David W Christianson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

154 papers	11,119 citations	54 h-index	103 g-index
160 ext. papers	12,457 ext. citations	9.2 avg, IF	6.83 L-index

#	Paper	IF	Citations
154	Identification of histone deacetylase 10 (HDAC10) inhibitors that modulate autophagy in transformed cells.. *European Journal of Medicinal Chemistry*, **2022**, 234, 114272	6.8	2
153	Engineering the Prenyltransferase Domain of a Bifunctional Assembly-Line Terpene Synthase. *Biochemistry*, **2021**, 60, 3162-3172	3.2	2
152	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	8.3	6
151	Structural insight on assembly-line catalysis in terpene biosynthesis. *Nature Communications*, **2021**, 12, 3487	17.4	6
150	Anchor extension: a structure-guided approach to design cyclic peptides targeting enzyme active sites. *Nature Communications*, **2021**, 12, 3384	17.4	12
149	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	8.3	5
148	Structural analysis of histone deacetylase 8 mutants associated with Cornelia de Lange Syndrome spectrum disorders. *Journal of Structural Biology*, **2021**, 213, 107681	3.4	1
147	X-ray Crystallographic Snapshots of Substrate Binding in the Active Site of Histone Deacetylase 10. *Biochemistry*, **2021**, 60, 303-313	3.2	4
146	Assembly-Line Catalysis in Bifunctional Terpene Synthases. *Accounts of Chemical Research*, **2021**, 54, 3780-3791	24.3	9
145	Visualizing transiently associated catalytic domains in assembly-line biosynthesis using cryo-electron microscopy. *Journal of Structural Biology*, **2021**, 213, 107802	3.4	1
144	Structural studies of geranylgeranylglyceryl phosphate synthase, a prenyltransferase found in thermophilic Euryarchaeota. *Acta Crystallographica Section D: Structural Biology*, **2020**, 76, 542-557	5.5	1
143	Structural determinants of affinity and selectivity in the binding of inhibitors to histone deacetylase 6. *Bioorganic and Medicinal Chemistry Letters*, **2020**, 30, 127023	2.9	20
142	Design and Synthesis of Dihydroxamic Acids as HDAC6/8/10 Inhibitors. *ChemMedChem*, **2020**, 15, 1163-1174	3.7	13
141	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	1.1	3
140	Exploring Structural Determinants of Inhibitor Affinity and Selectivity in Complexes with Histone Deacetylase 6. *Journal of Medicinal Chemistry*, **2020**, 63, 295-308	8.3	17
139	Spiroindoline-Capped Selective HDAC6 Inhibitors: Design, Synthesis, Structural Analysis, and Biological Evaluation. *ACS Medicinal Chemistry Letters*, **2020**, 11, 2268-2276	4.3	8
138	Higher-order oligomerization of a chimeric bifunctional diterpene synthase with prenyltransferase and class II cyclase activities is concentration-dependent. *Journal of Structural Biology*, **2020**, 210, 107463	3.4	6

137	Structural Basis for the Selective Inhibition of HDAC10, the Cytosolic Polyamine Deacetylase. *ACS Chemical Biology*, **2020**, 15, 2154-2163	4.9	8
136	An Aromatic Cluster in the Active Site of -Isozizaene Synthase Is an Electrostatic Toggle for Divergent Terpene Cyclization Pathways. *Biochemistry*, **2020**, 59, 4744-4754	3.2	3
135	Discovery of the cryptic function of terpene cyclases as aromatic prenyltransferases. *Nature Communications*, **2020**, 11, 3958	17.4	12
134	Multicomponent Synthesis, Binding Mode, and Structure-Activity Relationship of Selective Histone Deacetylase 6 (HDAC6) Inhibitors with Bifurcated Capping Groups. *Journal of Medicinal Chemistry*, **2020**, 63, 10339-10351	8.3	13
133	Structural Biology of Template-Directed Catalysis by Terpene Synthases **2020**, 613-643		
132	Structure and Function of the Acetylpolyamine Amidohydrolase from the Deep Earth Halophile. *Biochemistry*, **2019**, 58, 3755-3766	3.2	3
131	Crystal structure of F95Q epi-isozizaene synthase, an engineered sesquiterpene cyclase that generates biofuel precursors and curcumene. *Journal of Structural Biology*, **2019**, 207, 218-224	3.4	5
130	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	4.9	3
