

Andrew M Gulick

List of Publications by Year in descending order

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75
papers

4,064
citations

109321

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75
docs citations

75
times ranked

3689
citing authors

#	ARTICLE	IF	CITATIONS
1	An acyl-adenylate mimic reveals the structural basis for substrate recognition by the iterative siderophore synthetase DesD. <i>Journal of Biological Chemistry</i> , 2022, , 102166.	3.4	5
2	Siderophore natural products as pharmaceutical agents. <i>Current Opinion in Biotechnology</i> , 2021, 69, 242-251.	6.6	23
3	Anti-Zika candidates from a marine fungus with a remarkable biosynthetic repertoire. <i>Journal of Biological Chemistry</i> , 2021, 297, 101047.	3.4	2
4	p67: a cryptic lysosomal hydrolase in <i>Trypanosoma brucei</i> ?. <i>Parasitology</i> , 2020, 148, 1-6.	1.5	3
5	Modeling the Role of a Flexible Loop and Active Site Side Chains in Hydride Transfer Catalyzed by Glycerol-3-phosphate Dehydrogenase. <i>ACS Catalysis</i> , 2020, 10, 11253-11267.	11.2	14
6	Biosynthesis, Mechanism of Action, and Inhibition of the Enterotoxin Tilimycin Produced by the Opportunistic Pathogen <i>Klebsiella oxytoca</i> . <i>ACS Infectious Diseases</i> , 2020, 6, 1976-1997.	3.8	18
7	The Siderophore Synthetase <i>lucA</i> of the Aerobactin Biosynthetic Pathway Uses an Ordered Mechanism. <i>Biochemistry</i> , 2020, 59, 2143-2153.	2.5	11
8	Design, Synthesis, and Biophysical Evaluation of Mechanism-Based Probes for Condensation Domains of Nonribosomal Peptide Synthetases. <i>ACS Chemical Biology</i> , 2020, 15, 1813-1819.	3.4	9
9	The structural basis of N-acyl- β -amino- β -lactone formation catalyzed by a nonribosomal peptide synthetase. <i>Nature Communications</i> , 2019, 10, 3432.	12.8	50
10	Structure of a bound peptide phosphonate reveals the mechanism of nocardicin bifunctional thioesterase epimerase-hydrolase half-reactions. <i>Nature Communications</i> , 2019, 10, 3868.	12.8	16
11	Mutagenesis and Structural Studies Reveal the Basis for the Activity and Stability Properties That Distinguish the <i>Photinus</i> Luciferases <i>scintillans</i> and <i>pyralis</i> . <i>Biochemistry</i> , 2019, 58, 4293-4303.	2.5	10
12	Aerobactin Synthesis Proteins as Antivirulence Targets in Hypervirulent <i>Klebsiella pneumoniae</i> . <i>ACS Infectious Diseases</i> , 2019, 5, 1052-1054.	3.8	20
13	Human Glycerol 3-Phosphate Dehydrogenase: X-ray Crystal Structures That Guide the Interpretation of Mutagenesis Studies. <i>Biochemistry</i> , 2019, 58, 1061-1073.	2.5	15
14	Enzymes engineered to trap reaction intermediates. <i>Nature</i> , 2019, 565, 28-29.	27.8	2
15	Structural and functional delineation of aerobactin biosynthesis in hypervirulent <i>Klebsiella pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 7841-7852.	3.4	33
16	Crystal Structure of the Siderophore Binding Protein BauB Bound to an Unusual 2:1 Complex Between Acinetobactin and Ferric Iron. <i>Biochemistry</i> , 2018, 57, 6653-6661.	2.5	20
17	The Nitro Group as a Masked Electrophile in Covalent Enzyme Inhibition. <i>ACS Chemical Biology</i> , 2018, 13, 1470-1473.	3.4	23
18	Trapping interactions between catalytic domains and carrier proteins of modular biosynthetic enzymes with chemical probes. <i>Natural Product Reports</i> , 2018, 35, 1156-1184.	10.3	43

