

Peter J Stogios

List of Publications by Year in descending order

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60
papers

3,083
citations

172457

29
h-index

168389

53
g-index

63
all docs

63
docs citations

63
times ranked

5174
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel strigolactone receptor antagonist provides insights into the structural inhibition, conditioning, and germination of the crop parasite <i>Striga</i> . <i>Journal of Biological Chemistry</i> , 2022, , 101734.	3.4	7
2	Structural and molecular rationale for the diversification of resistance mediated by the Antibiotic_NAT family. <i>Communications Biology</i> , 2022, 5, 263.	4.4	3
3	Elucidating Sequence and Structural Determinants of Carbohydrate Esterases for Complete Deacetylation of Substituted Xylans. <i>Molecules</i> , 2022, 27, 2655.	3.8	3
4	Molecular analysis and essentiality of Aro1 shikimate biosynthesis multi-enzyme in <i>Candida albicans</i> . <i>Life Science Alliance</i> , 2022, 5, e202101358.	2.8	1
5	ApmA Is a Unique Aminoglycoside Antibiotic Acetyltransferase That Inactivates Apramycin. <i>MBio</i> , 2021, 12, .	4.1	12
6	Structural characterization of the family GH115 β -glucuronidase from <i>Amphibacillus xylanus</i> yields insight into its coordinated action with β -arabinofuranosidases. <i>New Biotechnology</i> , 2021, 62, 49-56.	4.4	8
7	Rapid and accurate agglutination-based testing for SARS-CoV-2 antibodies. <i>Cell Reports Methods</i> , 2021, 1, 100011.	2.9	11
8	Epitope-specific antibody responses differentiate COVID-19 outcomes and variants of concern. <i>JCI Insight</i> , 2021, 6, .	5.0	32
9	Three mutations repurpose a plant karrikin receptor to a strigolactone receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	27
10	A small molecule produced by <i>Lactobacillus</i> species blocks <i>Candida albicans</i> filamentation by inhibiting a DYRK1-family kinase. <i>Nature Communications</i> , 2021, 12, 6151.	12.8	50
11	Overcoming Fungal Echinocandin Resistance through Inhibition of the Non-essential Stress Kinase Yck2. <i>Cell Chemical Biology</i> , 2020, 27, 269-282.e5.	5.2	49
12	Structure of the full-length <i>Serratia marcescens</i> acetyltransferase AAC(3)-IIa in complex with coenzyme A. <i>Protein Science</i> , 2020, 29, 803-808.	7.6	1
13	One-Pot Biocatalytic Transformation of Adipic Acid to 6-Aminocaproic Acid and 1,6-Hexamethylenediamine Using Carboxylic Acid Reductases and Transaminases. <i>Journal of the American Chemical Society</i> , 2020, 142, 1038-1048.	13.7	66
14	Rational engineering of 2-deoxyribose-5-phosphate aldolases for the biosynthesis of (R)-1,3-butanediol. <i>Journal of Biological Chemistry</i> , 2020, 295, 597-609.	3.4	16
15	Molecular mechanisms of vancomycin resistance. <i>Protein Science</i> , 2020, 29, 654-669.	7.6	130
16	A novel C-terminal degron identified in bacterial aldehyde decarboxylases using directed evolution. <i>Biotechnology for Biofuels</i> , 2020, 13, 114.	6.2	8
17	A penicillin-binding protein that can promote advanced-generation cephalosporin resistance and genome adaptation in the opportunistic pathogen <i>Pseudomonas aeruginosa</i> . <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105896.	2.5	3
18	Structural characterization of aminoglycoside 4'-O-acetyltransferase ANT(4)-IIb from <i>Pseudomonas aeruginosa</i> . <i>Protein Science</i> , 2020, 29, 758-767.	7.6	5

