

Ann H West

List of Publications by Year in descending order

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56
papers

2,826
citations

257101

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174990

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3087
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights revealed by the co-crystal structure of the <i>Saccharomyces cerevisiae</i> histidine phosphotransfer protein Ypd1 and the receiver domain of its downstream response regulator Ssk1. <i>Protein Science</i> , 2019, 28, 2099-2111.	3.1	5
2	Role of the highly conserved G68 residue in the yeast phosphorelay protein Ypd1: implications for interactions between histidine phosphotransfer (HPT) and response regulator proteins. <i>BMC Biochemistry</i> , 2019, 20, 1.	4.4	6
3	Regulatory Targets of the Response Regulator RR_1586 from <i>Clostridioides difficile</i> Identified Using a Bacterial One-Hybrid Screen. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	5
4	Use of restrained molecular dynamics to predict the conformations of phosphorylated receiver domains in two-component signaling systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 155-176.	1.5	12
5	Crystal structure and DNA binding activity of a PadR family transcription regulator from hypervirulent <i>Clostridium difficile</i> R20291. <i>BMC Microbiology</i> , 2016, 16, 231.	1.3	13
6	Extended N-terminal region of the essential phosphorelay signaling protein Ypd1 from <i>Cryptococcus neoformans</i> contributes to structural stability, phosphostability and binding of calcium ions. <i>FEMS Yeast Research</i> , 2016, 16, fow068.	1.1	8
7	Crystal structures of two nitroreductases from hypervirulent <i>Clostridium difficile</i> and functionally related interactions with the antibiotic metronidazole. <i>Nitric Oxide - Biology and Chemistry</i> , 2016, 60, 32-39.	1.2	11
8	Evidence for an induced conformational change in the catalytic mechanism of homoisocitrate dehydrogenase for <i>Saccharomyces cerevisiae</i> : Characterization of the D271N mutant enzyme. <i>Archives of Biochemistry and Biophysics</i> , 2015, 584, 20-27.	1.4	0
9	Probing the chemical mechanism of saccharopine reductase from <i>Saccharomyces cerevisiae</i> using site-directed mutagenesis. <i>Archives of Biochemistry and Biophysics</i> , 2015, 584, 98-106.	1.4	4
10	Histidine Phosphotransfer Proteins in Fungal Two-Component Signal Transduction Pathways. <i>Eukaryotic Cell</i> , 2013, 12, 1052-1060.	3.4	53
11	Evidence in Support of Lysine 77 and Histidine 96 as Acid-Base Catalytic Residues in Saccharopine Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2012, 51, 857-866.	1.2	11
12	Supporting role of lysine 13 and glutamate 16 in the acid-base mechanism of saccharopine dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Archives of Biochemistry and Biophysics</i> , 2012, 522, 57-61.	1.4	6
13	Immunodominance of Antigenic Site B over Site A of Hemagglutinin of Recent H3N2 Influenza Viruses. <i>PLoS ONE</i> , 2012, 7, e41895.	1.1	92
14	The oxidation state of active site thiols determines activity of saccharopine dehydrogenase at low pH. <i>Archives of Biochemistry and Biophysics</i> , 2011, 513, 71-80.	1.4	3
15	Contribution of K99 and D319 to substrate binding and catalysis in the saccharopine dehydrogenase reaction. <i>Archives of Biochemistry and Biophysics</i> , 2011, 514, 8-15.	1.4	4
16	Kinetic and Chemical Mechanisms of Homocitrate Synthase from <i>Thermus thermophilus</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 29428-29439.	1.6	6
17	Fungal Skn7 Stress Responses and Their Relationship to Virulence. <i>Eukaryotic Cell</i> , 2011, 10, 156-167.	3.4	62
18	Glutamates 78 and 122 in the Active Site of Saccharopine Dehydrogenase Contribute to Reactant Binding and Modulate the Basicity of the Acid-Base Catalysts. <i>Journal of Biological Chemistry</i> , 2010, 285, 20756-20768.	1.6	7

