

# Irina Artsimovitch

## List of Publications by Year in descending order

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113  
papers

6,930  
citations

66343

42  
h-index

66911

78  
g-index

120  
all docs

120  
docs citations

120  
times ranked

4102  
citing authors

#	ARTICLE	IF	CITATIONS
1	A non-native C-terminal extension of the $\beta'$ subunit compromises RNA polymerase and Rho functions. <i>Molecular Microbiology</i> , 2022, , .	2.5	0
2	Positive supercoiling favors transcription elongation through lac repressor-mediated DNA loops. <i>Nucleic Acids Research</i> , 2022, 50, 2826-2835.	14.5	4
3	RfaH May Oppose Silencing by H-NS and YmoA Proteins during Transcription Elongation. <i>Journal of Bacteriology</i> , 2022, 204, e0059921.	2.2	6
4	High-throughput single-molecule experiments reveal heterogeneity, state switching, and three interconnected pause states in transcription. <i>Cell Reports</i> , 2022, 39, 110749.	6.4	18
5	Going Retro, Going Viral: Experiences and Lessons in Drug Discovery from COVID-19. <i>Molecules</i> , 2022, 27, 3815.	3.8	1
6	Allosteric couplings upon binding of RfaH to transcription elongation complexes. <i>Nucleic Acids Research</i> , 2022, 50, 6384-6397.	14.5	2
7	A Growing Gap between the RNAP and the Lead Ribosome. <i>Trends in Microbiology</i> , 2021, 29, 4-5.	7.7	4
8	Steps toward translocation-independent RNA polymerase inactivation by terminator ATPase $\beta'$ . <i>Science</i> , 2021, 371, .	12.6	78
9	A translational riboswitch coordinates nascent transcription-translation coupling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	38
10	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. <i>MBio</i> , 2021, 12, e0142321.	4.1	20
11	NMPylation and de-NMPylation of SARS-CoV-2 nsp9 by the NiRAN domain. <i>Nucleic Acids Research</i> , 2021, 49, 8822-8835.	14.5	30
12	Reductionism Ad Absurdum: The Misadventures of Structural Biology in the Time of Coronavirus. <i>ACS Infectious Diseases</i> , 2021, 7, 2948-2952.	3.8	1
13	Bacterial RNA synthesis: back to the limelight. <i>Transcription</i> , 2021, 12, 89-91.	3.1	0
14	Differential Local Stability Governs the Metamorphic Fold Switch of Bacterial Virulence Factor RfaH. <i>Biophysical Journal</i> , 2020, 118, 96-104.	0.5	22
15	Origins and Molecular Evolution of the NusG Paralog RfaH. <i>MBio</i> , 2020, 11, .	4.1	15
16	Benzyl and benzoyl benzoic acid inhibitors of bacterial RNA polymerase-sigma factor interaction. <i>European Journal of Medicinal Chemistry</i> , 2020, 208, 112671.	5.5	11
17	Discovery of Antibacterials That Inhibit Bacterial RNA Polymerase Interactions with Sigma Factors. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 7695-7720.	6.4	18
18	NusG, an Ancient Yet Rapidly Evolving Transcription Factor. <i>Frontiers in Microbiology</i> , 2020, 11, 619618.	3.5	30