129	Structure, mechanism, and inhibition of the zinc-dependent histone deacetylases. *Current Opinion in Structural Biology*, **2019**, 59, 9-18	8.1	38
128	Structural Basis of Tryptophan Reverse N-Prenylation Catalyzed by CymD. *Biochemistry*, **2019**, 58, 3232-3242	3.2	11
127	Methods for the expression, purification, and crystallization of histone deacetylase 6-inhibitor complexes. *Methods in Enzymology*, **2019**, 626, 447-474	1.7	10
126	Phosphorylation of Histone Deacetylase 8: Structural and Mechanistic Analysis of the Phosphomimetic S39E Mutant. *Biochemistry*, **2019**, 58, 4480-4493	3.2	5
125	Preparation of a new construct of human histone deacetylase 8 for the crystallization of enzyme-inhibitor complexes. *Methods in Enzymology*, **2019**, 626, 561-585	1.7	0
124	Binding of -Acetylspermidine Analogues to Histone Deacetylase 10 Reveals Molecular Strategies for Blocking Polyamine Deacetylation. *Biochemistry*, **2019**, 58, 4957-4969	3.2	9
123	Structural Basis of Catalysis and Inhibition of HDAC6 CD1, the Enigmatic Catalytic Domain of Histone Deacetylase 6. *Biochemistry*, **2019**, 58, 4912-4924	3.2	23
122	Synthesis and Biological Investigation of Phenothiazine-Based Benzhydroxamic Acids as Selective Histone Deacetylase 6 Inhibitors. *Journal of Medicinal Chemistry*, **2019**, 62, 1138-1166	8.3	52
121	Polyamine Deacetylase Structure and Catalysis: Prokaryotic Acetylpolyamine Amidohydrolase and Eukaryotic HDAC10. *Biochemistry*, **2018**, 57, 3105-3114	3.2	17
120	Histone Deacetylase 6-Selective Inhibitors and the Influence of Capping Groups on Hydroxamate-Zinc Denticity. *Journal of Medicinal Chemistry*, **2018**, 61, 8054-8060	8.3	55

119	Molecular Basis for the Selective Inhibition of Histone Deacetylase 6 by a Mercaptoacetamide Inhibitor. *ACS Medicinal Chemistry Letters*, **2018**, 9, 1301-1305	4.3	16
118	Discovery of the First-in-Class Dual Histone Deacetylase-Proteasome Inhibitor. *Journal of Medicinal Chemistry*, **2018**, 61, 10299-10309	8.3	46
117	Crystal Structure of Cucumene Synthase, a Terpenoid Cyclase That Generates a Linear Triquinane Sesquiterpene. *Biochemistry*, **2018**, 57, 6326-6335	3.2	8
116	Entropy as a Driver of Selectivity for Inhibitor Binding to Histone Deacetylase 6. *Biochemistry*, **2018**, 57, 3916-3924	3.2	32
115	Multicomponent Synthesis and Binding Mode of Imidazo[1,2- a]pyridine-Capped Selective HDAC6 Inhibitors. *Organic Letters*, **2018**, 20, 3255-3258	6.2	38
114	Histone deacetylase 10 structure and molecular function as a polyamine deacetylase. *Nature Communications*, **2017**, 8, 15368	17.4	88
113	Exploring the Influence of Domain Architecture on the Catalytic Function of Diterpene Synthases. *Biochemistry*, **2017**, 56, 2010-2023	3.2	35
112	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	3.2	12
111	Structural and Chemical Biology of Terpenoid Cyclases. *Chemical Reviews*, **2017**, 117, 11570-11648	68.1	416
110	Binding of the Microbial Cyclic Tetrapeptide Trapoxin A to the Class I Histone Deacetylase HDAC8. *ACS Chemical Biology*, **2017**, 12, 2281-2286	4.9	47
109	ARID1A-mutated ovarian cancers depend on HDAC6 activity. *Nature Cell Biology*, **2017**, 19, 962-973	23.4	124
108	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	11.5	91
107	Structural aspects of HDAC8 mechanism and dysfunction in Cornelia de Lange syndrome spectrum disorders. *Protein Science*, **2016**, 25, 1965-1976	6.3	21
106	Histone deacetylase 6 structure and molecular basis of catalysis and inhibition. *Nature Chemical Biology*, **2016**, 12, 741-7	11.7	242
105	Multi-domain terpenoid cyclase architecture and prospects for proximity in bifunctional catalysis. *Current Opinion in Structural Biology*, **2016**, 41, 27-37	8.1	21
104	Structure and Function of Fusicoccadiene Synthase, a Hexameric Bifunctional Diterpene Synthase. *ACS Chemical Biology*, **2016**, 11, 889-99	4.9	39
103	General Base-General Acid Catalysis in Human Histone Deacetylase 8. *Biochemistry*, **2016**, 55, 820-32	3.2	47
