

Emily J Parker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6975439/publications.pdf>

Version: 2024-02-01

93
papers

2,476
citations

257450

24
h-index

233421

45
g-index

96
all docs

96
docs citations

96
times ranked

2619
citing authors

#	ARTICLE	IF	CITATIONS
1	A symbiosis expressed non-ribosomal peptide synthetase from a mutualistic fungal endophyte of perennial ryegrass confers protection to the symbiotum from insect herbivory. <i>Molecular Microbiology</i> , 2005, 57, 1036-1050.	2.5	285
2	On the Temperature Dependence of Enzyme-Catalyzed Rates. <i>Biochemistry</i> , 2016, 55, 1681-1688.	2.5	233
3	Change in Heat Capacity for Enzyme Catalysis Determines Temperature Dependence of Enzyme Catalyzed Rates. <i>ACS Chemical Biology</i> , 2013, 8, 2388-2393.	3.4	164
4	The genetic basis for indole-diterpene chemical diversity in filamentous fungi. <i>Mycological Research</i> , 2008, 112, 184-199.	2.5	136
5	The Structure of 3-Deoxy-d-arabino-heptulosonate 7-phosphate Synthase from <i>Mycobacterium tuberculosis</i> Reveals a Common Catalytic Scaffold and Ancestry for Type I and Type II Enzymes. <i>Journal of Molecular Biology</i> , 2005, 354, 927-939.	4.2	74
6	Defining Paxilline Biosynthesis in <i>Penicillium paxilli</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 16829-16837.	3.4	65
7	Allosteric ACTION: the varied ACT domains regulating enzymes of amino-acid metabolism. <i>Current Opinion in Structural Biology</i> , 2014, 29, 102-111.	5.7	64
8	Synergistic Allostery, a Sophisticated Regulatory Network for the Control of Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 30567-30576.	3.4	63
9	Four gene products are required for the fungal synthesis of the indole-diterpene, paspaline. <i>FEBS Letters</i> , 2006, 580, 1625-1630.	2.8	62
10	Tyrosine Latching of a Regulatory Gate Affords Allosteric Control of Aromatic Amino Acid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2011, 286, 10216-10224.	3.4	56
11	Substrate Ambiguity and Crystal Structure of <i>Pyrococcus furiosus</i> 3-Deoxy-d-arabino-heptulosonate-7-phosphate Synthase: An Ancestral 3-Deoxyald-2-ulosonate-phosphate Synthase?. <i>Biochemistry</i> , 2005, 44, 11950-11962.	2.5	49
12	First structure of full-length mammalian phenylalanine hydroxylase reveals the architecture of an autoinhibited tetramer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2394-2399.	7.1	46
13	Engineering allosteric control to an unregulated enzyme by transfer of a regulatory domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2111-2116.	7.1	44
14	Selective Inhibition of Type II Dehydroquinases. <i>Journal of Organic Chemistry</i> , 1999, 64, 2612-2613.	3.2	42
15	MIDAS: A Modular DNA Assembly System for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2018, 7, 1018-1029.	3.8	42
16	Identification of 4-Amino-4-deoxychorismate Synthase as the Molecular Target for the Antimicrobial Action of (6S)-6-Fluoroshikimate. <i>Journal of the American Chemical Society</i> , 2004, 126, 9912-9913.	13.7	39
17	Dynamic Cross-Talk among Remote Binding Sites: The Molecular Basis for Unusual Synergistic Allostery. <i>Journal of Molecular Biology</i> , 2012, 415, 716-726.	4.2	39
18	Heterologous Biosynthesis of Nodulisporic Acid F. <i>Journal of the American Chemical Society</i> , 2018, 140, 582-585.	13.7	39

