

Vickery L Arcus

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/39358/publications.pdf>

Version: 2024-02-01

81
papers

3,620
citations

117625

34
h-index

149698

56
g-index

87
all docs

87
docs citations

87
times ranked

4409
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing thermal acclimation of soil microbial respiration using macromolecular rate theory. <i>Biogeochemistry</i> , 2022, 158, 131-141.	3.5	10
2	Sensing Enzyme Activation Heat Capacity at the Single-Molecule Level Using Gold-Nanorod-Based Optical Whispering Gallery Modes. <i>ACS Applied Nano Materials</i> , 2021, 4, 4576-4583.	5.0	20
3	pH-Independent Heat Capacity Changes during Phosphorolysis Catalyzed by the Pyrimidine Nucleoside Phosphorylase from <i>Geobacillus thermoglucosidasius</i> . <i>Biochemistry</i> , 2021, 60, 1573-1577.	2.5	5
4	Evolution of dynamical networks enhances catalysis in a designer enzyme. <i>Nature Chemistry</i> , 2021, 13, 1017-1022.	13.6	60
5	Separating the temperature response of soil respiration derived from soil organic matter and added labile carbon compounds. <i>Geoderma</i> , 2021, 400, 115128.	5.1	13
6	How close are we to the temperature tipping point of the terrestrial biosphere?. <i>Science Advances</i> , 2021, 7, .	10.3	102
7	Chemical Mapping Exposes the Importance of Active Site Interactions in Governing the Temperature Dependence of Enzyme Turnover. <i>ACS Catalysis</i> , 2021, 11, 14854-14863.	11.2	6
8	PhoH2 proteins couple RNA helicase and RNase activities. <i>Protein Science</i> , 2020, 29, 883-892.	7.6	10
9	Post-transcriptional modulation of the SigF regulon in <i>Mycobacterium smegmatis</i> by the PhoH2 toxin-antitoxin. <i>PLoS ONE</i> , 2020, 15, e0236551.	2.5	2
10	The Inflection Point Hypothesis: The Relationship between the Temperature Dependence of Enzyme-Catalyzed Reaction Rates and Microbial Growth Rates. <i>Biochemistry</i> , 2020, 59, 3562-3569.	2.5	20
11	Peptide cargo tunes a network of correlated motions in human leucocyte antigens. <i>FEBS Journal</i> , 2020, 287, 3777-3793.	4.7	6
12	Enzyme evolution and the temperature dependence of enzyme catalysis. <i>Current Opinion in Structural Biology</i> , 2020, 65, 96-101.	5.7	54
13	Contrasting temperature responses of soil respiration derived from soil organic matter and added plant litter. <i>Biogeochemistry</i> , 2020, 150, 45-59.	3.5	17
14	Temperature, Dynamics, and Enzyme-Catalyzed Reaction Rates. <i>Annual Review of Biophysics</i> , 2020, 49, 163-180.	10.0	74
15	Shifts in temperature response of soil respiration between adjacent irrigated and non-irrigated grazed pastures. <i>Agriculture, Ecosystems and Environment</i> , 2019, 285, 106620.	5.3	21
16	Tackling tuberculosis in the indigenous people of New Zealand. <i>Lancet Public Health</i> , The, 2019, 4, e496.	10.0	5
17	The three dimensional structure of Bovine Salivary Protein 30b (BSP30b) and its interaction with specific rumen bacteria. <i>PLoS ONE</i> , 2019, 14, e0206709.	2.5	1
18	Dispersal of <i>Mycobacterium tuberculosis</i> Driven by Historical European Trade in the South Pacific. <i>Frontiers in Microbiology</i> , 2019, 10, 2778.	3.5	28

