

Thomas J Santangelo

List of Publications by Year in descending order

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64
papers

2,765
citations

172457

29
h-index

189892

50
g-index

64
all docs

64
docs citations

64
times ranked

2190
citing authors

#	ARTICLE	IF	CITATIONS
1	Single molecule analysis of RNA polymerase elongation reveals uniform kinetic behavior. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13538-13543.	7.1	182
2	Termination and antitermination: RNA polymerase runs a stop sign. Nature Reviews Microbiology, 2011, 9, 319-329.	28.6	175
3	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. Nature, 2020, 583, 638-643.	27.8	175
4	Structure of histone-based chromatin in Archaea. Science, 2017, 357, 609-612.	12.6	149
5	SINGLE-MOLECULE ANALYSIS OF RNA POLYMERASE TRANSCRIPTION. Annual Review of Biophysics and Biomolecular Structure, 2006, 35, 343-360.	18.3	108
6	Forward Translocation Is the Natural Pathway of RNA Release at an Intrinsic Terminator. Molecular Cell, 2004, 14, 117-126.	9.7	102
7	Shuttle Vector Expression in <i>Thermococcus kodakaraensis</i> : Contributions of <i>cis</i> Elements to Protein Synthesis in a Hyperthermophilic Archaeon. Applied and Environmental Microbiology, 2008, 74, 3099-3104.	3.1	101
8	Primary transcriptome map of the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> . BMC Genomics, 2014, 15, 684.	2.8	99
9	Affinity Purification of an Archaeal DNA Replication Protein Network. MBio, 2010, 1, .	4.1	79
10	<i>Thermococcus kodakaraensis</i> Genetics: TK1827-Encoded β -Glycosidase, New Positive-Selection Protocol, and Targeted and Repetitive Deletion Technology. Applied and Environmental Microbiology, 2010, 76, 1044-1052.	3.1	78
11	Transcription and Translation are Coupled in Archaea. Molecular Biology and Evolution, 2007, 24, 893-895.	8.9	76
12	Archaeal Intrinsic Transcription Termination In Vivo. Journal of Bacteriology, 2009, 191, 7102-7108.	2.2	76
13	Archaeal RNA Polymerase is Sensitive to Intrinsic Termination Directed by Transcribed and Remote Sequences. Journal of Molecular Biology, 2006, 355, 196-210.	4.2	71
14	TFB1 or TFB2 Is Sufficient for <i>Thermococcus kodakaraensis</i> Viability and for Basal Transcription in Vitro. Journal of Molecular Biology, 2007, 367, 344-357.	4.2	70
15	Archaeal DNA Polymerase D but Not DNA Polymerase B Is Required for Genome Replication in <i>Thermococcus kodakaraensis</i> . Journal of Bacteriology, 2013, 195, 2322-2328.	2.2	70
16	A novel DNA nuclease is stimulated by association with the GINS complex. Nucleic Acids Research, 2011, 39, 6114-6123.	14.5	62
17	Genetics Techniques for <i>Thermococcus kodakaraensis</i> . Frontiers in Microbiology, 2012, 3, 195.	3.5	57
18	Polarity in Archaeal Operon Transcription in <i>Thermococcus kodakaraensis</i> . Journal of Bacteriology, 2008, 190, 2244-2248.	2.2	56

#	ARTICLE	IF	CITATIONS
19	Genetic Techniques for the Archaea. Annual Review of Genetics, 2013, 47, 539-561.	7.6	54
20	A Single-Molecule Technique to Study Sequence-Dependent Transcription Pausing. Biophysical Journal, 2004, 87, 3945-3953.	0.5	53
21	Archaeal nucleosome positioning in vivo and in vitro is directed by primary sequence motifs. BMC Genomics, 2013, 14, 391.	2.8	52
22	Transcription Regulation in Archaea. Journal of Bacteriology, 2016, 198, 1906-1917.	2.2	48
23	Archaeal RNA polymerase subunits E and F are not required for transcription <i>in vitro</i> , but a <i>Thermococcus kodakarensis</i> mutant lacking subunit F is temperature-sensitive. Molecular Microbiology, 2008, 70, 623-633.	2.5	43
24	An Archaeal Histone Is Required for Transformation of <i>Thermococcus kodakarensis</i> . Journal of Bacteriology, 2012, 194, 6864-6874.	2.2	43
25	Deletion of alternative pathways for reductant recycling in <i>Thermococcus kodakarensis</i> increases hydrogen production. Molecular Microbiology, 2011, 81, 897-911.	2.5	40
26	<i>Thermococcus kodakarensis</i> encodes three MCM homologs but only one is essential. Nucleic Acids Research, 2011, 39, 9671-9680.	14.5	40
27	The X-ray crystal structure of the euryarchaeal RNA polymerase in an open-clamp configuration. Nature Communications, 2014, 5, 5132.	12.8	36
28	Factor-dependent archaeal transcription termination. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6767-E6773.	7.1	35
29	Archaeal α F2B Interacts with Eukaryotic Translation Initiation Factors $eIF2\alpha$ and $eIF2B\beta$: Implications for α F2B Function and $eIF2B$ Regulation. Journal of Molecular Biology, 2009, 392, 701-722.	4.2	34
30	An Archaeal Fluoride-Responsive Riboswitch Provides an Inducible Expression System for Hyperthermophiles. Applied and Environmental Microbiology, 2018, 84, .	3.1	28
31	RNA polymerase mutations that impair conversion to a termination-resistant complex by Q antiterminator proteins. Genes and Development, 2003, 17, 1281-1292.	5.9	27
32	Defining the RNaseH2 enzyme-initiated ribonucleotide excision repair pathway in Archaea. Journal of Biological Chemistry, 2017, 292, 8835-8845.	3.4	26
33	Genome Replication in <i>Thermococcus kodakarensis</i> Independent of Cdc6 and an Origin of Replication. Frontiers in Microbiology, 2017, 8, 2084.	3.5	24
34	TFS and Spt4/5 accelerate transcription through archaeal histone-based chromatin. Molecular Microbiology, 2019, 111, 784-797.	2.5	24
35	FttA is a CPSF73 homologue that terminates transcription in Archaea. Nature Microbiology, 2020, 5, 545-553.	13.3	23
36	Kinetic Investigation of <i>Escherichia coli</i> RNA Polymerase Mutants That Influence Nucleotide Discrimination and Transcription Fidelity. Journal of Biological Chemistry, 2006, 281, 18677-18683.	3.4	22

