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	A chemical probe targeting the PWWP domain alters NSD2 nucleolar localization. Nature Chemical Biology, 2022, 18, 56-63.	3.9	41
2	Target 2035 â€“ update on the quest for a probe for every protein. RSC Medicinal Chemistry, 2022, 13, 13-21.	1.7	39
3	Prediction and Validation of a Proteinâ€™s Free Energy Surface Using Hydrogen Exchange and (Importantly) Its Denaturant Dependence. Journal of Chemical Theory and Computation, 2022, 18, 550-561.	2.3	8
4	The MYC oncoprotein directly interacts with its chromatin cofactor PNUTS to recruit PP1 phosphatase. Nucleic Acids Research, 2022, 50, 3505-3522.	6.5	11
5	Validating Small Molecule Chemical Probes for Biological Discovery. Annual Review of Biochemistry, 2022, 91, 61-87.	5.0	13
6	PRMT5 regulates ATF4 transcript splicing and oxidative stress response. Redox Biology, 2022, 51, 102282.	3.9	11
7	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer. Nature Chemical Biology, 2022, 18, 821-830.	3.9	43
8	Structure and activity of human TMPRSS2 protease implicated in SARS-CoV-2 activation. Nature Chemical Biology, 2022, 18, 963-971.	3.9	83
9	Identification of lysine isobutyrylation as a new histone modification mark. Nucleic Acids Research, 2021, 49, 177-189.	6.5	32
10	Identifying and Validating MYC:Protein Interactors in Pursuit of Novel Anti-MYC Therapies. Methods in Molecular Biology, 2021, 2318, 45-67.	0.4	0
11	A First-in-Class, Highly Selective and Cell-Active Allosteric Inhibitor of Protein Arginine Methyltransferase 6. Journal of Medicinal Chemistry, 2021, 64, 3697-3706.	2.9	15
12	Discovery of Small-Molecule Antagonists of the PWWP Domain of NSD2. Journal of Medicinal Chemistry, 2021, 64, 1584-1592.	2.9	29
13	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. Journal of Clinical Investigation, 2021, 131, .	3.9	38
14	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. Nature Communications, 2021, 12, 979.	5.8	77
15	Rational Design and Synthesis of Selective PRMT4 Inhibitors: A New Chemotype for Development of Cancer Therapeutics**. ChemMedChem, 2021, 16, 1116-1125.	1.6	4
16	Protein arginine methylation: from enigmatic functions to therapeutic targeting. Nature Reviews Drug Discovery, 2021, 20, 509-530.	21.5	186
17	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degraders. Journal of Medicinal Chemistry, 2021, 64, 10682-10710.	2.9	38
18	Discovery of the SMYD3 Inhibitor BAY-6035 Using Thermal Shift Assay (TSA)-Based High-Throughput Screening. SLAS Discovery, 2021, 26, 947-960.	1.4	14

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19	MYC protein interactors in gene transcription and cancer. Nature Reviews Cancer, 2021, 21, 579-591.	12.8	136
20	Structureâ€“Activity Relationship of USP5 Inhibitors. Journal of Medicinal Chemistry, 2021, 64, 15017-15036.	2.9	7
21	Chemical Genetics Screen Identifies COPB2 Tool Compounds That Alters ER Stress Response and Induces RTK Dysregulation in Lung Cancer Cells. Journal of Molecular Biology, 2021, 433, 167294.	2.0	4
22	Huntingtin structure is orchestrated by HAP40 and shows a polyglutamine expansion-specific interaction with exon 1. Communications Biology, 2021, 4, 1374.	2.0	22
23	HMCES Functions in the Alternative End-Joining Pathway of the DNA DSB Repair during Class Switch Recombination in B Cells. Molecular Cell, 2020, 77, 384-394.e4.	4.5	34
24	Epigenetics 2.0: Special Issue on Epigeneticsâ€”Call for Papers. Journal of Medicinal Chemistry, 2020, 63, 12129-12130.	2.9	1
25	LSD1 represses a neonatal/reparative gene program in adult intestinal epithelium. Science Advances, 2020, 6, .	4.7	18
26	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. Nature Communications, 2020, 11, 4205.	5.8	130
27	Discovery of a First-in-Class Protein Arginine Methyltransferase 6 (PRMT6) Covalent Inhibitor. Journal of Medicinal Chemistry, 2020, 63, 5477-5487.	2.9	24
28	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. Nature Communications, 2020, 11, 2396.	5.8	59
29	Epigenetic Switchâ€“Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. Cancer Discovery, 2020, 10, 1312-1329.	7.7	84
30	Alternative splicing and allosteric regulation modulate the chromatin binding of UHRF1. Nucleic Acids Research, 2020, 48, 7728-7747.	6.5	16
31	A Semi-automated Organoid Screening Method Demonstrates Epigenetic Control of Intestinal Epithelial Differentiation. Frontiers in Cell and Developmental Biology, 2020, 8, 618552.	1.8	13
32	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. Cell, 2020, 181, 1329-1345.e24.	13.5	79
33	Telomere dysfunction cooperates with epigenetic alterations to impair murine embryonic stem cell fate commitment. ELife, 2020, 9, .	2.8	12
34	The MLL1 trimeric catalytic complex is a dynamic conformational ensemble stabilized by multiple weak interactions. Nucleic Acids Research, 2019, 47, 9433-9447.	6.5	8
35	Selective, Small-Molecule Co-Factor Binding Site Inhibition of a Su(var)3â€“9, Enhancer of Zeste, Trithorax Domain Containing Lysine Methyltransferase. Journal of Medicinal Chemistry, 2019, 62, 7669-7683.	2.9	14
36	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. Cancer Cell, 2019, 36, 194-209.e9.	7.7	184

