

# Cheryl H Arrowsmith

## 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.

369  
papers

26,213  
citations

84  
h-index

149  
g-index

413  
ext. papers

30,280  
ext. citations

10  
avg, IF

6.45  
L-index

#	Paper	IF	Citations
369	Validating Small Molecule Chemical Probes for Biological Discovery.. <i>Annual Review of Biochemistry</i> , <b>2022</b> ,	29.1	3
368	PRMT5 regulates ATF4 transcript splicing and oxidative stress response.. <i>Redox Biology</i> , <b>2022</b> , 51, 102282	11.3	1
367	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer.. <i>Nature Chemical Biology</i> , <b>2022</b> ,	11.7	3
366	A chemical probe targeting the PWWP domain alters NSD2 nucleolar localization. <i>Nature Chemical Biology</i> , <b>2021</b> ,	11.7	6
365	Structure-Activity Relationship of USP5 Inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2021</b> , 64, 15017-15036	6.3	0
364	Chemical Genetics Screen Identifies COPB2 Tool Compounds That Alters ER Stress Response and Induces RTK Dysregulation in Lung Cancer Cells. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 167294	6.5	2
363	Protein arginine methylation: from enigmatic functions to therapeutic targeting. <i>Nature Reviews Drug Discovery</i> , <b>2021</b> , 20, 509-530	64.1	35
362	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degradere. <i>Journal of Medicinal Chemistry</i> , <b>2021</b> , 64, 10682-10710	8.3	9
361	Discovery of the SMYD3 Inhibitor BAY-6035 Using Thermal Shift Assay (TSA)-Based High-Throughput Screening. <i>SLAS Discovery</i> , <b>2021</b> , 26, 947-960	3.4	3
360	MYC protein interactors in gene transcription and cancer. <i>Nature Reviews Cancer</i> , <b>2021</b> , 21, 579-591	31.3	17
359	Identification of lysine isobutyrylation as a new histone modification mark. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 177-189	20.1	10
358	Identifying and Validating MYC:Protein Interactors in Pursuit of Novel Anti-MYC Therapies. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2318, 45-67	1.4	
357	A First-in-Class, Highly Selective and Cell-Active Allosteric Inhibitor of Protein Arginine Methyltransferase 6. <i>Journal of Medicinal Chemistry</i> , <b>2021</b> , 64, 3697-3706	8.3	4
356	Discovery of Small-Molecule Antagonists of the PWWP Domain of NSD2. <i>Journal of Medicinal Chemistry</i> , <b>2021</b> , 64, 1584-1592	8.3	8
355	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,	15.9	11
354	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 979	17.4	23
353	Rational Design and Synthesis of Selective PRMT4 Inhibitors: A New Chemotype for Development of Cancer Therapeutics*. <i>ChemMedChem</i> , <b>2021</b> , 16, 1116-1125	3.7	1

352	Huntingtin structure is orchestrated by HAP40 and shows a polyglutamine expansion-specific interaction with exon 1. <i>Communications Biology</i> , <b>2021</b> , 4, 1374	6.7	1
351	Discovery of a First-in-Class Protein Arginine Methyltransferase 6 (PRMT6) Covalent Inhibitor. <i>Journal of Medicinal Chemistry</i> , <b>2020</b> , 63, 5477-5487	8.3	9
350	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. <i>Nature Communications</i> , <b>2020</b> , 11, 2396	17.4	29
349	Epigenetic Switch-Induced Viral Mimicry Evasion in Chemotherapy-Resistant Breast Cancer. <i>Cancer Discovery</i> , <b>2020</b> , 10, 1312-1329	24.4	34
348	Alternative splicing and allosteric regulation modulate the chromatin binding of UHRF1. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 7728-7747	20.1	6
347	Telomere dysfunction cooperates with epigenetic alterations to impair murine embryonic stem cell fate commitment. <i>ELife</i> , <b>2020</b> , 9,	8.9	5
346	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , <b>2020</b> , 181, 1329-1345.e24	56.24	40
345	HMCES Functions in the Alternative End-Joining Pathway of the DNA DSB Repair during Class Switch Recombination in B Cells. <i>Molecular Cell</i> , <b>2020</b> , 77, 384-394.e4	17.6	17
344	LSD1 represses a neonatal/repairative gene program in adult intestinal epithelium. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	9
343	GLUT1 inhibition blocks growth of RB1-positive triple negative breast cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 4205	17.4	41
342	A Semi-automated Organoid Screening Method Demonstrates Epigenetic Control of Intestinal Epithelial Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , <b>2020</b> , 8, 618552	5.7	6
341	Targeting non-bromodomain chromatin readers. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 863-869	36.9	28
340	A Chemical Probe for Tudor Domain Protein Spindlin1 to Investigate Chromatin Function. <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 9008-9025	8.3	19
339	Structural basis of HMCES interactions with abasic DNA and multivalent substrate recognition. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 607-612	17.6	22
338	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. <i>Cancer Cell</i> , <b>2019</b> , 35, 782-797.e8	24.3	52
337	A chemical toolbox for the study of bromodomains and epigenetic signaling. <i>Nature Communications</i> , <b>2019</b> , 10, 1915	17.4	43
336	Discovery of selective activators of PRC2 mutant EED-I363M. <i>Scientific Reports</i> , <b>2019</b> , 9, 6524	4.9	10
335	AKT drives SOX2 overexpression and cancer cell stemness in esophageal cancer by protecting SOX2 from UBR5-mediated degradation. <i>Oncogene</i> , <b>2019</b> , 38, 5250-5264	9.2	40

