

Timothy R Hoover

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

51
papers

2,308
citations

25
h-index

47
g-index

53
ext. papers

2,502
ext. citations

6.3
avg, IF

4.48
L-index

#	Paper	IF	Citations
51	Phylogenetic Distribution, Ultrastructure, and Function of Bacterial Flagellar Sheaths. <i>Biomolecules</i> , 2020 , 10,	5.9	9
50	Crystal Structure of d-Ornithine/d-Lysine Decarboxylase, a Stereoinverting Decarboxylase: Implications for Substrate Specificity and Stereospecificity of Fold III Decarboxylases. <i>Biochemistry</i> , 2019 , 58, 1038-1042	3.2	6
49	Loss of a Cardiolipin Synthase in G27 Blocks Flagellum Assembly. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	2
48	Properties and mechanism of d-glucosaminatate-6-phosphate ammonia-lyase: An aminotransferase family enzyme with d-amino acid specificity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018 , 1866, 799-805	4	2
47	STM2360 encodes a d-ornithine/d-lysine decarboxylase in Salmonella enterica serovar typhimurium. <i>Archives of Biochemistry and Biophysics</i> , 2017 , 634, 83-87	4.1	3
46	Helicobacter pylori strains vary cell shape and flagellum number to maintain robust motility in viscous environments. <i>Molecular Microbiology</i> , 2016 , 99, 88-110	4.1	45
45	A Mannose Family Phosphotransferase System Permease and Associated Enzymes Are Required for Utilization of Fructoselysine and Glucoselysine in Salmonella enterica Serovar Typhimurium. <i>Journal of Bacteriology</i> , 2015 , 197, 2831-9	3.5	16
44	Helicobacter pylori FlhA Binds the Sensor Kinase and Flagellar Gene Regulatory Protein FlgS with High Affinity. <i>Journal of Bacteriology</i> , 2015 , 197, 1886-92	3.5	6
43	Basal Body Structures Differentially Affect Transcription of RpoN- and FliA-Dependent Flagellar Genes in Helicobacter pylori. <i>Journal of Bacteriology</i> , 2015 , 197, 1921-30	3.5	10
42	Requirement of the flagellar protein export apparatus component FliO for optimal expression of flagellar genes in Helicobacter pylori. <i>Journal of Bacteriology</i> , 2014 , 196, 2709-17	3.5	14
41	Themes and Variations: Regulation of RpoN-Dependent Flagellar Genes across Diverse Bacterial Species. <i>Scientifica</i> , 2014 , 2014, 681754	2.6	50
40	Use of a promiscuous, constitutively-active bacterial enhancer-binding protein to define the \square (RpoN) regulon of Salmonella Typhimurium LT2. <i>BMC Genomics</i> , 2013 , 14, 602	4.5	20
39	Salmonella utilizes D-glucosaminatate via a mannose family phosphotransferase system permease and associated enzymes. <i>Journal of Bacteriology</i> , 2013 , 195, 4057-66	3.5	21
38	Extracellular secretion of protease HtrA from Campylobacter jejuni is highly efficient and independent of its protease activity and flagellum. <i>European Journal of Microbiology and Immunology</i> , 2013 , 3, 163-73	4.6	22
37	Insertion mutations in Helicobacter pylori flhA reveal strain differences in RpoN-dependent gene expression. <i>Microbiology (United Kingdom)</i> , 2013 , 159, 58-67	2.9	11
36	The zinc-ribbon domain of Helicobacter pylori HP0958: requirement for RpoN accumulation and possible roles of homologs in other bacteria. <i>Microbial Informatics and Experimentation</i> , 2011 , 1, 1-10		8
35	Sense and sensibility: flagellum-mediated gene regulation. <i>Trends in Microbiology</i> , 2010 , 18, 30-7	12.4	71

