Julie A Maupin-Furlow

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. Nucleic Acids Research, 2022, 50, 4601-4615.	14.5	7
2	Lysine acetylation during oxidative stress response in the halophilic archaeon <i>Haloferax volcanii</i> . FASEB Journal, 2022, 36, .	0.5	0
3	Halophilic archaea and their potential to generate renewable fuels and chemicals. Biotechnology and Bioengineering, 2021, 118, 1066-1090.	3.3	19
4	Bacterial effectors mimicking ubiquitin-proteasome pathway tweak plant immunity. Microbiological Research, 2021, 250, 126810.	5.3	15
5	Expression and tandem affinity purification of 20S proteasomes and other multisubunit complexes in Haloferax volcanii. Methods in Enzymology, 2021, 659, 315-326.	1.0	3
6	High-level synthesis and secretion of laccase, a metalloenzyme biocatalyst, by the halophilic archaeon Haloferax volcanii. Methods in Enzymology, 2021, 659, 297-313.	1.0	3
7	Redox and Thiols in Archaea. Antioxidants, 2020, 9, 381.	5.1	20
8	The Antioxidant Enzyme Methionine Sulfoxide Reductase A (MsrA) Interacts with Jab1/CSN5 and Regulates Its Function. Antioxidants, 2020, 9, 452.	5.1	6
9	The Archaeal Proteome Project advances knowledge about archaeal cell biology through comprehensive proteomics. Nature Communications, 2020, 11, 3145.	12.8	40
10	Modification of the host ubiquitome by bacterial enzymes. Microbiological Research, 2020, 235, 126429.	5.3	10
11	Insights through Genetics of Halophilic Microorganisms and Their Viruses. Genes, 2020, 11, 388.	2.4	3
12	Gene Expression of Haloferax volcanii on Intermediate and Abundant Sources of Fixed Nitrogen. International Journal of Molecular Sciences, 2019, 20, 4784.	4.1	4
13	Alanine Tails Signal Proteolysis in Bacterial Ribosome-Associated Quality Control. Cell, 2019, 178, 76-90.e22.	28.9	81
14	Rhodanese-Like Domain Protein UbaC and Its Role in Ubiquitin-Like Protein Modification and Sulfur Mobilization in Archaea. Journal of Bacteriology, 2019, 201, .	2.2	3
15	Assays for ubiquitin-like protein ligation and proteasome function in archaea. Methods in Enzymology, 2019, 619, 161-178.	1.0	1
16	Stepping up protein degradation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 350-352.	7.1	0
17	Putting phage to work in deubiquitinase ligand discovery. Journal of Biological Chemistry, 2019, 294, 437-438.	3.4	0
18	RNA helicase homolog and its association with the JAMM2 metalloprotease required for targeted protein turnover in Archaea. FASEB Journal, 2019, 33, 631,36.	0.5	0

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19	Determining the association of the TrmBâ€ŀike protein OxsR to chromatin binding and oxidative stress in Haloferax volcanii. FASEB Journal, 2019, 33, 777.17.	0.5	0
20	Methionine Sulfoxide Reductases of Archaea. Antioxidants, 2018, 7, 124.	5.1	17
21	Proteolytic systems of archaea: slicing, dicing, and mincing in the extreme. Emerging Topics in Life Sciences, 2018, 2, 561-580.	2.6	7
22	Molecular Factors of Hypochlorite Tolerance in the Hypersaline Archaeon Haloferax volcanii. Genes, 2018, 9, 562.	2.4	5
23	A Cobalamin Activity-Based Probe Enables Microbial Cell Growth and Finds New Cobalamin-Protein Interactions across Domains. Applied and Environmental Microbiology, 2018, 84, .	3.1	15
24	Methionine sulfoxide reductase A (MsrA) mediates the ubiquitination of 14-3-3 protein isotypes in brain. Free Radical Biology and Medicine, 2018, 129, 600-607.	2.9	10
