

Andrew M Gulick

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	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
2	Structures of two distinct conformations of holo-non-ribosomal peptide synthetases. <i>Nature</i> , 2016, 529, 235-238.	27.8	210
3	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
4	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
5	X-ray Structures of the MgADP, MgATP ³ S, and MgAMPPNP Complexes of the <i>Dictyostelium discoideum</i> Myosin Motor Domain. <i>Biochemistry</i> , 1997, 36, 11619-11628.	2.5	194
6	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
7	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
8	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
9	Structure of PA1221, a Nonribosomal Peptide Synthetase Containing Adenylation and Peptidyl Carrier Protein Domains. <i>Biochemistry</i> , 2012, 51, 3252-3263.	2.5	121
10	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
11	Biochemical and Crystallographic Analysis of Substrate Binding and Conformational Changes in Acetyl-CoA Synthetase. <i>Biochemistry</i> , 2007, 46, 6536-6546.	2.5	113
12	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
13	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
14	Structural Biology of Nonribosomal Peptide Synthetases. <i>Methods in Molecular Biology</i> , 2016, 1401, 3-29.	0.9	96
15	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
16	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
17	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
18	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

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19	Nonribosomal peptide synthetase biosynthetic clusters of ESKAPE pathogens. <i>Natural Product Reports</i> , 2017, 34, 981-1009.	10.3	77
20	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
21	Mutational substitution of residues implicated by crystal structure in binding the substrate glutathione to human glutathione S-transferase ϵ . <i>Journal of Molecular Biology</i> , 1992, 226, 319-322.	4.2	58
22	Mechanism of 4-Chlorobenzoate:Coenzyme A Ligase Catalysis. <i>Biochemistry</i> , 2008, 47, 8026-8039.	2.5	58
23	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
24	Structural studies on myosin II: Communication between distant protein domains. <i>BioEssays</i> , 1997, 19, 561-569.	2.5	51
25	The structural basis of N-acyl-L-amino- β -lactone formation catalyzed by a nonribosomal peptide synthetase. <i>Nature Communications</i> , 2019, 10, 3432.	12.8	50
26	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
27	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
28	Evolution of Enzymatic Activities in the Enolase Superfamily: Crystallographic and Mutagenesis Studies of the Reaction Catalyzed by α -Glucarate Dehydratase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2000, 39, 4590-4602.	2.5	44
29	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
30	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
31	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
32	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
33	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
34	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
35	Mammalian glutathione S-transferase: Regulation of an enzyme system to achieve chemotherapeutic efficacy. , 1995, 66, 237-257.		39
36	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

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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	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
39	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
40	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
41	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
42	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
43	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
44	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
45	The Nitro Group as a Masked Electrophile in Covalent Enzyme Inhibition. <i>ACS Chemical Biology</i> , 2018, 13, 1470-1473.	3.4	23
46	Siderophore natural products as pharmaceutical agents. <i>Current Opinion in Biotechnology</i> , 2021, 69, 242-251.	6.6	23
47	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
48	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
49	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
50	Aerobactin Synthesis Proteins as Antivirulence Targets in Hypervirulent <i>Klebsiella pneumoniae</i> . <i>ACS Infectious Diseases</i> , 2019, 5, 1052-1054.	3.8	20
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	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
53	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
54	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

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55	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
56	Examining Reaction Specificity in PvcB, a Source of Diversity in Isonitrile-Containing Natural Products. <i>Biochemistry</i> , 2015, 54, 2659-2669.	2.5	16
57	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
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	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
68	Substrate Trapping in the Siderophore Tailoring Enzyme PvdQ. <i>ACS Chemical Biology</i> , 2017, 12, 643-647.	3.4	6
69	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
70	Ironing out a new siderophore synthesis strategy. <i>Nature Chemical Biology</i> , 2009, 5, 143-144.	8.0	5
71	An acyl-adenylate mimic reveals the structural basis for substrate recognition by the iterative siderophore synthetase <i>DesD</i> . <i>Journal of Biological Chemistry</i> , 2022, , 102166.	3.4	5
72	Insights into Resistance against Lincosamide Antibiotics. <i>Structure</i> , 2009, 17, 1549-1550.	3.3	3

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73	p67: a cryptic lysosomal hydrolase in <i>Trypanosoma brucei</i> ?. <i>Parasitology</i> , 2020, 148, 1-6.	1.5	3
74	Enzymes engineered to trap reaction intermediates. <i>Nature</i> , 2019, 565, 28-29.	27.8	2
75	Anti-Zika candidates from a marine fungus with a remarkable biosynthetic repertoire. <i>Journal of Biological Chemistry</i> , 2021, 297, 101047.	3.4	2