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37	Identification and characterization of the first fragment hits for SETDB1 Tudor domain. Bioorganic and Medicinal Chemistry, 2019, 27, 3866-3878.	1.4	9
38	Fragment-based discovery of a chemical probe for the PWWP1 domain of NSD3. Nature Chemical Biology, 2019, 15, 822-829.	3.9	59
39	Discovery of a Potent and Selective Fragment-like Inhibitor of Methyllysine Reader Protein Spindlin 1 (SPIN1). Journal of Medicinal Chemistry, 2019, 62, 8996-9007.	2.9	20
40	Target 2035: probing the human proteome. Drug Discovery Today, 2019, 24, 2111-2115.	3.2	103
41	Discovery of Small Molecule Antagonists of the USP5 Zinc Finger Ubiquitin-Binding Domain. Journal of Medicinal Chemistry, 2019, 62, 10144-10155.	2.9	10
42	Targeting non-bromodomain chromatin readers. Nature Structural and Molecular Biology, 2019, 26, 863-869.	3.6	49
43	A Chemical Probe for Tudor Domain Protein Spindlin1 to Investigate Chromatin Function. Journal of Medicinal Chemistry, 2019, 62, 9008-9025.	2.9	30
44	Structural basis of HMCES interactions with abasic DNA and multivalent substrate recognition. Nature Structural and Molecular Biology, 2019, 26, 607-612.	3.6	48
45	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. Cancer Cell, 2019, 35, 782-797.e8.	7.7	143
46	A chemical toolbox for the study of bromodomains and epigenetic signaling. Nature Communications, 2019, 10, 1915.	5.8	85
47	Discovery of selective activators of PRC2 mutant EED-I363M. Scientific Reports, 2019, 9, 6524.	1.6	12
48	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
49	Design and characterization of mutant and wildtype huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems. Journal of Biological Chemistry, 2019, 294, 6986-7001.	1.6	23
50	Targeting bivalency de-represses Indian Hedgehog and inhibits self-renewal of colorectal cancer-initiating cells. Nature Communications, 2019, 10, 1436.	5.8	33
51	Discovery of a chemical probe for PRDM9. Nature Communications, 2019, 10, 5759.	5.8	24
52	Direct interaction between the PRDM3 and PRDM16 tumor suppressors and the NuRD chromatin remodeling complex. Nucleic Acids Research, 2019, 47, 1225-1238.	6.5	32
53	A chemical biology toolbox to study protein methyltransferases and epigenetic signaling. Nature Communications, 2019, 10, 19.	5.8	113
54	Characterization of inv(3) cell line OCI-AML-20 with stroma-dependent CD34 expression. Experimental Hematology, 2019, 69, 27-36.	0.2	5

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55	Arginine methylation of FOXP3 is crucial for the suppressive function of regulatory T cells. Journal of Autoimmunity, 2019, 97, 10-21.	3.0	34
56	A chemical probe of CARM1 alters epigenetic plasticity against breast cancer cell invasion. ELife, 2019, 8, .	2.8	32
57	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
58	Discovery of Ubiquitin Deamidases in the Pathogenic Arsenal of Legionella pneumophila. Cell Reports, 2018, 23, 568-583.	2.9	43
59	Revealing the protein propionylation activity of the histone acetyltransferase MOF (males absent on) Tj ETQq1 1 0.784314 rgBT /Over	1.6	50
60	Discovery of Small-Molecule Antagonists of the H3K9me3 Binding to UHRF1 Tandem Tudor Domain. SLAS Discovery, 2018, 23, 930-940.	1.4	29
61	Discovery of Potent and Selective Allosteric Inhibitors of Protein Arginine Methyltransferase 3 (PRMT3). Journal of Medicinal Chemistry, 2018, 61, 1204-1217.	2.9	27
62	Guiding COMPASS: Dpy-30 Positions SET1/MLL Epigenetic Signaling. Structure, 2018, 26, 1567-1570.	1.6	0
63	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. Cancer Cell, 2018, 34, 579-595.e8.	7.7	94
64	Functional diversification of the NleG effector family in enterohemorrhagic Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10004-10009.	3.3	19
65	DOT1L inhibition attenuates graft-versus-host disease by allogeneic T cells in adoptive immunotherapy models. Nature Communications, 2018, 9, 1915.	5.8	21
66	Donated chemical probes for open science. ELife, 2018, 7, .	2.8	80
67	Identification of Rpl29 as a major substrate of the lysine methyltransferase Set7/9. Journal of Biological Chemistry, 2018, 293, 12770-12780.	1.6	24
68	Identification and Structureâ€“Activity Relationship of HDAC6 Zinc-Finger Ubiquitin Binding Domain Inhibitors. Journal of Medicinal Chemistry, 2018, 61, 4517-4527.	2.9	40
69	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. Journal of Cell Biology, 2018, 217, 2951-2974.	2.3	35
70	TP-064, a potent and selective small molecule inhibitor of PRMT4 for multiple myeloma. Oncotarget, 2018, 9, 18480-18493.	0.8	90
71	The SUV4-20 inhibitor A-196 verifies a role for epigenetics in genomic integrity. Nature Chemical Biology, 2017, 13, 317-324.	3.9	98
72	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

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73	The EED proteinâ€“protein interaction inhibitor A-395 inactivates the PRC2 complex. Nature Chemical Biology, 2017, 13, 389-395.	3.9	186
74	Discovery of Potent and Selective Inhibitors for G9a-Like Protein (GLP) Lysine Methyltransferase. Journal of Medicinal Chemistry, 2017, 60, 1876-1891.	2.9	54
75	Targeting human SET1/MLL family of proteins. Protein Science, 2017, 26, 662-676.	3.1	49
76	Discovery of Peptidomimetic Ligands of EED as Allosteric Inhibitors of PRC2. ACS Combinatorial Science, 2017, 19, 161-172.	3.8	43
77	The SMX DNA Repair Tri-nuclease. Molecular Cell, 2017, 65, 848-860.e11.	4.5	98
78	Early-life antibiotic treatment enhances the pathogenicity of CD4+ T cells during intestinal inflammation. Journal of Leukocyte Biology, 2017, 101, 893-900.	1.5	31
79	Conformational dynamics of the TTDâ€“PHD histone reader module of the UHRF1 epigenetic regulator reveals multiple histone-binding states, allosteric regulation, and druggability. Journal of Biological Chemistry, 2017, 292, 20947-20959.	1.6	36
80	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
81	Small Molecule Antagonists of the Interaction between the Histone Deacetylase 6 Zinc-Finger Domain and Ubiquitin. Journal of Medicinal Chemistry, 2017, 60, 9090-9096.	2.9	32
82	WD40 repeat domain proteins: a novel target class?. Nature Reviews Drug Discovery, 2017, 16, 773-786.	21.5	202
83	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	13.7	321
84	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. Cancer Research, 2017, 77, 5479-5490.	0.4	71
85	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
86	Structural and Functional Survey of Environmental Aminoglycoside Acetyltransferases Reveals Functionality of Resistance Enzymes. ACS Infectious Diseases, 2017, 3, 653-665.	1.8	9
87	Global analysis of protein folding using massively parallel design, synthesis, and testing. Science, 2017, 357, 168-175.	6.0	392
88	Assay interference and off-target liabilities of reported histone acetyltransferase inhibitors. Nature Communications, 2017, 8, 1527.	5.8	98
89	Structure-activity relationship studies of G9a-like protein (GLP) inhibitors. Bioorganic and Medicinal Chemistry, 2017, 25, 4414-4423.	1.4	24
90	A Suite of Biochemical Assays for Screening RNA Methyltransferase BCDIN3D. SLAS Discovery, 2017, 22, 32-39.	1.4	14