#	ARTICLE	IF	CITATIONS
19	Uncovering the Relationship between the Change in Heat Capacity for Enzyme Catalysis and Vibrational Frequency through Isotope Effect Studies. <i>ACS Catalysis</i> , 2018, 8, 5340-5349.	11.2	13
20	Dynamical origins of heat capacity changes in enzyme-catalysed reactions. <i>Nature Communications</i> , 2018, 9, 1177.	12.8	64
21	Macromolecular rate theory (<sc>MMRT</sc>) provides a thermodynamics rationale to underpin the convergent temperature response in plant leaf respiration. <i>Global Change Biology</i> , 2018, 24, 1538-1547.	9.5	35
22	Crystal structure of an inferred ancestral bacterial pyruvate decarboxylase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 179-186.	0.8	3
23	Structures and kinetics for plant nucleoside triphosphate diphosphohydrolases support a domain motion catalytic mechanism. <i>Protein Science</i> , 2017, 26, 1627-1638.	7.6	11
24	Rapid molecular diagnosis of the <i>Mycobacterium tuberculosis</i> Rangipo strain responsible for the largest recurring TB cluster in New Zealand. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 138-140.	1.8	8
25	Heat Capacity Changes for Transition-State Analogue Binding and Catalysis with Human 5â€²-Methylthioadenosine Phosphorylase. <i>ACS Chemical Biology</i> , 2017, 12, 464-473.	3.4	17
26	A complete thermodynamic analysis of enzyme turnover links the free energy landscape to enzyme catalysis. <i>FEBS Journal</i> , 2017, 284, 2829-2842.	4.7	39
27	Crystal structure of pyruvate decarboxylase from <i>Zymobacter palmae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 700-706.	0.8	8
28	Structure and Function of AmtR in <i>Mycobacterium smegmatis</i> : Implications for Post-Transcriptional Regulation of Urea Metabolism through a Small Antisense RNA. <i>Journal of Molecular Biology</i> , 2016, 428, 4315-4329.	4.2	8
29	Interdomain Conformational Changes Provide Allosteric Regulation en Route to Chorismate. <i>Journal of Biological Chemistry</i> , 2016, 291, 21836-21847.	3.4	22
30	On the Temperature Dependence of Enzyme-Catalyzed Rates. <i>Biochemistry</i> , 2016, 55, 1681-1688.	2.5	233
31	Prediction of the substrate for nonribosomal peptide synthetase (<sc>NRPS</sc>) adenylation domains by virtual screening. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2052-2066.	2.6	19
32	Biotechnological Uses of Archaeal Proteins. <i>Archaea</i> , 2015, 2015, 1-2.	2.3	1
33	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
34	The mycobacterial PhoH2 proteins are type II toxin antitoxins coupled to RNA helicase domains. <i>Tuberculosis</i> , 2015, 95, 385-394.	1.9	22
35	Change in heat capacity accurately predicts vibrational coupling in enzyme catalyzed reactions. <i>FEBS Letters</i> , 2015, 589, 2200-2206.	2.8	19
36	Reconstructed Ancestral Enzymes Impose a Fitness Cost upon Modern Bacteria Despite Exhibiting Favourable Biochemical Properties. <i>Journal of Molecular Evolution</i> , 2015, 81, 110-120.	1.8	16

