David W Christianson

List of Publications by Year
in descending order

155 papers	13,672 citations	22132 59 h-index	22147 113 g-index
160 all docs	160 docs citations	160 times ranked	10490 citing authors

#	Article	IF	Citations
1	Identification of histone deacetylase 10 (HDAC10) inhibitors that modulate autophagy in transformed cells. European Journal of Medicinal Chemistry, 2022, 234, 114272.	2.6	15
2	First Fluorescent Acetylspermidine Deacetylation Assay for HDAC10 Identifies Selective Inhibitors with Cellular Target Engagement**. ChemBioChem, 2022, 23, .	1.3	9
3	Structural analysis of histone deacetylase 8 mutants associated with Cornelia de Lange Syndrome spectrum disorders. Journal of Structural Biology, 2021, 213, 107681.	1.3	5
4	X-ray Crystallographic Snapshots of Substrate Binding in the Active Site of Histone Deacetylase 10. Biochemistry, 2021, 60, 303-313.	1.2	13
5	Structural insight on assembly-line catalysis in terpene biosynthesis. Nature Communications, 2021, 12, 3487.	5.8	22
6	Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites. Nature Communications, 2021, 12, 3384.	5.8	37
7	Harnessing the Role of HDAC6 in Idiopathic Pulmonary Fibrosis: Design, Synthesis, Structural Analysis, and Biological Evaluation of Potent Inhibitors. Journal of Medicinal Chemistry, 2021, 64, 9960-9988.	2.9	26
8	Assembly-Line Catalysis in Bifunctional Terpene Synthases. Accounts of Chemical Research, 2021, 54, 3780-3791.	7.6	33
9	Visualizing transiently associated catalytic domains in assembly-line biosynthesis using cryo-electron microscopy. Journal of Structural Biology, 2021, 213, 107802.	1.3	6
10	Unique Molecular Interaction with the Histone Deacetylase 6 Catalytic Tunnel: Crystallographic and Biological Characterization of a Model Chemotype. Journal of Medicinal Chemistry, 2021, 64, 2691-2704.	2.9	11
11	Engineering the Prenyltransferase Domain of a Bifunctional Assembly-Line Terpene Synthase. Biochemistry, 2021, 60, 3162-3172.	1.2	5
12	Structural Biology of Template-Directed Catalysis by Terpene Synthases. , 2020, , 613-643.		1
13	Exploring Structural Determinants of Inhibitor Affinity and Selectivity in Complexes with Histone Deacetylase 6. Journal of Medicinal Chemistry, 2020, 63, 295-308.	2.9	32
14	Spiroindoline-Capped Selective HDAC6 Inhibitors: Design, Synthesis, Structural Analysis, and Biological Evaluation. ACS Medicinal Chemistry Letters, 2020, 11, 2268-2276.	1.3	23
15	Higher-order oligomerization of a chimeric Î±Î²Î³ bifunctional diterpene synthase with prenyltransferase and class II cyclase activities is concentration-dependent. Journal of Structural Biology, 2020, 210, 107463.	1.3	11
16	Structural Basis for the Selective Inhibition of HDAC10, the Cytosolic Polyamine Deacetylase. ACS Chemical Biology, 2020, 15, 2154-2163.	1.6	16
17	An Aromatic Cluster in the Active Site of epi-Isozizaene Synthase Is an Electrostatic Toggle for Divergent Terpene Cyclization Pathways. Biochemistry, 2020, 59, 4744-4754.	1.2	14
18	Discovery of the cryptic function of terpene cyclases as aromatic prenyltransferases. Nature Communications, 2020, 11, 3958.	5.8	22

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19	Multicomponent Synthesis, Binding Mode, and Structureâ€“Activity Relationship of Selective Histone Deacetylase 6 (HDAC6) Inhibitors with Bifurcated Capping Groups. Journal of Medicinal Chemistry, 2020, 63, 10339-10351.	2.9	27
20	Structural studies of geranylgeranylglyceryl phosphate synthase, a prenyltransferase found in thermophilic Euryarchaeota. Acta Crystallographica Section D: Structural Biology, 2020, 76, 542-557.	1.1	2
21	Structural determinants of affinity and selectivity in the binding of inhibitors to histone deacetylase 6. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127023.	1.0	31