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91	Diverse modes of galacto-specific carbohydrate recognition by a family 31 glycoside hydrolase from Clostridium perfringens. PLoS ONE, 2017, 12, e0171606.	1.1	11
92	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. ELife, 2017, 6, .	2.8	44
93	Discovery of a Potent and Selective Coactivator Associated Arginine Methyltransferase 1 (CARM1) Inhibitor by Virtual Screening. Journal of Medicinal Chemistry, 2016, 59, 6838-6847.	2.9	43
94	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	7.7	191
95	A community resource of experimental data for <scp>NMR</scp> / <scp>X</scp>â€ray crystal structure pairs. Protein Science, 2016, 25, 30-45.	3.1	24
96	SETD7 Controls Intestinal Regeneration and Tumorigenesis by Regulating Wnt/Î²-Catenin and Hippo/YAP Signaling. Developmental Cell, 2016, 37, 47-57.	3.1	87
97	PR Domain-containing Protein 7 (PRDM7) Is a Histone 3 Lysine 4 Trimethyltransferase. Journal of Biological Chemistry, 2016, 291, 13509-13519.	1.6	25
98	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
99	An Integrative Proteomic Approach Identifies Novel Cellular SMYD2 Substrates. Journal of Proteome Research, 2016, 15, 2052-2059.	1.8	21
100	Structureâ€“Activity Relationship Studies for Enhancer of Zeste Homologue 2 (EZH2) and Enhancer of Zeste Homologue 1 (EZH1) Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 7617-7633.	2.9	46
101	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
102	Solution NMR structure of the HLTF HIRAN domain: a conserved module in SWI2/SNF2 DNA damage tolerance proteins. Journal of Biomolecular NMR, 2016, 66, 209-219.	1.6	13
103	Structure-Based Design of a Covalent Inhibitor of the SET Domain-Containing Protein 8 (SETD8) Lysine Methyltransferase. Journal of Medicinal Chemistry, 2016, 59, 9881-9889.	2.9	35
104	Methyltransferase inhibitors for modulation of the epigenome and beyond. Current Opinion in Chemical Biology, 2016, 33, 81-87.	2.8	24
105	Functional interdependence of BRD4 and DOT1L in MLL leukemia. Nature Structural and Molecular Biology, 2016, 23, 673-681.	3.6	92
106	Discovery of a Potent Class I Protein Arginine Methyltransferase Fragment Inhibitor. Journal of Medicinal Chemistry, 2016, 59, 1176-1183.	2.9	32
107	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. Genes and Development, 2016, 30, 772-785.	2.7	68
108	A cellular chemical probe targeting the chromodomains of Polycomb repressive complex 1. Nature Chemical Biology, 2016, 12, 180-187.	3.9	133

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109	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
110	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
111	A Potent, Selective, and Cell-Active Inhibitor of Human Type I Protein Arginine Methyltransferases. ACS Chemical Biology, 2016, 11, 772-781.	1.6	208
112	Design of a fluorescent ligand targeting the S-adenosylmethionine binding site of the histone methyltransferase MLL1. Organic and Biomolecular Chemistry, 2016, 14, 631-638.	1.5	12
113	BET bromodomain inhibition enhances T cell persistence and function in adoptive immunotherapy models. Journal of Clinical Investigation, 2016, 126, 3479-3494.	3.9	168
114	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. ELife, 2016, 5, .	2.8	111
115	Optimizing Production of Antigens and Fabs in the Context of Generating Recombinant Antibodies to Human Proteins. PLoS ONE, 2015, 10, e0139695.	1.1	26
116	Kinetic characterization of human histone H3 lysine 36 methyltransferases, ASH1L and SETD2. Biochimica Et Biophysica Acta - General Subjects, 2015, 1850, 1842-1848.	1.1	41
117	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
118	KCMF1 (potassium channel modulatory factor 1) Links RAD6 to UBR4 (ubiquitin N-recognin) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 T Proteomics, 2015, 14, 674-685.	2.5	31
119	Preclinical target validation using patient-derived cells. Nature Reviews Drug Discovery, 2015, 14, 149-150.	21.5	46
120	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
121	Pharmacological targeting of the Wdr5-MLL interaction in C/EBPÎ± N-terminal leukemia. Nature Chemical Biology, 2015, 11, 571-578.	3.9	227
122	The promise and peril of chemical probes. Nature Chemical Biology, 2015, 11, 536-541.	3.9	698
123	Probing the epigenome. Nature Chemical Biology, 2015, 11, 542-545.	3.9	33
124	Solution-state NMR structure of the putative morphogene protein BolA (PFE0790c) fromPlasmodium falciparum. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 514-521.	0.4	4
125	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. Nature Methods, 2015, 12, 725-731.	9.0	109
126	Discovery of a Dual PRMT5â€“PRMT7 Inhibitor. ACS Medicinal Chemistry Letters, 2015, 6, 408-412.	1.3	82

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127	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
128	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
129	Tackling reproducibility in academic preclinical drug discovery. Nature Reviews Drug Discovery, 2015, 14, 733-734.	21.5	62
130	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. Journal of Biomolecular NMR, 2015, 62, 413-424.	1.6	27
131	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
132	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
133	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
134	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICP0 of Herpes Simplex Virus-1. Journal of Biological Chemistry, 2015, 290, 22907-22918.	1.6	34
135	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. Nature, 2015, 525, 206-211.	13.7	386
136	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
137	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	1.1	13
138	Trimethylation of Histone H3 Lysine 36 by Human Methyltransferase PRDM9 Protein. Journal of Biological Chemistry, 2014, 289, 12177-12188.	1.6	100
139	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
140	(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
141	Structural Characterization of a Flexible Two-Domain Protein in Solution Using Small Angle X-Ray Scattering and NMR Data. Structure, 2014, 22, 1862-1874.	1.6	9
142	A global assessment of cancer genomic alterations in epigenetic mechanisms. Epigenetics and Chromatin, 2014, 7, 29.	1.8	64
143	Basic Tilted Helix Bundle â€“ A new protein fold in human FKBP25/FKBP3 and HectD1. Biochemical and Biophysical Research Communications, 2014, 447, 26-31.	1.0	14
144	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

