

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	Transcription Transcription Termination. , 2021, , 435-442.		0
2	The Hyperthermophilic Restriction-Modification Systems of <i>Thermococcus kodakarensis</i> Protect Genome Integrity. <i>Frontiers in Microbiology</i> , 2021, 12, 657356.	3.5	3
3	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
4	<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
5	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
6	Archaeal transcription. <i>Transcription</i> , 2020, 11, 199-210.	3.1	12
7	Archaeal DNA Repair Mechanisms. <i>Biomolecules</i> , 2020, 10, 1472.	4.0	20
8	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	27.8	175
9	FttA is a CPSF73 homologue that terminates transcription in Archaea. <i>Nature Microbiology</i> , 2020, 5, 545-553.	13.3	23
10	Archaeosine Modification of Archaeal tRNA: Role in Structural Stabilization. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	10
11	TFS and Spt4/5 accelerate transcription through archaeal histone-based chromatin. <i>Molecular Microbiology</i> , 2019, 111, 784-797.	2.5	24
12	A linear pathway for mevalonate production supports growth of <i>Thermococcus kodakarensis</i> . <i>Extremophiles</i> , 2019, 23, 229-238.	2.3	4
13	The Role of Archaeal Chromatin in Transcription. <i>Journal of Molecular Biology</i> , 2019, 431, 4103-4115.	4.2	19
14	Distinct Physiological Roles of the Three Ferredoxins Encoded in the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> . <i>MBio</i> , 2019, 10, .	4.1	20
15	An Archaeal Fluoride-Responsive Riboswitch Provides an Inducible Expression System for Hyperthermophiles. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	28
16	Defining the RNaseH2 enzyme-initiated ribonucleotide excision repair pathway in Archaea. <i>Journal of Biological Chemistry</i> , 2017, 292, 8835-8845.	3.4	26
17	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
18	Archaeal RNA polymerase arrests transcription at DNA lesions. <i>Transcription</i> , 2017, 8, 288-296.	3.1	13

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19	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
20	Structure of histone-based chromatin in Archaea. <i>Science</i> , 2017, 357, 609-612.	12.6	149
21	Factor-dependent archaeal transcription termination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6767-E6773.	7.1	35
22	Genome Replication in <i>Thermococcus kodakarensis</i> Independent of Cdc6 and an Origin of Replication. <i>Frontiers in Microbiology</i> , 2017, 8, 2084.	3.5	24
23	Markerless Gene Editing in the Hyperthermophilic Archaeon <i>Thermococcus kodakarensis</i> . <i>Bio-protocol</i> , 2017, 7, .	0.4	16
24	Transcription Regulation in Archaea. <i>Journal of Bacteriology</i> , 2016, 198, 1906-1917.	2.2	48
25	Bacterial Transcriptional Control. <i>Methods in Molecular Biology</i> , 2015, 1276, v.	0.9	1
26	Analyses of in vivo interactions between transcription factors and the archaeal RNA polymerase. <i>Methods</i> , 2015, 86, 73-79.	3.8	9
27	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
28	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
29	Primary transcriptome map of the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> . <i>BMC Genomics</i> , 2014, 15, 684.	2.8	99
30	The X-ray crystal structure of the euryarchaeal RNA polymerase in an open-clamp configuration. <i>Nature Communications</i> , 2014, 5, 5132.	12.8	36
31	Archaeal nucleosome positioning in vivo and in vitro is directed by primary sequence motifs. <i>BMC Genomics</i> , 2013, 14, 391.	2.8	52
32	<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
33	Genetic Techniques for the Archaea. <i>Annual Review of Genetics</i> , 2013, 47, 539-561.	7.6	54
34	Archaeal DNA Polymerase D but Not DNA Polymerase B Is Required for Genome Replication in <i>Thermococcus kodakarensis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2322-2328.	2.2	70
35	An Archaeal Histone Is Required for Transformation of <i>Thermococcus kodakarensis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 6864-6874.	2.2	43
36	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

