Cheryl H Arrowsmith

List of Publications by Year
in descending order

371	33,638	3149 92	5519 163
papers	citations	h-index	g-index

413	413	413	40136
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. Cell, 2012, 149, 214-231.	13.5	1,368
2	Epigenetic protein families: a new frontier for drug discovery. Nature Reviews Drug Discovery, 2012, 11, 384-400.	21.5	1,161
3	Consistent blind protein structure generation from NMR chemical shift data. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4685-4690.	3.3	776
4	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
5	The promise and peril of chemical probes. Nature Chemical Biology, 2015, 11, 536-541.	3.9	698
6	Ductal pancreatic cancer modeling and drug screening using human pluripotent stem cellâ€“ and patient-derived tumor organoids. Nature Medicine, 2015, 21, 1364-1371.	15.2	591
7	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	0.6	556
8	Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15835-15840.	3.3	526
9	A Suite of Triple Resonance NMR Experiments for the Backbone Assignment of 15N, 13C, 2H Labeled Proteins with High Sensitivity. Journal of the American Chemical Society, 1994, 116, 11655-11666.	6.6	513
10	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. Nature Chemical Biology, 2011, 7, 566-574.	3.9	465
11	Self-renewal as a therapeutic target in human colorectal cancer. Nature Medicine, 2014, 20, 29-36.	15.2	438
12	Structural basis for recognition of hemi-methylated DNA by the SRA domain of human UHRF1. Nature, 2008, 455, 822-825.	13.7	408
13	An Orally Bioavailable Chemical Probe of the Lysine Methyltransferases EZH2 and EZH1. ACS Chemical Biology, 2013, 8, 1324-1334.	1.6	399
14	Global analysis of protein folding using massively parallel design, synthesis, and testing. Science, 2017, 357, 168-175.	6.0	392
15	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. Nature, 2015, 525, 206-211.	13.7	386
16	ATM-dependent telomere loss in aging human diploid fibroblasts and DNA damage lead to the post-translational activation of p53 protein involving poly(ADP-ribose) polymerase. EMBO Journal, 1997, 16, 6018-6033.	3.5	343
17	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	13.7	321
18	Structure of the p53 Binding Domain of HAUSP/USP7 Bound to Epstein-Barr Nuclear Antigen 1. Molecular Cell, 2005, 18, 25-36.	4.5	317

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19	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. Nature Structural and Molecular Biology, 2012, 19, 1155-1160.	3.6	313
20	Structural proteomics of an archaeon. Nature Structural Biology, 2000, 7, 903-909.	9.7	272
21	Solution structure of the tetrameric minimum transforming domain of p53. Nature Structural and Molecular Biology, 1994, 1, 877-890.	3.6	267
22	Single-stranded DNA mimicry in the p53 transactivation domain interaction with replication protein A. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15412-15417.	3.3	266
23	A Small-Molecule Inhibitor of BCL6 Kills DLBCL Cells In Vitro and In Vivo. Cancer Cell, 2010, 17, 400-411.	7.7	263
24	Latent and active p53 are identical in conformation. Nature Structural Biology, 2001, 8, 756-760.	9.7	261
25	Molecular recognition of p53 and MDM2 by USP7/HAUSP. Nature Structural and Molecular Biology, 2006, 13, 285-291.	3.6	254
26	Recognition and Specificity Determinants of the Human Cbx Chromodomains. Journal of Biological Chemistry, 2011, 286, 521-529.	1.6	254
27	Genome-wide Analysis of Substrate Specificities of the Escherichia coli Haloacid Dehalogenase-like Phosphatase Family. Journal of Biological Chemistry, 2006, 281, 36149-36161.	1.6	249