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19	Development of a High-Throughput Biochemical Assay to Screen for Inhibitors of Aerobactin Synthetase <i>lucA</i> . <i>SLAS Discovery</i> , 2018, 23, 1070-1082.	2.7	6
20	Substrate Trapping in the Siderophore Tailoring Enzyme PvdQ. <i>ACS Chemical Biology</i> , 2017, 12, 643-647.	3.4	6
21	Nonribosomal peptide synthetase biosynthetic clusters of ESKAPE pathogens. <i>Natural Product Reports</i> , 2017, 34, 981-1009.	10.3	77
22	Cloning of the Orange Light-Producing Luciferase from <i>Photinus scintillans</i> —A New Proposal on how Bioluminescence Color is Determined. <i>Photochemistry and Photobiology</i> , 2017, 93, 479-485.	2.5	25
23	Structures of a Nonribosomal Peptide Synthetase Module Bound to MbtH-like Proteins Support a Highly Dynamic Domain Architecture. <i>Journal of Biological Chemistry</i> , 2016, 291, 22559-22571.	3.4	97
24	Structural insight into the necessary conformational changes of modular nonribosomal peptide synthetases. <i>Current Opinion in Chemical Biology</i> , 2016, 35, 89-96.	6.1	43
25	An Open and Shut Case: The Interaction of Magnesium with MST Enzymes. <i>Journal of the American Chemical Society</i> , 2016, 138, 9277-9293.	13.7	17
26	Structural and Functional Characterization of Aerobactin Synthetase <i>lucA</i> from a Hypervirulent Pathotype of <i>Klebsiella pneumoniae</i> . <i>Biochemistry</i> , 2016, 55, 3559-3570.	2.5	21
27	1.2-Å resolution crystal structure of the periplasmic aminotransferase PvdN from <i>Pseudomonas aeruginosa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 403-408.	0.8	10
28	Structures of two distinct conformations of holo-non-ribosomal peptide synthetases. <i>Nature</i> , 2016, 529, 235-238.	27.8	210
29	Structural Biology of Nonribosomal Peptide Synthetases. <i>Methods in Molecular Biology</i> , 2016, 1401, 3-29.	0.9	96
30	The Role of Phosphate in a Multistep Enzymatic Reaction: Reactions of the Substrate and Intermediate in Pieces. <i>Journal of the American Chemical Society</i> , 2015, 137, 2748-2756.	13.7	20
31	Experimental Support for a Single Electron-Transfer Oxidation Mechanism in Firefly Bioluminescence. <i>Journal of the American Chemical Society</i> , 2015, 137, 7592-7595.	13.7	85
32	Examining Reaction Specificity in PvcB, a Source of Diversity in Isonitrile-Containing Natural Products. <i>Biochemistry</i> , 2015, 54, 2659-2669.	2.5	16
33	The structure of <i>S. lividans</i> acetoacetyl-CoA synthetase shows a novel interaction between the C-terminal extension and the N-terminal domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 575-581.	2.6	6
34	Alteration of the Flexible Loop in 1-Deoxy-xylulose-5-phosphate Reductoisomerase Boosts Enthalpy-Driven Inhibition by Fosmidomycin. <i>Biochemistry</i> , 2014, 53, 3423-3431.	2.5	10
35	Identification of Inhibitors of PvdQ, an Enzyme Involved in the Synthesis of the Siderophore Pyoverdine. <i>ACS Chemical Biology</i> , 2014, 9, 1536-1544.	3.4	36
36	Structural and bioinformatic characterization of an <i>Acinetobacter baumannii</i> type II carrier protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1718-1725.	2.5	18