334	Design and characterization of mutant and wildtype huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 6986-7001	5.4	12
333	Targeting bivalency de-represses Indian Hedgehog and inhibits self-renewal of colorectal cancer-initiating cells. <i>Nature Communications</i> , <b>2019</b> , 10, 1436	17.4	21
332	The MLL1 trimeric catalytic complex is a dynamic conformational ensemble stabilized by multiple weak interactions. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 9433-9447	20.1	7
331	Selective, Small-Molecule Co-Factor Binding Site Inhibition of a Su(var)3-9, Enhancer of Zeste, Trithorax Domain Containing Lysine Methyltransferase. <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 7669-7683	8.3	10
330	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. <i>Cancer Cell</i> , <b>2019</b> , 36, 194-209.e9	24.3	92
329	Identification and characterization of the first fragment hits for SETDB1 Tudor domain. <i>Bioorganic and Medicinal Chemistry</i> , <b>2019</b> , 27, 3866-3878	3.4	4
328	Fragment-based discovery of a chemical probe for the PWWP1 domain of NSD3. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 822-829	11.7	26
327	Discovery of a Potent and Selective Fragment-like Inhibitor of Methyllysine Reader Protein Spindlin 1 (SPIN1). <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 8996-9007	8.3	11
326	Target 2035: probing the human proteome. <i>Drug Discovery Today</i> , <b>2019</b> , 24, 2111-2115	8.8	62
325	Discovery of Small Molecule Antagonists of the USP5 Zinc Finger Ubiquitin-Binding Domain. <i>Journal of Medicinal Chemistry</i> , <b>2019</b> , 62, 10144-10155	8.3	2
324	A chemical probe of CARM1 alters epigenetic plasticity against breast cancer cell invasion. <i>ELife</i> , <b>2019</b> , 8,	8.9	14
323	Discovery of a chemical probe for PRDM9. <i>Nature Communications</i> , <b>2019</b> , 10, 5759	17.4	13
322	Direct interaction between the PRDM3 and PRDM16 tumor suppressors and the NuRD chromatin remodeling complex. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 1225-1238	20.1	16
321	A chemical biology toolbox to study protein methyltransferases and epigenetic signaling. <i>Nature Communications</i> , <b>2019</b> , 10, 19	17.4	69
320	Characterization of inv(3) cell line OCI-AML-20 with stroma-dependent CD34 expression. <i>Experimental Hematology</i> , <b>2019</b> , 69, 27-36	3.1	2
319	Arginine methylation of FOXP3 is crucial for the suppressive function of regulatory T cells. <i>Journal of Autoimmunity</i> , <b>2019</b> , 97, 10-21	15.5	21
318	LLY-283, a Potent and Selective Inhibitor of Arginine Methyltransferase 5, PRMT5, with Antitumor Activity. <i>ACS Medicinal Chemistry Letters</i> , <b>2018</b> , 9, 612-617	4.3	75
317	Discovery of Ubiquitin Deamidases in the Pathogenic Arsenal of Legionella pneumophila. <i>Cell Reports</i> , <b>2018</b> , 23, 568-583	10.6	25

316	Revealing the protein propionylation activity of the histone acetyltransferase MOF (males absent on the first). <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 3410-3420	5-4	31
315	Discovery of Small-Molecule Antagonists of the H3K9me3 Binding to UHRF1 Tandem Tudor Domain. <i>SLAS Discovery</i> , <b>2018</b> , 23, 930-940	3-4	16
314	Identification of Rpl29 as a major substrate of the lysine methyltransferase Set7/9. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 12770-12780	5-4	10
313	Identification and Structure-Activity Relationship of HDAC6 Zinc-Finger Ubiquitin Binding Domain Inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2018</b> , 61, 4517-4527	8-3	27
312	Mammary molecular portraits reveal lineage-specific features and progenitor cell vulnerabilities. <i>Journal of Cell Biology</i> , <b>2018</b> , 217, 2951-2974	7-3	20
311	TP-064, a potent and selective small molecule inhibitor of PRMT4 for multiple myeloma. <i>Oncotarget</i> , <b>2018</b> , 9, 18480-18493	3-3	53
310	Discovery of Potent and Selective Allosteric Inhibitors of Protein Arginine Methyltransferase 3 (PRMT3). <i>Journal of Medicinal Chemistry</i> , <b>2018</b> , 61, 1204-1217	8-3	17
309	Guiding COMPASS: Dpy-30 Positions SET1/MLL Epigenetic Signaling. <i>Structure</i> , <b>2018</b> , 26, 1567-1570	5-2	
308	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , <b>2018</b> , 34, 579-595.e8	24-3	52
307	Functional diversification of the NleG effector family in enterohemorrhagic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 10004-10009	11-5	11
306	DOT1L inhibition attenuates graft-versus-host disease by allogeneic T cells in adoptive immunotherapy models. <i>Nature Communications</i> , <b>2018</b> , 9, 1915	17-4	14
305	Donated chemical probes for open science. <i>ELife</i> , <b>2018</b> , 7,	8-9	48
304	The SUV4-20 inhibitor A-196 verifies a role for epigenetics in genomic integrity. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 317-324	11-7	62
303	Epigenetic siRNA and Chemical Screens Identify SETD8 Inhibition as a Therapeutic Strategy for p53 Activation in High-Risk Neuroblastoma. <i>Cancer Cell</i> , <b>2017</b> , 31, 50-63	24-3	54
302	The EED protein-protein interaction inhibitor A-395 inactivates the PRC2 complex. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 389-395	11-7	139
301	Discovery of Potent and Selective Inhibitors for G9a-Like Protein (GLP) Lysine Methyltransferase. <i>Journal of Medicinal Chemistry</i> , <b>2017</b> , 60, 1876-1891	8-3	35
300	Targeting human SET1/MLL family of proteins. <i>Protein Science</i> , <b>2017</b> , 26, 662-676	6-3	33
299	Discovery of Peptidomimetic Ligands of EED as Allosteric Inhibitors of PRC2. <i>ACS Combinatorial Science</i> , <b>2017</b> , 19, 161-172	3-9	36