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145	The study of epigenetic mechanisms based on the analysis of histone modification patterns by flow cytoametry. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 78-87.	1.1	24
146	Self-renewal as a therapeutic target in human colorectal cancer. Nature Medicine, 2014, 20, 29-36.	15.2	438
147	A Basic Post-SET Extension of NSDs Is Essential for Nucleosome Binding In Vitro. Journal of Biomolecular Screening, 2014, 19, 928-935.	2.6	34
148	Discovery of a Selective, Substrate-Competitive Inhibitor of the Lysine Methyltransferase SETD8. Journal of Medicinal Chemistry, 2014, 57, 6822-6833.	2.9	81
149	An Unusual Mode of Galactose Recognition by a Family 32 Carbohydrate-Binding Module. Journal of Molecular Biology, 2014, 426, 869-880.	2.0	18
150	Screening Proteins for NMR Suitability. Methods in Molecular Biology, 2014, 1140, 169-178.	0.4	4
151	Structure and function of dioxygenases in histone demethylation and DNA/RNA demethylation. IUCrJ, 2014, 1, 540-549.	1.0	26
152	Methyltransferase G9A regulates T cell differentiation during murine intestinal inflammation. Journal of Clinical Investigation, 2014, 124, 1945-1955.	3.9	81
153	Control of the Hippo Pathway by Set7-Dependent Methylation of Yap. Developmental Cell, 2013, 26, 188-194.	3.1	130
154	The structureâ€“activity relationships of L3MBTL3 inhibitors: flexibility of the dimer interface. MedChemComm, 2013, 4, 1501.	3.5	24
155	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
156	Small-Molecule Ligands of Methyl-Lysine Binding Proteins: Optimization of Selectivity for L3MBTL3. Journal of Medicinal Chemistry, 2013, 56, 7358-7371.	2.9	66
157	Structural Insights into Aldosterone Synthase Substrate Specificity and Targeted Inhibition. Molecular Endocrinology, 2013, 27, 315-324.	3.7	116
158	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
159	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. Nature Chemical Biology, 2013, 9, 184-191.	3.9	160
160	Exploiting an Allosteric Binding Site of PRMT3 Yields Potent and Selective Inhibitors. Journal of Medicinal Chemistry, 2013, 56, 2110-2124.	2.9	64
161	An Orally Bioavailable Chemical Probe of the Lysine Methyltransferases EZH2 and EZH1. ACS Chemical Biology, 2013, 8, 1324-1334.	1.6	399
162	Bromo-deaza-SAH: A potent and selective DOT1L inhibitor. Bioorganic and Medicinal Chemistry, 2013, 21, 1787-1794.	1.4	62

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163	Synthesis, Optimization, and Evaluation of Novel Small Molecules as Antagonists of WDR5-MLL Interaction. ACS Medicinal Chemistry Letters, 2013, 4, 353-357.	1.3	51
164	Small-molecule inhibition of MLL activity by disruption of its interaction with WDR5. Biochemical Journal, 2013, 449, 151-159.	1.7	133
165	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
166	Ubiquitin-specific Protease 7 Is a Regulator of Ubiquitin-conjugating Enzyme UbE2E1. Journal of Biological Chemistry, 2013, 288, 16975-16985.	1.6	35
167	The ZIP5 Ectodomain Co-Localizes with PrP and May Acquire a PrP-Like Fold That Assembles into a Dimer. PLoS ONE, 2013, 8, e72446.	1.1	23
168	Solution NMR Structure and Histone Binding of the PHD Domain of Human MLL5. PLoS ONE, 2013, 8, e77020.	1.1	26
169	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
170	Solution NMR Structure of Hypothetical Protein CV_2116 Encoded by a Viral Prophage Element in Chromobacterium violaceum. International Journal of Molecular Sciences, 2012, 13, 7354-7364.	1.8	1
171	Structural and Biochemical Characterization of Phage Î» FI Protein (gpFI) Reveals a Novel Mechanism of DNA Packaging Chaperone Activity. Journal of Biological Chemistry, 2012, 287, 32085-32095.	1.6	8
172	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
173	Fluorescence-Based Methods for Screening Writers and Readers of Histone Methyl Marks. Journal of Biomolecular Screening, 2012, 17, 71-84.	2.6	45
174	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. Nucleic Acids Research, 2012, 40, 6353-6366.	6.5	97
175	A Human Ubiquitin Conjugating Enzyme (E2)-HECT E3 Ligase Structure-function Screen. Molecular and Cellular Proteomics, 2012, 11, 329-341.	2.5	95
176	Sequence-Specific Recognition of a PxLPxI/L Motif by an Ankyrin Repeat Tumbler Lock. Science Signaling, 2012, 5, ra39.	1.6	42
177	Structural Analysis of HopPmaL Reveals the Presence of a Second Adaptor Domain Common to the HopAB Family of Pseudomonas syringae Type III Effectors. Biochemistry, 2012, 51, 1-3.	1.2	8
178	An Allosteric Inhibitor of Protein Arginine Methyltransferase 3. Structure, 2012, 20, 1425-1435.	1.6	80
179	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. Nature Structural and Molecular Biology, 2012, 19, 1155-1160.	3.6	313
180	Preferential binding of IFI16 protein to cruciform structure and superhelical DNA. Biochemical and Biophysical Research Communications, 2012, 422, 716-720.	1.0	62