22	Design and Synthesis of Dihydroxamic Acids as HDAC6/8/10 Inhibitors. ChemMedChem, 2020, 15, 1163-1174.	1.6	21
23	Binding of inhibitors to active-site mutants of CD1, the enigmatic catalytic domain of histone deacetylase 6. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 428-437.	0.4	5
24	Structural Basis of Tryptophan Reverse N-Prenylation Catalyzed by CymD. Biochemistry, 2019, 58, 3232-3242.	1.2	14
25	Methods for the expression, purification, and crystallization of histone deacetylase 6â€“inhibitor complexes. Methods in Enzymology, 2019, 626, 447-474.	0.4	17
26	Phosphorylation of Histone Deacetylase 8: Structural and Mechanistic Analysis of the Phosphomimetic S39E Mutant. Biochemistry, 2019, 58, 4480-4493.	1.2	8
27	Structure and Function of the Acetylpolyamine Amidohydrolase from the Deep Earth Halophile Marinobacter subterrani. Biochemistry, 2019, 58, 3755-3766.	1.2	8
28	Crystal structure of F95Q epi-isozizaene synthase, an engineered sesquiterpene cyclase that generates biofuel precursors Î²- and Î³-curcumene. Journal of Structural Biology, 2019, 207, 218-224.	1.3	7
29	Structure of Sesquisabinene Synthase 1, a Terpenoid Cyclase That Generates a Strained [3.1.0] Bridged-Bicyclic Product. ACS Chemical Biology, 2019, 14, 1011-1019.	1.6	5
30	Structure, mechanism, and inhibition of the zinc-dependent histone deacetylases. Current Opinion in Structural Biology, 2019, 59, 9-18.	2.6	74
31	Preparation of a new construct of human histone deacetylase 8 for the crystallization of enzyme-inhibitor complexes. Methods in Enzymology, 2019, 626, 561-585.	0.4	2
32	Binding of N⁸-Acetylspermidine Analogues to Histone Deacetylase 10 Reveals Molecular Strategies for Blocking Polyamine Deacetylation. Biochemistry, 2019, 58, 4957-4969.	1.2	19
33	Structural Basis of Catalysis and Inhibition of HDAC6 CD1, the Enigmatic Catalytic Domain of Histone Deacetylase 6. Biochemistry, 2019, 58, 4912-4924.	1.2	42
34	Synthesis and Biological Investigation of Phenothiazine-Based Benzhydroxamic Acids as Selective Histone Deacetylase 6 Inhibitors. Journal of Medicinal Chemistry, 2019, 62, 1138-1166.	2.9	75
35	Polyamine Deacetylase Structure and Catalysis: Prokaryotic Acetylpolyamine Amidohydrolase and Eukaryotic HDAC10. Biochemistry, 2018, 57, 3105-3114.	1.2	27
36	Molecular Basis for the Selective Inhibition of Histone Deacetylase 6 by a Mercaptoacetamide Inhibitor. ACS Medicinal Chemistry Letters, 2018, 9, 1301-1305.	1.3	24

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37	Discovery of the First-in-Class Dual Histone Deacetylaseâ€“Proteasome Inhibitor. Journal of Medicinal Chemistry, 2018, 61, 10299-10309.	2.9	62
38	Crystal Structure of Cucumene Synthase, a Terpenoid Cyclase That Generates a Linear Triquinane Sesquiterpene. Biochemistry, 2018, 57, 6326-6335.	1.2	14
39	Entropy as a Driver of Selectivity for Inhibitor Binding to Histone Deacetylase 6. Biochemistry, 2018, 57, 3916-3924.	1.2	40
40	Multicomponent Synthesis and Binding Mode of Imidazo[1,2-a]pyridine-Capped Selective HDAC6 Inhibitors. Organic Letters, 2018, 20, 3255-3258.	2.4	43
41	Histone Deacetylase 6-Selective Inhibitors and the Influence of Capping Groups on Hydroxamate-Zinc Denticity. Journal of Medicinal Chemistry, 2018, 61, 8054-8060.	2.9	76
42	Histone deacetylase 10 structure and molecular function as a polyamine deacetylase. Nature Communications, 2017, 8, 15368.	5.8	139
43	Exploring the Influence of Domain Architecture on the Catalytic Function of Diterpene Synthases. Biochemistry, 2017, 56, 2010-2023.	1.2	56