298	The SMX DNA Repair Tri-nuclease. <i>Molecular Cell</i> , <b>2017</b> , 65, 848-860.e11	17.6	70
297	Early-life antibiotic treatment enhances the pathogenicity of CD4 T cells during intestinal inflammation. <i>Journal of Leukocyte Biology</i> , <b>2017</b> , 101, 893-900	6.5	19
296	Conformational dynamics of the TTD-PHD histone reader module of the UHRF1 epigenetic regulator reveals multiple histone-binding states, allosteric regulation, and druggability. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 20947-20959	5.4	23
295	A p53 Super-tumor Suppressor Reveals a Tumor Suppressive p53-Ptpn14-Yap Axis in Pancreatic Cancer. <i>Cancer Cell</i> , <b>2017</b> , 32, 460-473.e6	24.3	93
294	Small Molecule Antagonists of the Interaction between the Histone Deacetylase 6 Zinc-Finger Domain and Ubiquitin. <i>Journal of Medicinal Chemistry</i> , <b>2017</b> , 60, 9090-9096	8.3	18
293	WD40 repeat domain proteins: a novel target class?. <i>Nature Reviews Drug Discovery</i> , <b>2017</b> , 16, 773-786	64.1	101
292	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. <i>Nature</i> , <b>2017</b> , 549, 227-232	30.4	197
291	LSD1-Mediated Epigenetic Reprogramming Drives CENPE Expression and Prostate Cancer Progression. <i>Cancer Research</i> , <b>2017</b> , 77, 5479-5490	10.1	53
290	ASCL1 Reorganizes Chromatin to Direct Neuronal Fate and Suppress Tumorigenicity of Glioblastoma Stem Cells. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 209-224.e7	18	78
289	Structural and Functional Survey of Environmental Aminoglycoside Acetyltransferases Reveals Functionality of Resistance Enzymes. <i>ACS Infectious Diseases</i> , <b>2017</b> , 3, 653-665	5.5	6
288	Global analysis of protein folding using massively parallel design, synthesis, and testing. <i>Science</i> , <b>2017</b> , 357, 168-175	33.3	241
287	Assay interference and off-target liabilities of reported histone acetyltransferase inhibitors. <i>Nature Communications</i> , <b>2017</b> , 8, 1527	17.4	64
286	Structure-activity relationship studies of G9a-like protein (GLP) inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , <b>2017</b> , 25, 4414-4423	3.4	13
285	A Suite of Biochemical Assays for Screening RNA Methyltransferase BCDIN3D. <i>SLAS Discovery</i> , <b>2017</b> , 22, 32-39	3.4	7
284	Diverse modes of galacto-specific carbohydrate recognition by a family 31 glycoside hydrolase from <i>Clostridium perfringens</i> . <i>PLoS ONE</i> , <b>2017</b> , 12, e0171606	3.7	10
283	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. <i>ELife</i> , <b>2017</b> , 6,	8.9	30
282	Discovery of a Potent, Selective, and Cell-Active Dual Inhibitor of Protein Arginine Methyltransferase 4 and Protein Arginine Methyltransferase 6. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 9124-9139	8.3	45
281	Solution NMR structure of the HLTF HIRAN domain: a conserved module in SWI2/SNF2 DNA damage tolerance proteins. <i>Journal of Biomolecular NMR</i> , <b>2016</b> , 66, 209-219	3	11

280	Structure-Based Design of a Covalent Inhibitor of the SET Domain-Containing Protein 8 (SETD8) Lysine Methyltransferase. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 9881-9889	8.3	26
279	Methyltransferase inhibitors for modulation of the epigenome and beyond. <i>Current Opinion in Chemical Biology</i> , <b>2016</b> , 33, 81-7	9.7	13
278	Functional interdependence of BRD4 and DOT1L in MLL leukemia. <i>Nature Structural and Molecular Biology</i> , <b>2016</b> , 23, 673-81	17.6	69
277	Discovery of a Potent Class I Protein Arginine Methyltransferase Fragment Inhibitor. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 1176-83	8.3	28
276	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. <i>Genes and Development</i> , <b>2016</b> , 30, 772-85	12.6	54
275	A cellular chemical probe targeting the chromodomains of Polycomb repressive complex 1. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 180-7	11.7	100
274	Structure-Based Optimization of a Small Molecule Antagonist of the Interaction Between WD Repeat-Containing Protein 5 (WDR5) and Mixed-Lineage Leukemia 1 (MLL1). <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 2478-96	8.3	48
273	A Radioactivity-Based Assay for Screening Human m6A-RNA Methyltransferase, METTL3-METTL14 Complex, and Demethylase ALKBH5. <i>Journal of Biomolecular Screening</i> , <b>2016</b> , 21, 290-7		47
272	A Potent, Selective, and Cell-Active Inhibitor of Human Type I Protein Arginine Methyltransferases. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 772-781	4.9	131
271	Design of a fluorescent ligand targeting the S-adenosylmethionine binding site of the histone methyltransferase MLL1. <i>Organic and Biomolecular Chemistry</i> , <b>2016</b> , 14, 631-638	3.9	6
270	BET bromodomain inhibition enhances T cell persistence and function in adoptive immunotherapy models. <i>Journal of Clinical Investigation</i> , <b>2016</b> , 126, 3479-94	15.9	118
269	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , <b>2016</b> , 5,	8.9	80
268	Discovery of a Potent and Selective Coactivator Associated Arginine Methyltransferase 1 (CARM1) Inhibitor by Virtual Screening. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 6838-47	8.3	32
267	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , <b>2016</b> , 30, 891-908	24.3	135
266	A community resource of experimental data for NMR / X-ray crystal structure pairs. <i>Protein Science</i> , <b>2016</b> , 25, 30-45	6.3	10
265	SETD7 Controls Intestinal Regeneration and Tumorigenesis by Regulating Wnt/ECatenin and Hippo/YAP Signaling. <i>Developmental Cell</i> , <b>2016</b> , 37, 47-57	10.2	64
264	PR Domain-containing Protein 7 (PRDM7) Is a Histone 3 Lysine 4 Trimethyltransferase. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 13509-19	5.4	18
263	Discovery and Characterization of a Highly Potent and Selective Aminopyrazoline-Based in Vivo Probe (BAY-598) for the Protein Lysine Methyltransferase SMYD2. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 4578-600	8.3	52

262	An Integrative Proteomic Approach Identifies Novel Cellular SMYD2 Substrates. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 2052-9	5.6	17
261	Structure-Activity Relationship Studies for Enhancer of Zeste Homologue 2 (EZH2) and Enhancer of Zeste Homologue 1 (EZH1) Inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 7617-33	8.3	23
260	Preclinical target validation using patient-derived cells. <i>Nature Reviews Drug Discovery</i> , <b>2015</b> , 14, 149-50	64.1	40
259	A potent, selective and cell-active allosteric inhibitor of protein arginine methyltransferase 3 (PRMT3). <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 5166-70	16.4	78
258	Pharmacological targeting of the Wdr5-MLL interaction in C/EBP $\beta$ -terminal leukemia. <i>Nature Chemical Biology</i> , <b>2015</b> , 11, 571-578	11.7	159
257	The promise and peril of chemical probes. <i>Nature Chemical Biology</i> , <b>2015</b> , 11, 536-41	11.7	523
256	Probing the epigenome. <i>Nature Chemical Biology</i> , <b>2015</b> , 11, 542-5	11.7	29
255	Solution-state NMR structure of the putative morphogene protein Bola (PFE0790c) from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 514-21	1.1	4
254	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , <b>2015</b> , 12, 725-31	21.6	86
253	Discovery of a Dual PRMT5-PRMT7 Inhibitor. <i>ACS Medicinal Chemistry Letters</i> , <b>2015</b> , 6, 408-12	4.3	59
252	Cbx2 targets PRC1 to constitutive heterochromatin in mouse zygotes in a parent-of-origin-dependent manner. <i>Molecular Cell</i> , <b>2015</b> , 58, 157-71	17.6	52
251	Discovery of A-893, A New Cell-Active Benzoxazinone Inhibitor of Lysine Methyltransferase SMYD2. <i>ACS Medicinal Chemistry Letters</i> , <b>2015</b> , 6, 695-700	4.3	49
250	Tackling reproducibility in academic preclinical drug discovery. <i>Nature Reviews Drug Discovery</i> , <b>2015</b> , 14, 733-4	64.1	49
249	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. <i>Journal of Biomolecular NMR</i> , <b>2015</b> , 62, 413-24	3	21
248	Ductal pancreatic cancer modeling and drug screening using human pluripotent stem cell- and patient-derived tumor organoids. <i>Nature Medicine</i> , <b>2015</b> , 21, 1364-71	50.5	403
247	LLY-507, a Cell-active, Potent, and Selective Inhibitor of Protein-lysine Methyltransferase SMYD2. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 13641-53	5.4	83
246	WDR5 Supports an N-Myc Transcriptional Complex That Drives a Protumorigenic Gene Expression Signature in Neuroblastoma. <i>Cancer Research</i> , <b>2015</b> , 75, 5143-54	10.1	52
245	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICP0 of Herpes Simplex Virus-1. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 22907-18	5.4	26