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19	The $\beta'$ subunit and NTPase HelD institute a two-pronged mechanism for RNA polymerase recycling. Nature Communications, 2020, 11, 6418.	12.8	32
20	The dormancy-specific regulator, SutA, is intrinsically disordered and modulates transcription initiation in <i>Pseudomonas aeruginosa</i> . Molecular Microbiology, 2019, 112, 992-1009.	2.5	11
21	The Mechanisms of Substrate Selection, Catalysis, and Translocation by the Elongating RNA Polymerase. Journal of Molecular Biology, 2019, 431, 3975-4006.	4.2	56
22	Ancient Transcription Factors in the News. MBio, 2019, 10, .	4.1	23
23	Reversible fold-switching controls the functional cycle of the antitermination factor RfaH. Nature Communications, 2019, 10, 702.	12.8	50
24	RNA synthesis is a team effort. Nature Microbiology, 2019, 4, 1776-1777.	13.3	0
25	Uneven Braking Spins RNA Polymerase into a Pause. Molecular Cell, 2018, 69, 723-725.	9.7	4
26	Rebuilding the bridge between transcription and translation. Molecular Microbiology, 2018, 108, 467-472.	2.5	29
27	Locking the nontemplate DNA to control transcription. Molecular Microbiology, 2018, 109, 445-457.	2.5	16
28	Ligand Modulates Cross-Coupling between Riboswitch Folding and Transcriptional Pausing. Molecular Cell, 2018, 72, 541-552.e6.	9.7	48
29	Global DNA Compaction in Stationary-Phase Bacteria Does Not Affect Transcription. Cell, 2018, 174, 1188-1199.e14.	28.9	81
30	In silico discovery of small molecules that inhibit RfaH recruitment to RNA polymerase. Molecular Microbiology, 2018, 110, 128-142.	2.5	11
31	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. Molecular Cell, 2018, 71, 911-922.e4.	9.7	65
32	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. Cell, 2018, 173, 1650-1662.e14.	28.9	143
33	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. ELife, 2018, 7, .	6.0	45
34	A Screen for <i>rfaH</i> Suppressors Reveals a Key Role for a Connector Region of Termination Factor Rho. MBio, 2017, 8, .	4.1	23
35	Distributed biotin-streptavidin transcription roadblocks for mapping cotranscriptional RNA folding. Nucleic Acids Research, 2017, 45, e109-e109.	14.5	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.	14.5	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.	7.1	20
38	Maintenance of Transcription-Translation Coupling by Elongation Factor P. MBio, 2016, 7, .	4.1	24
39	Initial Events in Bacterial Transcription Initiation. Biomolecules, 2015, 5, 1035-1062.	4.0	157
40	pH Dependence of the Stress Regulator DksA. PLoS ONE, 2015, 10, e0120746.	2.5	22
41	Interdomain Contacts Control Native State Switching of RfaH on a Dual-Funneled Landscape. PLoS Computational Biology, 2015, 11, e1004379.	3.2	47
42	E. coli RNA Polymerase Determinants of Open Complex Lifetime and Structure. Journal of Molecular Biology, 2015, 427, 2435-2450.	4.2	45
43	Ubiquitous transcription factors display structural plasticity and diverse functions. BioEssays, 2015, 37, 324-334.	2.5	25
44	Creative Math of RNA Polymerase III Termination: Sense Plus Antisense Makes More Sense. Molecular Cell, 2015, 58, 974-976.	9.7	1
45	Regulation of Transcript Elongation. Annual Review of Microbiology, 2015, 69, 49-69.	7.3	64
46	Purification of Bacterial RNA Polymerase: Tools and Protocols. Methods in Molecular Biology, 2015, 1276, 13-29.	0.9	123
47	CBR antimicrobials alter coupling between the bridge helix and the $\beta^2$ subunit in RNA polymerase. Nature Communications, 2014, 5, 3408.	12.8	34
48	Interplay between the trigger loop and the F loop during RNA polymerase catalysis. Nucleic Acids Research, 2014, 42, 544-552.	14.5	25
49	The tug of DNA repair. Nature, 2014, 505, 298-299.	27.8	15
50	Toward a General Mechanism for Transcription Initiation. Biophysical Journal, 2014, 106, 488a.	0.5	0
51	NusG-Spt5 Proteinsâ€™ Universal Tools for Transcription Modification and Communication. Chemical Reviews, 2013, 113, 8604-8619.	47.7	54
52	An Insertion in the Catalytic Trigger Loop Gates the Secondary Channel of RNA Polymerase. Journal of Molecular Biology, 2013, 425, 82-93.	4.2	37
53	DksA2, a zincâ€independent structural analog of the transcription factor DksA. FEBS Letters, 2013, 587, 614-619.	2.8	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.	14.5	49