25	GlpR Is a Direct Transcriptional Repressor of Fructose Metabolic Genes in Haloferax volcanii. Journal of Bacteriology, 2018, 200, .	2.2	14
26	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. Environmental Microbiology, 2018, 20, 385-401.	3.8	21
27	In vitro Analysis of Ubiquitin-like Protein Modification in Archaea. Bio-protocol, 2018, 8, .	0.4	1
28	RPT., 2018,, 4756-4762.		0
29	Cdc48a AAAâ€ATPase and its association with ubiquitinâ€like SAMP1 and DNA repair in Archaea. FASEB Journal, 2018, 32, 786.10.	0.5	Ο
30	ThiN as a Versatile Domain of Transcriptional Repressors and Catalytic Enzymes of Thiamine Biosynthesis. Journal of Bacteriology, 2017, 199, .	2.2	11
31	Structural Insight into Ubiquitin-Like Protein Recognition and Oligomeric States of JAMM/MPN+ Proteases. Structure, 2017, 25, 823-833.e6.	3.3	16
32	Methionine Sulfoxide Reductase A (MsrA) and Its Function in Ubiquitin-Like Protein Modification in <i>Archaea</i> . MBio, 2017, 8, .	4.1	20
33	Chase Assay of Protein Stability in Haloferax volcanii. Bio-protocol, 2017, 7, .	0.4	1
34	Proteome targets of ubiquitinâ€like samp1ylation are associated with sulfur metabolism and oxidative stress in <i>Haloferax volcanii</i> . Proteomics, 2016, 16, 1100-1110.	2.2	16
35	Ubiquitin-Like Proteasome System Represents a Eukaryotic-Like Pathway for Targeted Proteolysis in Archaea. MBio, 2016, 7, .	4.1	28
36	Mechanistic insight into protein modification and sulfur mobilization activities of noncanonical E1 and associated ubiquitinâ€like proteins of Archaea. FEBS Journal, 2016, 283, 3567-3586.	4.7	21

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37	Archaeal Inorganic Pyrophosphatase Displays Robust Activity under High-Salt Conditions and in Organic Solvents. Applied and Environmental Microbiology, 2016, 82, 538-548.	3.1	13
38	Ubiquitin-Like Protein SAMP1 and JAMM/MPN+ Metalloprotease HvJAMM1 Constitute a System for Reversible Regulation of Metabolic Enzyme Activity in Archaea. PLoS ONE, 2015, 10, e0128399.	2.5	14
39	Archaeal Tuc1/Ncs6 Homolog Required for Wobble Uridine tRNA Thiolation Is Associated with Ubiquitin-Proteasome, Translation, and RNA Processing System Homologs. PLoS ONE, 2014, 9, e99104.	2.5	32
40	Conserved active site cysteine residue of archaeal THI4 homolog is essential for thiamine biosynthesis in Haloferax volcanii. BMC Microbiology, 2014, 14, 260.	3.3	14
41	Archaeal Ubiquitin-like SAMP3 is Isopeptide-linked to Proteins via a UbaA-dependent Mechanism. Molecular and Cellular Proteomics, 2014, 13, 220-239.	3.8	25
42	Structural and biochemical properties of an extreme â€~salt-loving' proteasome activating nucleotidase from the archaeon Haloferax volcanii. Extremophiles, 2014, 18, 283-293.	2.3	10
43	Prokaryotic Ubiquitin-Like Protein Modification. Annual Review of Microbiology, 2014, 68, 155-175.	7.3	47
44	Functional Proteomic Discovery of Slr0110 as a Central Regulator of Carbohydrate Metabolism in Synechocystis Species PCC6803. Molecular and Cellular Proteomics, 2014, 13, 204-219.	3.8	22
45	Post-translation modification in Archaea: lessons from <i>Haloferax volcanii</i> and other haloarchaea. FEMS Microbiology Reviews, 2013, 37, 583-606.	8.6	34
46	Ubiquitin-like proteins and their roles in archaea. Trends in Microbiology, 2013, 21, 31-38.	7.7	43
47	Prokaryotic Proteasomes: Nanocompartments of Degradation. Journal of Molecular Microbiology and Biotechnology, 2013, 23, 321-334.	1.0	24