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19	Substrate specificity, regiospecificity, and processivity in glycoside hydrolase family 74. <i>Journal of Biological Chemistry</i> , 2019, 294, 13233-13247.	3.4	25
20	An interbacterial toxin inhibits target cell growth by synthesizing (p)ppApp. <i>Nature</i> , 2019, 575, 674-678.	27.8	118
21	Substrate Recognition by a Colistin Resistance Enzyme from <i>Moraxella catarrhalis</i> . <i>ACS Chemical Biology</i> , 2018, 13, 1322-1332.	3.4	15
22	Plazomicin Retains Antibiotic Activity against Most Aminoglycoside Modifying Enzymes. <i>ACS Infectious Diseases</i> , 2018, 4, 980-987.	3.8	91
23	Rox, a Rifamycin Resistance Enzyme with an Unprecedented Mechanism of Action. <i>Cell Chemical Biology</i> , 2018, 25, 403-412.e5.	5.2	48
24	The <i>Legionella pneumophila</i> effector Ceg4 is a phosphotyrosine phosphatase that attenuates activation of eukaryotic MAPK pathways. <i>Journal of Biological Chemistry</i> , 2018, 293, 3307-3320.	3.4	12
25	The evolution of substrate discrimination in macrolide antibiotic resistance enzymes. <i>Nature Communications</i> , 2018, 9, 112.	12.8	50
26	Determinants and Prediction of Esterase Substrate Promiscuity Patterns. <i>ACS Chemical Biology</i> , 2018, 13, 225-234.	3.4	106
27	Structural enzymology reveals the molecular basis of substrate regiospecificity and processivity of an exemplar bacterial glycoside hydrolase family 74 endo-xyloglucanase. <i>Biochemical Journal</i> , 2018, 475, 3963-3978.	3.7	15
28	Identification and characterization of a large family of superbinding bacterial SH2 domains. <i>Nature Communications</i> , 2018, 9, 4549.	12.8	17
29	A novel acetyl xylan esterase enabling complete deacetylation of substituted xylans. <i>Biotechnology for Biofuels</i> , 2018, 11, 74.	6.2	53
30	Structural and Functional Survey of Environmental Aminoglycoside Acetyltransferases Reveals Functionality of Resistance Enzymes. <i>ACS Infectious Diseases</i> , 2017, 3, 653-665.	3.8	9
31	Structural and Biochemical Characterization of <i>Acinetobacter</i> spp. Aminoglycoside Acetyltransferases Highlights Functional and Evolutionary Variation among Antibiotic Resistance Enzymes. <i>ACS Infectious Diseases</i> , 2017, 3, 132-143.	3.8	17
32	Rifampin phosphotransferase is an unusual antibiotic resistance kinase. <i>Nature Communications</i> , 2016, 7, 11343.	12.8	36
33	Diverse mechanisms of metaeffector activity in an intracellular bacterial pathogen, <i>Legionella pneumophila</i> . <i>Molecular Systems Biology</i> , 2016, 12, 893.	7.2	108
34	<i>Legionella pneumophila</i> S1P-lyase targets host sphingolipid metabolism and restrains autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1901-1906.	7.1	115
35	l-Hydroxyproline and d-Proline Catabolism in <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2016, 198, 1171-1181.	2.2	20
36	Structure-Function Analysis of a Mixed-linkage β -Glucanase/Xyloglucanase from the Key Ruminant Bacteroidetes <i>Prevotella bryantii</i> B14. <i>Journal of Biological Chemistry</i> , 2016, 291, 1175-1197.	3.4	38