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55	Interdomain contacts control folding of transcription factor RfaH. Nucleic Acids Research, 2013, 41, 10077-10085.	14.5	37
56	Response to Klyuyev and Vassilyev: On the mechanism of tagetitoxin inhibition of transcription. Transcription, 2012, 3, 51-55.	3.1	3
57	Transformer proteins. Cell Cycle, 2012, 11, 4289-4290.	2.6	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.	7.1	42
59	Fidaxomicin Is an Inhibitor of the Initiation of Bacterial RNA Synthesis. Clinical Infectious Diseases, 2012, 55, S127-S131.	5.8	85
60	Transcription initiation factor DksA has diverse effects on RNA chain elongation. Nucleic Acids Research, 2012, 40, 3392-3402.	14.5	47
61	Transformation. RNA Biology, 2012, 9, 1418-1423.	3.1	11
62	An $\alpha$ Helix to $\beta$ Barrel Domain Switch Transforms the Transcription Factor RfaH into a Translation Factor. Cell, 2012, 150, 291-303.	28.9	201
63	Interplay of DNA repair with transcription: from structures to mechanisms. Trends in Biochemical Sciences, 2012, 37, 543-552.	7.5	12
64	E. Coli RNA Polymerase: A Molecular DNA Opening Machine. Biophysical Journal, 2012, 102, 286a.	0.5	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.	7.1	93
66	Termination and antitermination: RNA polymerase runs a stop sign. Nature Reviews Microbiology, 2011, 9, 319-329.	28.6	175
67	The $\beta$ Subunit Gate Loop Is Required for RNA Polymerase Modification by RfaH and NusG. Molecular Cell, 2011, 43, 253-262.	9.7	96
68	Role of a Zn-independent DksA in Zn homeostasis and stringent response. Molecular Microbiology, 2011, 79, 700-715.	2.5	68
69	Tagetitoxin Inhibits RNA Polymerase through Trapping of the Trigger Loop. Journal of Biological Chemistry, 2011, 286, 40395-40400.	3.4	31
70	Functional regions of the N-terminal domain of the antiterminator RfaH. Molecular Microbiology, 2010, 76, 286-301.	2.5	63
71	A processive riboantiterminator seeks a switch to make biofilms. Molecular Microbiology, 2010, 76, 535-539.	2.5	4
72	Functional analysis of Thermus thermophilus transcription factor NusG. Nucleic Acids Research, 2010, 38, 7432-7445.	14.5	44

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73	Multiple roles of the RNA polymerase $\beta$ SW2 region in transcription initiation, promoter escape, and RNA elongation. Nucleic Acids Research, 2010, 38, 5784-5796.	14.5	25
74	Modulation of RNA polymerase activity through the trigger loop folding. Transcription, 2010, 1, 89-94.	3.1	9
75	The $\beta$ Subunit Gate Loop Mediates Antitermination Modification of RNA Polymerase. FASEB Journal, 2010, 24, .	0.5	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.	7.1	41
77	Functional specialization of transcription elongation factors. EMBO Journal, 2009, 28, 112-122.	7.8	114
78	Transcription inactivation through local refolding of the RNA polymerase structure. Nature, 2009, 457, 332-335.	27.8	131
79	Mechanism of chromatin remodeling and recovery during passage of RNA polymerase II. Nature Structural and Molecular Biology, 2009, 16, 1272-1278.	8.2	162
80	In vitro approaches to analysis of transcription termination. Methods, 2009, 47, 37-43.	3.8	42
81	Post-initiation control by the initiation factor sigma. Molecular Microbiology, 2008, 68, 1-3.	2.5	13
82	The elongation factor RfaH and the initiation factor $\sigma$ 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.	7.1	60
83	Allosteric control of the RNA polymerase by the elongation factor RfaH. Nucleic Acids Research, 2007, 35, 5694-5705.	14.5	68
84	Structural Basis for Converting a General Transcription Factor into an Operon-Specific Virulence Regulator. Molecular Cell, 2007, 26, 117-129.	9.7	191
85	The carboxy-terminal coiled-coil of the RNA polymerase $\beta$ subunit is the main binding site for Gre factors. EMBO Reports, 2007, 8, 1038-1043.	4.5	53
86	Merging the RNA and DNA worlds. Nature Structural and Molecular Biology, 2007, 14, 1122-1123.	8.2	3
87	Structural basis for substrate loading in bacterial RNA polymerase. Nature, 2007, 448, 163-168.	27.8	333
88	Structural basis for transcription elongation by bacterial RNA polymerase. Nature, 2007, 448, 157-162.	27.8	380
89	Is It Easy to Stop RNA Polymerase?. Cell Cycle, 2006, 5, 399-404.	2.6	22
90	Regulation through the RNA Polymerase Secondary Channel. Journal of Biological Chemistry, 2006, 281, 1309-1312.	3.4	39