#	ARTICLE	IF	CITATIONS
19	Three Sites and You Are Out: Ternary Synergistic Allostery Controls Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2013, 425, 1582-1592.	4.2	38
20	Potent Inhibitors of a Shikimate Pathway Enzyme from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 16197-16207.	3.4	37
21	Enzymatic synthesis of (6R)- and (6S)-fluoroshikimic acids. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1995, 5, 2347-2352.	2.2	32
22	Expression, purification, and characterization of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase from <i>Pyrococcus furiosus</i> . <i>Protein Expression and Purification</i> , 2004, 34, 17-27.	1.3	32
23	Cloning and characterisation of dihydrodipicolinate synthase from the pathogen <i>Neisseria meningitidis</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1168-1174.	2.3	32
24	Deletion and Gene Expression Analyses Define the Paxilline Biosynthetic Gene Cluster in <i>Penicillium paxilli</i> . <i>Toxins</i> , 2013, 5, 1422-1446.	3.4	29
25	Exploring modular allostery via interchangeable regulatory domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3006-3011.	7.1	27
26	<i>Neisseria meningitidis</i> expresses a single 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase that is inhibited primarily by phenylalanine. <i>Protein Science</i> , 2013, 22, 1087-1099.	7.6	26
27	Complex Formation between Two Biosynthetic Enzymes Modifies the Allosteric Regulatory Properties of Both. <i>Journal of Biological Chemistry</i> , 2015, 290, 18187-18198.	3.4	26
28	Characterization of a recombinant type II 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from <i>Helicobacter pylori</i> . <i>Biochemical Journal</i> , 2005, 390, 223-230.	3.7	23
29	The Substrate Capture Mechanism of <i>Mycobacterium tuberculosis</i> Anthranilate Phosphoribosyltransferase Provides a Mode for Inhibition. <i>Biochemistry</i> , 2013, 52, 1776-1787.	2.5	23
30	Interdomain Conformational Changes Provide Allosteric Regulation en Route to Chorismate. <i>Journal of Biological Chemistry</i> , 2016, 291, 21836-21847.	3.4	22
31	Mechanistic divergence of two closely related aldol-like enzyme-catalysed reactions. <i>Organic and Biomolecular Chemistry</i> , 2005, 3, 4046.	2.8	20
32	Screening of New Zealand Native White-Rot Isolates for PCP Degradation. <i>Bioremediation Journal</i> , 2003, 7, 119-128.	2.0	19
33	Removal of the C-Terminal Regulatory Domain of \pm -Isopropylmalate Synthase Disrupts Functional Substrate Binding. <i>Biochemistry</i> , 2012, 51, 2289-2297.	2.5	18
34	Biochemical and structural characterisation of dehydroquinase synthase from the New Zealand kiwifruit <i>Actinidia chinensis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2013, 537, 185-191.	3.0	18
35	Alternative substrates reveal catalytic cycle and key binding events in the reaction catalysed by anthranilate phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2014, 461, 87-98.	3.7	18
36	Calculated pK_a Variations Expose Dynamic Allosteric Communication Networks. <i>Journal of the American Chemical Society</i> , 2016, 138, 2036-2045.	13.7	18

#	ARTICLE	IF	CITATIONS
37	Quaternary structure is an essential component that contributes to the sophisticated allosteric regulation mechanism in a key enzyme from <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2017, 12, e0180052.	2.5	18
38	Synthesis and evaluation of a mechanism-based inhibitor of a 3-deoxy-d-arabino heptulosonate 7-phosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2006, 16, 2951-2954.	2.2	16
39	Reversing Evolution: Re-establishing Obligate Metal Ion Dependence in a Metal-independent KDO8P Synthase. <i>Journal of Molecular Biology</i> , 2009, 390, 646-661.	4.2	15
40	<i>Campylobacter jejuni</i> adenosine triphosphate phosphoribosyltransferase is an active hexamer that is allosterically controlled by the twisting of a regulatory tail. <i>Protein Science</i> , 2016, 25, 1492-1506.	7.6	15
41	Substrate and reaction intermediate mimics as inhibitors of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 3031.	2.8	14
42	A Pseudoisostuctural Type II DAH7PS Enzyme from <i>Pseudomonas aeruginosa</i> : Alternative Evolutionary Strategies to Control Shikimate Pathway Flux. <i>Biochemistry</i> , 2018, 57, 2667-2678.	2.5	14
43	Structural and functional characterisation of the entry point to pyocyanin biosynthesis in <i>Pseudomonas aeruginosa</i> defines a new 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase subclass. <i>Bioscience Reports</i> , 2018, 38, .	2.4	14
44	Synthesis and evaluation of dual site inhibitors of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 5092-5097.	2.2	13
45	Destabilization of the Homotetrameric Assembly of 3-Deoxy-d-Arabino-Heptulosonate-7-Phosphate Synthase from the Hyperthermophile <i>Pyrococcus furiosus</i> Enhances Enzymatic Activity. <i>Journal of Molecular Biology</i> , 2014, 426, 656-673.	4.2	13
46	A single amino acid substitution uncouples catalysis and allostery in an essential biosynthetic enzyme in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 6252-6262.	3.4	13
47	Derailing Dehydroquinase Synthase by Introducing a Stabilizing Stereoelectronic Effect in a Reaction Intermediate. <i>Journal of Organic Chemistry</i> , 1997, 62, 8582-8585.	3.2	12
48	Mechanistic studies on type I and type II dehydroquinase with (6 R)- and (6 S)-6-fluoro-3-dehydroquinic acids. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2000, 10, 231-234.	2.2	12
49	Substrate Deactivation of Phenylalanine-Sensitive 3-Deoxy-d-arabino-heptulosonate 7-Phosphate Synthase by Erythrose 4-Phosphate. <i>Biochemistry</i> , 2001, 40, 14821-14828.	2.5	12
50	The C-terminal regulatory domain is required for catalysis by <i>Neisseria meningitidis</i> L-isopropylmalate synthase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 168-173.	2.1	12
51	Modifying the determinants of L-ketoacid substrate selectivity in <i>mycobacterium tuberculosis</i> L-isopropylmalate synthase. <i>FEBS Letters</i> , 2014, 588, 1603-1607.	2.8	12
52	Independent catalysis of the short form HisG from <i>Lactococcus lactis</i> . <i>FEBS Letters</i> , 2016, 590, 2603-2610.	2.8	12
53	Transition State Analysis of Adenosine Triphosphate Phosphoribosyltransferase. <i>ACS Chemical Biology</i> , 2017, 12, 2662-2670.	3.4	12
54	A dimeric catalytic core relates the short and long forms of ATP-phosphoribosyltransferase. <i>Biochemical Journal</i> , 2018, 475, 247-260.	3.7	12