48	Nitrogen regulation of protein–protein interactions and transcript levels of GlnK <scp>PII</scp> regulator and AmtB ammonium transporter homologs in Archaea. MicrobiologyOpen, 2013, 2, 826-840.	3.0	18
49	Crystal structure of the ubiquitinâ€like small archaeal modifier protein 2 from <i>Haloferax volcanii</i> . Protein Science, 2013, 22, 1206-1217.	7.6	8
50	Archaeal Proteasomes and Sampylation. Sub-Cellular Biochemistry, 2013, 66, 297-327.	2.4	14
51	Characterization of an archaeal ubiquitinâ€like protein SAMP1. FASEB Journal, 2013, 27, 782.8.	0.5	0
52	Enhanced archaeal laccase production in recombinant <i>Escherichia coli</i> by modification of N-terminal propeptide and twin arginine translocation motifs. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 1523-1532.	3.0	13
53	Proteasomes and protein conjugation across domains of life. Nature Reviews Microbiology, 2012, 10, 100-111.	28.6	98
54	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon Natrialba magadii ATCC 43099T. BMC Genomics, 2012, 13, 165.	2.8	36

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55	Archaeal <scp>JAB</scp> 1/ <scp>MPN</scp> / <scp>MOV</scp> 34 metalloenzyme (<scp>HvJAMM</scp> 1) cleaves ubiquitinâ€like small archaeal modifier proteins (<scp>SAMP</scp> s) from proteinâ€conjugates. Molecular Microbiology, 2012, 86, 971-987.	2.5	39
56	Extreme challenges and advances in archaeal proteomics. Current Opinion in Microbiology, 2012, 15, 351-356.	5.1	15
57	Chemical crossâ€linking, mass spectrometry, and in silico modeling of proteasomal 20 <scp>S</scp> core particles of the haloarchaeon <i><scp>H</scp>aloferax volcanii</i> . Proteomics, 2012, 12, 1806-1814.	2.2	16
58	Microbial diversity of the hypersaline Sidi Ameur and Himalatt Salt Lakes of the Algerian Sahara. Journal of Arid Environments, 2011, 75, 909-916.	2.4	39
59	Activity and Transcriptional Regulation of Bacterial Protein-Like Glycerol-3-Phosphate Dehydrogenase of the Haloarchaea in Haloferax volcanii. Journal of Bacteriology, 2011, 193, 4469-4476.	2.2	27
60	Activity and Transcriptional Regulation of Bacterial Protein-Like Glycerol-3-Phosphate Dehydrogenase of the Haloarchaea in Haloferax volcanii. Journal of Bacteriology, 2011, 193, 6110-6110.	2.2	1
61	E1- and ubiquitin-like proteins provide a direct link between protein conjugation and sulfur transfer in archaea. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4417-4422.	7.1	83
62	Ubiquitin-like small archaeal modifier proteins (SAMPs) in Haloferax volcanii. Nature, 2010, 463, 54-60.	27.8	170
63	Phosphorylation and Methylation of Proteasomal Proteins of the Haloarcheon <i>Haloferax volcanii</i> . Archaea, 2010, 2010, 1-10.	2.3	25
64	Archaeal Protein Biogenesis: Posttranslational Modification and Degradation. Archaea, 2010, 2010, 1-2.	2.3	1
65	The Complete Genome Sequence of Haloferax volcanii DS2, a Model Archaeon. PLoS ONE, 2010, 5, e9605.	2.5	234
66	Hydrophobic carboxy-terminal residues dramatically reduce protein levels in the haloarchaeon Haloferax volcanii. Microbiology (United Kingdom), 2010, 156, 248-255.	1.8	14
67	GlpR Represses Fructose and Glucose Metabolic Enzymes at the Level of Transcription in the Haloarchaeon <i>Haloferax volcanii</i> . Journal of Bacteriology, 2010, 192, 6251-6260.	2.2	33
68	LccA, an Archaeal Laccase Secreted as a Highly Stable Glycoprotein into the Extracellular Medium by <i>Haloferax volcanii</i> . Applied and Environmental Microbiology, 2010, 76, 733-743.	3.1	117