#	ARTICLE	IF	CITATIONS
37	Toward More Accurate Ancestral Protein Genotypeâ€“Phenotype Reconstructions with the Use of Species Tree-Aware Gene Trees. <i>Molecular Biology and Evolution</i> , 2015, 32, 13-22.	8.9	43
38	Thermodynamic theory explains the temperature optima of soil microbial processes and high Q_{10} values at low temperatures. <i>Global Change Biology</i> , 2014, 20, 3578-3586.	9.5	163
39	<i>Mycobacterium tuberculosis</i> Rv2179c Protein Establishes a New Exoribonuclease Family with Broad Phylogenetic Distribution. <i>Journal of Biological Chemistry</i> , 2014, 289, 2139-2147.	3.4	13
40	Tracking Molecular Recognition at the Atomic Level with a New Protein Scaffold Based on the OB-Fold. <i>PLoS ONE</i> , 2014, 9, e86050.	2.5	20
41	Ribonucleases in bacterial toxinâ€“antitoxin systems. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 523-531.	1.9	77
42	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
43	Structure and function of an acetyl xylan esterase (Est2A) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 911-917.	2.6	21
44	Infinite stacking of alternating polyfluoroaryl rings and bromide anions. <i>CrystEngComm</i> , 2013, 15, 9841.	2.6	13
45	Type II Toxin-Antitoxins: Structural and Functional Aspects of Type II Loci in <i>Mycobacteria</i> . , 2013, , 137-156.		0
46	A VapBC Toxin-Antitoxin Module Is a Posttranscriptional Regulator of Metabolic Flux in <i>Mycobacteria</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2189-2204.	2.2	75
47	Toxin-Antitoxin Systems of <i>Mycobacterium smegmatis</i> Are Essential for Cell Survival. <i>Journal of Biological Chemistry</i> , 2012, 287, 5340-5356.	3.4	59
48	On the Origin and Evolution of Thermophily: Reconstruction of Functional Precambrian Enzymes from Ancestors of <i>Bacillus</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 825-835.	8.9	83
49	The Structure of the Oligomerization Domain of Lsr2 from <i>Mycobacterium tuberculosis</i> Reveals a Mechanism for Chromosome Organization and Protection. <i>PLoS ONE</i> , 2012, 7, e38542.	2.5	37
50	Determination of ribonuclease sequence-specificity using Pentaproboscids and mass spectrometry. <i>Rna</i> , 2012, 18, 1267-1278.	3.5	39
51	Identification of extracellular siderophores and a related peptide from the endophytic fungus <i>Epichloa festucae</i> in culture and endophyte-infected <i>Lolium perenne</i> . <i>Phytochemistry</i> , 2012, 75, 128-139.	2.9	42
52	Expression, purification and characterisation of GIGANTEA: A circadian clock-controlled regulator of photoperiodic flowering in plants. <i>Protein Expression and Purification</i> , 2011, 76, 197-204.	1.3	11
53	VapC Toxins from <i>Mycobacterium tuberculosis</i> Are Ribonucleases that Differentially Inhibit Growth and Are Neutralized by Cognate VapB Antitoxins. <i>PLoS ONE</i> , 2011, 6, e21738.	2.5	78
54	The PIN-domain ribonucleases and the prokaryotic VapBC toxin-antitoxin array. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 33-40.	2.1	148