244	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. <i>Nature</i> , <b>2015</b> , 525, 206-11	50.4	294
243	MLL5 Orchestrates a Cancer Self-Renewal State by Repressing the Histone Variant H3.3 and Globally Reorganizing Chromatin. <i>Cancer Cell</i> , <b>2015</b> , 28, 715-729	24.3	64
242	A Potent, Selective and Cell-Active Allosteric Inhibitor of Protein Arginine Methyltransferase 3 (PRMT3). <i>Angewandte Chemie</i> , <b>2015</b> , 127, 5255-5259	3.6	2
241	Optimizing Production of Antigens and Fabs in the Context of Generating Recombinant Antibodies to Human Proteins. <i>PLoS ONE</i> , <b>2015</b> , 10, e0139695	3.7	20
240	Kinetic characterization of human histone H3 lysine 36 methyltransferases, ASH1L and SETD2. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2015</b> , 1850, 1842-8	4	31
239	Identification of a fragment-like small molecule ligand for the methyl-lysine binding protein, 53BP1. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 1072-81	4.9	44
238	KCMF1 (potassium channel modulatory factor 1) Links RAD6 to UBR4 (ubiquitin N-recognin domain-containing E3 ligase 4) and lysosome-mediated degradation. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 674-85	7.6	17
237	The study of epigenetic mechanisms based on the analysis of histone modification patterns by flow cytometry. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , <b>2014</b> , 85, 78-87	4.6	10
236	Self-renewal as a therapeutic target in human colorectal cancer. <i>Nature Medicine</i> , <b>2014</b> , 20, 29-36	50.5	361
235	A Basic Post-SET Extension of NSDs Is Essential for Nucleosome Binding In Vitro. <i>Journal of Biomolecular Screening</i> , <b>2014</b> , 19, 928-35		21
234	Discovery of a selective, substrate-competitive inhibitor of the lysine methyltransferase SETD8. <i>Journal of Medicinal Chemistry</i> , <b>2014</b> , 57, 6822-33	8.3	61
233	An unusual mode of galactose recognition by a family 32 carbohydrate-binding module. <i>Journal of Molecular Biology</i> , <b>2014</b> , 426, 869-80	6.5	15
232	Structural and functional characterization of DUF1471 domains of Salmonella proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , <b>2014</b> , 9, e101787	3.7	8
231	Trimethylation of histone H3 lysine 36 by human methyltransferase PRDM9 protein. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 12177-12188	5.4	76
230	RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 686-695	17.6	54
229	(R)-PFI-2 is a potent and selective inhibitor of SETD7 methyltransferase activity in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 12853-8	11.5	120
228	Structural characterization of a flexible two-domain protein in solution using small angle X-ray scattering and NMR data. <i>Structure</i> , <b>2014</b> , 22, 1862-1874	5.2	6
227	A global assessment of cancer genomic alterations in epigenetic mechanisms. <i>Epigenetics and Chromatin</i> , <b>2014</b> , 7, 29	5.8	46

226	Basic Tilted Helix Bundle - a new protein fold in human FKBP25/FKBP3 and HectD1. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 447, 26-31	3.4	12
225	Accessibility of different histone H3-binding domains of UHRF1 is allosterically regulated by phosphatidylinositol 5-phosphate. <i>Molecular Cell</i> , <b>2014</b> , 54, 905-19	17.6	86
224	Structure and function of dioxygenases in histone demethylation and DNA/RNA demethylation. <i>IUCrJ</i> , <b>2014</b> , 1, 540-9	4.7	21
223	Methyltransferase G9A regulates T cell differentiation during murine intestinal inflammation. <i>Journal of Clinical Investigation</i> , <b>2014</b> , 124, 1945-55	15.9	57
222	Screening proteins for NMR suitability. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1140, 169-78	1.4	3
221	Control of the hippo pathway by Set7-dependent methylation of Yap. <i>Developmental Cell</i> , <b>2013</b> , 26, 188-94	14.2	100
220	The structure-activity relationships of L3MBTL3 inhibitors: flexibility of the dimer interface. <i>MedChemComm</i> , <b>2013</b> , 4, 1501-1507	5	22
219	Discovery of an in vivo chemical probe of the lysine methyltransferases G9a and GLP. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 8931-42	8.3	155
218	Small-molecule ligands of methyl-lysine binding proteins: optimization of selectivity for L3MBTL3. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 7358-71	8.3	57
217	Structural insights into aldosterone synthase substrate specificity and targeted inhibition. <i>Molecular Endocrinology</i> , <b>2013</b> , 27, 315-24		97
216	Nahuoic acid A produced by a <i>Streptomyces</i> sp. isolated from a marine sediment is a selective SAM-competitive inhibitor of the histone methyltransferase SETD8. <i>Organic Letters</i> , <b>2013</b> , 15, 414-7	6.2	56
215	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. <i>Nature Chemical Biology</i> , <b>2013</b> , 9, 184-91	11.7	129
214	Exploiting an allosteric binding site of PRMT3 yields potent and selective inhibitors. <i>Journal of Medicinal Chemistry</i> , <b>2013</b> , 56, 2110-24	8.3	58
213	An orally bioavailable chemical probe of the Lysine Methyltransferases EZH2 and EZH1. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 1324-34	4.9	313
212	Bromo-deaza-SAH: a potent and selective DOT1L inhibitor. <i>Bioorganic and Medicinal Chemistry</i> , <b>2013</b> , 21, 1787-1794	3.4	54
211	Synthesis, Optimization, and Evaluation of Novel Small Molecules as Antagonists of WDR5-MLL Interaction. <i>ACS Medicinal Chemistry Letters</i> , <b>2013</b> , 4, 353-7	4.3	39
210	Small-molecule inhibition of MLL activity by disruption of its interaction with WDR5. <i>Biochemical Journal</i> , <b>2013</b> , 449, 151-9	3.8	100
209	Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for the epigenetic inheritance of DNA methylation. <i>Genes and Development</i> , <b>2013</b> , 27, 1288-98	12.6	129