69	Glycerol-Mediated Repression of Glucose Metabolism and Glycerol Kinase as the Sole Route of Glycerol Catabolism in the Haloarchaeon <i>Haloferax volcanii</i> . Journal of Bacteriology, 2009, 191, 4307-4315.	2.2	37
70	Stabilization of an archaeal DNA-sliding clamp protein, PCNA, by proteasome-activating nucleotidase gene knockout inHaloferax volcanii. FEMS Microbiology Letters, 2009, 294, 32-36.	1.8	8
71	The N-Terminal Penultimate Residue of 20S Proteasome α1 Influences its N α Acetylation and Protein Levels as Well as Growth Rate and Stress Responses of Haloferax volcanii. Journal of Bacteriology, 2009, 191, 3794-3803.	2.2	40
72	Gene cloning and heterologous synthesis of a haloalkaliphilic extracellular protease of Natrialba magadii (Nep). Extremophiles, 2008, 12, 677-687.	2.3	60

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73	Shotgun Proteomics of the Haloarchaeon Haloferax volcanii. Journal of Proteome Research, 2008, 7, 5033-5039.	3.7	51
74	Proteasomal Components Required for Cell Growth and Stress Responses in the Haloarchaeon <i>Haloferax volcanii</i> . Journal of Bacteriology, 2008, 190, 8096-8105.	2.2	55
75	Genetic and Proteomic Analyses of a Proteasome-Activating Nucleotidase A Mutant of the Haloarchaeon <i>Haloferax volcanii</i> . Journal of Bacteriology, 2008, 190, 193-205.	2.2	37
76	Proteomic analysis of Haloferax volcanii reveals salinity-mediated regulation of the stress response protein PspA. Microbiology (United Kingdom), 2008, 154, 1436-1443.	1.8	45
77	Effect of proteasome inhibitor clasto-lactacystin-β-lactone on the proteome of the haloarchaeon Haloferax volcanii. Microbiology (United Kingdom), 2007, 153, 2271-2280.	1.8	18
78	Transcriptional linkage of Haloferax volcanii proteasomal genes with non-proteasomal gene neighbours including RNase P, MOSC domain and SAM-methyltransferase homologues. Microbiology (United Kingdom), 2007, 153, 3009-3022.	1.8	7
79	Proteasomes from Structure to Function: Perspectives from Archaea. Current Topics in Developmental Biology, 2006, 75, 125-169.	2.2	50
80	Haloarchaeal proteases and proteolytic systems. FEMS Microbiology Reviews, 2006, 30, 17-35.	8.6	69
81	Haloarchaeal proteases and proteolytic systems. FEMS Microbiology Reviews, 2006, 30, 649-649.	8.6	1
82	Trizol-based method for sample preparation and isoelectric focusing of halophilic proteins. Analytical Biochemistry, 2006, 351, 254-259.	2.4	62
83	Proteasomes and Other Nanocompartmentalized Proteases of Archaea. Microbiology Monographs, 2006, , 23-46.	0.6	1
84	Haloferax volcanii PitA: an example of functional interaction between the Pfam chlorite dismutase and antibiotic biosynthesis monooxygenase families?. Bioinformatics, 2006, 22, 671-675.	4.1	35
85	Posttranslational Modification of the 20S Proteasomal Proteins of the Archaeon Haloferax volcanii. Journal of Bacteriology, 2006, 188, 7521-7530.	2.2	27
86	Improvement of two-dimensional gel electrophoresis proteome maps of the haloarchaeonHaloferax volcanii. Proteomics, 2005, 5, 354-359.	2.2	30
87	Recombinant production ofZymomonas mobilispyruvate decarboxylase in the haloarchaeonHaloferax volcanii. Archaea, 2005, 1, 327-334.	2.3	21
88	Construction and expression of an ethanol production operon in Gram-positive bacteria. Microbiology (United Kingdom), 2005, 151, 4023-4031.	1.8	43
89	Archaeal proteasomes and other regulatory proteases. Current Opinion in Microbiology, 2005, 8, 720-728.	5.1	38
90	Proteasomes: perspectives from the archaea. Frontiers in Bioscience - Landmark, 2004, 9, 1743.	3.0	29