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37	Cyclic AMP Receptor Protein and RhaR Synergistically Activate Transcription from the I-Rhamnose-Responsive rhaSR Promoter in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6708-6718.	2.2	20
38	Distinct Physiological Roles of the Three Ferredoxins Encoded in the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> . <i>MBio</i> , 2019, 10, .	4.1	20
39	Archaeal DNA Repair Mechanisms. <i>Biomolecules</i> , 2020, 10, 1472.	4.0	20
40	The Role of Archaeal Chromatin in Transcription. <i>Journal of Molecular Biology</i> , 2019, 431, 4103-4115.	4.2	19
41	Archaeal Minichromosome Maintenance (MCM) Helicase Can Unwind DNA Bound by Archaeal Histones and Transcription Factors. <i>Journal of Biological Chemistry</i> , 2007, 282, 4908-4915.	3.4	18
42	Association of a multi- ϵ -synthetase complex with translating ribosomes in the archaeon <i>Thermococcus kodakarensis</i> . <i>FEBS Letters</i> , 2012, 586, 2232-2238.	2.8	18
43	The GAN Exonuclease or the Flap Endonuclease Fen1 and RNase HII Are Necessary for Viability of <i>Thermococcus kodakarensis</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	18
44	Markerless Gene Editing in the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> . <i>Bio-protocol</i> , 2017, 7, .	0.4	16
45	Bacteriophage N4 virion RNA polymerase interaction with its promoter DNA hairpin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7033-7038.	7.1	15
46	Deletion of Switch 3 Results in an Archaeal RNA Polymerase That Is Defective in Transcript Elongation. <i>Journal of Biological Chemistry</i> , 2010, 285, 23908-23915.	3.4	15
47	<i>Thermococcus kodakarensis</i> has two functional PCNA homologs but only one is required for viability. <i>Extremophiles</i> , 2013, 17, 453-461.	2.3	13
48	A novel mechanism for regulating the activity of proliferating cell nuclear antigen by a small protein. <i>Nucleic Acids Research</i> , 2014, 42, 5776-5789.	14.5	13
49	Archaeal RNA polymerase arrests transcription at DNA lesions. <i>Transcription</i> , 2017, 8, 288-296.	3.1	13
50	Extended Archaeal Histone-Based Chromatin Structure Regulates Global Gene Expression in <i>Thermococcus kodakarensis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 681150.	3.5	13
51	RfaH, a Bacterial Transcription Antiterminator. <i>Molecular Cell</i> , 2002, 9, 698-700.	9.7	12
52	BosR Is A Novel Fur Family Member Responsive to Copper and Regulating Copper Homeostasis in <i>Borrelia burgdorferi</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	12
53	Archaeal transcription. <i>Transcription</i> , 2020, 11, 199-210.	3.1	12
54	Biochemical reconstitution and genetic characterization of the major oxidative damage base excision DNA repair pathway in <i>Thermococcus kodakarensis</i> . <i>DNA Repair</i> , 2020, 86, 102767.	2.8	11

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55	Manipulating Archaeal Systems to Permit Analyses of Transcription Elongation-Termination Decisions In Vitro. <i>Methods in Molecular Biology</i> , 2015, 1276, 263-279.	0.9	11
56	Archaeosine Modification of Archaeal tRNA: Role in Structural Stabilization. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	10
57	Analyses of in vivo interactions between transcription factors and the archaeal RNA polymerase. <i>Methods</i> , 2015, 86, 73-79.	3.8	9
58	Formation of Long DNA Templates Containing Site-Specific Alkane-Disulfide DNA Interstrand Cross-Links for Use in Transcription Reactions. <i>Methods in Enzymology</i> , 2003, 371, 120-132.	1.0	4
59	Genetic Tools and Manipulations of the Hyperthermophilic Heterotrophic Archaeon <i>Thermococcus kodakarensis</i> . , 2011, , 567-582.		4
60	A linear pathway for mevalonate production supports growth of <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2019, 23, 229-238.	2.3	4
61	The Hyperthermophilic Restriction-Modification Systems of <i>Thermococcus kodakarensis</i> Protect Genome Integrity. <i>Frontiers in Microbiology</i> , 2021, 12, 657356.	3.5	3
62	<i>Thermococcus kodakarensis</i> provides a versatile hyperthermophilic archaeal platform for protein expression. <i>Methods in Enzymology</i> , 2021, 659, 243-273.	1.0	3
63	Bacterial Transcriptional Control. <i>Methods in Molecular Biology</i> , 2015, 1276, v.	0.9	1
64	Transcription Transcription Termination. , 2021, , 435-442.		0