102	Structural and Functional Influence of the Glycine-Rich Loop GGGGY on the Catalytic Tyrosine of Histone Deacetylase 8. *Biochemistry*, **2016**, 55, 6718-6729	3.2	18

101	Mechanism of Germacradien-4-ol Synthase-Controlled Water Capture. *Biochemistry*, **2016**, 55, 2112-21	3.2	23
100	Probing the Role of Active Site Water in the Sesquiterpene Cyclization Reaction Catalyzed by Aristolochene Synthase. *Biochemistry*, **2016**, 55, 2864-74	3.2	19
99	Crystal structures of Leishmania mexicana arginase complexed with □disubstituted boronic amino-acid inhibitors. *Acta Crystallographica Section F, Structural Biology Communications*, **2016**, 72, 300-6	1.1	10
98	General base-general acid catalysis by terpenoid cyclases. *Journal of Antibiotics*, **2016**, 69, 486-93	3.7	13
97	Variable active site loop conformations accommodate the binding of macrocyclic largazole analogues to HDAC8. *Biochemistry*, **2015**, 54, 2126-35	3.2	47
96	Biochemical and structural characterization of HDAC8 mutants associated with Cornelia de Lange syndrome spectrum disorders. *Biochemistry*, **2015**, 54, 6501-13	3.2	32
95	Design, Synthesis, and Evaluation of Polyamine Deacetylase Inhibitors, and High-Resolution Crystal Structures of Their Complexes with Acetylpolyamine Amidohydrolase. *Biochemistry*, **2015**, 54, 4692-703	3.2	9
94	Structural Studies of Geosmin Synthase, a Bifunctional Sesquiterpene Synthase with □Domain Architecture That Catalyzes a Unique Cyclization-Fragmentation Reaction Sequence. *Biochemistry*, **2015**, 54, 7142-55	3.2	28
93	Crystal structure of an arginase-like protein from Trypanosoma brucei that evolved without a binuclear manganese cluster. *Biochemistry*, **2015**, 54, 458-71	3.2	13
92	Reprogramming the chemodiversity of terpenoid cyclization by remolding the active site contour of epi-isozizaene synthase. *Biochemistry*, **2014**, 53, 1155-68	3.2	43
91	Crystal structure of Schistosoma mansoni arginase, a potential drug target for the treatment of schistosomiasis. *Biochemistry*, **2014**, 53, 4671-84	3.2	13
90	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, 2888-900	5.6	99
89	Compromised structure and function of HDAC8 mutants identified in Cornelia de Lange Syndrome spectrum disorders. *ACS Chemical Biology*, **2014**, 9, 2157-64	4.9	47
88	1.55□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, 184-90	4	40
87	Mechanistic insights from the binding of substrate and carbocation intermediate analogues to aristolochene synthase. *Biochemistry*, **2013**, 52, 5441-53	3.2	44
86	Synthesis and evaluation of N□acetylspermidine analogues as inhibitors of bacterial acetylpolyamine amidohydrolase. *Bioorganic and Medicinal Chemistry*, **2013**, 21, 4530-40	3.4	11
85	Energetically unfavorable amide conformations for N6-acetyllysine side chains in refined protein structures. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1051-7	4.2	9
84	Formiminoglutamase from Trypanosoma cruzi is an arginase-like manganese metalloenzyme. *Biochemistry*, **2013**, 52, 9294-309	3.2	7

83	Unexpected reactivity of 2-fluorolinalyl diphosphate in the active site of crystalline 2-methylisoborneol synthase. *Biochemistry*, **2013**, 52, 5247-55	3.2	10
82	Probing the mechanism of 1,4-conjugate elimination reactions catalyzed by terpene synthases. *Journal of the American Chemical Society*, **2012**, 134, 20844-8	16.4	17
81	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. *Nature*, **2012**, 489, 313-7	50.4	398
80	Structure of 2-methylisoborneol synthase from Streptomyces coelicolor and implications for the cyclization of a noncanonical C-methylated monoterpenoid substrate. *Biochemistry*, **2012**, 51, 3011-20	3.2	32
79	Structure of geranyl diphosphate C-methyltransferase from Streptomyces coelicolor and implications for the mechanism of isoprenoid modification. *Biochemistry*, **2012**, 51, 3003-10	3.2	27