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91	Differential Regulation of the PanA and PanB Proteasome-Activating Nucleotidase and 20S Proteasomal Proteins of the Haloarchaeon Haloferax volcanii. Journal of Bacteriology, 2004, 186, 7763-7772.	2.2	56
92	Analysis of Proteasome-Dependent Proteolysis in Haloferax volcanii Cells, Using Short-Lived Green Fluorescent Proteins. Applied and Environmental Microbiology, 2004, 70, 7530-7538.	3.1	83
93	Archaeal proteasomes:. Metabolic Engineering, 2003, 5, 151-163.	7.0	5
94	Subunit Topology of Two 20S Proteasomes from Haloferax volcanii. Journal of Bacteriology, 2003, 185, 165-174.	2.2	49
95	Cloning and Characterization of the Zymobacter palmae Pyruvate Decarboxylase Gene (pdc) and Comparison to Bacterial Homologues. Applied and Environmental Microbiology, 2002, 68, 2869-2876.	3.1	63
96	Archaeal proteasomes: Proteolytic nanocompartments of the cell. Advances in Applied Microbiology, 2001, 50, 279-338.	2.4	13
97	Pyruvate decarboxylase: a key enzyme for the oxidative metabolism of lactic acid by Acetobacter pasteurianus. Archives of Microbiology, 2001, 176, 443-451.	2.2	57
98	Production of the Gram-positive Sarcina ventriculi pyruvate decarboxylase in Escherichia coli The GenBank accession number for the sequence reported in this paper is AF354297 Microbiology (United) Tj ETQq	0 0 .0 rgB1	/Overlock 10
99	Proteasomes in the archaea from structure to function. Frontiers in Bioscience - Landmark, 2000, 5, d837-865.	3.0	3
100	Biochemical and Physical Properties of the Methanococcus jannaschii 20S Proteasome and PAN, a Homolog of the ATPase (Rpt) Subunits of the Eucaryal 26S Proteasome. Journal of Bacteriology, 2000, 182, 1680-1692.	2.2	82
101	Proteasomes in the archaea: from structure to function. Frontiers in Bioscience - Landmark, 2000, 5, d837.	3.0	40
102	Halophilic 20S Proteasomes of the Archaeon <i>Haloferax volcanii</i> : Purification, Characterization, and Gene Sequence Analysis. Journal of Bacteriology, 1999, 181, 5814-5824.	2.2	57
103	Biochemical Characterization of the 20S Proteasome from the Methanoarchaeon <i>Methanosarcina thermophila</i> . Journal of Bacteriology, 1998, 180, 1480-1487.	2.2	60
104	Biochemical Characterization of the 20S Proteasome from the Methanoarchaeon <i>Methanosarcina thermophila</i> . Journal of Bacteriology, 1998, 180, 3017-3017.	2.2	0
105	Characterization of the cdhD and cdhE genes encoding subunits of the corrinoid/iron-sulfur enzyme of the CO dehydrogenase complex from Methanosarcina thermophila. Journal of Bacteriology, 1996, 178, 340-346.	2.2	36
106	Analysis of the CO dehydrogenase/acetyl-coenzyme A synthase operon of Methanosarcina thermophila. Journal of Bacteriology, 1996, 178, 6849-6856.	2.2	51
107	Analysis of genes in the pathway for the fermentation of acetate to methane by Methanosarcina thermophila. , 1996, , 64-71.		2
108	Genetic analysis of the modABCD (molybdate transport) operon of Escherichia coli. Journal of Bacteriology, 1995, 177, 4851-4856.	2.2	104

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109	Molybdate and regulation of mod (molybdate transport), fdhF, and hyc (formate hydrogenlyase) operons in Escherichia coli. Journal of Bacteriology, 1995, 177, 4857-4864.	2.2	85
110	A Proteasome from the Methanogenic Archaeon Methanosarcina thermophila. Journal of Biological Chemistry, 1995, 270, 28617-28622.	3.4	77
111	Vitamin B1 (Thiamine) Metabolism and Regulation in Archaea. , 0, , .		13