28	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. Nature Communications, 2012, 3, 1288.	5.8	247
29	Human HDAC7 Harbors a Class IIa Histone Deacetylase-specific Zinc Binding Motif and Cryptic Deacetylase Activity. Journal of Biological Chemistry, 2008, 283, 11355-11363.	1.6	239
30	Placental Transforming Growth Factor-Î² Is a Downstream Mediator of the Growth Arrest and Apoptotic Response of Tumor Cells to DNA Damage and p53 Overexpression. Journal of Biological Chemistry, 2000, 275, 20127-20135.	1.6	232
31	Pharmacological targeting of the Wdr5-MLL interaction in C/EBPÎ± N-terminal leukemia. Nature Chemical Biology, 2015, 11, 571-578.	3.9	227
32	Discovery of an in Vivo Chemical Probe of the Lysine Methyltransferases G9a and GLP. Journal of Medicinal Chemistry, 2013, 56, 8931-8942.	2.9	220
33	Structural Biology of Human H3K9 Methyltransferases. PLoS ONE, 2010, 5, e8570.	1.1	218
34	Genome-scale protein expression and structural biology of Plasmodium falciparum and related Apicomplexan organisms. Molecular and Biochemical Parasitology, 2007, 151, 100-110.	0.5	216
35	A Potent, Selective, and Cell-Active Inhibitor of Human Type I Protein Arginine Methyltransferases. ACS Chemical Biology, 2016, 11, 772-781.	1.6	208
36	Discovery of a 2,4-Diamino-7-aminoalkoxyquinazoline as a Potent and Selective Inhibitor of Histone Lysine Methyltransferase G9a. Journal of Medicinal Chemistry, 2009, 52, 7950-7953.	2.9	206

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37	Cruciform structures are a common DNA feature important for regulating biological processes. BMC Molecular Biology, 2011, 12, 33.	3.0	206
38	WD40 repeat domain proteins: a novel target class?. Nature Reviews Drug Discovery, 2017, 16, 773-786.	21.5	202
39	In situ proteolysis for protein crystallization and structure determination. Nature Methods, 2007, 4, 1019-1021.	9.0	197
40	An NMR approach to structural proteomics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1825-1830.	3.3	195
41	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	7.7	191
42	Structural and Chemical Profiling of the Human Cytosolic Sulfotransferases. PLoS Biology, 2007, 5, e97.	2.6	187
43	The EED proteinâ€“protein interaction inhibitor A-395 inactivates the PRC2 complex. Nature Chemical Biology, 2017, 13, 389-395.	3.9	186
44	Protein arginine methylation: from enigmatic functions to therapeutic targeting. Nature Reviews Drug Discovery, 2021, 20, 509-530.	21.5	186
45	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. Cancer Cell, 2019, 36, 194-209.e9.	7.7	184
46	L3MBTL1 recognition of mono- and dimethylated histones. Nature Structural and Molecular Biology, 2007, 14, 1229-1230.	3.6	180
47	Protein Lysine Methyltransferase G9a Inhibitors: Design, Synthesis, and Structure Activity Relationships of 2,4-Diamino-7-aminoalkoxy-quinazolines.. Journal of Medicinal Chemistry, 2010, 53, 5844-5857.	2.9	177
48	Recognition of Multivalent Histone States Associated with Heterochromatin by UHRF1 Protein. Journal of Biological Chemistry, 2011, 286, 24300-24311.	1.6	177
49	Structural basis for molecular recognition and presentation of histone H3 By WDR5. EMBO Journal, 2006, 25, 4245-4252.	3.5	169
50	Protein Aggregates Are Recruited to Aggresome by Histone Deacetylase 6 via Unanchored Ubiquitin C Termini. Journal of Biological Chemistry, 2012, 287, 2317-2327.	1.6	169
51	BET bromodomain inhibition enhances T cell persistence and function in adoptive immunotherapy models. Journal of Clinical Investigation, 2016, 126, 3479-3494.	3.9	168
