

# David W Christianson

## List of Publications by Year in descending order

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papers

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160  
docs citations

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times ranked

10490  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and Chemical Biology of Terpenoid Cyclases. <i>Chemical Reviews</i> , 2017, 117, 11570-11648.	23.0	720
2	Structural Biology and Chemistry of the Terpenoid Cyclases. <i>Chemical Reviews</i> , 2006, 106, 3412-3442.	23.0	682
3	Carboxypeptidase A. <i>Accounts of Chemical Research</i> , 1989, 22, 62-69.	7.6	654
4	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. <i>Nature</i> , 2012, 489, 313-317.	13.7	488
5	Carbonic Anhydrase: Evolution of the Zinc Binding Site by Nature and by Design. <i>Accounts of Chemical Research</i> , 1996, 29, 331-339.	7.6	471
6	Crystal Structure of Pentalenene Synthase: Mechanistic Insights on Terpenoid Cyclization Reactions in Biology. <i>Science</i> , 1997, 277, 1820-1824.	6.0	447
7	Structure of a unique binuclear manganese cluster in arginase. <i>Nature</i> , 1996, 383, 554-557.	13.7	425
8	Histone deacetylase 6 structure and molecular basis of catalysis and inhibition. <i>Nature Chemical Biology</i> , 2016, 12, 741-747.	3.9	351
9	Catalysis By Metal-Activated Hydroxide in Zinc and Manganese Metalloenzymes. <i>Annual Review of Biochemistry</i> , 1999, 68, 33-57.	5.0	345
10	Unearthing the roots of the terpenome. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 141-150.	2.8	302
11	Taxadiene synthase structure and evolution of modular architecture in terpene biosynthesis. <i>Nature</i> , 2011, 469, 116-120.	13.7	290
12	Hydrogen bond stereochemistry in protein structure and function. <i>Journal of Molecular Biology</i> , 1990, 215, 457-471.	2.0	275
13	Nonlinear partial differential equations and applications: Bornyl diphosphate synthase: Structure and strategy for carbocation manipulation by a terpenoid cyclase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15375-15380.	3.3	272
14	Structure, mechanism, and inhibition of histone deacetylases and related metalloenzymes. <i>Current Opinion in Structural Biology</i> , 2011, 21, 735-743.	2.6	225
15	Crystal Structure Determination of Aristolochene Synthase from the Blue Cheese Mold, <i>Penicillium roqueforti</i> *. <i>Journal of Biological Chemistry</i> , 2000, 275, 25533-25539.	1.6	185
16	Structural Studies of Human Histone Deacetylase 8 and Its Site-Specific Variants Complexed with Substrate and Inhibitors. <i>Biochemistry</i> , 2008, 47, 13554-13563.	1.2	180
17	ARID1A-mutated ovarian cancers depend on HDAC6 Activity. <i>Nature Cell Biology</i> , 2017, 19, 962-973.	4.6	173
18	Crystal structure of an uncleaved serpin reveals the conformation of an inhibitory reactive loop. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 251-258.	3.6	167