34	An ATPase R-finger leaves its print on transcriptional activation. <i>Structure</i> , 2010 , 18, 1391-2	5.2	2
33	Novel features of the polysaccharide-digesting gliding bacterium <i>Flavobacterium johnsoniae</i> as revealed by genome sequence analysis. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6864-75	4.8	177
32	Deciphering bacterial flagellar gene regulatory networks in the genomic era. <i>Advances in Applied Microbiology</i> , 2009 , 67, 257-95	4.9	64
31	<i>Helicobacter pylori</i> FlhB processing-deficient variants affect flagellar assembly but not flagellar gene expression. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 1170-1180	2.9	17
30	The human gastric pathogen <i>Helicobacter pylori</i> has a potential acetone carboxylase that enhances its ability to colonize mice. <i>BMC Microbiology</i> , 2008 , 8, 14	4.5	17
29	Survival in nuclear waste, extreme resistance, and potential applications gleaned from the genome sequence of <i>Kineococcus radiotolerans</i> SRS30216. <i>PLoS ONE</i> , 2008 , 3, e3878	3.7	47
28	Direct analysis of the extracellular proteome from two strains of <i>Helicobacter pylori</i> . <i>Proteomics</i> , 2007 , 7, 2240-5	4.8	28
27	Insights into the complex regulation of <i>rpoS</i> in <i>Borrelia burgdorferi</i> . <i>Molecular Microbiology</i> , 2007 , 65, 277-93	4.1	101
26	ATP ground- and transition states of bacterial enhancer binding AAA+ ATPases support complex formation with their target protein, sigma54. <i>Structure</i> , 2007 , 15, 429-40	5.2	62
25	Look, no hands! Unconventional transcriptional activators in bacteria. <i>Trends in Microbiology</i> , 2007 , 15, 530-7	12.4	37
24	Comparative genomic evidence for a close relationship between the dimorphic prosthecate bacteria <i>Hyphomonas neptunium</i> and <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2006 , 188, 6841-50	3.5	52
23	The structural basis for regulated assembly and function of the transcriptional activator NtrC. <i>Genes and Development</i> , 2006 , 20, 1485-95	12.6	97
22	Characterization of <i>Helicobacter pylori</i> sigma54 promoter-binding activity. <i>FEMS Microbiology Letters</i> , 2006 , 259, 20-6	2.9	4
21	Stable accumulation of sigma54 in <i>Helicobacter pylori</i> requires the novel protein HP0958. <i>Journal of Bacteriology</i> , 2005 , 187, 4463-9	3.5	28
20	Purification and characterization of the AAA+ domain of <i>Sinorhizobium meliloti</i> DctD, a sigma54-dependent transcriptional activator. <i>Journal of Bacteriology</i> , 2004 , 186, 3499-507	3.5	25
19	<i>Helicobacter pylori</i> FlgR is an enhancer-independent activator of sigma54-RNA polymerase holoenzyme. <i>Journal of Bacteriology</i> , 2004 , 186, 4535-42	3.5	47
18	Novel substitutions in the sigma54-dependent activator DctD that increase dependence on upstream activation sequences or uncouple ATP hydrolysis from transcriptional activation. <i>Molecular Microbiology</i> , 2004 , 54, 32-44	4.1	4
17	Nucleotide-dependent conformational changes in the sigma54-dependent activator DctD. <i>Journal of Bacteriology</i> , 2003 , 185, 6215-9	3.5	8

16	Synergistic transcriptional activation by one regulatory protein in response to two metabolites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7693-8	11.5	76
15	Transcriptional regulation at a distance in bacteria. <i>Current Opinion in Microbiology</i> , 2001 , 4, 138-44	7.9	102
14	The amino terminus of Salmonella enterica serovar Typhimurium sigma(54) is required for interactions with an enhancer-binding protein and binding to fork junction DNA. <i>Journal of Bacteriology</i> , 2000 , 182, 513-7	3.5	13
13	Transcription initiation-defective forms of sigma(54) that differ in ability To function with a heteroduplex DNA template. <i>Journal of Bacteriology</i> , 2000 , 182, 6503-8	3.5	5
12	A rhizobial homolog of IHF stimulates transcription of dctA in Rhizobium leguminosarum but not in Sinorhizobium meliloti. <i>Gene</i> , 1999 , 238, 489-500	3.8	3
11	Mutant forms of Salmonella typhimurium sigma54 defective in transcription initiation but not promoter binding activity. <i>Journal of Bacteriology</i> , 1999 , 181, 3351-7	3.5	12
10	Cloning and characterization of Planctomyces limnophilus rpoN: complementation of a Salmonella typhimurium rpoN mutant strain. <i>Gene</i> , 1998 , 221, 151-7	3.8	17
9	Mutational analysis of the phosphate-binding loop of Rhizobium meliloti DctD, a sigma54-dependent activator. <i>Journal of Bacteriology</i> , 1998 , 180, 2792-5	3.5	9
8	A conserved region in the sigma54-dependent activator DctD is involved in both binding to RNA polymerase and coupling ATP hydrolysis to activation. <i>Molecular Microbiology</i> , 1997 , 26, 373-86	4.1	48
7	Rhizobium meliloti DctD, a sigma 54-dependent transcriptional activator, may be negatively controlled by a subdomain in the C-terminal end of its two-component receiver module. <i>Molecular Microbiology</i> , 1994 , 13, 51-66	4.1	52
6	Role of integration host factor in stimulating transcription from the sigma 54-dependent nifH promoter. <i>Journal of Molecular Biology</i> , 1992 , 227, 602-20	6.5	98
5	The integration host factor stimulates interaction of RNA polymerase with NIFA, the transcriptional activator for nitrogen fixation operons. <i>Cell</i> , 1990 , 63, 11-22	56.2	343
4	Homocitrate is a component of the iron-molybdenum cofactor of nitrogenase. <i>Biochemistry</i> , 1989 , 28, 2768-71	3.2	126
3	Substrate reduction properties of dinitrogenase activated in vitro are dependent upon the presence of homocitrate or its analogues during iron-molybdenum cofactor synthesis. <i>Biochemistry</i> , 1989 , 28, 7796-9	3.2	86
2	Dinitrogenase with altered substrate specificity results from the use of homocitrate analogues for in vitro synthesis of the iron-molybdenum cofactor. <i>Biochemistry</i> , 1988 , 27, 3647-52	3.2	48
1	Identification of the V factor needed for synthesis of the iron-molybdenum cofactor of nitrogenase as homocitrate. <i>Nature</i> , 1987 , 329, 855-7	50.4	136