#	Article	IF	Citations
181	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. Cell, 2012, 149, 214-231.	13.5	1,368
182	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. Nature Communications, 2012, 3, 1288.	5.8	247
183	Histone Recognition by Human Malignant Brain Tumor Domains. Journal of Molecular Biology, 2012, 423, 702-718.	2.0	58
184	Tandem Protein Interaction Modules Organize the Ubiquitin-Dependent Response to DNA Double-Strand Breaks. Molecular Cell, 2012, 47, 383-395.	4.5	124
185	Epigenetic protein families: a new frontier for drug discovery. Nature Reviews Drug Discovery, 2012, 11, 384-400.	21.5	1,161
186	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
187	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. Nature Chemical Biology, 2011, 7, 566-574.	3.9	465
188	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
189	Interferon-Inducible Protein 16: Insight into the Interaction with Tumor Suppressor p53. Structure, 2011, 19, 418-429.	1.6	82
190	Small-Molecule Ligands of Methyl-Lysine Binding Proteins. Journal of Medicinal Chemistry, 2011, 54, 2504-2511.	2.9	115
191	Optimization of Cellular Activity of G9a Inhibitors 7-Aminoalkoxy-quinazolines. Journal of Medicinal Chemistry, 2011, 54, 6139-6150.	2.9	127
192	A novel strategy for NMR resonance assignment and protein structure determination. Journal of Biomolecular NMR, 2011, 49, 27-38.	1.6	46
193	Zn-binding AZUL domain of human ubiquitin protein ligase Ube3A. Journal of Biomolecular NMR, 2011, 51, 185-190.	1.6	23
194	Cruciform structures are a common DNA feature important for regulating biological processes. BMC Molecular Biology, 2011, 12, 33.	3.0	206
195	Solution structure of MTH1821, a putative structure homologue to RNA polymerase Î± subunit from Methanobacterium thermoautotrophicum. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1347-1351.	1.5	2
196	Crystal Structure of Fushi Tarazu Factor 1 Ligand Binding Domain/Fushi Tarazu Peptide Complex Identifies New Class of Nuclear Receptors. Journal of Biological Chemistry, 2011, 286, 31225-31231.	1.6	16
197	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
198	Structural and Functional Comparison of the RING Domains of Two p53 E3 Ligases, Mdm2 and Pirh2. Journal of Biological Chemistry, 2011, 286, 4796-4808.	1.6	32

#	Article	IF	Citations
199	Recognition and Specificity Determinants of the Human Cbx Chromodomains. Journal of Biological Chemistry, 2011, 286, 521-529.	1.6	254
200	Recognition of Multivalent Histone States Associated with Heterochromatin by UHRF1 Protein. Journal of Biological Chemistry, 2011, 286, 24300-24311.	1.6	177
201	Role of Pirh2 in Mediating the Regulation of p53 and c-Myc. PLoS Genetics, 2011, 7, e1002360.	1.5	65
202	A Small-Molecule Inhibitor of BCL6 Kills DLBCL Cells In Vitro and In Vivo. Cancer Cell, 2010, 17, 400-411.	7.7	263
203	Four p(53)s in a pod. Nature Structural and Molecular Biology, 2010, 17, 390-391.	3.6	2
204	Structural Biology of Human H3K9 Methyltransferases. PLoS ONE, 2010, 5, e8570.	1.1	218
205	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
206	Structural Basis of E2â€“25K/UBB+1 Interaction Leading to Proteasome Inhibition and Neurotoxicity. Journal of Biological Chemistry, 2010, 285, 36070-36080.	1.6	47
207	NleG Type 3 Effectors from Enterohaemorrhagic Escherichia coli Are U-Box E3 Ubiquitin Ligases. PLoS Pathogens, 2010, 6, e1000960.	2.1	74
208	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
209	Biophysical characterization of recombinant proteins: A key to higher structural genomics success. Journal of Structural Biology, 2010, 172, 107-119.	1.3	63
210	Further Insight into Substrate Recognition by USP7: Structural and Biochemical Analysis of the HdmX and Hdm2 Interactions with USP7. Journal of Molecular Biology, 2010, 402, 825-837.	2.0	39
211	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
212	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
213	Unique opportunities for NMR methods in structural genomics. Journal of Structural and Functional Genomics, 2009, 10, 101-106.	1.2	25
214	A novel member of the YchN-like fold: Solution structure of the hypothetical protein Tm0979 from Thermotoga maritima. Protein Science, 2009, 14, 216-223.	3.1	8
215	Ring1B Contains a Ubiquitin-Like Docking Module for Interaction with Cbx Proteins[,]. Biochemistry, 2009, 48, 10542-10548.	1.2	37
216	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

#	Article	IF	Citations
217	The Central Region of BRCA1 Binds Preferentially to Supercoiled DNA. Journal of Biomolecular Structure and Dynamics, 2009, 27, 97-103.	2.0	10
218	Characterization of binding-induced changes in dynamics suggests a model for sequence-nonspecific binding of ssDNA by replication protein A. Protein Science, 2009, 11, 2316-2325.	3.1	17
219	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. Nucleic Acids Research, 2009, 37, 2204-2210.	6.5	85
220	A survey of proteins encoded by non-synonymous single nucleotide polymorphisms reveals a significant fraction with altered stability and activity. Biochemical Journal, 2009, 424, 15-26.	1.7	43
221	Sequence specific resonance assignment via Multicanonical Monte Carlo search using an ABACUS approach. Journal of Biomolecular NMR, 2008, 41, 29-41.	1.6	39
222	Structural genomics and drug discovery: all in the family. Current Opinion in Chemical Biology, 2008, 12, 32-39.	2.8	38
223	The solution structure of ribosomal protein S17E from Methanobacterium thermoautotrophicum: A structural homolog of the FF domain. Protein Science, 2008, 17, 583-588.	3.1	3
224	Solution structure of ribosomal protein L40E, a unique C4 zinc finger protein encoded by archaeon Sulfolobus solfataricus. Protein Science, 2008, 17, 589-596.	3.1	8
225	Structural basis for recognition of hemi-methylated DNA by the SRA domain of human UHRF1. Nature, 2008, 455, 822-825.	13.7	408
226	Molecular basis of Pirh2-mediated p53 ubiquitylation. Nature Structural and Molecular Biology, 2008, 15, 1334-1342.	3.6	93
227	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
228	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
229	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
230	Biochemical and Structural Characterization of a Novel Family of Cystathionine Î²-Synthase Domain Proteins Fused to a Zn Ribbon-Like Domain. Journal of Molecular Biology, 2008, 375, 301-315.	2.0	44
231	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. Molecular Cell, 2008, 32, 259-275.	4.5	87
232	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
233	High Throughput Screening of Purified Proteins for Enzymatic Activity. Methods in Molecular Biology, 2008, 426, 331-341.	0.4	17
234	Analysis of binding site similarity, small-molecule similarity and experimental binding profiles in the human cytosolic sulfotransferase family. Bioinformatics, 2007, 23, e104-e109.	1.8	33