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19	Structure and mechanism of the diterpene cyclase ent-copalyl diphosphate synthase. <i>Nature Chemical Biology</i> , 2011, 7, 431-433.	3.9	166
20	Crystal structure of human arginase I at 1.29-Å resolution and exploration of inhibition in the immune response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13058-13063.	3.3	164
21	Probing Erectile Function: S-(2-Boronoethyl)-L-Cysteine Binds to Arginase as a Transition State Analogue and Enhances Smooth Muscle Relaxation in Human Penile Corpus Cavernosum. <i>Biochemistry</i> , 2001, 40, 2678-2688.	1.2	163
22	X-ray Crystal Structure of Aristolochene Synthase from <i>Aspergillus terreus</i> and Evolution of Templates for the Cyclization of Farnesyl Diphosphate. <i>Biochemistry</i> , 2007, 46, 1941-1951.	1.2	161
23	Arginase: Structure, Mechanism, and Physiological Role in Male and Female Sexual Arousal. <i>Accounts of Chemical Research</i> , 2005, 38, 191-201.	7.6	158
24	Arginase-boronic acid complex highlights a physiological role in erectile function. <i>Nature Structural Biology</i> , 1999, 6, 1043-1047.	9.7	157
25	Purification and characterization of <i>Klebsiella aerogenes</i> UreE protein: A nickel-binding protein that functions in urease metallocenter assembly. <i>Protein Science</i> , 1993, 2, 1042-1052.	3.1	156
26	Pentalene Synthase. Analysis of Active Site Residues by Site-Directed Mutagenesis. <i>Journal of the American Chemical Society</i> , 2002, 124, 7681-7689.	6.6	147
27	Structural Basis of the Antiproliferative Activity of Largazole, a Depsipeptide Inhibitor of the Histone Deacetylases. <i>Journal of the American Chemical Society</i> , 2011, 133, 12474-12477.	6.6	141
28	Histone deacetylase 10 structure and molecular function as a polyamine deacetylase. <i>Nature Communications</i> , 2017, 8, 15368.	5.8	139
29	Structure of Epi-Isozizaene Synthase from <i>Streptomyces coelicolor</i> A3(2), a Platform for New Terpenoid Cyclization Templates. <i>Biochemistry</i> , 2010, 49, 1787-1797.	1.2	137
30	Contribution of Fluorine to Protein-Ligand Affinity in the Binding of Fluoroaromatic Inhibitors to Carbonic Anhydrase II. <i>Journal of the American Chemical Society</i> , 2000, 122, 12125-12134.	6.6	136
31	Human Arginase II: Crystal Structure and Physiological Role in Male and Female Sexual Arousal. <i>Biochemistry</i> , 2003, 42, 8445-8451.	1.2	131
32	Unusual zinc-binding mode of HDAC6-selective hydroxamate inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13459-13464.	3.3	127
33	Inhibition of Mn <sup>2+</sup> -Arginase by Borate Leads to the Design of a Transition State Analogue Inhibitor, 2(S)-Amino-6-borono-hexanoic Acid. <i>Journal of the American Chemical Society</i> , 1997, 119, 8107-8108.	6.6	123
34	Crystal Structure of (+)-Î-Cadinene Synthase from <i>Gossypium arboreum</i> and Evolutionary Divergence of Metal Binding Motifs for Catalysis. <i>Biochemistry</i> , 2009, 48, 6175-6183.	1.2	122
35	Loss-of-function HDAC8 mutations cause a phenotypic spectrum of Cornelia de Lange syndrome-like features, ocular hypertelorism, large fontanelle and X-linked inheritance. <i>Human Molecular Genetics</i> , 2014, 23, 2888-2900.	1.4	120
36	Trinuclear metal clusters in catalysis by terpenoid synthases. <i>Pure and Applied Chemistry</i> , 2010, 82, 1585-1597.	0.9	116