78	Conversion of human steroid 5β-reductase (AKR1D1) into 3β-hydroxysteroid dehydrogenase by single point mutation E120H: example of perfect enzyme engineering. *Journal of Biological Chemistry*, **2012**, 287, 16609-22	5.4	15
77	Structural basis of the antiproliferative activity of largazole, a depsipeptide inhibitor of the histone deacetylases. *Journal of the American Chemical Society*, **2011**, 133, 12474-7	16.4	125
76	Structure of prokaryotic polyamine deacetylase reveals evolutionary functional relationships with eukaryotic histone deacetylases. *Biochemistry*, **2011**, 50, 1808-17	3.2	40
75	Structure and mechanism of the diterpene cyclase ent-copalyl diphosphate synthase. *Nature Chemical Biology*, **2011**, 7, 431-3	11.7	125
74	Taxadiene synthase structure and evolution of modular architecture in terpene biosynthesis. *Nature*, **2011**, 469, 116-20	50.4	229
73	Structure, mechanism, and inhibition of histone deacetylases and related metalloenzymes. *Current Opinion in Structural Biology*, **2011**, 21, 735-43	8.1	181
72	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, 5854-8	2.9	21
71	Binding of α,α-disubstituted amino acids to arginase suggests new avenues for inhibitor design. *Journal of Medicinal Chemistry*, **2011**, 54, 5432-43	8.3	50
70	Crystal structures of complexes with cobalt-reconstituted human arginase I. *Biochemistry*, **2011**, 50, 8018-27	3.2	15
69	Trinuclear Metal Clusters in Catalysis by Terpenoid Synthases. *Pure and Applied Chemistry*, **2010**, 82, 1585-1597	2.1	92
68	2-aminoimidazole amino acids as inhibitors of the binuclear manganese metalloenzyme human arginase I. *Journal of Medicinal Chemistry*, **2010**, 53, 4266-76	8.3	35
67	Structure of epi-isozizaene synthase from Streptomyces coelicolor A3(2), a platform for new terpenoid cyclization templates. *Biochemistry*, **2010**, 49, 1787-97	3.2	114
66	Structure of isoprene synthase illuminates the chemical mechanism of teragram atmospheric carbon emission. *Journal of Molecular Biology*, **2010**, 402, 363-73	6.5	87

65	Structures of metal-substituted human histone deacetylase 8 provide mechanistic inferences on biological function. *Biochemistry*, **2010**, 49, 5048-56	3.2	65
64	Design and synthesis of C60Benzenesulfonamide conjugates. *Tetrahedron Letters*, **2010**, 51, 3645-3648	2	4
63	Aldo-keto reductases in which the conserved catalytic histidine is substituted. *Chemico-Biological Interactions*, **2009**, 178, 127-33	5	13
62	Crystal structure of (+)-delta-cadinene synthase from Gossypium arboreum and evolutionary divergence of metal binding motifs for catalysis. *Biochemistry*, **2009**, 48, 6175-83	3.2	89
61	Structure and catalytic mechanism of human steroid 5beta-reductase (AKR1D1). *Molecular and Cellular Endocrinology*, **2009**, 301, 191-8	4.4	29
60	Inhibition of human steroid 5beta-reductase (AKR1D1) by finasteride and structure of the enzyme-inhibitor complex. *Journal of Biological Chemistry*, **2009**, 284, 19786-90	5.4	41
59	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-Mg2+B motif. *Archives of Biochemistry and Biophysics*, **2008**, 469, 184-94	4.1	62
58	Structural studies of human histone deacetylase 8 and its site-specific variants complexed with substrate and inhibitors. *Biochemistry*, **2008**, 47, 13554-63	3.2	164
57	X-ray crystallographic studies of substrate binding to aristolochene synthase suggest a metal ion binding sequence for catalysis. *Journal of Biological Chemistry*, **2008**, 283, 15431-9	5.4	63
56	Crystal structure of human liver Delta4-3-ketosteroid 5beta-reductase (AKR1D1) and implications for substrate binding and catalysis. *Journal of Biological Chemistry*, **2008**, 283, 16830-9	5.4	60
55	Unearthing the roots of the terpenome. *Current Opinion in Chemical Biology*, **2008**, 12, 141-50	9.7	256
54	X-ray crystal structure of aristolochene synthase from Aspergillus terreus and evolution of templates for the cyclization of farnesyl diphosphate. *Biochemistry*, **2007**, 46, 1941-51	3.2	123
53	Chemistry. Roots of biosynthetic diversity. *Science*, **2007**, 316, 60-1	33.3	60