44	Substitution of Aromatic Residues with Polar Residues in the Active Site Pocket of epi-Isozizaene Synthase Leads to the Generation of New Cyclic Sesquiterpenes. Biochemistry, 2017, 56, 5798-5811.	1.2	21
45	Structural and Chemical Biology of Terpenoid Cyclases. Chemical Reviews, 2017, 117, 11570-11648.	23.0	720
46	Binding of the Microbial Cyclic Tetrapeptide Trapoxin A to the Class I Histone Deacetylase HDAC8. ACS Chemical Biology, 2017, 12, 2281-2286.	1.6	57
47	ARID1A-mutated ovarian cancers depend on HDAC6Âactivity. Nature Cell Biology, 2017, 19, 962-973.	4.6	173
48	Unusual zinc-binding mode of HDAC6-selective hydroxamate inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13459-13464.	3.3	127
49	Structural and Functional Influence of the Glycine-Rich Loop G³⁰²GGGY on the Catalytic Tyrosine of Histone Deacetylase 8. Biochemistry, 2016, 55, 6718-6729.	1.2	22
50	Mechanism of Germacradien-4-ol Synthase-Controlled Water Capture. Biochemistry, 2016, 55, 2112-2121.	1.2	25
51	Probing the Role of Active Site Water in the Sesquiterpene Cyclization Reaction Catalyzed by Aristolochene Synthase. Biochemistry, 2016, 55, 2864-2874.	1.2	22
52	Crystal structures ofLeishmania mexicanaarginase complexed with Î±,Î±-disubstituted boronic amino-acid inhibitors. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 300-306.	0.4	15
53	General base-general acid catalysis by terpenoid cyclases. Journal of Antibiotics, 2016, 69, 486-493.	1.0	18
54	Structural aspects of HDAC8 mechanism and dysfunction in Cornelia de Lange syndrome spectrum disorders. Protein Science, 2016, 25, 1965-1976.	3.1	30

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55	Editorial overview: Catalysis and regulation: enzyme structure, mechanism, and biosynthetic pathways. Current Opinion in Structural Biology, 2016, 41, viii-x.	2.6	0
56	Histone deacetylase 6 structure and molecular basis of catalysis and inhibition. Nature Chemical Biology, 2016, 12, 741-747.	3.9	351
57	Multi-domain terpenoid cyclase architecture and prospects for proximity in bifunctional catalysis. Current Opinion in Structural Biology, 2016, 41, 27-37.	2.6	28
58	Structure and Function of Fusicoccadiene Synthase, a Hexameric Bifunctional Diterpene Synthase. ACS Chemical Biology, 2016, 11, 889-899.	1.6	59
59	General Baseâ€“General Acid Catalysis in Human Histone Deacetylase 8. Biochemistry, 2016, 55, 820-832.	1.2	61
60	Structural Studies of Geosmin Synthase, a Bifunctional Sesquiterpene Synthase with Î±Î± Domain Architecture That Catalyzes a Unique Cyclizationâ€“Fragmentation Reaction Sequence. Biochemistry, 2015, 54, 7142-7155.	1.2	36
61	Crystal Structure of an Arginase-like Protein from Trypanosoma brucei That Evolved without a Binuclear Manganese Cluster. Biochemistry, 2015, 54, 458-471.	1.2	26
62	Variable Active Site Loop Conformations Accommodate the Binding of Macrocyclic Largazole Analogues to HDAC8. Biochemistry, 2015, 54, 2126-2135.	1.2	55
63	Biochemical and Structural Characterization of HDAC8 Mutants Associated with Cornelia de Lange Syndrome Spectrum Disorders. Biochemistry, 2015, 54, 6501-6513.	1.2	41
64	Design, Synthesis, and Evaluation of Polyamine Deacetylase Inhibitors, and High-Resolution Crystal Structures of Their Complexes with Acetylpolyamine Amidohydrolase. Biochemistry, 2015, 54, 4692-4703.	1.2	12
65	Reprogramming the Chemodiversity of Terpenoid Cyclization by Remolding the Active Site Contour of epi-Isozizaene Synthase. Biochemistry, 2014, 53, 1155-1168.	1.2	62
66	Crystal Structure of Schistosoma mansoni Arginase, a Potential Drug Target for the Treatment of Schistosomiasis. Biochemistry, 2014, 53, 4671-4684.	1.2	18
67	Loss-of-function HDAC8 mutations cause a phenotypic spectrum of Cornelia de Lange syndrome-like features, ocular hypertelorism, large fontanelle and X-linked inheritance. Human Molecular Genetics, 2014, 23, 2888-2900.	1.4	120