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91	Structural basis for transcription inhibition by tagetitoxin. Nature Structural and Molecular Biology, 2005, 12, 1086-1093.	8.2	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.	4.2	23
93	Allosteric Modulation of the RNA Polymerase Catalytic Reaction Is an Essential Component of Transcription Control by Rifamycins. Cell, 2005, 122, 351-363.	28.9	156
94	Tracking RNA Polymerase, One Step at a Time. Cell, 2005, 123, 977-979.	28.9	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.	2.2	31
96	Discrimination against Deoxyribonucleotide Substrates by Bacterial RNA Polymerase. Journal of Biological Chemistry, 2004, 279, 38087-38090.	3.4	52
97	Cloning, expression, purification, crystallization and initial crystallographic analysis of transcription factor DksA from Escherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1611-1613.	2.5	11
98	Regulation through the Secondary Channel – Structural Framework for ppGpp-DksA Synergism during Transcription. Cell, 2004, 118, 297-309.	28.9	318
99	Structural Basis for Transcription Regulation by Alarmone ppGpp. Cell, 2004, 117, 299-310.	28.9	261
100	A New Class of Bacterial RNA Polymerase Inhibitor Affects Nucleotide Addition. Science, 2003, 302, 650-654.	12.6	95
101	Transcription termination control of the S box system: Direct measurement of <i>S</i> -adenosylmethionine by the leader RNA. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3083-3088.	7.1	242
102	Co-overexpression of Escherichia coli RNA Polymerase Subunits Allows Isolation and Analysis of Mutant Enzymes Lacking Lineage-specific Sequence Insertions. Journal of Biological Chemistry, 2003, 278, 12344-12355.	3.4	132
103	Mutations of Bacterial RNA Polymerase Leading to Resistance to Microcin J25. Journal of Biological Chemistry, 2002, 277, 50867-50875.	3.4	134
104	The Downstream DNA Jaw of Bacterial RNA Polymerase Facilitates Both Transcriptional Initiation and Pausing. Journal of Biological Chemistry, 2002, 277, 37456-37463.	3.4	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.	28.9	229
106	Binding of the Initiation Factor $\sigma^{70}$ to Core RNA Polymerase Is a Multistep Process. Molecular Cell, 2001, 8, 21-31.	9.7	61
107	Allosteric Control of RNA Polymerase by a Site That Contacts Nascent RNA Hairpins. Science, 2001, 292, 730-733.	12.6	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.	2.2	0

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109	RNA Polymerases from <i>Bacillus subtilis</i> and <i>Escherichia coli</i> Differ in Recognition of Regulatory Signals In Vitro. <i>Journal of Bacteriology</i> , 2000, 182, 6027-6035.	2.2	93
110	Rapid Purification of His6-Tagged <i>Bacillus subtilis</i> Core RNA Polymerase. <i>Protein Expression and Purification</i> , 2000, 19, 350-354.	1.3	32
111	Information Processing by RNA Polymerase: Recognition of Regulatory Signals during RNA Chain Elongation. <i>Journal of Bacteriology</i> , 1998, 180, 3265-3275.	2.2	132
112	Transcription Activation by the Bacteriophage Mu Mor Protein Requires the C-terminal Regions of Both $\sigma^{70}$ and $\sigma^{32}$ Subunits of <i>Escherichia coli</i> RNA Polymerase. <i>Journal of Biological Chemistry</i> , 1996, 271, 32343-32348.	3.4	52
113	Control of Transcription Termination and Antitermination. , 0, , 311-326.		1