52	Expression, purification, assay, and crystal structure of perdeuterated human arginase I. *Archives of Biochemistry and Biophysics*, **2007**, 465, 82-9	4.1	56
51	Exploring biosynthetic diversity with trichodiene synthase. *Archives of Biochemistry and Biophysics*, **2007**, 466, 260-6	4.1	50
50	Crystal structure of lactaldehyde dehydrogenase from Escherichia coli and inferences regarding substrate and cofactor specificity. *Journal of Molecular Biology*, **2007**, 366, 481-93	6.5	44
49	Biochemistry. Five golden rings. *Science*, **2006**, 311, 1382-3	33.3	13
48	Structural biology and chemistry of the terpenoid cyclases. *Chemical Reviews*, **2006**, 106, 3412-42	68.1	618

47	Binding of uridine 5Rdiphosphate in the "basic patch" of the zinc deacetylase LpxC and implications for substrate binding. *Biochemistry*, **2006**, 45, 15216-23	3.2	20
46	Stereochemistry of guanidine-metal interactions: implications for L-arginine-metal interactions in protein structure and function. *Proteins: Structure, Function and Bioinformatics*, **2006**, 65, 637-42	4.2	32
45	Molecular recognition of the substrate diphosphate group governs product diversity in trichodiene synthase mutants. *Biochemistry*, **2005**, 44, 6153-63	3.2	53
44	Role of arginine-304 in the diphosphate-triggered active site closure mechanism of trichodiene synthase. *Biochemistry*, **2005**, 44, 12719-27	3.2	46
43	Arginase: structure, mechanism, and physiological role in male and female sexual arousal. *Accounts of Chemical Research*, **2005**, 38, 191-201	24.3	139
42	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, 13058-63	11.5	137
41	Design of amino acid aldehydes as transition-state analogue inhibitors of arginase. *Journal of the American Chemical Society*, **2004**, 126, 10278-84	16.4	26
40	Human arginase II: crystal structure and physiological role in male and female sexual arousal. *Biochemistry*, **2003**, 42, 8445-51	3.2	108
39	Structural and functional importance of first-shell metal ligands in the binuclear manganese cluster of arginase I. *Biochemistry*, **2003**, 42, 7748-58	3.2	40
38	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, 15375-80	11.5	232
37	X-ray crystal structures of D100E trichodiene synthase and its pyrophosphate complex reveal the basis for terpene product diversity. *Biochemistry*, **2002**, 41, 1732-41	3.2	76
36	Pentalenene synthase. Analysis of active site residues by site-directed mutagenesis. *Journal of the American Chemical Society*, **2002**, 124, 7681-9	16.4	135
35	Mechanistic and metabolic inferences from the binding of substrate analogues and products to arginase. *Biochemistry*, **2001**, 40, 2689-701	3.2	69
34	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. *Biochemistry*, **2001**, 40, 2678-88	3.2	150
33	Fluoroaromatic-fluoroaromatic interactions between inhibitors bound in the crystal lattice of human carbonic anhydrase II. *Journal of the American Chemical Society*, **2001**, 123, 9620-7	16.4	78
32	Crystal structure determination of aristolochene synthase from the blue cheese mold, Penicillium roqueforti. *Journal of Biological Chemistry*, **2000**, 275, 25533-9	5.4	142
31	Contribution of Fluorine to Protein□Ligand Affinity in the Binding of Fluoroaromatic Inhibitors to Carbonic Anhydrase II. *Journal of the American Chemical Society*, **2000**, 122, 12125-12134	16.4	124
30	Arginase-boronic acid complex highlights a physiological role in erectile function. *Nature Structural Biology*, **1999**, 6, 1043-7		137

29	Konvergenz der Mechanismen eines katalytischen Antik□pers und einer Terpen-Cyclase: eine durch Carbokation-□Elektronen-Wechselwirkung gesteuerte Polyencyclisierung. *Angewandte Chemie*, **1999**, 111, 1859-1864	3.6	10
28	Convergence of Catalytic Antibody and Terpene Cyclase Mechanisms: Polyene Cyclization Directed by Carbocation-□Interactions. *Angewandte Chemie - International Edition*, **1999**, 38, 1743-1747	16.4	37