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37	The activity of CouR, a MarR family transcriptional regulator, is modulated through a novel molecular mechanism. <i>Nucleic Acids Research</i> , 2016, 44, 595-607.	14.5	44
38	Structural and Functional Characterization of a Ketosteroid Transcriptional Regulator of <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 872-882.	3.4	29
39	Pressure adaptation is linked to thermal adaptation in salt-saturated marine habitats. <i>Environmental Microbiology</i> , 2015, 17, 332-345.	3.8	40
40	Structural and Molecular Basis for Resistance to Aminoglycoside Antibiotics by the Adenylyltransferase ANT(2-ae)-Ia. <i>MBio</i> , 2015, 6, .	4.1	49
41	Molecular Characterization of LubX: Functional Divergence of the U-Box Fold by <i>Legionella pneumophila</i> . <i>Structure</i> , 2015, 23, 1459-1469.	3.3	34
42	Structural and Functional Plasticity of Antibiotic Resistance Nucleotidyltransferases Revealed by Molecular Characterization of Lincosamide Nucleotidyltransferases Lnu(A) and Lnu(D). <i>Journal of Molecular Biology</i> , 2015, 427, 2229-2243.	4.2	7
43	Structural and Functional Adaptation of Vancomycin Resistance VanT Serine Racemases. <i>MBio</i> , 2015, 6, e00806.	4.1	18
44	Structure-function analysis identifies highly sensitive strigolactone receptors in <i>Striga</i> . <i>Science</i> , 2015, 350, 203-207.	12.6	227
45	Multiple histidines in the periplasmic domain of the <i>S. almonella enterica</i> sensor kinase SsrA enhance signaling in response to extracellular acidification. <i>Molecular Microbiology</i> , 2015, 95, 678-691.	2.5	27
46	Multiple Influenza A (H3N2) Mutations Conferring Resistance to Neuraminidase Inhibitors in a Bone Marrow Transplant Recipient. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7188-7197.	3.2	53
47	Structural basis for the evolution of vancomycin resistance D-peptidases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5872-5877.	7.1	28
48	Potential for Reduction of Streptogramin A Resistance Revealed by Structural Analysis of Acetyltransferase VatA. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7083-7092.	3.2	19
49	Elucidation of the Molecular Basis for Arabinoxylan-Debranching Activity of a Thermostable Family GH62 α -Arabinofuranosidase from <i>Streptomyces thermoviolaceus</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 5317-5329.	3.1	44
50	Structure of the LdcB LD-Carboxypeptidase Reveals the Molecular Basis of Peptidoglycan Recognition. <i>Structure</i> , 2014, 22, 949-960.	3.3	31
51	Single residues dictate the co-evolution of dual esterases: MCP hydrolases from the α / β hydrolase family. <i>Biochemical Journal</i> , 2013, 454, 157-166.	3.7	34
52	Structure-guided optimization of protein kinase inhibitors reverses aminoglycoside antibiotic resistance. <i>Biochemical Journal</i> , 2013, 454, 191-200.	3.7	43
53	An Inserted α Subdomain Shapes the Catalytic Pocket of <i>Lactobacillus johnsonii</i> Cinnamoyl Esterase. <i>PLoS ONE</i> , 2011, 6, e23269.	2.5	46
54	A Small Molecule Discrimination Map of the Antibiotic Resistance Kinome. <i>Chemistry and Biology</i> , 2011, 18, 1591-1601.	6.0	72

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55	Structure and Function of APH(4)-Ia, a Hygromycin B Resistance Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 1966-1975.	3.4	30
56	Insights into Strand Exchange in BTB Domain Dimers from the Crystal Structures of FAZF and Miz1. <i>Journal of Molecular Biology</i> , 2010, 400, 983-997.	4.2	25
57	Crystal structure of the BTB domain from the LRF/ZBTB7 transcriptional regulator. <i>Protein Science</i> , 2006, 16, 336-342.	7.6	56
58	Sequence and structural analysis of BTB domain proteins. <i>Genome Biology</i> , 2005, 6, R82.	9.6	575
59	Dramatic acceleration of protein folding by stabilization of a nonnative backbone conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7954-7959.	7.1	79
60	The BACK domain in BTB-kelch proteins. <i>Trends in Biochemical Sciences</i> , 2004, 29, 634-637.	7.5	146