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37	Analysis of the linker region joining the adenylation and carrier protein domains of the modular nonribosomal peptide synthetases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2691-2702.	2.6	39
38	Aerobactin Mediates Virulence and Accounts for Increased Siderophore Production under Iron-Limiting Conditions by Hypervirulent (Hypermucoviscous) <i>Klebsiella pneumoniae</i> . <i>Infection and Immunity</i> , 2014, 82, 2356-2367.	2.2	198
39	Characterization of AusA: A Dimodular Nonribosomal Peptide Synthetase Responsible for the Production of Aureusimine Pyrazinones. <i>Biochemistry</i> , 2013, 52, 926-937.	2.5	44
40	Structure-based engineering of streptavidin monomer with a reduced biotin dissociation rate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1621-1633.	2.6	44
41	Non-Nucleoside Inhibitors of BasE, an Adenylating Enzyme in the Siderophore Biosynthetic Pathway of the Opportunistic Pathogen <i>Acinetobacter baumannii</i> . <i>Journal of Medicinal Chemistry</i> , 2013, 56, 2385-2405.	6.4	48
42	Structure determination of the functional domain interaction of a chimeric nonribosomal peptide synthetase from a challenging crystal with noncrystallographic translational symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1482-1492.	2.5	23
43	Computational Screening of the Human TF-Glycome Provides a Structural Definition for the Specificity of Anti-Tumor Antibody JAA-F11. <i>PLoS ONE</i> , 2013, 8, e54874.	2.5	29
44	Crystal Structure of Firefly Luciferase in a Second Catalytic Conformation Supports a Domain Alternation Mechanism. <i>Biochemistry</i> , 2012, 51, 6493-6495.	2.5	119
45	Structure of PA1221, a Nonribosomal Peptide Synthetase Containing Adenylation and Peptidyl Carrier Protein Domains. <i>Biochemistry</i> , 2012, 51, 3252-3263.	2.5	121
46	Rational Design of Proteolytically Stable, Cell-Permeable Peptide-Based Selective Mcl-1 Inhibitors. <i>Journal of the American Chemical Society</i> , 2012, 134, 14734-14737.	13.7	143
47	Structural and Functional Investigation of the Intermolecular Interaction between NRPS Adenylation and Carrier Protein Domains. <i>Chemistry and Biology</i> , 2012, 19, 188-198.	6.0	130
48	Structural Characterization and High-Throughput Screening of Inhibitors of PvdQ, an NTN Hydrolase Involved in Pyoverdine Synthesis. <i>ACS Chemical Biology</i> , 2011, 6, 1277-1286.	3.4	83
49	Biochemical and Structural Characterization of Bisubstrate Inhibitors of BasE, the Self-Standing Nonribosomal Peptide Synthetase Adenylate-Forming Enzyme of Acinetobactin Synthesis. <i>Biochemistry</i> , 2010, 49, 9292-9305.	2.5	52
50	Insights into Resistance against Lincosamide Antibiotics. <i>Structure</i> , 2009, 17, 1549-1550.	3.3	3
51	The 2.1 Å crystal structure of an acyl-CoA synthetase from <i>Methanosarcina acetivorans</i> reveals an alternate acyl-binding pocket for small branched acyl substrates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 685-698.	2.6	18
52	Ironing out a new siderophore synthesis strategy. <i>Nature Chemical Biology</i> , 2009, 5, 143-144.	8.0	5
53	The Mechanism of Domain Alternation in the Acyl-Adenylate Forming Ligase Superfamily Member 4-Chlorobenzoate: Coenzyme A Ligase. <i>Biochemistry</i> , 2009, 48, 4115-4125.	2.5	43
54	Conformational Dynamics in the Acyl-CoA Synthetases, Adenylation Domains of Non-ribosomal Peptide Synthetases, and Firefly Luciferase. <i>ACS Chemical Biology</i> , 2009, 4, 811-827.	3.4	360