52	An HNCA Pulse Scheme for the Backbone Assignment of 15N,13C,2H-Labeled Proteins: Application to a 37-kDa Trp Repressor-DNA Complex. Journal of the American Chemical Society, 1994, 116, 6464-6465.	6.6	167
53	Protein production: feeding the crystallographers and NMR spectroscopists. Nature Structural Biology, 2000, 7, 970-972.	9.7	160
54	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. Nature Chemical Biology, 2013, 9, 184-191.	3.9	160

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55	(R)-PFI-2 is a potent and selective inhibitor of SETD7 methyltransferase activity in cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12853-12858.	3.3	158
56	Characterization of Segments from the Central Region of BRCA1: An Intrinsically Disordered Scaffold for Multiple Proteinâ€“Protein and Proteinâ€“DNA Interactions?. Journal of Molecular Biology, 2005, 345, 275-287.	2.0	157
57	A pulsed field gradient isotope-filtered 3D 13 C HMQC-NOESY experiment for extracting intermolecular NOE contacts in molecular complexes. FEBS Letters, 1994, 350, 87-90.	1.3	156
58	Protein Interaction Domains of the Ubiquitin-specific Protease, USP7/HAUSP. Journal of Biological Chemistry, 2003, 278, 47753-47761.	1.6	155
59	Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for the epigenetic inheritance of DNA methylation. Genes and Development, 2013, 27, 1288-1298.	2.7	155
60	Biological and Structural Basis for Aha1 Regulation of Hsp90 ATPase Activity in Maintaining Proteostasis in the Human Disease Cystic Fibrosis. Molecular Biology of the Cell, 2010, 21, 871-884.	0.9	150
61	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. Cell Stem Cell, 2017, 21, 209-224.e7.	5.2	150
62	Simultaneous prediction of protein folding and docking at high resolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18978-18983.	3.3	145
63	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. Cancer Cell, 2019, 35, 782-797.e8.	7.7	143
64	A p53 Super-tumor Suppressor Reveals a Tumor Suppressive p53-Ptpn14-Yap Axis in Pancreatic Cancer. Cancer Cell, 2017, 32, 460-473.e6.	7.7	142
65	MYC protein interactors in gene transcription and cancer. Nature Reviews Cancer, 2021, 21, 579-591.	12.8	136
66	p73 and p63 Are Homotetramers Capable of Weak Heterotypic Interactions with Each Other but Not with p53. Journal of Biological Chemistry, 1999, 274, 18709-18714.	1.6	133
67	Small-molecule inhibition of MLL activity by disruption of its interaction with WDR5. Biochemical Journal, 2013, 449, 151-159.	1.7	133
68	A cellular chemical probe targeting the chromodomains of Polycomb repressive complex 1. Nature Chemical Biology, 2016, 12, 180-187.	3.9	133
69	Assignment of 15N, 13CÎ±, 13CÎ², and HN Resonances in an 15N,13C,2H Labeled 64 kDa Trp Repressorâ•Operator Complex Using Triple-Resonance NMR Spectroscopy and 2H-Decoupling. Journal of the American Chemical Society, 1996, 118, 6570-6579.	6.6	131
70	Thermodynamic analysis of the structural stability of the tetrameric oligomerization domain of p53 tumor suppressor. Biochemistry, 1995, 34, 5309-5316.	1.2	130
71	Control of the Hippo Pathway by Set7-Dependent Methylation of Yap. Developmental Cell, 2013, 26, 188-194.	3.1	130
72	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. Nature Communications, 2020, 11, 4205.	5.8	130

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73	Optimization of Cellular Activity of G9a Inhibitors 7-Aminoalkoxy-quinazolines. Journal of Medicinal Chemistry, 2011, 54, 6139-6150.	2.9	127