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37	Managing and manipulating carbocations in biology: terpenoid cyclase structure and mechanism. <i>Current Opinion in Structural Biology</i> , 1998, 8, 695-703.	2.6	114
38	Structure of Isoprene Synthase Illuminates the Chemical Mechanism of Teragram Atmospheric Carbon Emission. <i>Journal of Molecular Biology</i> , 2010, 402, 363-373.	2.0	101
39	Novel Binding Mode of Hydroxamate Inhibitors to Human Carbonic Anhydrase II. <i>Journal of the American Chemical Society</i> , 1997, 119, 850-851.	6.6	100
40	Structural analysis of inhibitor binding to human carbonic anhydrase II. <i>Protein Science</i> , 1998, 7, 2483-2489.	3.1	99
41	Histidine $\hat{+}$ Carboxamide Ligand Substitutions in the Zinc Binding Site of Carbonic Anhydrase II Alter Metal Coordination Geometry but Retain Catalytic Activity. <i>Biochemistry</i> , 1997, 36, 15780-15791.	1.2	96
42	X-ray Crystal Structures of D100E Trichodiene Synthase and Its Pyrophosphate Complex Reveal the Basis for Terpene Product Diversity. <i>Biochemistry</i> , 2002, 41, 1732-1741.	1.2	90
43	Altering the Binuclear Manganese Cluster of Arginase Diminishes Thermostability and Catalytic Function. <i>Biochemistry</i> , 1997, 36, 10558-10565.	1.2	84
44	Fluoroaromatic $\hat{\sim}$ Fluoroaromatic Interactions between Inhibitors Bound in the Crystal Lattice of Human Carbonic Anhydrase II. <i>Journal of the American Chemical Society</i> , 2001, 123, 9620-9627.	6.6	84
45	Complex between carboxypeptidase A and a possible transition-state analog: mechanistic inferences from high-resolution x-ray structures of enzyme-inhibitor complexes. <i>Journal of the American Chemical Society</i> , 1986, 108, 4998-5003.	6.6	78
46	Structures of murine carbonic anhydrase IV and human carbonic anhydrase II complexed with brinzolamide: Molecular basis of isozyme $\hat{e}$ drug discrimination. <i>Protein Science</i> , 1998, 7, 556-563.	3.1	77
47	Mechanistic and Metabolic Inferences from the Binding of Substrate Analogues and Products to Arginase. <i>Biochemistry</i> , 2001, 40, 2689-2701.	1.2	77
48	CHEMISTRY: Roots of Biosynthetic Diversity. <i>Science</i> , 2007, 316, 60-61.	6.0	76
49	Histone Deacetylase 6-Selective Inhibitors and the Influence of Capping Groups on Hydroxamate-Zinc Denticity. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 8054-8060.	2.9	76
50	Synthesis and Biological Investigation of Phenothiazine-Based Benzhydroxamic Acids as Selective Histone Deacetylase 6 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 1138-1166.	2.9	75
51	Structure, mechanism, and inhibition of the zinc-dependent histone deacetylases. <i>Current Opinion in Structural Biology</i> , 2019, 59, 9-18.	2.6	74
52	Structural and mechanistic analysis of trichodiene synthase using site-directed mutagenesis: Probing the catalytic function of tyrosine-295 and the asparagine-225/serine-229/glutamate-233. $\hat{e}$ $\langle$ mml:math altimg="sl3.gif" display="inline" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.. Archives of Biochemistry	1.4	71
53	Structures of Metal-Substituted Human Histone Deacetylase 8 Provide Mechanistic Inferences on Biological Function. <i>Biochemistry</i> , 2010, 49, 5048-5056.	1.2	71
54	X-ray Crystallographic Studies of Substrate Binding to Aristolochene Synthase Suggest a Metal Ion Binding Sequence for Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 15431-15439.	1.6	67