#	Article	IF	Citations
235	Structural and Chemical Profiling of the Human Cytosolic Sulfotransferases. PLoS Biology, 2007, 5, e97.	2.6	187
236	CUL7 Is a Novel Antiapoptotic Oncogene. Cancer Research, 2007, 67, 9616-9622.	0.4	50
237	The Conserved CPH Domains of Cul7 and PARC Are Protein-Protein Interaction Modules That Bind the Tetramerization Domain of p53. Journal of Biological Chemistry, 2007, 282, 11300-11307.	1.6	45
238	NMR structure of hypothetical protein TA0938 from Thermoplasma acidophilum. Proteins: Structure, Function and Bioinformatics, 2007, 67, 1185-1188.	1.5	0
239	In situ proteolysis for protein crystallization and structure determination. Nature Methods, 2007, 4, 1019-1021.	9.0	197
240	L3MBTL1 recognition of mono- and dimethylated histones. Nature Structural and Molecular Biology, 2007, 14, 1229-1230.	3.6	180
241	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
242	The hypothetical protein Atu4866 from Agrobacterium tumefaciens adopts a streptavidin-like fold. Protein Science, 2007, 17, 154-158.	3.1	1
243	Backbone and side chain 1H, 13C, and 15N resonance assignments of AF2241 from Archaeoglobus fulgidus. Journal of Biomolecular NMR, 2007, 38, 183-183.	1.6	1
244	Hypothetical protein AF2241 from Archaeoglobus fulgidus adopts a cyclophilin-like fold. Journal of Biomolecular NMR, 2007, 38, 353-358.	1.6	2
245	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
246	Solution structure of acyl carrier protein from Nitrosomonas europaea. Proteins: Structure, Function and Bioinformatics, 2006, 64, 800-803.	1.5	3
247	Solution structure of TA1092, a ribosomal protein S24e from Thermoplasma acidophilum. Proteins: Structure, Function and Bioinformatics, 2006, 64, 1095-1097.	1.5	7
248	NMR structure of protein PA2021 fromPseudomonas aeruginosa. Proteins: Structure, Function and Bioinformatics, 2006, 65, 767-770.	1.5	1
249	Solution structure of TA0895, a MoaD homologue from Thermoplasma acidophilum. Proteins: Structure, Function and Bioinformatics, 2006, 65, 1055-1057.	1.5	1
250	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
251	Molecular recognition of p53 and MDM2 by USP7/HAUSP. Nature Structural and Molecular Biology, 2006, 13, 285-291.	3.6	254
252	Structural basis for molecular recognition and presentation of histone H3 By WDR5. EMBO Journal, 2006, 25, 4245-4252.	3.5	169

#	Article	IF	Citations
253	Sequence Specific Resonance Assignment of a Hypothetical Protein PA0128 from Pseudomonas Aeruginosa. Journal of Biomolecular NMR, 2006, 36, 27-27.	1.6	3
254	MTH187 from Methanobacterium thermoautotrophicum has three HEAT-like Repeats. Journal of Biomolecular NMR, 2006, 35, 149-154.	1.6	5
255	Resonance Assignments for the Hypothetical Protein TA0938 from Termoplasma Acidophilum. Journal of Biomolecular NMR, 2006, 36, 36-36.	1.6	1
256	The solution structure of the protein ydhA from Escherichia coli. Journal of Biomolecular NMR, 2006, 35, 295-300.	1.6	11
257	Solution NMR in structural genomics. Current Opinion in Structural Biology, 2006, 16, 611-617.	2.6	43
258	p53 Transcriptional Activation Domain: A Molecular Chameleon?. Cell Cycle, 2006, 5, 489-494.	1.3	31
259	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
260	NMR Spectroscopy in Structural Genomics. , 2005, , 49-60.		0
261	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	87
262	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. FEMS Microbiology Reviews, 2005, 29, 263-279.	3.9	104
263	Solution Structure of MTH0776 from Methanobacterium Thermoautotrophicum. Journal of Biomolecular NMR, 2005, 33, 51-56.	1.6	4
264	High-throughput production of prokaryotic membrane proteins. Journal of Structural and Functional Genomics, 2005, 6, 33-50.	1.2	41
265	NMR solution structure of Thermotoga maritima protein TM1509 reveals a Zn-metalloprotease-like tertiary structure. Journal of Structural and Functional Genomics, 2005, 6, 51-62.	1.2	21
266	NMR structure of the conserved novel-fold protein TA0743 from Thermoplasma acidophilum. Proteins: Structure, Function and Bioinformatics, 2005, 62, 819-821.	1.5	2
267	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
268	An Integrated Platform for Automated Analysis of Protein NMR Structures. Methods in Enzymology, 2005, 394, 111-141.	0.4	67
269	The Shwachman-Bodian-Diamond Syndrome Protein Family Is Involved in RNA Metabolism. Journal of Biological Chemistry, 2005, 280, 19213-19220.	1.6	100
270	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

#	Article	IF	Citations
271	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
272	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
273	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
274	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
275	The Structural Basis for Methylmalonic Aciduria. Journal of Biological Chemistry, 2004, 279, 23646-23653.	1.6	43
276	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
277	Solution structure of a novel calcium binding protein, MTH1880, fromMethanobacterium thermoautotrophicum. Protein Science, 2004, 13, 1148-1154.	3.1	10
278	Structure of the archaeal translation initiation factor aIF2Â from Methanobacterium thermoautotrophicum: Implications for translation initiation. Protein Science, 2004, 13, 659-667.	3.1	27
279	Letter to the Editor: Solution structure of hypothetical protein TA1414 from Thermoplasma acidophilum. Journal of Biomolecular NMR, 2004, 28, 81-84.	1.6	1
280	Letter to the Editor:1H,13C and15N Assignments of Single-Stranded DNA Binding Domains from the 70ÂkDa Subunit of Human Replication Protein A. Journal of Biomolecular NMR, 2004, 28, 195-196.	1.6	9
281	Letter to the Editor: Complete 1H, 13C and 15N NMR assignments of MTH0776 from Methanobacterium thermoautotrophicum. Journal of Biomolecular NMR, 2004, 30, 459-460.	1.6	1
282	Structural proteomics: a tool for genome annotation. Current Opinion in Chemical Biology, 2004, 8, 42-48.	2.8	70
283	Structure- and Function-based Characterization of a New Phosphoglycolate Phosphatase from Thermoplasma acidophilum. Journal of Biological Chemistry, 2004, 279, 517-526.	1.6	49
284	Solution structure of the hypothetical protein Mth677 fromMethanobacterium thermoautotrophicum: A novel Î±+Î² fold. Protein Science, 2004, 13, 1458-1465.	3.1	2
285	Solution structure of the yeast ubiquitin-like modifier protein Hub1. Journal of Structural and Functional Genomics, 2003, 4, 25-30.	1.2	27
286	1H(C) and 1H(N) total NOE correlations in a single 3D NMR experiment. 15N and 13C time-sharing in t1 and t2 dimensions for simultaneous data acquisition. Journal of Biomolecular NMR, 2003, 27, 193-203.	1.6	26
287	A novel member of the split Î²Î±Î² fold: Solution structure of the hypothetical protein YML108W fromSaccharomyces cerevisiae. Protein Science, 2003, 12, 1136-1140.	3.1	27
288	Structure of Escherichia coli Ribose-5-Phosphate Isomerase. Structure, 2003, 11, 31-42.	1.6	110