208	Ubiquitin-specific protease 7 is a regulator of ubiquitin-conjugating enzyme UbE2E1. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 16975-16985	5.4	29
207	The ZIP5 ectodomain co-localizes with PrP and may acquire a PrP-like fold that assembles into a dimer. <i>PLoS ONE</i> , <b>2013</b> , 8, e72446	3.7	19
206	Solution NMR structure and histone binding of the PHD domain of human MLL5. <i>PLoS ONE</i> , <b>2013</b> , 8, e77020	7.0	21
205	Structure of the catalytic domain of EZH2 reveals conformational plasticity in cofactor and substrate binding sites and explains oncogenic mutations. <i>PLoS ONE</i> , <b>2013</b> , 8, e83737	3.7	88
204	Blind testing of routine, fully automated determination of protein structures from NMR data. <i>Structure</i> , <b>2012</b> , 20, 227-36	5.2	64
203	A human ubiquitin conjugating enzyme (E2)-HECT E3 ligase structure-function screen. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 329-41	7.6	81
202	Sequence-specific recognition of a PxLPxI/L motif by an ankyrin repeat tumbler lock. <i>Science Signaling</i> , <b>2012</b> , 5, ra39	8.8	33
201	Structural analysis of HopPmaL reveals the presence of a second adaptor domain common to the HopAB family of <i>Pseudomonas syringae</i> type III effectors. <i>Biochemistry</i> , <b>2012</b> , 51, 1-3	3.2	8
200	An allosteric inhibitor of protein arginine methyltransferase 3. <i>Structure</i> , <b>2012</b> , 20, 1425-35	5.2	72
199	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 1155-60	17.6	253
198	Preferential binding of IFI16 protein to cruciform structure and superhelical DNA. <i>Biochemical and Biophysical Research Communications</i> , <b>2012</b> , 422, 716-20	3.4	54
197	Histone recognition and large-scale structural analysis of the human bromodomain family. <i>Cell</i> , <b>2012</b> , 149, 214-31	56.2	1054
196	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. <i>Nature Communications</i> , <b>2012</b> , 3, 1288	17.4	209
195	Histone recognition by human malignant brain tumor domains. <i>Journal of Molecular Biology</i> , <b>2012</b> , 423, 702-18	6.5	45
194	Tandem protein interaction modules organize the ubiquitin-dependent response to DNA double-strand breaks. <i>Molecular Cell</i> , <b>2012</b> , 47, 383-95	17.6	106
193	Epigenetic protein families: a new frontier for drug discovery. <i>Nature Reviews Drug Discovery</i> , <b>2012</b> , 11, 384-400	64.1	1003
192	Solution NMR structure of hypothetical protein CV_2116 encoded by a viral prophage element in <i>Chromobacterium violaceum</i> . <i>International Journal of Molecular Sciences</i> , <b>2012</b> , 13, 7354-64	6.3	1
191	Structural and biochemical characterization of phage $\Phi$ I protein (gpFI) reveals a novel mechanism of DNA packaging chaperone activity. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 32085-95	5.4	5

190	Protein aggregates are recruited to aggresome by histone deacetylase 6 via unanchored ubiquitin C termini. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 2317-27	5.4	141
189	Fluorescence-based methods for screening writers and readers of histone methyl marks. <i>Journal of Biomolecular Screening</i> , <b>2012</b> , 17, 71-84		37
188	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 6353-66	20.1	75
187	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. <i>Nature Chemical Biology</i> , <b>2011</b> , 7, 566-74	11.7	386
186	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , <b>2011</b> , 117, 2451-9	2.2	458
185	Interferon-inducible protein 16: insight into the interaction with tumor suppressor p53. <i>Structure</i> , <b>2011</b> , 19, 418-29	5.2	69
184	Small-molecule ligands of methyl-lysine binding proteins. <i>Journal of Medicinal Chemistry</i> , <b>2011</b> , 54, 2504-8.3	8.3	106
183	Optimization of cellular activity of G9a inhibitors 7-aminoalkoxy-quinazolines. <i>Journal of Medicinal Chemistry</i> , <b>2011</b> , 54, 6139-50	8.3	103
182	A novel strategy for NMR resonance assignment and protein structure determination. <i>Journal of Biomolecular NMR</i> , <b>2011</b> , 49, 27-38	3	35
181	Zn-binding AZUL domain of human ubiquitin protein ligase Ube3A. <i>Journal of Biomolecular NMR</i> , <b>2011</b> , 51, 185-90	3	18
180	Cruciform structures are a common DNA feature important for regulating biological processes. <i>BMC Molecular Biology</i> , <b>2011</b> , 12, 33	4.5	155
179	Solution structure of MTH1821, a putative structure homologue to RNA polymerase $\beta$ subunit from <i>Methanobacterium thermoautotrophicum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1347-51	4.2	2
178	Crystal structure of Fushi tarazu factor 1 ligand binding domain/Fushi tarazu peptide complex identifies new class of nuclear receptors. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 31225-31	5.4	15
177	Anti-Ro52 autoantibodies from patients with Sjögren's syndrome inhibit the Ro52 E3 ligase activity by blocking the E3/E2 interface. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 36478-91	5.4	47
176	Structural and functional comparison of the RING domains of two p53 E3 ligases, Mdm2 and Pirh2. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 4796-808	5.4	29
175	Recognition and specificity determinants of the human cbx chromodomains. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 521-9	5.4	205
174	Recognition of multivalent histone states associated with heterochromatin by UHRF1 protein. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 24300-11	5.4	149
173	Role of Pirh2 in mediating the regulation of p53 and c-Myc. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002360	6	51