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37	Genetics Techniques for <i>Thermococcus kodakarensis</i> . <i>Frontiers in Microbiology</i> , 2012, 3, 195.	3.5	57
38	Genetic Tools and Manipulations of the Hyperthermophilic Heterotrophic Archaeon <i>Thermococcus kodakarensis</i> . , 2011, , 567-582.		4
39	Termination and antitermination: RNA polymerase runs a stop sign. <i>Nature Reviews Microbiology</i> , 2011, 9, 319-329.	28.6	175
40	Deletion of alternative pathways for reductant recycling in <i>Thermococcus kodakarensis</i> increases hydrogen production. <i>Molecular Microbiology</i> , 2011, 81, 897-911.	2.5	40
41	A novel DNA nuclease is stimulated by association with the GINS complex. <i>Nucleic Acids Research</i> , 2011, 39, 6114-6123.	14.5	62
42	<i>Thermococcus kodakarensis</i> encodes three MCM homologs but only one is essential. <i>Nucleic Acids Research</i> , 2011, 39, 9671-9680.	14.5	40
43	Affinity Purification of an Archaeal DNA Replication Protein Network. <i>MBio</i> , 2010, 1, .	4.1	79
44	<i>Thermococcus kodakarensis</i> Genetics: TK1827-Encoded β -Glycosidase, New Positive-Selection Protocol, and Targeted and Repetitive Deletion Technology. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1044-1052.	3.1	78
45	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
46	Archaeal Intrinsic Transcription Termination In Vivo. <i>Journal of Bacteriology</i> , 2009, 191, 7102-7108.	2.2	76
47	Archaeal α F2B Interacts with Eukaryotic Translation Initiation Factors $eIF2\beta$ and $eIF2B\beta$: Implications for α F2B Function and $eIF2B$ Regulation. <i>Journal of Molecular Biology</i> , 2009, 392, 701-722.	4.2	34
48	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. <i>Molecular Microbiology</i> , 2008, 70, 623-633.	2.5	43
49	Shuttle Vector Expression in <i>Thermococcus kodakaraensis</i> : Contributions of <i>cis</i> Elements to Protein Synthesis in a Hyperthermophilic Archaeon. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3099-3104.	3.1	101
50	Polarity in Archaeal Operon Transcription in <i>Thermococcus kodakaraensis</i> . <i>Journal of Bacteriology</i> , 2008, 190, 2244-2248.	2.2	56
51	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
52	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
53	Transcription and Translation are Coupled in Archaea. <i>Molecular Biology and Evolution</i> , 2007, 24, 893-895.	8.9	76
54	TFB1 or TFB2 Is Sufficient for <i>Thermococcus kodakaraensis</i> Viability and for Basal Transcription in Vitro. <i>Journal of Molecular Biology</i> , 2007, 367, 344-357.	4.2	70

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55	Archaeal RNA Polymerase is Sensitive to Intrinsic Termination Directed by Transcribed and Remote Sequences. <i>Journal of Molecular Biology</i> , 2006, 355, 196-210.	4.2	71
56	SINGLE-MOLECULE ANALYSIS OF RNA POLYMERASE TRANSCRIPTION. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 343-360.	18.3	108
57	Kinetic Investigation of Escherichia coli RNA Polymerase Mutants That Influence Nucleotide Discrimination and Transcription Fidelity. <i>Journal of Biological Chemistry</i> , 2006, 281, 18677-18683.	3.4	22
58	Cyclic AMP Receptor Protein and RhaR Synergistically Activate Transcription from the I-Rhamnose-Responsive rhaSR Promoter in Escherichia coli. <i>Journal of Bacteriology</i> , 2005, 187, 6708-6718.	2.2	20
59	A Single-Molecule Technique to Study Sequence-Dependent Transcription Pausing. <i>Biophysical Journal</i> , 2004, 87, 3945-3953.	0.5	53
60	Forward Translocation Is the Natural Pathway of RNA Release at an Intrinsic Terminator. <i>Molecular Cell</i> , 2004, 14, 117-126.	9.7	102
61	RNA polymerase mutations that impair conversion to a termination-resistant complex by Q antiterminator proteins. <i>Genes and Development</i> , 2003, 17, 1281-1292.	5.9	27
62	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
63	Single molecule analysis of RNA polymerase elongation reveals uniform kinetic behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13538-13543.	7.1	182
64	RfaH, a Bacterial Transcription Antiterminator. <i>Molecular Cell</i> , 2002, 9, 698-700.	9.7	12