74	LLY-283, a Potent and Selective Inhibitor of Arginine Methyltransferase 5, PRMT5, with Antitumor Activity. ACS Medicinal Chemistry Letters, 2018, 9, 612-617.	1.3	127
75	The Solution Structures of the trp Repressor-Operator DNA Complex. Journal of Molecular Biology, 1994, 238, 592-614.	2.0	124
76	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. Nature Structural Biology, 2002, 9, 27-31.	9.7	124
77	Tandem Protein Interaction Modules Organize the Ubiquitin-Dependent Response to DNA Double-Strand Breaks. Molecular Cell, 2012, 47, 383-395.	4.5	124
78	Eme1 is involved in DNA damage processing and maintenance of genomic stability in mammalian cells. EMBO Journal, 2003, 22, 6137-6147.	3.5	118
79	Structural Insights into Aldosterone Synthase Substrate Specificity and Targeted Inhibition. Molecular Endocrinology, 2013, 27, 315-324.	3.7	116
80	Integrating Structure, Bioinformatics, and Enzymology to Discover Function. Journal of Biological Chemistry, 2003, 278, 26039-26045.	1.6	115
81	Small-Molecule Ligands of Methyl-Lysine Binding Proteins. Journal of Medicinal Chemistry, 2011, 54, 2504-2511.	2.9	115
82	A chemical biology toolbox to study protein methyltransferases and epigenetic signaling. Nature Communications, 2019, 10, 19.	5.8	113
83	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. ELife, 2016, 5, .	2.8	111
84	Structure of Escherichia coli Ribose-5-Phosphate Isomerase. Structure, 2003, 11, 31-42.	1.6	110
85	Sequence-specific proton NMR assignments and secondary structure in solution of Escherichia coli trp repressor. Biochemistry, 1990, 29, 6332-6341.	1.2	109
86	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. Nature Methods, 2015, 12, 725-731.	9.0	109
87	NMR data collection and analysis protocol for high-throughput protein structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10487-10492.	3.3	108
88	Accessibility of Different Histone H3-Binding Domains of UHRF1 Is Allosterically Regulated by Phosphatidylinositol 5-Phosphate. Molecular Cell, 2014, 54, 905-919.	4.5	108
89	Structure of the Catalytic Domain of EZH2 Reveals Conformational Plasticity in Cofactor and Substrate Binding Sites and Explains Oncogenic Mutations. PLoS ONE, 2013, 8, e83737.	1.1	108
90	Characterization of the oligomerization defects of two p53 mutants found in families with Liâ€“Fraumeni and Liâ€“Fraumeni-like syndrome. Oncogene, 1998, 17, 651-656.	2.6	104

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91	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	104
92	LLY-507, a Cell-active, Potent, and Selective Inhibitor of Protein-lysine Methyltransferase SMYD2. Journal of Biological Chemistry, 2015, 290, 13641-13653.	1.6	104
93	Target 2035: probing the human proteome. Drug Discovery Today, 2019, 24, 2111-2115.	3.2	103
94	The Shwachman-Bodian-Diamond Syndrome Protein Family Is Involved in RNA Metabolism. Journal of Biological Chemistry, 2005, 280, 19213-19220.	1.6	100
95	Trimethylation of Histone H3 Lysine 36 by Human Methyltransferase PRDM9 Protein. Journal of Biological Chemistry, 2014, 289, 12177-12188.	1.6	100
96	The SUV4-20 inhibitor A-196 verifies a role for epigenetics in genomic integrity. Nature Chemical Biology, 2017, 13, 317-324.	3.9	98
97	The SMX DNA Repair Tri-nuclease. Molecular Cell, 2017, 65, 848-860.e11.	4.5	98
98	Assay interference and off-target liabilities of reported histone acetyltransferase inhibitors. Nature Communications, 2017, 8, 1527.	5.8	98
99	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. Nucleic Acids Research, 2012, 40, 6353-6366.	6.5	97