172	Structural biology of human H3K9 methyltransferases. <i>PLoS ONE</i> , <b>2010</b> , 5, e8570	3.7	184
171	Screening for inhibitors of low-affinity epigenetic peptide-protein interactions: an AlphaScreen-based assay for antagonists of methyl-lysine binding proteins. <i>Journal of Biomolecular Screening</i> , <b>2010</b> , 15, 62-71		75
170	Structural basis of E2-25K/UBB+1 interaction leading to proteasome inhibition and neurotoxicity. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 36070-80	5.4	38
169	NleG Type 3 effectors from enterohaemorrhagic <i>Escherichia coli</i> are U-Box E3 ubiquitin ligases. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000960	7.6	66
168	Biological and structural basis for Aha1 regulation of Hsp90 ATPase activity in maintaining proteostasis in the human disease cystic fibrosis. <i>Molecular Biology of the Cell</i> , <b>2010</b> , 21, 871-84	3.5	137
167	Biophysical characterization of recombinant proteins: a key to higher structural genomics success. <i>Journal of Structural Biology</i> , <b>2010</b> , 172, 107-19	3.4	46
166	Further insight into substrate recognition by USP7: structural and biochemical analysis of the HdmX and Hdm2 interactions with USP7. <i>Journal of Molecular Biology</i> , <b>2010</b> , 402, 825-37	6.5	35
165	Protein lysine methyltransferase G9a inhibitors: design, synthesis, and structure activity relationships of 2,4-diamino-7-aminoalkoxy-quinazolines. <i>Journal of Medicinal Chemistry</i> , <b>2010</b> , 53, 5844-57	8.7	156
164	A small-molecule inhibitor of BCL6 kills DLBCL cells in vitro and in vivo. <i>Cancer Cell</i> , <b>2010</b> , 17, 400-11	24.3	230
163	Simultaneous prediction of protein folding and docking at high resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 18978-83	11.5	127
162	Unique opportunities for NMR methods in structural genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2009</b> , 10, 101-6		15
161	Ring1B contains a ubiquitin-like docking module for interaction with Cbx proteins. <i>Biochemistry</i> , <b>2009</b> , 48, 10542-8	3.2	34
160	Discovery of a 2,4-diamino-7-aminoalkoxyquinazoline as a potent and selective inhibitor of histone lysine methyltransferase G9a. <i>Journal of Medicinal Chemistry</i> , <b>2009</b> , 52, 7950-3	8.3	184
159	The central region of BRCA1 binds preferentially to supercoiled DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2009</b> , 27, 97-104	3.6	10
158	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 2204-10	20.1	77
157	A survey of proteins encoded by non-synonymous single nucleotide polymorphisms reveals a significant fraction with altered stability and activity. <i>Biochemical Journal</i> , <b>2009</b> , 424, 15-26	3.8	42
156	Structural basis for recognition of hemi-methylated DNA by the SRA domain of human UHRF1. <i>Nature</i> , <b>2008</b> , 455, 822-5	50.4	353
155	Molecular basis of Pirh2-mediated p53 ubiquitylation. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 1334-42	17.6	74

154	Protein production and purification. <i>Nature Methods</i> , <b>2008</b> , 5, 135-46	21.6	655
153	A SPOT on the chromatin landscape? Histone peptide arrays as a tool for epigenetic research. <i>Trends in Biochemical Sciences</i> , <b>2008</b> , 33, 305-13	10.3	63
152	Consistent blind protein structure generation from NMR chemical shift data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 4685-90	11.5	665
151	Biochemical and structural characterization of a novel family of cystathionine beta-synthase domain proteins fused to a Zn ribbon-like domain. <i>Journal of Molecular Biology</i> , <b>2008</b> , 375, 301-15	6.5	43
150	Atomic structure of the KEOPS complex: an ancient protein kinase-containing molecular machine. <i>Molecular Cell</i> , <b>2008</b> , 32, 259-75	17.6	72
149	Human HDAC7 harbors a class IIa histone deacetylase-specific zinc binding motif and cryptic deacetylase activity. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 11355-63	5.4	214
148	The hypothetical protein Atu4866 from <i>Agrobacterium tumefaciens</i> adopts a streptavidin-like fold. <i>Protein Science</i> , <b>2008</b> , 17, 154-8	6.3	
147	Sequence specific resonance assignment via Multicanonical Monte Carlo search using an ABACUS approach. <i>Journal of Biomolecular NMR</i> , <b>2008</b> , 41, 29-41	3	33
146	Structural genomics and drug discovery: all in the family. <i>Current Opinion in Chemical Biology</i> , <b>2008</b> , 12, 32-9	9.7	34
145	The solution structure of ribosomal protein S17E from <i>Methanobacterium thermoautotrophicum</i> : a structural homolog of the FF domain. <i>Protein Science</i> , <b>2008</b> , 17, 583-8	6.3	3
144	Solution structure of ribosomal protein L40E, a unique C4 zinc finger protein encoded by archaeon <i>Sulfolobus solfataricus</i> . <i>Protein Science</i> , <b>2008</b> , 17, 589-96	6.3	8
143	High throughput screening of purified proteins for enzymatic activity. <i>Methods in Molecular Biology</i> , <b>2008</b> , 426, 331-41	1.4	16
142	NMR structure of hypothetical protein TA0938 from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 67, 1185-8	4.2	
141	In situ proteolysis for protein crystallization and structure determination. <i>Nature Methods</i> , <b>2007</b> , 4, 1019-21	21.6	181
140	L3MBTL1 recognition of mono- and dimethylated histones. <i>Nature Structural and Molecular Biology</i> , <b>2007</b> , 14, 1229-30	17.6	159
139	Genome-scale protein expression and structural biology of <i>Plasmodium falciparum</i> and related Apicomplexan organisms. <i>Molecular and Biochemical Parasitology</i> , <b>2007</b> , 151, 100-10	1.9	199
138	Backbone and side chain 1H, 13C, and 15N resonance assignments of AF2241 from <i>Archaeoglobus fulgidus</i> . <i>Journal of Biomolecular NMR</i> , <b>2007</b> , 38, 183	3	1
137	Hypothetical protein AF2241 from <i>Archaeoglobus fulgidus</i> adopts a cyclophilin-like fold. <i>Journal of Biomolecular NMR</i> , <b>2007</b> , 38, 353-8	3	2