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55	Three-dimensional Structures of <i>Pseudomonas aeruginosa</i> PvcA and PvcB, Two Proteins Involved in the Synthesis of 2-Isocyano-6,7-dihydroxycoumarin. <i>Journal of Molecular Biology</i> , 2008, 384, 193-205.	4.2	34
56	Structural Characterization of a 140° Domain Movement in the Two-Step Reaction Catalyzed by 4-Chlorobenzoate:CoA Ligase. <i>Biochemistry</i> , 2008, 47, 8016-8025.	2.5	121
57	Mechanism of 4-Chlorobenzoate:Coenzyme A Ligase Catalysis. <i>Biochemistry</i> , 2008, 47, 8026-8039.	2.5	58
58	The 1.8 Å... Crystal Structure of PA2412, an MbtH-like Protein from the Pyoverdine Cluster of <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 20425-20434.	3.4	69
59	Biochemical and Crystallographic Analysis of Substrate Binding and Conformational Changes in Acetyl-CoA Synthetase,. <i>Biochemistry</i> , 2007, 46, 6536-6546.	2.5	113
60	Rational Redesign of the 4-Chlorobenzoate Binding Site of 4-Chlorobenzoate: Coenzyme A Ligase for Expanded Substrate Range. <i>Biochemistry</i> , 2007, 46, 14487-14499.	2.5	17
61	Determination of the crystal structure of EntA, a 2,3-dihydro-2,3-dihydroxybenzoic acid dehydrogenase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 734-740.	2.5	14
62	Structure of the EntB Multidomain Nonribosomal Peptide Synthetase and Functional Analysis of Its Interaction with the EntE Adenylation Domain. <i>Chemistry and Biology</i> , 2006, 13, 409-419.	6.0	89
63	Crystal Structure of 4-Chlorobenzoate:CoA Ligase/Synthetase in the Unliganded and Aryl Substrate-Bound States–. <i>Biochemistry</i> , 2004, 43, 8670-8679.	2.5	86
64	The 1.75 Å... Crystal Structure of Acetyl-CoA Synthetase Bound to Adenosine-5–propylphosphate and Coenzyme A–. <i>Biochemistry</i> , 2003, 42, 2866-2873.	2.5	208
65	Pentaerythritol propoxylate: a new crystallization agent and cryoprotectant induces crystal growth of 2-methylcitrate dehydratase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 306-309.	2.5	25
66	Evolution of Enzymatic Activities in the Enolase Superfamily:– Crystal Structures of the l-Ala-d/l-Glu Epimerases from <i>Escherichia coli</i> and <i>Bacillus subtilis</i> ,. <i>Biochemistry</i> , 2001, 40, 15716-15724.	2.5	39
67	X-ray Structures of the <i>Dictyostelium discoideum</i> Myosin Motor Domain with Six Non-nucleotide Analogs. <i>Journal of Biological Chemistry</i> , 2000, 275, 398-408.	3.4	44
68	Evolution of Enzymatic Activities in the Enolase Superfamily:– Crystallographic and Mutagenesis Studies of the Reaction Catalyzed by d-Glucarate Dehydratase from <i>Escherichia coli</i> –. <i>Biochemistry</i> , 2000, 39, 4590-4602.	2.5	44
69	X-ray Crystal Structure of the Yeast Kar3 Motor Domain Complexed with Mg–ADP to 2.3 Å... Resolution,., <i>Biochemistry</i> , 1998, 37, 1769-1776.	2.5	97
70	Molecular Structures of the S124A, S124T, and S124V Site-Directed Mutants of UDP-galactose 4-Epimerase from <i>Escherichia coli</i> –. <i>Biochemistry</i> , 1997, 36, 10685-10695.	2.5	40
71	X-ray Structures of the MgADP, MgATP–S, and MgAMPPNP Complexes of the <i>Dictyostelium discoideum</i> Myosin Motor Domain–. <i>Biochemistry</i> , 1997, 36, 11619-11628.	2.5	194
72	High-level production and purification of biologically active proteins from bacterial and mammalian cells using the tandem pGFLEX expression system. <i>Gene</i> , 1997, 193, 229-237.	2.2	6

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73	Structural studies on myosin II: Communication between distant protein domains. <i>BioEssays</i> , 1997, 19, 561-569.	2.5	51
74	Mammalian glutathione S-transferase: Regulation of an enzyme system to achieve chemotherapeutic efficacy. , 1995, 66, 237-257.		39
75	Mutational substitution of residues implicated by crystal structure in binding the substrate glutathione to human glutathione S-transferase I€. <i>Journal of Molecular Biology</i> , 1992, 226, 319-322.	4.2	58