100	Structural Proteomics:â€‰ Toward High-Throughput Structural Biology as a Tool in Functional Genomics. Accounts of Chemical Research, 2003, 36, 183-189.	7.6	96
101	A Human Ubiquitin Conjugating Enzyme (E2)-HECT E3 Ligase Structure-function Screen. Molecular and Cellular Proteomics, 2012, 11, 329-341.	2.5	95
102	A Potent, Selective and Cellâ€Active Allosteric Inhibitor of Protein Arginine Methyltransferaseâ€…3 (PRMT3). Angewandte Chemie - International Edition, 2015, 54, 5166-5170.	7.2	95
103	A Radioactivity-Based Assay for Screening Human m6A-RNA Methyltransferase, METTL3-METTL14 Complex, and Demethylase ALKBH5. Journal of Biomolecular Screening, 2016, 21, 290-297.	2.6	95
104	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. Cancer Cell, 2018, 34, 579-595.e8.	7.7	94
105	Molecular basis of Pirh2-mediated p53 ubiquitylation. Nature Structural and Molecular Biology, 2008, 15, 1334-1342.	3.6	93
106	Functional interdependence of BRD4 and DOT1L in MLL leukemia. Nature Structural and Molecular Biology, 2016, 23, 673-681.	3.6	92
107	A Structure-based Model of the c-Myc/Bin1 Protein Interaction Shows Alternative Splicing of Bin1 and c-Myc Phosphorylation are Key Binding Determinants. Journal of Molecular Biology, 2005, 351, 182-194.	2.0	90
108	MLL5 Orchestrates a Cancer Self-Renewal State by Repressing the Histone Variant H3.3 and Globally Reorganizing Chromatin. Cancer Cell, 2015, 28, 715-729.	7.7	90

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109	TP-064, a potent and selective small molecule inhibitor of PRMT4 for multiple myeloma. Oncotarget, 2018, 9, 18480-18493.	0.8	90
110	DNA Binding Specificity Studies of Four ETS Proteins Support an Indirect Read-out Mechanism of Protein-DNA Recognition. Journal of Biological Chemistry, 2000, 275, 28363-28370.	1.6	89
111	NMR and X-ray Crystallography, Complementary Tools in Structural Proteomics of Small Proteins. Journal of the American Chemical Society, 2005, 127, 16512-16517.	6.6	88
112	Screening for Inhibitors of Low-Affinity Epigenetic Peptide-Protein Interactions: An AlphaScreenâ„¢-Based Assay for Antagonists of Methyl-Lysine Binding Proteins. Journal of Biomolecular Screening, 2010, 15, 62-71.	2.6	88
113	WDR5 Supports an N-Myc Transcriptional Complex That Drives a Protumorigenic Gene Expression Signature in Neuroblastoma. Cancer Research, 2015, 75, 5143-5154.	0.4	88
114	Data mining crystallization databases: Knowledge-based approaches to optimize protein crystal screens. Proteins: Structure, Function and Bioinformatics, 2003, 51, 562-568.	1.5	87
115	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	87
116	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. Molecular Cell, 2008, 32, 259-275.	4.5	87
117	SETD7 Controls Intestinal Regeneration and Tumorigenesis by Regulating Wnt/Î²-Catenin and Hippo/YAP Signaling. Developmental Cell, 2016, 37, 47-57.	3.1	87
118	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. Nucleic Acids Research, 2009, 37, 2204-2210.	6.5	85
119	A chemical toolbox for the study of bromodomains and epigenetic signaling. Nature Communications, 2019, 10, 1915.	5.8	85
120	Epigenetic Switchâ€“Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. Cancer Discovery, 2020, 10, 1312-1329.	7.7	84
121	Structure and activity of human TMPRSS2 protease implicated in SARS-CoV-2 activation. Nature Chemical Biology, 2022, 18, 963-971.	3.9	83
122	Interferon-Inducible Protein 16: Insight into the Interaction with Tumor Suppressor p53. Structure, 2011, 19, 418-429.	1.6	82
123	Discovery of a Dual PRMT5â€“PRMT7 Inhibitor. ACS Medicinal Chemistry Letters, 2015, 6, 408-412.	1.3	82