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55	Crystal Structure of Human Liver $\beta$ -4-3-Ketosteroid $5\beta$ -Reductase (AKR1D1) and Implications for Substrate Binding and Catalysis. <i>Journal of Biological Chemistry</i> , 2008, 283, 16830-16839.	1.6	67
56	Expression, purification, assay, and crystal structure of perdeuterated human arginase I. <i>Archives of Biochemistry and Biophysics</i> , 2007, 465, 82-89.	1.4	65
57	Positions of His64 and a bound water in human carbonic anhydrase II upon binding three structurally related inhibitors. <i>Protein Science</i> , 1994, 3, 118-125.	3.1	62
58	Binding of $\beta$ , $\gamma$ -Disubstituted Amino Acids to Arginase Suggests New Avenues for Inhibitor Design. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 5432-5443.	2.9	62
59	Reprogramming the Chemodiversity of Terpenoid Cyclization by Remolding the Active Site Contour of $\epsilon$ -Isozizaene Synthase. <i>Biochemistry</i> , 2014, 53, 1155-1168.	1.2	62
60	Discovery of the First-in-Class Dual Histone Deacetylase-Proteasome Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10299-10309.	2.9	62
61	General Base-General Acid Catalysis in Human Histone Deacetylase 8. <i>Biochemistry</i> , 2016, 55, 820-832.	1.2	61
62	Molecular Recognition of the Substrate Diphosphate Group Governs Product Diversity in Trichodiene Synthase Mutants. <i>Biochemistry</i> , 2005, 44, 6153-6163.	1.2	59
63	Structure and Function of Fusicoccadiene Synthase, a Hexameric Bifunctional Diterpene Synthase. <i>ACS Chemical Biology</i> , 2016, 11, 889-899.	1.6	59
64	Binding of the Microbial Cyclic Tetrapeptide Trapoxin A to the Class I Histone Deacetylase HDAC8. <i>ACS Chemical Biology</i> , 2017, 12, 2281-2286.	1.6	57
65	Exploring biosynthetic diversity with trichodiene synthase. <i>Archives of Biochemistry and Biophysics</i> , 2007, 466, 260-266.	1.4	56
66	Compromised Structure and Function of HDAC8 Mutants Identified in Cornelia de Lange Syndrome Spectrum Disorders. <i>ACS Chemical Biology</i> , 2014, 9, 2157-2164.	1.6	56
67	Exploring the Influence of Domain Architecture on the Catalytic Function of Diterpene Synthases. <i>Biochemistry</i> , 2017, 56, 2010-2023.	1.2	56
68	Structure and energetics of a non-proline cis-peptidyl linkage in a proline-202 .fwdarw. alanine carbonic anhydrase II variant. <i>Biochemistry</i> , 1993, 32, 10944-10949.	1.2	55
69	Mechanistic Insights from the Binding of Substrate and Carbocation Intermediate Analogues to Aristolochene Synthase. <i>Biochemistry</i> , 2013, 52, 5441-5453.	1.2	55
70	Variable Active Site Loop Conformations Accommodate the Binding of Macrocyclic Largazole Analogues to HDAC8. <i>Biochemistry</i> , 2015, 54, 2126-2135.	1.2	55
71	Mapping Protein-Peptide Affinity: Binding of Peptidylsulfonamide Inhibitors to Human Carbonic Anhydrase II. <i>Journal of the American Chemical Society</i> , 1994, 116, 5063-5068.	6.6	52
72	1.55Å-resolution structure of ent-copalyl diphosphate synthase and exploration of general acid function by site-directed mutagenesis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 184-190.	1.1	52