#	ARTICLE	IF	CITATIONS
55	Structural and functional characterization of a promiscuous feruloyl esterase (Est1E) from the rumen bacterium <i>Butyrivibrio proteoclasticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1457-1469.	2.6	62
56	Structure of a Eukaryotic Nonribosomal Peptide Synthetase Adenylation Domain That Activates a Large Hydroxamate Amino Acid in Siderophore Biosynthesis. <i>Journal of Biological Chemistry</i> , 2010, 285, 2415-2427.	3.4	57
57	Expression and purification of an adenylation domain from a eukaryotic nonribosomal peptide synthetase: Using structural genomics tools for a challenging target. <i>Protein Expression and Purification</i> , 2010, 74, 162-168.	1.3	5
58	The vapBC Operon from <i>Mycobacterium smegmatis</i> Is An Autoregulated Toxin-Antitoxin Module That Controls Growth via Inhibition of Translation. <i>Journal of Molecular Biology</i> , 2009, 390, 353-367.	4.2	96
59	A Structural Basis for the Reduced Toxicity of Dinophysistoxin-2. <i>Chemical Research in Toxicology</i> , 2009, 22, 1782-1786.	3.3	39
60	Crystal structure of PAE0151 from <i>Pyrobaculum aerophilum</i> , a PIN domain (VapC) protein from a toxin-antitoxin operon. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 510-518.	2.6	45
61	Clarification of the C-35 Stereochemistries of Dinophysistoxin-1 and Dinophysistoxin-2 and Its Consequences for Binding to Protein Phosphatase. <i>Chemical Research in Toxicology</i> , 2007, 20, 868-875.	3.3	52
62	The potential impact of structural genomics on tuberculosis drug discovery. <i>Drug Discovery Today</i> , 2006, 11, 28-34.	6.4	42
63	Structure of naphthoate synthase (MenB) from <i>Mycobacterium tuberculosis</i> in both native and product-bound forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1199-1206.	2.5	19
64	A flexible and economical medium-throughput strategy for protein production and crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1378-1385.	2.5	67
65	The PIN-domain toxin-antitoxin array in mycobacteria. <i>Trends in Microbiology</i> , 2005, 13, 360-365.	7.7	111
66	Crystallographic and Mutational Data Show That the Streptococcal Pyrogenic Exotoxin J Can Use a Common Binding Surface for T-cell Receptor Binding and Dimerization. <i>Journal of Biological Chemistry</i> , 2004, 279, 38571-38576.	3.4	18
67	Distant Structural Homology Leads to the Functional Characterization of an Archaeal PIN Domain as an Exonuclease. <i>Journal of Biological Chemistry</i> , 2004, 279, 16471-16478.	3.4	103
68	Crystallization and preliminary X-ray analysis of a conserved hypothetical protein PAE2754 from <i>Pyrobaculum aerophilum</i> and of a double Leu ¹ Met mutant engineered for MAD phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 733-735.	2.5	4
69	Crystal Structure of a Putative Methyltransferase from <i>Mycobacterium tuberculosis</i> : Misannotation of a Genome Clarified by Protein Structural Analysis. <i>Journal of Bacteriology</i> , 2003, 185, 4057-4065.	2.2	29
70	Protein structure prediction and analysis as a tool for functional genomics. <i>Applied Bioinformatics</i> , 2003, 2, S3-10.	1.6	9
71	The Three-dimensional Structure of a Superantigen-like Protein, SET3, from a Pathogenicity Island of the <i>Staphylococcus aureus</i> Genome. <i>Journal of Biological Chemistry</i> , 2002, 277, 32274-32281.	3.4	77
72	OB-fold domains: a snapshot of the evolution of sequence, structure and function. <i>Current Opinion in Structural Biology</i> , 2002, 12, 794-801.	5.7	195

#	ARTICLE	IF	CITATIONS
73	LISA: an intranet-based flexible database for protein crystallography project management. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1341-1343.	2.5	10
74	Structure of HisF, a histidine biosynthetic protein from Pyrobaculum aerophilum. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1518-1525.	2.5	9
75	Immunological and Biochemical Characterization of Streptococcal Pyrogenic Exotoxins I and J (SPE-I) Tj ETQq1 1 0.784314 rgBT /Over 0.8 48	0.8	48
76	Superantigens â€“ powerful modifiers of the immune system. Trends in Molecular Medicine, 2000, 6, 125-132.	2.6	147
77	Conservation and variation in superantigen structure and activity highlighted by the three-dimensional structures of two new superantigens from Streptococcus pyogenes 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 299, 157-168.	4.2	69
78	The dependence of chemical exchange on boundary selection in a fibronectin type III domain from human tenascin. Journal of Molecular Biology, 1998, 282, 181-194.	4.2	22
79	A Comparison of the pH, Urea, and Temperature-denatured States of Barnase by Heteronuclear NMR: Implications for the Initiation of Protein Folding. Journal of Molecular Biology, 1995, 254, 305-321.	4.2	134
80	ortho-Directed electrophilic boronation of a benzyl ketone: the preparation, X-ray crystal structure, and some reactions of 4-ethyl-1-hydroxy-3-(4-hydroxyphenyl)-2-oxa-1-boranaphthalene. Journal of Organometallic Chemistry, 1993, 460, 139-147.	1.8	40
81	Superantigen Architecture: Functional Decoration on a Conserved Scaffold. , 0, , 91-102.		0