68	Compromised Structure and Function of HDAC8 Mutants Identified in Cornelia de Lange Syndrome Spectrum Disorders. ACS Chemical Biology, 2014, 9, 2157-2164.	1.6	56
69	1.55Ã…-resolution structure of ent-copalyl diphosphate synthase and exploration of general acid function by site-directed mutagenesis. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 184-190.	1.1	52
70	Mechanistic Insights from the Binding of Substrate and Carbocation Intermediate Analogues to Aristolochene Synthase. Biochemistry, 2013, 52, 5441-5453.	1.2	55
71	Synthesis and evaluation of N8-acetylspermidine analogues as inhibitors of bacterial acetylpolyamine amidohydrolase. Bioorganic and Medicinal Chemistry, 2013, 21, 4530-4540.	1.4	14
72	Energetically unfavorable amide conformations for N6â€acetyllysine side chains in refined protein structures. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1051-1057.	1.5	10

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73	Formiminoglutamase fromTrypanosoma CruziIs An Arginase-Like Manganese Metalloenzyme. Biochemistry, 2013, 52, 9294-9309.	1.2	8
74	Unexpected Reactivity of 2-Fluorolinalyl Diphosphate in the Active Site of Crystalline 2-Methylisoborneol Synthase. Biochemistry, 2013, 52, 5247-5255.	1.2	12
75	Probing the Mechanism of 1,4-Conjugate Elimination Reactions Catalyzed by Terpene Synthases. Journal of the American Chemical Society, 2012, 134, 20844-20848.	6.6	19
76	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. Nature, 2012, 489, 313-317.	13.7	488
77	Structure of 2-Methylisoborneol Synthase from Streptomyces coelicolor and Implications for the Cyclization of a Noncanonical C-Methylated Monoterpenoid Substrate. Biochemistry, 2012, 51, 3011-3020.	1.2	42
78	Structure of Geranyl Diphosphate C-Methyltransferase from Streptomyces coelicolor and Implications for the Mechanism of Isoprenoid Modification. Biochemistry, 2012, 51, 3003-3010.	1.2	41
79	Conversion of Human Steroid 5Î²-Reductase (AKR1D1) into 3Î²-Hydroxysteroid Dehydrogenase by Single Point Mutation E120H. Journal of Biological Chemistry, 2012, 287, 16609-16622.	1.6	18
80	Binding of Î±,Î±-Disubstituted Amino Acids to Arginase Suggests New Avenues for Inhibitor Design. Journal of Medicinal Chemistry, 2011, 54, 5432-5443.	2.9	62
81	Crystal Structures of Complexes with Cobalt-Reconstituted Human Arginase I. Biochemistry, 2011, 50, 8018-8027.	1.2	17
82	Structural Basis of the Antiproliferative Activity of Largazole, a Depsipeptide Inhibitor of the Histone Deacetylases. Journal of the American Chemical Society, 2011, 133, 12474-12477.	6.6	141
83	Structure of Prokaryotic Polyamine Deacetylase Reveals Evolutionary Functional Relationships with Eukaryotic Histone Deacetylases,. Biochemistry, 2011, 50, 1808-1817.	1.2	45
84	Structure and mechanism of the diterpene cyclase ent-copalyl diphosphate synthase. Nature Chemical Biology, 2011, 7, 431-433.	3.9	166
85	Taxadiene synthase structure and evolution of modular architecture in terpene biosynthesis. Nature, 2011, 469, 116-120.	13.7	290
86	Structure, mechanism, and inhibition of histone deacetylases and related metalloenzymes. Current Opinion in Structural Biology, 2011, 21, 735-743.	2.6	225
87	Synthesis of a new trifluoromethylketone analogue of l-arginine and contrasting inhibitory activity against human arginase I and histone deacetylase 8. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 5854-5858.	1.0	25
88	Design and synthesis of C60â€“benzenesulfonamide conjugates. Tetrahedron Letters, 2010, 51, 3645-3648.	0.7	4
89	Trinuclear metal clusters in catalysis by terpenoid synthases. Pure and Applied Chemistry, 2010, 82, 1585-1597.	0.9	116