#	Article	IF	Citations
289	Structural Proteomics: Toward High-Throughput Structural Biology as a Tool in Functional Genomics. ChemInform, 2003, 34, no.	0.1	0
290	Data mining crystallization databases: Knowledge-based approaches to optimize protein crystal screens. Proteins: Structure, Function and Bioinformatics, 2003, 51, 562-568.	1.5	87
291	Crystal structures of MTH1187 and its yeast ortholog YBL001c. Proteins: Structure, Function and Bioinformatics, 2003, 52, 478-480.	1.5	8
292	X-ray crystal structure of CutA from Thermotoga maritima at 1.4 Ã... resolution. Proteins: Structure, Function and Bioinformatics, 2003, 54, 162-165.	1.5	14
293	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
294	Solution structure of ribosomal protein S28E fromMethanobacterium thermoautotrophicum. Protein Science, 2003, 12, 2831-2837.	3.1	15
295	Refolding out of guanidine hydrochloride is an effective approach for high-throughput structural studies of small proteins. Protein Science, 2003, 12, 2073-2080.	3.1	39
296	Eme1 is involved in DNA damage processing and maintenance of genomic stability in mammalian cells. EMBO Journal, 2003, 22, 6137-6147.	3.5	118
297	Chemical shift changes provide evidence for overlapping single-stranded DNA- and XPA-binding sites on the 70 kDa subunit of human replication protein A. Nucleic Acids Research, 2003, 31, 4176-4183.	6.5	46
298	Structure and function of the PWI motif: a novel nucleic acid-binding domain that facilitates pre-mRNA processing. Genes and Development, 2003, 17, 461-475.	2.7	47
299	Aspartate Dehydrogenase, a Novel Enzyme Identified from Structural and Functional Studies of TM1643. Journal of Biological Chemistry, 2003, 278, 8804-8808.	1.6	70
300	Protein Interaction Domains of the Ubiquitin-specific Protease, USP7/HAUSP. Journal of Biological Chemistry, 2003, 278, 47753-47761.	1.6	155
301	Integrating Structure, Bioinformatics, and Enzymology to Discover Function. Journal of Biological Chemistry, 2003, 278, 26039-26045.	1.6	115
302	Producing Proteins. , 2003, , 9-25.		1
303	A novel member of the split betaalphabeta fold: Solution structure of the hypothetical protein YML108W from Saccharomyces cerevisiae. Protein Science, 2003, 12, 1136-40.	3.1	1
304	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
305	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
306	Identification of a Novel Archaebacterial Thioredoxin:â€‰ Determination of Function through Structure. Biochemistry, 2002, 41, 4760-4770.	1.2	25

#	Article	IF	Citations
307	Zinc is required for structural stability of the C-terminus of archaeal translation initiation factor aIF2Î². FEBS Letters, 2002, 517, 155-158.	1.3	9
308	The Solution Structure of the Bacteriophage Î» Headâ€“Tail Joining Protein, gpFII. Journal of Molecular Biology, 2002, 318, 1395-1404.	2.0	38
309	Myxoma Virus Immunomodulatory Protein M156R is a Structural Mimic of Eukaryotic Translation Initiation Factor eIF2Î±. Journal of Molecular Biology, 2002, 322, 943-954.	2.0	45
310	NMR structure of the hypothetical protein encoded by the YjbJ gene fromEscherichia coli. Proteins: Structure, Function and Bioinformatics, 2002, 47, 572-574.	1.5	9
311	Crystal structure ofMethanobacterium thermoautotrophicum conserved protein MTH1020 reveals an NTN-hydrolase fold. Proteins: Structure, Function and Bioinformatics, 2002, 48, 141-143.	1.5	9
312	Crystal structure of MTH169, a crucial component of phosphoribosylformylglycinamidine synthetase. Proteins: Structure, Function and Bioinformatics, 2002, 49, 285-288.	1.5	14
313	NMR structure of theEscherichia coli protein YacG: A novel sequence motif in the zinc-finger family of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 49, 289-293.	1.5	11
314	Deep trefoil knot implicated in RNA binding found in an archaebacterial protein. Proteins: Structure, Function and Bioinformatics, 2002, 50, 177-183.	1.5	40
315	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. Nature Structural Biology, 2002, 9, 27-31.	9.7	124
316	1H, 13C, and 15N resonance assignments and secondary structure of the PWI domain from SRm160 using reduced dimensionality NMR. Journal of Biomolecular NMR, 2002, 22, 299-300.	1.6	4
317	Solution structure of the hypothetical protein MTH0637 from Methanobacterium thermoautotrophicum. Journal of Biomolecular NMR, 2002, 22, 291-294.	1.6	3
318	Novel projected 4D triple resonance experiments for polypeptide backbone chemical shift assignment. Journal of Biomolecular NMR, 2002, 24, 41-50.	1.6	18
319	The crystal structure of hypothetical protein MTH1491 fromMethanobacterium thermoautotrophicum. Protein Science, 2002, 11, 1409-1414.	3.1	15
320	Structure and functionality of a designed p53 dimer11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 307, 605-617.	2.0	71
321	The solution structure of bacteriophage Î» protein W, a small morphogenetic protein possessing a novel fold11Edited by P. E. Wright. Journal of Molecular Biology, 2001, 308, 9-14.	2.0	41
322	Solution structure and dynamics of yeast elongin C in complex with a von hippel-lindau peptide 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2001, 312, 177-186.	2.0	30
323	X-ray crystal structure of MTH938 fromMethanobacterium thermoautotrophicumat 2.2 Ã… resolution reveals a novel tertiary protein fold. Proteins: Structure, Function and Bioinformatics, 2001, 45, 486-488.	1.5	5
324	NMR-based structure of the conserved protein MTH865 from the archaeon Methanobacterium thermoautotrophicum. Journal of Biomolecular NMR, 2001, 21, 63-66.	1.6	3