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73	Structure of the complex between an unexpectedly hydrolyzed phosphoramidate inhibitor and carboxypeptidase A. <i>Journal of the American Chemical Society</i> , 1986, 108, 545-546.	6.6	50
74	Inhibition of Human Steroid 5 $\beta$ -Reductase (AKR1D1) by Finasteride and Structure of the Enzyme-Inhibitor Complex. <i>Journal of Biological Chemistry</i> , 2009, 284, 19786-19790.	1.6	50
75	Role of Arginine-304 in the Diphosphate-Triggered Active Site Closure Mechanism of Trichodiene Synthase. <i>Biochemistry</i> , 2005, 44, 12719-12727.	1.2	49
76	Crystal Structure of Lactaldehyde Dehydrogenase from <i>Escherichia coli</i> and Inferences Regarding Substrate and Cofactor Specificity. <i>Journal of Molecular Biology</i> , 2007, 366, 481-493.	2.0	49
77	X-ray Crystallographic Studies of Alanine-65 Variants of Carbonic Anhydrase II Reveal the Structural Basis of Compromised Proton Transfer in Catalysis. <i>Biochemistry</i> , 1996, 35, 16429-16434.	1.2	46
78	Convergence of Catalytic Antibody and Terpene Cyclase Mechanisms: Polyene Cyclization Directed by Carbocation- $\pi$ Interactions. <i>Angewandte Chemie - International Edition</i> , 1999, 38, 1743-1747.	7.2	45
79	Structure of Prokaryotic Polyamine Deacetylase Reveals Evolutionary Functional Relationships with Eukaryotic Histone Deacetylases. <i>Biochemistry</i> , 2011, 50, 1808-1817.	1.2	45
80	Multicomponent Synthesis and Binding Mode of Imidazo[1,2- <i>a</i> ]pyridine-Capped Selective HDAC6 Inhibitors. <i>Organic Letters</i> , 2018, 20, 3255-3258.	2.4	43
81	Structural and Functional Importance of First-Shell Metal Ligands in the Binuclear Manganese Cluster of Arginase. <i>Biochemistry</i> , 2003, 42, 7748-7758.	1.2	42
82	2-Aminoimidazole Amino Acids as Inhibitors of the Binuclear Manganese Metalloenzyme Human Arginase I. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 4266-4276.	2.9	42
83	Structure of 2-Methylisoborneol Synthase from <i>Streptomyces coelicolor</i> and Implications for the Cyclization of a Noncanonical C-Methylated Monoterpenoid Substrate. <i>Biochemistry</i> , 2012, 51, 3011-3020.	1.2	42
84	Structural Basis of Catalysis and Inhibition of HDAC6 CD1, the Enigmatic Catalytic Domain of Histone Deacetylase 6. <i>Biochemistry</i> , 2019, 58, 4912-4924.	1.2	42
85	Structure of Geranyl Diphosphate C-Methyltransferase from <i>Streptomyces coelicolor</i> and Implications for the Mechanism of Isoprenoid Modification. <i>Biochemistry</i> , 2012, 51, 3003-3010.	1.2	41
86	Biochemical and Structural Characterization of HDAC8 Mutants Associated with Cornelia de Lange Syndrome Spectrum Disorders. <i>Biochemistry</i> , 2015, 54, 6501-6513.	1.2	41
87	Entropy as a Driver of Selectivity for Inhibitor Binding to Histone Deacetylase 6. <i>Biochemistry</i> , 2018, 57, 3916-3924.	1.2	40
88	Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites. <i>Nature Communications</i> , 2021, 12, 3384.	5.8	37
89	Structural Studies of Geosmin Synthase, a Bifunctional Sesquiterpene Synthase with $\beta$ Domain Architecture That Catalyzes a Unique Cyclization-Fragmentation Reaction Sequence. <i>Biochemistry</i> , 2015, 54, 7142-7155.	1.2	36
90	Arginine substitutions in the hinge region of antichymotrypsin affect serpin $\beta$ -sheet rearrangement. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 888-893.	3.6	35