90	2-Aminoimidazole Amino Acids as Inhibitors of the Binuclear Manganese Metalloenzyme Human Arginase I. Journal of Medicinal Chemistry, 2010, 53, 4266-4276.	2.9	42

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91	Structure of Epi-Isozizaene Synthase from Streptomyces coelicolor A3(2), a Platform for New Terpenoid Cyclization Templates[,]. Biochemistry, 2010, 49, 1787-1797.	1.2	137
92	Structure of Isoprene Synthase Illuminates the Chemical Mechanism of Teragram Atmospheric Carbon Emission. Journal of Molecular Biology, 2010, 402, 363-373.	2.0	101
93	Structures of Metal-Substituted Human Histone Deacetylase 8 Provide Mechanistic Inferences on Biological Function,. Biochemistry, 2010, 49, 5048-5056.	1.2	71
94	Aldo-keto reductases in which the conserved catalytic histidine is substituted. Chemico-Biological Interactions, 2009, 178, 127-133.	1.7	17
95	Crystal Structure of (+)-Î´-Cadinene Synthase from Gossypium arboreum and Evolutionary Divergence of Metal Binding Motifs for Catalysis. Biochemistry, 2009, 48, 6175-6183.	1.2	122
96	Structure and catalytic mechanism of human steroid 5Î²-reductase (AKR1D1). Molecular and Cellular Endocrinology, 2009, 301, 191-198.	1.6	31
97	Inhibition of Human Steroid 5Î²-Reductase (AKR1D1) by Finasteride and Structure of the Enzyme-Inhibitor Complex. Journal of Biological Chemistry, 2009, 284, 19786-19790.	1.6	50
98	Unearthing the roots of the terpenome. Current Opinion in Chemical Biology, 2008, 12, 141-150.	2.8	302
99	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-233a€"<mml:math altimg="si3.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
100	Structural Studies of Human Histone Deacetylase 8 and Its Site-Specific Variants Complexed with Substrate and Inhibitors[,]. Biochemistry, 2008, 47, 13554-13563.	1.2	180
101	X-ray Crystallographic Studies of Substrate Binding to Aristolochene Synthase Suggest a Metal Ion Binding Sequence for Catalysis. Journal of Biological Chemistry, 2008, 283, 15431-15439.	1.6	67
102	Crystal Structure of Human Liver Î"4-3-Ketosteroid 5Î²-Reductase (AKR1D1) and Implications for Substrate Binding and Catalysis. Journal of Biological Chemistry, 2008, 283, 16830-16839.	1.6	67
103	CHEMISTRY: Roots of Biosynthetic Diversity. Science, 2007, 316, 60-61.	6.0	76
104	Expression, purification, assay, and crystal structure of perdeuterated human arginase I. Archives of Biochemistry and Biophysics, 2007, 465, 82-89.	1.4	65
105	Exploring biosynthetic diversity with trichodiene synthase. Archives of Biochemistry and Biophysics, 2007, 466, 260-266.	1.4	56
106	Crystal Structure of Lactaldehyde Dehydrogenase from Escherichia coli and Inferences Regarding Substrate and Cofactor Specificity. Journal of Molecular Biology, 2007, 366, 481-493.	2.0	49
107	X-ray Crystal Structure of Aristolochene Synthase from Aspergillus terreus and Evolution of Templates for the Cyclization of Farnesyl Diphosphate,. Biochemistry, 2007, 46, 1941-1951.	1.2	161
108	Structural Biology and Chemistry of the Terpenoid Cyclases. Chemical Reviews, 2006, 106, 3412-3442.	23.0	682

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109	Binding of Uridine 5â€˜-Diphosphate in the â€œBasic Patchâ€•of the Zinc Deacetylase LpxC and Implications for Substrate Bindingâ€,â€¡. Biochemistry, 2006, 45, 15216-15223.	1.2	23
110	Stereochemistry of guanidine-metal interactions: Implications for L-arginine-metal interactions in protein structure and function. Proteins: Structure, Function and Bioinformatics, 2006, 65, 637-642.	1.5	34
111	BIOCHEMISTRY: Five Golden Rings. Science, 2006, 311, 1382-1383.	6.0	14
112	Crystal structure of human arginase I at 1.29-A resolution and exploration of inhibition in the immune response. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13058-13063.	3.3	164