#	Article	IF	Citations
325	1H, 13C and 15N resonance assignments and secondary structure of the c-Myc binding domain (MBD) and the SH3 domain of the tumor suppressor Bin1. , 2001, 19, 191-192.		4
326	Latent and active p53 are identical in conformation. Nature Structural Biology, 2001, 8, 756-760.	9.7	261
327	The weak interdomain coupling observed in the 70 kDa subunit of human replication protein A is unaffected by ssDNA binding. Nucleic Acids Research, 2001, 29, 3270-3276.	6.5	43
328	Protein production: feeding the crystallographers and NMR spectroscopists. Nature Structural Biology, 2000, 7, 970-972.	9.7	160
329	Structural proteomics of an archaeon. Nature Structural Biology, 2000, 7, 903-909.	9.7	272
330	Structural proteomics: prospects for high throughput sample preparation. Progress in Biophysics and Molecular Biology, 2000, 73, 339-345.	1.4	78
331	Assignment of 1H(N), 15N, 13C(alpha), 13CO and 13C(beta) resonances in a 67 kDa p53 dimer using 4D-TROSY NMR spectroscopy. Journal of Biomolecular NMR, 2000, 18, 173-176.	1.6	30
332	NMR structure determination and structure-based functional characterization of conserved hypothetical protein MTH1175 from Methanobacterium thermoautotrophicum. Journal of Structural and Functional Genomics, 2000, 1, 15-25.	1.2	22
333	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
334	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
335	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
336	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
337	Elongin from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2000, 275, 11174-11180.	1.6	21
338	Structure-based functional classification of hypothetical protein MTH538 from Methanobacterium thermoautotrophicum 1 1Edited by P. Wright. Journal of Molecular Biology, 2000, 302, 189-203.	2.0	27
339	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
340	Subunit-specific backbone NMR assignments of a 64 kDa trp repressor/DNA complex: a role for N-terminal residues in tandem binding. Journal of Biomolecular NMR, 1998, 11, 307-318.	1.6	19
341	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
342	NMR of large (s> 25 kDa) proteins and protein complexes. Progress in Nuclear Magnetic Resonance Spectroscopy, 1998, 32, 277-286.	3.9	25

#	Article	IF	Citations
343	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
344	New perceptions of transcription factor properties from NMR. Biochemistry and Cell Biology, 1998, 76, 368-378.	0.9	7
345	Quantitative Hydroxyl Radical Footprinting Reveals Cooperative Interactions between DNA-Binding Subdomains of PU.1 and IRF4â€. Biochemistry, 1998, 37, 9802-9811.	1.2	22
346	Hydroxyl Radical Footprinting of DNA Complexes of the Ets Domain of PU.1 and Its Comparison to the Crystal Structureâ€. Biochemistry, 1998, 37, 5129-5135.	1.2	14
347	Cooperative interaction between the DNA-binding domains of PU.1 and IRF4. Journal of Molecular Biology, 1998, 279, 1075-1083.	2.0	34
348	Yeast Transcript Elongation Factor (TFIIS), Structure and Function. Journal of Biological Chemistry, 1998, 273, 22589-22594.	1.6	44
349	Yeast Transcript Elongation Factor (TFIIS), Structure and Function. Journal of Biological Chemistry, 1998, 273, 22595-22605.	1.6	71
350	Quantitative Determination of Conformational, Dynamic, and Kinetic Parameters of a Ligand-Protein/DNA Complex from a Complete Relaxation and Conformational Exchange Matrix Analysis of Intermolecular Transferred NOESYâ€. Biochemistry, 1997, 36, 5293-5299.	1.2	21
351	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
352	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
353	Toward the solution structure of large (>30 kDa) proteins and macromolecular complexes. Techniques in Protein Chemistry, 1995, 6, 503-510.	0.3	1
354	Thermodynamic analysis of the structural stability of the tetrameric oligomerization domain of p53 tumor suppressor. Biochemistry, 1995, 34, 5309-5316.	1.2	130
355	Secretion and Circular Dichroism Analysis of the C-Terminal Signal Peptides of HlyA and LktA. Biochemistry, 1995, 34, 4193-4201.	1.2	52
356	Structural analysis and comparison of the C-terminal transport signal domains of hemolysin A and leukotoxin A. FEBS Letters, 1995, 366, 1-5.	1.3	26
357	Solution structure of the tetrameric minimum transforming domain of p53. Nature Structural and Molecular Biology, 1994, 1, 877-890.	3.6	267
358	The Solution Structures of the trp Repressor-Operator DNA Complex. Journal of Molecular Biology, 1994, 238, 592-614.	2.0	124
359	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
360	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

#	Article	IF	Citations
361	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
362	The effect of selective deuteration on magnetization transfer in larger proteins. Journal of Biomolecular NMR, 1992, 2, 183-194.	1.6	36
363	The solution structures of Escherichia coli trp repressor and trp aporepressor at an intermediate resolution. FEBS Journal, 1991, 202, 53-66.	0.2	60
364	Segmental differences in the stability of thetrp-repressor peptide backbone. Journal of Biomolecular NMR, 1991, 1, 349-361.	1.6	38
365	Determination of Large Protein Structures from NMR Data: Definition of the Solution Structure of the TRP Repressor. , 1991, , 363-374.		1
366	The use of selective deuteration for the sequence specific ¹H NMR assignment of larger proteins. Makromolekulare Chemie Macromolecular Symposia, 1990, 34, 33-46.	0.6	5
367	Sequence-specific proton NMR assignments and secondary structure in solution of Escherichia coli trp repressor. Biochemistry, 1990, 29, 6332-6341.	1.2	109
368	NMR studies of the Escherichia coli trp aporepressor. Sequence-specific assignment of the aromatic proton resonances. FEBS Journal, 1989, 183, 545-553.	0.2	14
369	NMR assignments for the amino-terminal residues of trp repressor and their role in DNA binding. Biochemistry, 1989, 28, 3875-3879.	1.2	30
370	A correlation between .beta.-hydrogen isotope effects on carbon-13 NMR chemical shifts in unsaturated systems and the strength of hyperconjugative interactions. Journal of the American Chemical Society, 1986, 108, 7918-7920.	6.6	25
371	Tritium isotope effects on carbon-13 NMR chemical shifts. Journal of the American Chemical Society, 1986, 108, 1356-1357.	6.6	14