136	Analysis of binding site similarity, small-molecule similarity and experimental binding profiles in the human cytosolic sulfotransferase family. <i>Bioinformatics</i> , <b>2007</b> , 23, e104-9	7.2	30
135	Structural and chemical profiling of the human cytosolic sulfotransferases. <i>PLoS Biology</i> , <b>2007</b> , 5, e97	9.7	153
134	CUL7 is a novel antiapoptotic oncogene. <i>Cancer Research</i> , <b>2007</b> , 67, 9616-22	10.1	45
133	The conserved CPH domains of Cul7 and PARC are protein-protein interaction modules that bind the tetramerization domain of p53. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 11300-7	5.4	40
132	NMR structure and binding studies confirm that PA4608 from <i>Pseudomonas aeruginosa</i> is a PilZ domain and a c-di-GMP binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2007</b> , 66, 266-71	4.2	63
131	Solution NMR in structural genomics. <i>Current Opinion in Structural Biology</i> , <b>2006</b> , 16, 611-7	8.1	41
130	p53 transcriptional activation domain: a molecular chameleon?. <i>Cell Cycle</i> , <b>2006</b> , 5, 489-94	4.7	30
129	Genome-wide analysis of substrate specificities of the <i>Escherichia coli</i> haloacid dehalogenase-like phosphatase family. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 36149-61	5.4	198
128	Chemical screening methods to identify ligands that promote protein stability, protein crystallization, and structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 15835-40	11.5	478
127	Solution structure of acyl carrier protein from <i>Nitrosomonas europaea</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 64, 800-3	4.2	2
126	Solution structure of TA1092, a ribosomal protein S24e from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 64, 1095-7	4.2	6
125	NMR structure of protein PA2021 from <i>Pseudomonas aeruginosa</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 65, 767-70	4.2	1
124	Solution structure of TA0895, a MoaD homologue from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 65, 1055-7	4.2	1
123	Molecular recognition of p53 and MDM2 by USP7/HAUSP. <i>Nature Structural and Molecular Biology</i> , <b>2006</b> , 13, 285-91	17.6	201
122	Structural basis for molecular recognition and presentation of histone H3 by WDR5. <i>EMBO Journal</i> , <b>2006</b> , 25, 4245-52	13	143
121	MTH187 from <i>Methanobacterium thermoautotrophicum</i> has three HEAT-like repeats. <i>Journal of Biomolecular NMR</i> , <b>2006</b> , 35, 149-54	3	5
120	Resonance assignments for the hypothetical protein TA0938 from <i>Thermoplasma acidophilum</i> . <i>Journal of Biomolecular NMR</i> , <b>2006</b> , 36 Suppl 1, 36	3	1
119	The solution structure of the protein ydhA from <i>Escherichia coli</i> . <i>Journal of Biomolecular NMR</i> , <b>2006</b> , 35, 295-300	3	11

118	NMR structure of the conserved novel-fold protein TA0743 from <i>Thermoplasma acidophilum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 819-21	4.2	2
117	A novel member of the YchN-like fold: solution structure of the hypothetical protein Tm0979 from <i>Thermotoga maritima</i> . <i>Protein Science</i> , <b>2005</b> , 14, 216-23	6.3	8
116	Characterization of segments from the central region of BRCA1: an intrinsically disordered scaffold for multiple protein-protein and protein-DNA interactions?. <i>Journal of Molecular Biology</i> , <b>2005</b> , 345, 275-87	6.5	141
115	A structure-based model of the c-Myc/Bin1 protein interaction shows alternative splicing of Bin1 and c-Myc phosphorylation are key binding determinants. <i>Journal of Molecular Biology</i> , <b>2005</b> , 351, 182-94	6.5	77
114	Structure of the p53 binding domain of HAUSP/USP7 bound to Epstein-Barr nuclear antigen 1 implications for EBV-mediated immortalization. <i>Molecular Cell</i> , <b>2005</b> , 18, 25-36	17.6	264
113	NMR and X-ray crystallography, complementary tools in structural proteomics of small proteins. <i>Journal of the American Chemical Society</i> , <b>2005</b> , 127, 16512-7	16.4	75
112	NMR Spectroscopy in Structural Genomics <b>2005</b> , 49-60		
111	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. <i>FEMS Microbiology Reviews</i> , <b>2005</b> , 29, 263-279	15.1	81
110	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. <i>FEMS Microbiology Reviews</i> , <b>2005</b> , 29, 263-79	15.1	89
109	Solution Structure of MTH0776 from <i>Methanobacterium thermoautotrophicum</i> . <i>Journal of Biomolecular NMR</i> , <b>2005</b> , 33, 51-6	3	4
108	High-throughput production of prokaryotic membrane proteins. <i>Journal of Structural and Functional Genomics</i> , <b>2005</b> , 6, 33-50		39
107	NMR solution structure of <i>Thermotoga maritima</i> protein TM1509 reveals a Zn-metalloprotease-like tertiary structure. <i>Journal of Structural and Functional Genomics</i> , <b>2005</b> , 6, 51-62		19
106	Single-stranded DNA mimicry in the p53 transactivation domain interaction with replication protein A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 15412-7	11.5	226
105	An integrated platform for automated analysis of protein NMR structures. <i>Methods in Enzymology</i> , <b>2005</b> , 394, 111-41	1.7	59
104	The Shwachman-Bodian-Diamond syndrome protein family is involved in RNA metabolism. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 19213-20	5.4	89
103	NMR data collection and analysis protocol for high-throughput protein structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 10487-92	11.5	101
102	The structural basis for methylmalonic aciduria. The crystal structure of archaeal ATP:cobalamin adenosyltransferase. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 23646-53	5.4	36
101	The HD domain of the <i>Escherichia coli</i> tRNA nucleotidyltransferase has 2P3Pcyclic phosphodiesterase, 2Pnucleotidase, and phosphatase activities. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 36819-27	5.4	68