124	Discovery of a Selective, Substrate-Competitive Inhibitor of the Lysine Methyltransferase SETD8. Journal of Medicinal Chemistry, 2014, 57, 6822-6833.	2.9	81
125	Methyltransferase G9A regulates T cell differentiation during murine intestinal inflammation. Journal of Clinical Investigation, 2014, 124, 1945-1955.	3.9	81
126	An Allosteric Inhibitor of Protein Arginine Methyltransferase 3. Structure, 2012, 20, 1425-1435.	1.6	80

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127	Donated chemical probes for open science. ELife, 2018, 7, .	2.8	80
128	Epigenetic siRNA and Chemical Screens Identify SETD8 Inhibition as a Therapeutic Strategy for p53 Activation in High-Risk Neuroblastoma. Cancer Cell, 2017, 31, 50-63.	7.7	79
129	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. Cell, 2020, 181, 1329-1345.e24.	13.5	79
130	Structural proteomics: prospects for high throughput sample preparation. Progress in Biophysics and Molecular Biology, 2000, 73, 339-345.	1.4	78
131	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. Nature Communications, 2021, 12, 979.	5.8	77
132	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
133	Study of a noncovalent trp repressor: DNA operator complex by electrospray ionization timeâ€ofâ€flight mass spectrometry. Protein Science, 1998, 7, 1388-1395.	3.1	74
134	The HD Domain of the Escherichia coli tRNA Nucleotidyltransferase Has 2â€²,3â€²-Cyclic Phosphodiesterase, 2â€²-Nucleotidase, and Phosphatase Activities. Journal of Biological Chemistry, 2004, 279, 36819-36827.	1.6	74
135	NMR structure and binding studies confirm that PA4608 from Pseudomonas aeruginosa is a PilZ domain and a c-di-GMP binding protein. Proteins: Structure, Function and Bioinformatics, 2006, 66, 266-271.	1.5	74
136	NleG Type 3 Effectors from Enterohaemorrhagic Escherichia coli Are U-Box E3 Ubiquitin Ligases. PLoS Pathogens, 2010, 6, e1000960.	2.1	74
137	AKT drives SOX2 overexpression and cancer cell stemness in esophageal cancer by protecting SOX2 from UBR5-mediated degradation. Oncogene, 2019, 38, 5250-5264.	2.6	73
138	RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. Nature Structural and Molecular Biology, 2014, 21, 686-695.	3.6	72
139	Yeast Transcript Elongation Factor (TFIIS), Structure and Function. Journal of Biological Chemistry, 1998, 273, 22595-22605.	1.6	71
140	Structure and functionality of a designed p53 dimer11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 307, 605-617.	2.0	71
141	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. Cancer Research, 2017, 77, 5479-5490.	0.4	71
142	Aspartate Dehydrogenase, a Novel Enzyme Identified from Structural and Functional Studies of TM1643. Journal of Biological Chemistry, 2003, 278, 8804-8808.	1.6	70
143	Structural proteomics: a tool for genome annotation. Current Opinion in Chemical Biology, 2004, 8, 42-48.	2.8	70
144	A SPOT on the chromatin landscape? Histone peptide arrays as a tool for epigenetic research. Trends in Biochemical Sciences, 2008, 33, 305-313.	3.7	70

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145	Cbx2 Targets PRC1 to Constitutive Heterochromatin in Mouse Zygotes in a Parent-of-Origin-Dependent Manner. Molecular Cell, 2015, 58, 157-171.	4.5	70
146	Discovery and Characterization of a Highly Potent and Selective Aminopyrazoline-Based in Vivo Probe (BAY-598) for the Protein Lysine Methyltransferase SMYD2. Journal of Medicinal Chemistry, 2016, 59, 4578-4600.	2.9	69
147	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. Genes and Development, 2016, 30, 772-785.	2.7	68
