxin. Nature Structural and Molecular Biology, 2005, 12, 1086-1093.	3.6	67
92	Transcriptional Pausing in Vivo: A Nascent RNA Hairpin Restricts Lateral Movements of RNA Polymerase in Both Forward and Reverse Directions. Journal of Molecular Biology, 2005, 351, 39-51.	2.0	23
93	Allosteric Modulation of the RNA Polymerase Catalytic Reaction Is an Essential Component of Transcription Control by Rifamycins. Cell, 2005, 122, 351-363.	13.5	156
94	Tracking RNA Polymerase, One Step at a Time. Cell, 2005, 123, 977-979.	13.5	13
95	Highly Divergent RfaH Orthologs from Pathogenic Proteobacteria Can Substitute for Escherichia coli RfaH both In Vivo and In Vitro. Journal of Bacteriology, 2004, 186, 2829-2840.	1.0	31
96	Discrimination against Deoxyribonucleotide Substrates by Bacterial RNA Polymerase. Journal of Biological Chemistry, 2004, 279, 38087-38090.	1.6	52
97	Cloning, expression, purification, crystallization and initial crystallographic analysis of transcription factor DksA fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1611-1613.	2.5	11
98	Regulation through the Secondary Channelâ€"Structural Framework for ppGpp-DksA Synergism during Transcription. Cell, 2004, 118, 297-309.	13.5	318
99	Structural Basis for Transcription Regulation by Alarmone ppGpp. Cell, 2004, 117, 299-310.	13.5	261
100	A New Class of Bacterial RNA Polymerase Inhibitor Affects Nucleotide Addition. Science, 2003, 302, 650-654.	6.0	95
101	Transcription termination control of the S box system: Direct measurement of S-adenosylmethionine by the leader RNA. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3083-3088.	3.3	242
102	Co-overexpression of Escherichia coliRNA Polymerase Subunits Allows Isolation and Analysis of Mutant Enzymes Lacking Lineage-specific Sequence Insertions. Journal of Biological Chemistry, 2003, 278, 12344-12355.	1.6	132
103	Mutations of Bacterial RNA Polymerase Leading to Resistance to Microcin J25. Journal of Biological Chemistry, 2002, 277, 50867-50875.	1.6	134
104	The Downstream DNA Jaw of Bacterial RNA Polymerase Facilitates Both Transcriptional Initiation and Pausing. Journal of Biological Chemistry, 2002, 277, 37456-37463.	1.6	86
105	The Transcriptional Regulator RfaH Stimulates RNA Chain Synthesis after Recruitment to Elongation Complexes by the Exposed Nontemplate DNA Strand. Cell, 2002, 109, 193-203.	13.5	229
106	Binding of the Initiation Factor Ïƒ70 to Core RNA Polymerase Is a Multistep Process. Molecular Cell, 2001, 8, 21-31.	4.5	61
107	Allosteric Control of RNA Polymerase by a Site That Contacts Nascent RNA Hairpins. Science, 2001, 292, 730-733.	6.0	205
108	RNA Polymerases from <i>Bacillus subtilis</i> and <i>Escherichia coli</i> Differ in Recognition of Regulatory Signals In Vitro. Journal of Bacteriology, 2001, 183, 1504-1504.	1.0	0

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109	RNA Polymerases from Bacillus subtilisand Escherichia coli Differ in Recognition of Regulatory Signals In Vitro. Journal of Bacteriology, 2000, 182, 6027-6035.	1.0	93
110	Rapid Purification of His6-Tagged Bacillus subtilis Core RNA Polymerase. Protein Expression and Purification, 2000, 19, 350-354.	0.6	32
111	Information Processing by RNA Polymerase: Recognition of Regulatory Signals during RNA Chain Elongation. Journal of Bacteriology, 1998, 180, 3265-3275.	1.0	132
112	Transcription Activation by the Bacteriophage Mu Mor Protein Requires the C-terminal Regions of Both Î± and Ïƒ70 Subunits of Escherichia coli RNA Polymerase. Journal of Biological Chemistry, 1996, 271, 32343-32348.	1.6	52
113	Control of Transcription Termination and Antitermination. , 0, , 311-326.		1