27	Catalysis by metal-activated hydroxide in zinc and manganese metalloenzymes. *Annual Review of Biochemistry*, **1999**, 68, 33-57	29.1	317
26	Structures of murine carbonic anhydrase IV and human carbonic anhydrase II complexed with brinzolamide: molecular basis of isozyme-drug discrimination. *Protein Science*, **1998**, 7, 556-63	6.3	70
25	Structural analysis of inhibitor binding to human carbonic anhydrase II. *Protein Science*, **1998**, 7, 2483-9	6.3	89
24	Managing and manipulating carbocations in biology: terpenoid cyclase structure and mechanism. *Current Opinion in Structural Biology*, **1998**, 8, 695-703	8.1	108
23	Engineering an anion-binding cavity in antichymotrypsin modulates the "spring-loaded" serpin-protease interaction. *Biochemistry*, **1998**, 37, 3297-304	3.2	11
22	Novel Binding Mode of Hydroxamate Inhibitors to Human Carbonic Anhydrase II. *Journal of the American Chemical Society*, **1997**, 119, 850-851	16.4	91
21	Crystal structure of pentalenene synthase: mechanistic insights on terpenoid cyclization reactions in biology. *Science*, **1997**, 277, 1820-4	33.3	375
20	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	16.4	103
19	Altering the binuclear manganese cluster of arginase diminishes thermostability and catalytic function. *Biochemistry*, **1997**, 36, 10558-65	3.2	72
18	Histidine --> carboxamide ligand substitutions in the zinc binding site of carbonic anhydrase II alter metal coordination geometry but retain catalytic activity. *Biochemistry*, **1997**, 36, 15780-91	3.2	87
17	X-ray crystallographic studies of alanine-65 variants of carbonic anhydrase II reveal the structural basis of compromised proton transfer in catalysis. *Biochemistry*, **1996**, 35, 16429-34	3.2	42
16	Carbonic Anhydrase: Evolution of the Zinc Binding Site by Nature and by Design. *Accounts of Chemical Research*, **1996**, 29, 331-339	24.3	422
15	Is the binding of □amyloid protein to antichymotrypsin in Alzheimer plaques mediated by a □strand insertion?. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 420-424	4.2	
14	Arginine substitutions in the hinge region of antichymotrypsin affect serpin beta-sheet rearrangement. *Nature Structural and Molecular Biology*, **1996**, 3, 888-93	17.6	33
13	Structure of a unique binuclear manganese cluster in arginase. *Nature*, **1996**, 383, 554-7	50.4	378
12	Crystallization and preliminary X-ray diffraction analysis of recombinant pentalenene synthase. *Protein Science*, **1995**, 4, 2436-8	6.3	9

11	Positions of His-64 and a bound water in human carbonic anhydrase II upon binding three structurally related inhibitors. *Protein Science*, **1994**, 3, 118-25	6.3	54
10	Crystal structure of an uncleaved serpin reveals the conformation of an inhibitory reactive loop. *Nature Structural and Molecular Biology*, **1994**, 1, 251-8	17.6	151
9	Mapping Protein-Peptide Affinity: Binding of Peptidylsulfonamide Inhibitors to Human Carbonic Anhydrase II. *Journal of the American Chemical Society*, **1994**, 116, 5063-5068	16.4	52
8	Structure and energetics of a non-proline cis-peptidyl linkage in a proline-202-->alanine carbonic anhydrase II variant. *Biochemistry*, **1993**, 32, 10944-9	3.2	52
7	Purification and characterization of Klebsiella aerogenes UreE protein: a nickel-binding protein that functions in urease metallocenter assembly. *Protein Science*, **1993**, 2, 1042-52	6.3	145
6	Crystallographic studies of azide binding to human carbonic anhydrase II. *FEBS Journal*, **1993**, 213, 507-15		19
5	Another catalytic triad?. *Nature*, **1990**, 346, 225	50.4	25
4	Hydrogen bond stereochemistry in protein structure and function. *Journal of Molecular Biology*, **1990**, 215, 457-71	6.5	250
3	Carboxypeptidase A. *Accounts of Chemical Research*, **1989**, 22, 62-69	24.3	598
2	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	16.4	68
1	Structure of the complex between an unexpectedly hydrolyzed phosphonamidate inhibitor and carboxypeptidase A. *Journal of the American Chemical Society*, **1986**, 108, 545-6	16.4	46