113	Molecular Recognition of the Substrate Diphosphate Group Governs Product Diversity in Trichodiene Synthase Mutants,. Biochemistry, 2005, 44, 6153-6163.	1.2	59
114	Role of Arginine-304 in the Diphosphate-Triggered Active Site Closure Mechanism of Trichodiene Synthase,. Biochemistry, 2005, 44, 12719-12727.	1.2	49
115	Arginase:â€‰ Structure, Mechanism, and Physiological Role in Male and Female Sexual Arousal. Accounts of Chemical Research, 2005, 38, 191-201.	7.6	158
116	Design of Amino Acid Aldehydes as Transition-State Analogue Inhibitors of Arginase. Journal of the American Chemical Society, 2004, 126, 10278-10284.	6.6	32
117	Human Arginase II:Â Crystal Structure and Physiological Role in Male and Female Sexual Arousalâ€,â€¡. Biochemistry, 2003, 42, 8445-8451.	1.2	131
118	Structural and Functional Importance of First-Shell Metal Ligands in the Binuclear Manganese Cluster of Arginase Iâ€,â€¡. Biochemistry, 2003, 42, 7748-7758.	1.2	42
119	Nonlinear partial differential equations and applications: Bornyl diphosphate synthase: Structure and strategy for carbocation manipulation by a terpenoid cyclase. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15375-15380.	3.3	272
120	X-ray Crystal Structures of D100E Trichodiene Synthase and Its Pyrophosphate Complex Reveal the Basis for Terpene Product Diversityâ€,â€¡. Biochemistry, 2002, 41, 1732-1741.	1.2	90
121	Pentalenene Synthase. Analysis of Active Site Residues by Site-Directed Mutagenesis. Journal of the American Chemical Society, 2002, 124, 7681-7689.	6.6	147
122	Mechanistic and Metabolic Inferences from the Binding of Substrate Analogues and Products to Arginaseâ€,â€¡. Biochemistry, 2001, 40, 2689-2701.	1.2	77
123	Probing Erectile Function:ÂS-(2-Boronoethyl)-l-Cysteine Binds to Arginase as a Transition State Analogue and Enhances Smooth Muscle Relaxation in Human Penile Corpus Cavernosumâ€,â€¡. Biochemistry, 2001, 40, 2678-2688.	1.2	163
124	Fluoroaromaticâ^'Fluoroaromatic Interactions between Inhibitors Bound in the Crystal Lattice of Human Carbonic Anhydrase II. Journal of the American Chemical Society, 2001, 123, 9620-9627.	6.6	84
125	Crystal Structure Determination of Aristolochene Synthase from the Blue Cheese Mold, Penicillium roqueforti*. Journal of Biological Chemistry, 2000, 275, 25533-25539.	1.6	185
126	Contribution of Fluorine to Proteinâ^'Ligand Affinity in the Binding of Fluoroaromatic Inhibitors to Carbonic Anhydrase II. Journal of the American Chemical Society, 2000, 122, 12125-12134.	6.6	136

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127	Arginase-boronic acid complex highlights a physiological role in erectile function. Nature Structural Biology, 1999, 6, 1043-1047.	9.7	157
128	Convergence of Catalytic Antibody and Terpene Cyclase Mechanisms: Polyene Cyclization Directed by Carbocation-Ï€ Interactions. Angewandte Chemie - International Edition, 1999, 38, 1743-1747.	7.2	45
129	Catalysis By Metal-Activated Hydroxide in Zinc and Manganese Metalloenzymes. Annual Review of Biochemistry, 1999, 68, 33-57.	5.0	345
130	Structures of murine carbonic anhydrase IV and human carbonic anhydrase II complexed with brinzolamide: Molecular basis of isozymeâ€drug discrimination. Protein Science, 1998, 7, 556-563.	3.1	77
131	Structural analysis of inhibitor binding to human carbonic anhydrase II. Protein Science, 1998, 7, 2483-2489.	3.1	99
132	Managing and manipulating carbocations in biology: terpenoid cyclase structure and mechanism. Current Opinion in Structural Biology, 1998, 8, 695-703.	2.6	114