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91	Stereochemistry of guanidine-metal interactions: Implications for L-arginine-metal interactions in protein structure and function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 637-642.	1.5	34
92	Assembly-Line Catalysis in Bifunctional Terpene Synthases. <i>Accounts of Chemical Research</i> , 2021, 54, 3780-3791.	7.6	33
93	Design of Amino Acid Aldehydes as Transition-State Analogue Inhibitors of Arginase. <i>Journal of the American Chemical Society</i> , 2004, 126, 10278-10284.	6.6	32
94	Exploring Structural Determinants of Inhibitor Affinity and Selectivity in Complexes with Histone Deacetylase 6. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 295-308.	2.9	32
95	Structure and catalytic mechanism of human steroid 5 $\beta$ -reductase (AKR1D1). <i>Molecular and Cellular Endocrinology</i> , 2009, 301, 191-198.	1.6	31
96	Structural determinants of affinity and selectivity in the binding of inhibitors to histone deacetylase 6. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020, 30, 127023.	1.0	31
97	Another catalytic triad?. <i>Nature</i> , 1990, 346, 225-225.	13.7	30
98	Structural aspects of HDAC8 mechanism and dysfunction in Cornelia de Lange syndrome spectrum disorders. <i>Protein Science</i> , 2016, 25, 1965-1976.	3.1	30
99	Multi-domain terpenoid cyclase architecture and prospects for proximity in bifunctional catalysis. <i>Current Opinion in Structural Biology</i> , 2016, 41, 27-37.	2.6	28
100	Polyamine Deacetylase Structure and Catalysis: Prokaryotic Acetylpolyamine Amidohydrolase and Eukaryotic HDAC10. <i>Biochemistry</i> , 2018, 57, 3105-3114.	1.2	27
101	Multicomponent Synthesis, Binding Mode, and Structure-Activity Relationship of Selective Histone Deacetylase 6 (HDAC6) Inhibitors with Bifurcated Capping Groups. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 10339-10351.	2.9	27
102	Crystal Structure of an Arginase-like Protein from <i>Trypanosoma brucei</i> That Evolved without a Binuclear Manganese Cluster. <i>Biochemistry</i> , 2015, 54, 458-471.	1.2	26
103	Harnessing the Role of HDAC6 in Idiopathic Pulmonary Fibrosis: Design, Synthesis, Structural Analysis, and Biological Evaluation of Potent Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 9960-9988.	2.9	26
104	Synthesis of a new trifluoromethylketone analogue of L-arginine and contrasting inhibitory activity against human arginase I and histone deacetylase 8. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2011, 21, 5854-5858.	1.0	25
105	Mechanism of Germacradien-4-ol Synthase-Controlled Water Capture. <i>Biochemistry</i> , 2016, 55, 2112-2121.	1.2	25
106	Crystallographic studies of azide binding to human carbonic anhydrase II. <i>FEBS Journal</i> , 1993, 213, 507-515.	0.2	24
107	Molecular Basis for the Selective Inhibition of Histone Deacetylase 6 by a Mercaptoacetamide Inhibitor. <i>ACS Medicinal Chemistry Letters</i> , 2018, 9, 1301-1305.	1.3	24
108	Binding of Uridine 5'-Diphosphate in the "Basic Patch" of the Zinc Deacetylase LpxC and Implications for Substrate Binding. <i>Biochemistry</i> , 2006, 45, 15216-15223.	1.2	23

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109	Spiroindoline-Capped Selective HDAC6 Inhibitors: Design, Synthesis, Structural Analysis, and Biological Evaluation. <i>ACS Medicinal Chemistry Letters</i> , 2020, 11, 2268-2276.	1.3	23
110	Structural and Functional Influence of the Glycine-Rich Loop G <sup>302</sup> GGGY on the Catalytic Tyrosine of Histone Deacetylase 8. <i>Biochemistry</i> , 2016, 55, 6718-6729.	1.2	22
111	Probing the Role of Active Site Water in the Sesquiterpene Cyclization Reaction Catalyzed by Aristolochene Synthase. <i>Biochemistry</i> , 2016, 55, 2864-2874.	1.2	22
112	Discovery of the cryptic function of terpene cyclases as aromatic prenyltransferases. <i>Nature Communications</i> , 2020, 11, 3958.	5.8	22
113	Structural insight on assembly-line catalysis in terpene biosynthesis. <i>Nature Communications</i> , 2021, 12, 3487.	5.8	22
114	Substitution of Aromatic Residues with Polar Residues in the Active Site Pocket of <i>epi</i> -Isozizaene Synthase Leads to the Generation of New Cyclic Sesquiterpenes. <i>Biochemistry</i> , 2017, 56, 5798-5811.	1.2	21
115	Design and Synthesis of Dihydroxamic Acids as HDAC6/8/10 Inhibitors. <i>ChemMedChem</i> , 2020, 15, 1163-1174.	1.6	21
116	Probing the Mechanism of 1,4-Conjugate Elimination Reactions Catalyzed by Terpene Synthases. <i>Journal of the American Chemical Society</i> , 2012, 134, 20844-20848.	6.6	19
117	Binding of <i>N</i> <sup>8</sup> -Acetylspermidine Analogues to Histone Deacetylase 10 Reveals Molecular Strategies for Blocking Polyamine Deacetylation. <i>Biochemistry</i> , 2019, 58, 4957-4969.	1.2	19
118	Conversion of Human Steroid 5 $\beta$ -Reductase (AKR1D1) into 3 $\beta$ -Hydroxysteroid Dehydrogenase by Single Point Mutation E120H. <i>Journal of Biological Chemistry</i> , 2012, 287, 16609-16622.	1.6	18
119	Crystal Structure of <i>Schistosoma mansoni</i> Arginase, a Potential Drug Target for the Treatment of Schistosomiasis. <i>Biochemistry</i> , 2014, 53, 4671-4684.	1.2	18
120	General base-general acid catalysis by terpenoid cyclases. <i>Journal of Antibiotics</i> , 2016, 69, 486-493.	1.0	18
121	Engineering an Anion-Binding Cavity in Antichymotrypsin Modulates the "Spring-Loaded" Serpin <sup>Protease</sup> Interaction. <i>Biochemistry</i> , 1998, 37, 3297-3304.	1.2	17
122	Aldo-keto reductases in which the conserved catalytic histidine is substituted. <i>Chemico-Biological Interactions</i> , 2009, 178, 127-133.	1.7	17
123	Crystal Structures of Complexes with Cobalt-Reconstituted Human Arginase I. <i>Biochemistry</i> , 2011, 50, 8018-8027.	1.2	17
124	Methods for the expression, purification, and crystallization of histone deacetylase "inhibitor complexes. <i>Methods in Enzymology</i> , 2019, 626, 447-474.	0.4	17
125	Structural Basis for the Selective Inhibition of HDAC10, the Cytosolic Polyamine Deacetylase. <i>ACS Chemical Biology</i> , 2020, 15, 2154-2163.	1.6	16
126	Crystal structures of <i>Leishmania mexicana</i> arginase complexed with $\hat{I}_{\pm}$ -disubstituted boronic amino-acid inhibitors. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 300-306.	0.4	15

