

Wayne M Patrick

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

2,417
citations

257450

24
h-index

214800

47
g-index

65
all docs

65
docs citations

65
times ranked

3570
citing authors

#	ARTICLE	IF	CITATIONS
1	Dan Tawfik's Lessons for Protein Engineers about Enzymes Adapting to New Substrates. <i>Biochemistry</i> , 2023, 62, 158-162.	2.5	2
2	Assessing the effectiveness of oxathiapiprolin toward <i>Phytophthora agathidicida</i> , the causal agent of kauri dieback disease. <i>FEMS Microbes</i> , 2022, 2, .	2.1	5
3	Complex Loop Dynamics Underpin Activity, Specificity, and Evolvability in the β -Barrel Enzymes of Histidine and Tryptophan Biosynthesis. <i>Jacs Au</i> , 2022, 2, 943-960.	7.9	10
4	Draft Genome Sequence of a Novel <i>Rhizobium</i> Species Isolated from the Marine Macroalga <i>Codium fragile</i> (Oyster Thief). <i>Microbiology Resource Announcements</i> , 2022, 11, e0003022.	0.6	1
5	Uniform binding and negative catalysis at the origin of enzymes. <i>Protein Science</i> , 2022, 31, .	7.6	5
6	Structures and kinetics of <i>Thermotoga maritima</i> MetY reveal new insights into the predominant sulfurylation enzyme of bacterial methionine biosynthesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100797.	3.4	14
7	Quantifying the taxonomic bias in enzymology. <i>Protein Science</i> , 2021, 30, 914-921.	7.6	5
8	Enzyme-based amperometric biosensors for malic acid – A review. <i>Analytica Chimica Acta</i> , 2021, 1156, 338218.	5.4	24
9	Enzyme promiscuity in natural environments: alkaline phosphatase in the ocean. <i>ISME Journal</i> , 2021, 15, 3375-3383.	9.8	30
10	Complete Genome Sequence of a Novel <i>Pseudomonas fluorescens</i> Strain Isolated from the Flower of <i>Kalanchoe pinnatifida</i> (Pomaderris kumeraho). <i>Microbiology Resource Announcements</i> , 2021, 10, e0062921.	0.6	0
11	Methods for competitive enrichment and evaluation of superior DNA ligases. <i>Methods in Enzymology</i> , 2020, 644, 209-225.	1.0	5
12	Structure and kinetics of indole-3-glycerol phosphate synthase from <i>Pseudomonas aeruginosa</i> : Decarboxylation is not essential for indole formation. <i>Journal of Biological Chemistry</i> , 2020, 295, 15948-15956.	3.4	1
13	Distinct pseudokinase domain conformations underlie divergent activation mechanisms among vertebrate MLKL orthologues. <i>Nature Communications</i> , 2020, 11, 3060.	12.8	47
14	Intracellular complexities of acquiring a new enzymatic function revealed by mass-randomisation of active-site residues. <i>ELife</i> , 2020, 9, .	6.0	8
15	Metagenome-guided screening of New Zealand native plants reveals flavonoids from <i>Kunzea</i> (<i>Kunzea</i>) Tj ETQq1 1 0.784314 rgBT /Cv 49, 137-154.	1.9	24
16	A Large-Scale Whole-Genome Comparison Shows that Experimental Evolution in Response to Antibiotics Predicts Changes in Naturally Evolved Clinical <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	31
17	The uncharacterized bacterial protein YejG has the same architecture as domain III of elongation factor G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 699-705.	2.6	0
18	Assessment of Phenotype Microarray plates for rapid and high-throughput analysis of collateral sensitivity networks. <i>PLoS ONE</i> , 2019, 14, e0219879.	2.5	5

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19	Mechanisms of ciprofloxacin resistance in <i>Pseudomonas aeruginosa</i> : new approaches to an old problem. <i>Journal of Medical Microbiology</i> , 2019, 68, 1-10.	1.8	137
20	Genomic and phenotypic comparison of environmental and patient-derived isolates of <i>Pseudomonas aeruginosa</i> suggest that antimicrobial resistance is rare within the environment. <i>Journal of Medical Microbiology</i> , 2019, 68, 1591-1595.	1.8	16
21	The BRD3 ET domain recognizes a short peptide motif through a mechanism that is conserved across chromatin remodelers and transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2018, 293, 7160-7175.	3.4	39
22	Enzyme evolution: innovation is easy, optimization is complicated. <i>Current Opinion in Structural Biology</i> , 2018, 48, 110-116.	5.7	70
23	Structural and functional innovations in the real-time evolution of new (β ₈) barrel enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4727-4732.	7.1	26
24	<i>Biochemical Evolution: The Pursuit of Perfection</i> . Second Edition. By Athel Cornish-Bowden. New York: Garland Science (Taylor & Francis Group). \$49.95 (paper). xviii + 274 p.; ill.; index. ISBN: 978-0-8153-4552-7. 2016.. <i>Quarterly Review of Biology</i> , 2017, 92, 332-333.	0.1	0
25	An Engineered Glycerol Dehydratase With Improved Activity for the Conversion of <i>meso</i> -2,3-butanediol to Butanone. <i>Biotechnology Journal</i> , 2017, 12, 1700480.	3.5	9
26	Primordial-like enzymes from bacteria with reduced genomes. <i>Molecular Microbiology</i> , 2017, 105, 508-524.	2.5	28
27	High-Throughput Chemical Screening Identifies Compounds that Inhibit Different Stages of the <i>Phytophthora agathidicida</i> and <i>Phytophthora cinnamomi</i> Life Cycles. <i>Frontiers in Microbiology</i> , 2017, 8, 1340.	3.5	22
28	Mechanistic and Evolutionary Insights from the Reciprocal Promiscuity of Two Pyridoxal Phosphate-dependent Enzymes. <i>Journal of Biological Chemistry</i> , 2016, 291, 19873-19887.	3.4	26
29	Whither life? Conjectures on the future evolution of biochemistry. <i>Biology Letters</i> , 2016, 12, 20160269.	2.3	1
30	The <i>in vitro</i> and <i>in vivo</i> effects of constitutive light expression on a bioluminescent strain of the mouse enteropathogen <i>Citrobacter rodentium</i> . <i>PeerJ</i> , 2016, 4, e2130.	2.0	6
31	Archaeal Nucleic Acid Ligases and Their Potential in Biotechnology. <i>Archaea</i> , 2015, 2015, 1-10.	2.3	12
32	Rapid bursts and slow declines: on the possible evolutionary trajectories of enzymes. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150036.	3.4	26
33	Substitutions at the cofactor phosphate-binding site of a clostridial alcohol dehydrogenase lead to unexpected changes in substrate specificity. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 251-258.	2.1	25
34	Two-step Ligand Binding in a (β ₈) Barrel Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 24657-24668.	3.4	16
35	Genetic Code Evolution Started with the Incorporation of Glycine, Followed by Other Small Hydrophilic Amino Acids. <i>Journal of Molecular Evolution</i> , 2014, 78, 307-309.	1.8	25
36	Bacterial methionine biosynthesis. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1571-1584.	1.8	178