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19	Kinetic Studies of the Yeast His-Asp Phosphorelay Signaling Pathway. <i>Methods in Enzymology</i> , 2010, 471, 59-75.	0.4	8
20	Genetic and Biochemical Analysis of the SLN1 Pathway in <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2010, 471, 291-317.	0.4	17
21	Effects of Osmolytes on the SLN1-YPD1-SSK1 Phosphorelay System from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2009, 48, 8044-8050.	1.2	27
22	Site-Directed Mutagenesis as a Probe of the Acid-Base Catalytic Mechanism of Homoisocitrate Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2009, 48, 7305-7312.	1.2	12
23	Chemical Mechanism of Saccharopine Reductase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2009, 48, 5899-5907.	1.2	13
24	Crystal structures of manganese- and cobalt-substituted myoglobin in complex with NO and nitrite reveal unusual ligand conformations. <i>Journal of Inorganic Biochemistry</i> , 2008, 102, 216-233.	1.5	40
25	Crystal Structure of a Complex between the Phosphorelay Protein YPD1 and the Response Regulator Domain of SLN1 Bound to a Phosphoryl Analog. <i>Journal of Molecular Biology</i> , 2008, 375, 1141-1151.	2.0	47
26	Overall Kinetic Mechanism of Saccharopine Dehydrogenase (N ⁶ -Glutamate Forming) from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2008, 47, 5417-5423.	1.2	6
27	Chemical Mechanism of Homoisocitrate Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2008, 47, 4169-4180.	1.2	20
28	Potassium Is an Activator of Homoisocitrate Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2008, 47, 10809-10815.	1.2	13
29	Evidence for a Catalytic Dyad in the Active Site of Homocitrate Synthase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2008, 47, 6851-6858.	1.2	21
30	Complete Kinetic Mechanism of Homoisocitrate Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2007, 46, 890-898.	1.2	17
31	A Proposed Proton Shuttle Mechanism for Saccharopine Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2007, 46, 871-882.	1.2	19
32	Determinants of Substrate Specificity for Saccharopine Dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2007, 46, 7625-7636.	1.2	5
33	Functional characterization of the phosphorelay protein Mpr1p from <i>Schizosaccharomyces pombe</i> . <i>FEMS Yeast Research</i> , 2007, 7, 912-921.	1.1	8
34	Functional studies of the Ssk1p response regulator protein of <i>Candida albicans</i> as determined by phenotypic analysis of receiver domain point mutants. <i>Molecular Microbiology</i> , 2006, 62, 997-1013.	1.2	33
35	Crystal structures of the nitrite and nitric oxide complexes of horse heart myoglobin. <i>Journal of Inorganic Biochemistry</i> , 2006, 100, 1413-1425.	1.5	103
36	Crystal Structure of the His-Tagged Saccharopine Reductase From <i>Saccharomyces cerevisiae</i> at 1.7-Å Resolution. <i>Cell Biochemistry and Biophysics</i> , 2006, 46, 17-26.	0.9	8

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37	The β -Aminoadipate Pathway for Lysine Biosynthesis in Fungi. <i>Cell Biochemistry and Biophysics</i> , 2006, 46, 43-64.	0.9	135
38	A common docking site for response regulators on the yeast phosphorelay protein YPD1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1748, 138-145.	1.1	23
39	Regulatory Mechanism of Histidine-tagged Homocitrate Synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 31624-31632.	1.6	24
40	Kinetic Analysis of YPD1-Dependent Phosphotransfer Reactions in the Yeast Osmoregulatory Phosphorelay System. <i>Biochemistry</i> , 2005, 44, 377-386.	1.2	50
41	Stabilization and characterization of histidine-tagged homocitrate synthase from <i>Saccharomyces cerevisiae</i> . <i>Archives of Biochemistry and Biophysics</i> , 2004, 421, 243-254.	1.4	24
42	The Yeast YPD1/SLN1 Complex. <i>Structure</i> , 2003, 11, 1569-1581.	1.6	65
43	Co-crystallization of the yeast phosphorelay protein YPD1 with the SLN1 response-regulator domain and preliminary X-ray diffraction analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 927-929.	2.5	3
44	Crystal structures of ferrous horse heart myoglobin complexed with nitric oxide and nitrosoethane. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 182-192.	1.5	45
45	Ssk1p Response Regulator Binding Surface on Histidine-Containing Phosphotransfer Protein Ypd1p. <i>Eukaryotic Cell</i> , 2003, 2, 27-33.	3.4	20
46	Interactions of Organic Nitroso Compounds with Metals. <i>Chemical Reviews</i> , 2002, 102, 1019-1066.	23.0	230
47	Histidine kinases and response regulator proteins in two-component signaling systems. <i>Trends in Biochemical Sciences</i> , 2001, 26, 369-376.	3.7	841
48	Functional roles of conserved amino acid residues surrounding the phosphorylatable histidine of the yeast phosphorelay protein YPD1. <i>Molecular Microbiology</i> , 2000, 37, 136-144.	1.2	45
49	Novel Role for an HPT Domain in Stabilizing the Phosphorylated State of a Response Regulator Domain. <i>Journal of Bacteriology</i> , 2000, 182, 6673-6678.	1.0	50
50	Purification, crystallization and preliminary X-ray diffraction analysis of the yeast phosphorelay protein YPD1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 291-293.	2.5	13
51	Conservation of structure and function among histidine-containing phosphotransfer (HPT) domains as revealed by the crystal structure of YPD1 1. Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 292, 1039-1050.	2.0	87
52	Differential Stabilities of Phosphorylated Response Regulator Domains Reflect Functional Roles of the Yeast Osmoregulatory SLN1 and SSK1 Proteins. <i>Journal of Bacteriology</i> , 1999, 181, 411-417.	1.0	52
53	Purification, crystallization, and preliminary X-ray diffraction analyses of the bacterial chemotaxis receptor modifying enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 345-350.	1.5	11
54	Crystal Structure of the Catalytic Domain of the Chemotaxis Receptor Methyltransferase, CheB. <i>Journal of Molecular Biology</i> , 1995, 250, 276-290.	2.0	70

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55	Structure of the magnesium-bound form of CheY and mechanism of phosphoryl transfer in bacterial chemotaxis. <i>Biochemistry</i> , 1993, 32, 13375-13380.	1.2	229
56	Proteins encoded by the trans-acting replication and maintenance regions of broad host range plasmid RK2. <i>Plasmid</i> , 1984, 11, 48-57.	0.4	57