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127	Identification of histone deacetylase 10 (HDAC10) inhibitors that modulate autophagy in transformed cells. <i>European Journal of Medicinal Chemistry</i> , 2022, 234, 114272.	2.6	15
128	BIOCHEMISTRY: Five Golden Rings. <i>Science</i> , 2006, 311, 1382-1383.	6.0	14
129	Synthesis and evaluation of N8-acetylspermidine analogues as inhibitors of bacterial acetylpolyamine amidohydrolase. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 4530-4540.	1.4	14
130	Crystal Structure of Cucumene Synthase, a Terpenoid Cyclase That Generates a Linear Triquinane Sesquiterpene. <i>Biochemistry</i> , 2018, 57, 6326-6335.	1.2	14
131	Structural Basis of Tryptophan Reverse N-Prenylation Catalyzed by CymD. <i>Biochemistry</i> , 2019, 58, 3232-3242.	1.2	14
132	An Aromatic Cluster in the Active Site of <i>ε</i> -Isozoaene Synthase Is an Electrostatic Toggle for Divergent Terpene Cyclization Pathways. <i>Biochemistry</i> , 2020, 59, 4744-4754.	1.2	14
133	X-ray Crystallographic Snapshots of Substrate Binding in the Active Site of Histone Deacetylase 10. <i>Biochemistry</i> , 2021, 60, 303-313.	1.2	13
134	Unexpected Reactivity of 2-Fluorolinalyl Diphosphate in the Active Site of Crystalline 2-Methylisoborneol Synthase. <i>Biochemistry</i> , 2013, 52, 5247-5255.	1.2	12
135	Design, Synthesis, and Evaluation of Polyamine Deacetylase Inhibitors, and High-Resolution Crystal Structures of Their Complexes with Acetylpolyamine Amidohydrolase. <i>Biochemistry</i> , 2015, 54, 4692-4703.	1.2	12
136	Crystallization and preliminary X-ray diffraction analysis of recombinant pentalenene synthase. <i>Protein Science</i> , 1995, 4, 2436-2438.	3.1	11
137	Higher-order oligomerization of a chimeric $\hat{1}^2\hat{1}^3$ bifunctional diterpene synthase with prenyltransferase and class II cyclase activities is concentration-dependent. <i>Journal of Structural Biology</i> , 2020, 210, 107463.	1.3	11
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