133	Engineering an Anion-Binding Cavity in Antichymotrypsin Modulates the â€œSpring-Loadedâ€• Serpinâ^'Protease Interactionâ€. Biochemistry, 1998, 37, 3297-3304.	1.2	17
134	Novel Binding Mode of Hydroxamate Inhibitors to Human Carbonic Anhydrase II. Journal of the American Chemical Society, 1997, 119, 850-851.	6.6	100
135	Crystal Structure of Pentalenene Synthase: Mechanistic Insights on Terpenoid Cyclization Reactions in Biology. Science, 1997, 277, 1820-1824.	6.0	447
136	Inhibition of Mn2+2-Arginase by Borate Leads to the Design of a Transition State Analogue Inhibitor, 2(S)-Amino-6-boronohexanoic Acid. Journal of the American Chemical Society, 1997, 119, 8107-8108.	6.6	123
137	Altering the Binuclear Manganese Cluster of Arginase Diminishes Thermostability and Catalytic Function. Biochemistry, 1997, 36, 10558-10565.	1.2	84
138	Histidine â†' Carboxamide Ligand Substitutions in the Zinc Binding Site of Carbonic Anhydrase II Alter Metal Coordination Geometry but Retain Catalytic Activityâ€. Biochemistry, 1997, 36, 15780-15791.	1.2	96
139	X-ray Crystallographic Studies of Alanine-65 Variants of Carbonic Anhydrase II Reveal the Structural Basis of Compromised Proton Transfer in Catalysisâ€. Biochemistry, 1996, 35, 16429-16434.	1.2	46
140	Carbonic Anhydrase:â€‰ Evolution of the Zinc Binding Site by Nature and by Design. Accounts of Chemical Research, 1996, 29, 331-339.	7.6	471
141	Is the binding of Î²-amyloid protein to antichymotrypsin in Alzheimer plaques mediated by a Î²-strand insertion?. Proteins: Structure, Function and Bioinformatics, 1996, 25, 420-424.	1.5	0
142	Arginine substitutions in the hinge region of antichymotrypsin affect serpin Î²-sheet rearrangement. Nature Structural and Molecular Biology, 1996, 3, 888-893.	3.6	35
143	Structure of a unique binuclear manganese cluster in arginase. Nature, 1996, 383, 554-557.	13.7	425
144	Crystallization and preliminary Xâ€ray diffraction analysis of recombinant pentalenene synthase. Protein Science, 1995, 4, 2436-2438.	3.1	11

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145	Positions of Hisâ€64 and a bound water in human carbonic anhydrase II upon binding three structurally related inhibitors. Protein Science, 1994, 3, 118-125.	3.1	62
146	Crystal structure of an uncleaved serpin reveals the conformation of an inhibitory reactive loop. Nature Structural and Molecular Biology, 1994, 1, 251-258.	3.6	167
147	Mapping Protein-Peptide Affinity: Binding of Peptidylsulfonamide Inhibitors to Human Carbonic Anhydrase II. Journal of the American Chemical Society, 1994, 116, 5063-5068.	6.6	52
148	Purification and characterization of Klebsiella aerogenes UreE protein: A nickelâ€binding protein that functions in urease metallocenter assembly. Protein Science, 1993, 2, 1042-1052.	3.1	156
149	Crystallographic studies of azide binding to human carbonic anhydrase II. FEBS Journal, 1993, 213, 507-515.	0.2	24
150	Structure and energetics of a non-proline cis-peptidyl linkage in a proline-202 .fwdarw. alanine carbonic anhydrase II variant. Biochemistry, 1993, 32, 10944-10949.	1.2	55
151	Another catalytic triad?. Nature, 1990, 346, 225-225.	13.7	30
152	Hydrogen bond stereochemistry in protein structure and function. Journal of Molecular Biology, 1990, 215, 457-471.	2.0	275
153	Carboxypeptidase A. Accounts of Chemical Research, 1989, 22, 62-69.	7.6	654
154	Complex between carboxypeptidase A and a possible transition-state analog: mechanistic inferences from high-resolution x-ray structures of enzyme-inhibitor complexes. Journal of the American Chemical Society, 1986, 108, 4998-5003.	6.6	78
155	Structure of the complex between an unexpectedly hydrolyzed phosphonamidate inhibitor and carboxypeptidase A. Journal of the American Chemical Society, 1986, 108, 545-546.	6.6	50