148	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	0.4	67
149	Structure-Based Optimization of a Small Molecule Antagonist of the Interaction Between WD Repeat-Containing Protein 5 (WDR5) and Mixed-Lineage Leukemia 1 (MLL1). Journal of Medicinal Chemistry, 2016, 59, 2478-2496.	2.9	67
150	Small-Molecule Ligands of Methyl-Lysine Binding Proteins: Optimization of Selectivity for L3MBTL3. Journal of Medicinal Chemistry, 2013, 56, 7358-7371.	2.9	66
151	Role of Pirh2 in Mediating the Regulation of p53 and c-Myc. PLoS Genetics, 2011, 7, e1002360.	1.5	65
152	Nahuoic Acid A Produced by a Streptomyces sp. Isolated From a Marine Sediment Is a Selective SAM-Competitive Inhibitor of the Histone Methyltransferase SETD8. Organic Letters, 2013, 15, 414-417.	2.4	65
153	Anti-Ro52 Autoantibodies from Patients with SjÃ¶gren's Syndrome Inhibit the Ro52 E3 Ligase Activity by Blocking the E3/E2 Interface. Journal of Biological Chemistry, 2011, 286, 36478-36491.	1.6	64
154	Exploiting an Allosteric Binding Site of PRMT3 Yields Potent and Selective Inhibitors. Journal of Medicinal Chemistry, 2013, 56, 2110-2124.	2.9	64
155	A global assessment of cancer genomic alterations in epigenetic mechanisms. Epigenetics and Chromatin, 2014, 7, 29.	1.8	64
156	Discovery of a Potent, Selective, and Cell-Active Dual Inhibitor of Protein Arginine Methyltransferase 4 and Protein Arginine Methyltransferase 6. Journal of Medicinal Chemistry, 2016, 59, 9124-9139.	2.9	64
157	Crystal Structure of Thermotoga maritima 0065, a Member of the IclR Transcriptional Factor Family. Journal of Biological Chemistry, 2002, 277, 19183-19190.	1.6	63
158	Biophysical characterization of recombinant proteins: A key to higher structural genomics success. Journal of Structural Biology, 2010, 172, 107-119.	1.3	63
159	Preferential binding of IFI16 protein to cruciform structure and superhelical DNA. Biochemical and Biophysical Research Communications, 2012, 422, 716-720.	1.0	62
160	Bromo-deaza-SAH: A potent and selective DOT1L inhibitor. Bioorganic and Medicinal Chemistry, 2013, 21, 1787-1794.	1.4	62
161	Tackling reproducibility in academic preclinical drug discovery. Nature Reviews Drug Discovery, 2015, 14, 733-734.	21.5	62
162	The solution structures of Escherichia coli trp repressor and trp aporepressor at an intermediate resolution. FEBS Journal, 1991, 202, 53-66.	0.2	60

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163	Fragment-based discovery of a chemical probe for the PWWP1 domain of NSD3. Nature Chemical Biology, 2019, 15, 822-829.	3.9	59
164	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. Nature Communications, 2020, 11, 2396.	5.8	59
165	Histone Recognition by Human Malignant Brain Tumor Domains. Journal of Molecular Biology, 2012, 423, 702-718.	2.0	58
166	Discovery of A-893, A New Cell-Active Benzoxazinone Inhibitor of Lysine Methyltransferase SMYD2. ACS Medicinal Chemistry Letters, 2015, 6, 695-700.	1.3	58
167	Crystal Structure of dTDP-4-keto-6-deoxy-d-hexulose 3,5-Epimerase fromMethanobacterium thermoautotrophicum Complexed with dTDP. Journal of Biological Chemistry, 2000, 275, 24608-24612.	1.6	57
168	Identification of a Fragment-like Small Molecule Ligand for the Methyl-lysine Binding Protein, 53BP1. ACS Chemical Biology, 2015, 10, 1072-1081.	1.6	56
169	Structure of a Conserved Domain Common to the Transcription Factors TFIIS, Elongin A, and CRSP70. Journal of Biological Chemistry, 2000, 275, 31266-31268.	1.6	55
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