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37	Reconstruction of an Acetogenic 2,3-Butanediol Pathway Involving a Novel NADPH-Dependent Primary-Secondary Alcohol Dehydrogenase. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3394-3403.	3.1	89
38	Error-Prone PCR and Effective Generation of Gene Variant Libraries for Directed Evolution. <i>Methods in Molecular Biology</i> , 2014, 1179, 3-22.	0.9	47
39	ITCHY: Incremental Truncation for the Creation of Hybrid Enzymes. <i>Methods in Molecular Biology</i> , 2014, 1179, 225-244.	0.9	4
40	Construction and Analysis of Randomized Protein-Encoding Libraries Using Error-Prone PCR. <i>Methods in Molecular Biology</i> , 2013, 996, 251-267.	0.9	24
41	Desalting DNA by Drop Dialysis Increases Library Size upon Transformation. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 402-404.	1.3	8
42	Engineered DNA ligases with improved activities in vitro. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 471-478.	2.1	18
43	New rRNA Gene-Based Phylogenies of the Alphaproteobacteria Provide Perspective on Major Groups, Mitochondrial Ancestry and Phylogenetic Instability. <i>PLoS ONE</i> , 2013, 8, e83383.	2.5	106
44	Characterization of the indole-3-glycerol phosphate synthase from <i>Pseudomonas aeruginosa</i> PAO1. <i>Protein Journal</i> , 2012, 31, 359-365.	1.6	7
45	The Structure of a Truncated Phosphoribosylanthranilate Isomerase Suggests a Unified Model for Evolution of the (β ₂) ₈ Barrel Fold. <i>Journal of Molecular Biology</i> , 2011, 408, 291-303.	4.2	17
46	Artificial gene amplification reveals an abundance of promiscuous resistance determinants in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1484-1489.	7.1	144
47	Carbohydrate binding sites in <i>Candida albicans</i> exo-1,3-glucanase and the role of the Phe ¹³ -Phe ¹⁴ -clamp TM at the active site entrance. <i>FEBS Journal</i> , 2010, 277, 4549-4561.	4.7	29
48	A Study in Molecular Contingency: Glutamine Phosphoribosylpyrophosphate Amidotransferase is a Promiscuous and Evolvable Phosphoribosylanthranilate Isomerase. <i>Journal of Molecular Biology</i> , 2008, 377, 323-336.	4.2	46
49	GLUE-IT and PEDEL-AA: new programmes for analyzing protein diversity in randomized libraries. <i>Nucleic Acids Research</i> , 2008, 36, W281-W285.	14.5	168
50	Multicopy Suppression Underpins Metabolic Evolvability. <i>Molecular Biology and Evolution</i> , 2007, 24, 2716-2722.	8.9	154
51	Natural history as a predictor of protein evolvability. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 439-442.	2.1	51
52	Strategies and computational tools for improving randomized protein libraries. <i>New Biotechnology</i> , 2005, 22, 105-112.	2.7	113
53	In vitro selection and characterization of a stable subdomain of phosphoribosylanthranilate isomerase. <i>FEBS Journal</i> , 2005, 272, 3684-3697.	4.7	18
54	Statistics of protein library construction. <i>Bioinformatics</i> , 2005, 21, 3314-3315.	4.1	74

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55	A second-generation system for unbiased reading frame selection. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 595-602.	2.1	32
56	Novel methods for directed evolution of enzymes: quality, not quantity. <i>Current Opinion in Biotechnology</i> , 2004, 15, 291-297.	6.6	214
57	User-friendly algorithms for estimating completeness and diversity in randomized protein-encoding libraries. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 451-457.	2.1	143
58	Site-Directed Mutagenesis of Tyr354 in <i>Geobacillus stearothermophilus</i> Alanine Racemase Identifies a Role in Controlling Substrate Specificity and a Possible Role in the Evolution of Antibiotic Resistance. <i>ChemBioChem</i> , 2002, 3, 789.	2.6	28