#	ARTICLE	IF	CITATIONS
55	Crystallization and preliminary X-ray crystallographic analysis of 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 403-406.	0.7	11
56	Using a Combination of Computational and Experimental Techniques to Understand the Molecular Basis for Protein Allostery. <i>Advances in Protein Chemistry and Structural Biology</i> , 2012, 87, 391-413.	2.3	11
57	Structures of <i>Mycobacterium tuberculosis</i> Anthranilate Phosphoribosyltransferase Variants Reveal the Conformational Changes That Facilitate Delivery of the Substrate to the Active Site. <i>Biochemistry</i> , 2015, 54, 6082-6092.	2.5	11
58	Diverse allosteric componentry and mechanisms control entry into aromatic metabolite biosynthesis. <i>Current Opinion in Structural Biology</i> , 2020, 65, 159-167.	5.7	11
59	Arabinose 5-phosphate analogues as mechanistic probes for <i>Neisseria meningitidis</i> 3-deoxy-d-manno-octulosonate 8-phosphate synthase. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 9830-9836.	3.0	10
60	â€˜Tetheringâ€™ fragment-based drug discovery to identify inhibitors of the essential respiratory membrane protein type II NADH dehydrogenase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 2239-2243.	2.2	10
61	Stereospecific deuteration of 2-deoxyerythrose 4-phosphate using 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2005, 15, 2339-2342.	2.2	9
62	Specificity and mutational analysis of the metal-dependent 3-deoxy-d-manno-octulosonate 8-phosphate synthase from <i>Acidithiobacillus ferrooxidans</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 1526-1536.	2.3	9
63	Allosteric inhibitor specificity of <i>Thermotoga maritima</i> 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase. <i>FEBS Letters</i> , 2013, 587, 3063-3068.	2.8	9
64	Arg314 Is Essential for Catalysis by <i>N</i> -Acetyl Neuraminic Acid Synthase from <i>Neisseria meningitidis</i> . <i>Biochemistry</i> , 2013, 52, 2609-2619.	2.5	9
65	Synthesis and evaluation of tetrahedral intermediate mimic inhibitors of 3-deoxy-d-manno-octulosonate 8-phosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2012, 22, 907-911.	2.2	8
66	Draft Genome Sequence of the Filamentous Fungus <i>Hypoxylon pulicidum</i> ATCC 74245. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
67	Domain cross-talk within a bifunctional enzyme provides catalytic and allosteric functionality in the biosynthesis of aromatic amino acids. <i>Journal of Biological Chemistry</i> , 2019, 294, 4828-4842.	3.4	8
68	Nodulisporic acid E biosynthesis: in vivo characterisation of NodD1, an indole-diterpene prenyltransferase that acts on an emindole SB derived indole-diterpene scaffold. <i>MedChemComm</i> , 2019, 10, 1160-1164.	3.4	8
69	Key Targets and Relevant Inhibitors for the Drug Discovery of Tuberculosis. <i>Current Drug Targets</i> , 2013, 14, 676-699.	2.1	8
70	Molecular Modeling Studies of Peptide Inhibitors Highlight the Importance of Conformational Prearrangement for Inhibition of Calpain. <i>Biochemistry</i> , 2010, 49, 5533-5539.	2.5	7
71	Targeting the Role of a Key Conserved Motif for Substrate Selection and Catalysis by 3-Deoxy-d-manno-octulosonate 8-Phosphate Synthase. <i>Biochemistry</i> , 2011, 50, 3686-3695.	2.5	7
72	Amino-acid substitutions at the domain interface affect substrate and allosteric inhibitor binding in Î±-isopropylmalate synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013, 433, 249-254.	2.1	7

#	ARTICLE	IF	CITATIONS
73	Structural analysis of substrate-mimicking inhibitors in complex with <i>Neisseria meningitidis</i> 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase – The importance of accommodating the active site water. <i>Bioorganic Chemistry</i> , 2014, 57, 242-250.	4.1	7
74	Aminoacylation of Indole Diterpenes by Cluster-Specific Monomodular NRPS-like Enzymes. <i>Organic Letters</i> , 2022, 24, 2332-2337.	4.6	7
75	The Molecular Basis for the Substrate Specificity of Protein Tyrosine Phosphatase PTPN3. <i>Structure</i> , 2015, 23, 608-609.	3.3	6
76	Probing the Sophisticated Synergistic Allosteric Regulation of Aromatic Amino Acid Biosynthesis in <i>Mycobacterium tuberculosis</i> Using – Amino Acids. <i>PLoS ONE</i> , 2016, 11, e0152723.	2.5	6
77	The Functional Unit of <i>Neisseria meningitidis</i> 3-Deoxy-–Arabino-Heptulosonate 7-Phosphate Synthase Is Dimeric. <i>PLoS ONE</i> , 2016, 11, e0145187.	2.5	6
78	An Extended –7 Substrate-Binding Loop Is Essential for Efficient Catalysis by 3-Deoxy-–manno-Octulosonate 8-Phosphate Synthase. <i>Biochemistry</i> , 2011, 50, 9318-9327.	2.5	5
79	Anthranilate phosphoribosyltransferase: Binding determinants for 5-phospho-alpha-d-ribose-1-pyrophosphate (PRPP) and the implications for inhibitor design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 264-274.	2.3	5
80	Investigating the role of the hydroxyl groups of substrate erythrose 4-phosphate in the reaction catalysed by the first enzyme of the shikimate pathway. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 6838-6841.	2.2	4
81	Probing the determinants of phosphorylated sugar-substrate binding for human sialic acid synthase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2257-2264.	2.3	4
82	Examining the Role of Intersubunit Contacts in Catalysis by 3-Deoxy-–manno-octulosonate 8-Phosphate Synthase. <i>Biochemistry</i> , 2013, 52, 4676-4686.	2.5	3
83	Hinge Twists and Population Shifts Deliver Regulated Catalysis for ATP-PRT in Histidine Biosynthesis. <i>Biophysical Journal</i> , 2019, 116, 1887-1897.	0.5	3
84	Enzymic synthesis of 3-[3-13C]dehydroquinic acid. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 3271.	2.8	2
85	Fluorinated substrates result in variable leakage of a reaction intermediate during catalysis by dehydroquinase synthase. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 2861.	2.8	2
86	Expression, Purification, and Characterisation of Dehydroquinase Synthase from <i>Pyrococcus furiosus</i> . <i>Enzyme Research</i> , 2011, 2011, 1-10.	1.8	2
87	Active site plasticity of a critical enzyme from <i>Mycobacterium tuberculosis</i> . <i>RSC Advances</i> , 2013, 3, 3209.	3.6	2
88	Substrate-mediated control of the conformation of an ancillary domain delivers a competent catalytic site for N-acetylneuraminic acid synthase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2054-2066.	2.6	2
89	Datasets, processing and refinement details for <i>Mtb</i> -AnPRT: inhibitor structures with various space groups. <i>Data in Brief</i> , 2017, 15, 1019-1029.	1.0	2
90	Reciprocal allostery arising from a hienzyme assembly controls aromatic amino acid biosynthesis in <i>Prevotella nigrescens</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101038.	3.4	2

#	ARTICLE	IF	CITATIONS
91	Erratum to "Reversing Evolution: Re-establishing Obligate Metal Ion Dependence in a Metal-independent KDO8P Synthase" [J. Mol. Biol. 390 (2009) 646-661]. Journal of Molecular Biology, 2009, 393, 1004-1005.	4.2	0
92	Editorial overview: Catalysis and regulation: Enzyme catalysis, biosynthetic pathways and regulation. Current Opinion in Structural Biology, 2014, 29, iv-v.	5.7	0
93	Editorial overview: Catalysis and regulation. Current Opinion in Structural Biology, 2020, 65, iii-iv.	5.7	0