100	Solution structure of a novel calcium binding protein, MTH1880, from Methanobacterium thermoautotrophicum. <i>Protein Science</i> , <b>2004</b> , 13, 1148-54	6.3	9
99	Structure of the archaeal translation initiation factor aIF2 beta from Methanobacterium thermoautotrophicum: implications for translation initiation. <i>Protein Science</i> , <b>2004</b> , 13, 659-67	6.3	25
98	Solution structure of hypothetical protein TA1414 from Thermoplasma acidophilum. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 28, 81-4	3	1
97	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N assignments of single-stranded DNA binding domains from the 70 kDa subunit of human replication protein A. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 28, 195-6	3	7
96	Complete <sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N NMR assignments of MTH0776 from Methanobacterium thermoautotrophicum. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 30, 459-60	3	1
95	Structural proteomics: a tool for genome annotation. <i>Current Opinion in Chemical Biology</i> , <b>2004</b> , 8, 42-8	9.7	66
94	Structure- and function-based characterization of a new phosphoglycolate phosphatase from Thermoplasma acidophilum. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 517-26	5.4	39
93	Solution structure of the hypothetical protein Mth677 from Methanobacterium thermoautotrophicum: a novel alpha+beta fold. <i>Protein Science</i> , <b>2004</b> , 13, 1458-65	6.3	1
92	X-ray crystal structure of CutA from Thermotoga maritima at 1.4 A resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 54, 162-5	4.2	13
91	Aspartate dehydrogenase, a novel enzyme identified from structural and functional studies of TM1643. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 8804-8	5.4	50
90	Protein interaction domains of the ubiquitin-specific protease, USP7/HAUSP. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 47753-61	5.4	125
89	Integrating structure, bioinformatics, and enzymology to discover function: BioH, a new carboxylesterase from Escherichia coli. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 26039-45	5.4	103
88	Producing Proteins <b>2003</b> , 9-25		1
87	Deep trefoil knot implicated in RNA binding found in an archaeobacterial protein. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 50, 177-83	4.2	38
86	Solution structure of the yeast ubiquitin-like modifier protein Hub1. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 25-30		25
85	<sup>1</sup> H(C) and <sup>1</sup> H(N) total NOE correlations in a single 3D NMR experiment. <sup>15</sup> N and <sup>13</sup> C time-sharing in t1 and t2 dimensions for simultaneous data acquisition. <i>Journal of Biomolecular NMR</i> , <b>2003</b> , 27, 193-203	3	26
84	Arresting and releasing Staphylococcal alpha-hemolysin at intermediate stages of pore formation by engineered disulfide bonds. <i>Protein Science</i> , <b>2003</b> , 12, 997-1006	6.3	26
83	Structure of Escherichia coli ribose-5-phosphate isomerase: a ubiquitous enzyme of the pentose phosphate pathway and the Calvin cycle. <i>Structure</i> , <b>2003</b> , 11, 31-42	5.2	82

82	Data mining crystallization databases: knowledge-based approaches to optimize protein crystal screens. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 51, 562-8	4.2	69
81	Crystal structures of MTH1187 and its yeast ortholog YBL001c. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 52, 478-80	4.2	6
80	Structural proteomics: toward high-throughput structural biology as a tool in functional genomics. <i>Accounts of Chemical Research</i> , <b>2003</b> , 36, 183-9	24.3	84
79	Solution structure of ribosomal protein S28E from <i>Methanobacterium thermoautotrophicum</i> . <i>Protein Science</i> , <b>2003</b> , 12, 2831-7	6.3	15
78	Refolding out of guanidine hydrochloride is an effective approach for high-throughput structural studies of small proteins. <i>Protein Science</i> , <b>2003</b> , 12, 2073-80	6.3	37
77	Eme1 is involved in DNA damage processing and maintenance of genomic stability in mammalian cells. <i>EMBO Journal</i> , <b>2003</b> , 22, 6137-47	13	106
76	Chemical shift changes provide evidence for overlapping single-stranded DNA- and XPA-binding sites on the 70 kDa subunit of human replication protein A. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 4176-83	20.1	43
75	Structure and function of the PWI motif: a novel nucleic acid-binding domain that facilitates pre-mRNA processing. <i>Genes and Development</i> , <b>2003</b> , 17, 461-75	12.6	40
74	A novel member of the split betaalpha fold: Solution structure of the hypothetical protein YML108W from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , <b>2003</b> , 12, 1136-40	6.3	1
73	Characterization of binding-induced changes in dynamics suggests a model for sequence-nonspecific binding of ssDNA by replication protein A. <i>Protein Science</i> , <b>2002</b> , 11, 2316-25	6.3	15
72	NMR structure of the hypothetical protein encoded by the YjbJ gene from <i>Escherichia coli</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 47, 572-4	4.2	9
71	Crystal structure of <i>Methanobacterium thermoautotrophicum</i> conserved protein MTH1020 reveals an NTN-hydrolase fold. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 48, 141-3	4.2	7
70	Crystal structure of MTH169, a crucial component of phosphoribosylformylglycinamide synthetase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 49, 285-8	4.2	13
69	NMR structure of the <i>Escherichia coli</i> protein YacG: a novel sequence motif in the zinc-finger family of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2002</b> , 49, 289-93	4.2	10
68	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 27-31		115
67	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments and secondary structure of the PWI domain from SRm160 using reduced dimensionality NMR. <i>Journal of Biomolecular NMR</i> , <b>2002</b> , 22, 299-300	3	4
66	Solution structure of the hypothetical protein MTH0637 from <i>Methanobacterium thermoautotrophicum</i> . <i>Journal of Biomolecular NMR</i> , <b>2002</b> , 22, 291-4	3	3
65	Novel projected 4D triple resonance experiments for polypeptide backbone chemical shift assignment. <i>Journal of Biomolecular NMR</i> , <b>2002</b> , 24, 41-50	3	16

64	The crystal structure of hypothetical protein MTH1491 from Methanobacterium thermoautotrophicum. <i>Protein Science</i> , <b>2002</b> , 11, 1409-14	6.3	15
63	An NMR approach to structural proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 1825-30	11.5	180
62	Crystal structure of Thermotoga maritima 0065, a member of the IclR transcriptional factor family. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 19183-90	5.4	58
61	Identification of a novel archaeobacterial thioredoxin: determination of function through structure. <i>Biochemistry</i> , <b>2002</b> , 41, 4760-70	3.2	25
60	Zinc is required for structural stability of the C-terminus of archaeal translation initiation factor aIF2beta. <i>FEBS Letters</i> , <b>2002</b> , 517, 155-8	3.8	9
59	The solution structure of the bacteriophage lambda head-tail joining protein, gpFII. <i>Journal of Molecular Biology</i> , <b>2002</b> , 318, 1395-404	6.5	31
58	Myxoma virus immunomodulatory protein M156R is a structural mimic of eukaryotic translation initiation factor eIF2alpha. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 943-54	6.5	38
57	X-ray crystal structure of MTH938 from Methanobacterium thermoautotrophicum at 2.2 Å resolution reveals a novel tertiary protein fold. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , 45, 486-8	4.2	4
56	NMR-based structure of the conserved protein MTH865 from the archaeon Methanobacterium thermoautotrophicum. <i>Journal of Biomolecular NMR</i> , <b>2001</b> , 21, 63-6	3	1
55	<sup>1</sup> H, <sup>13</sup> C and <sup>15</sup> N resonance assignments and secondary structure of the c-Myc binding domain (MBD) and the SH3 domain of the tumor suppressor Bin1. <i>Journal of Biomolecular NMR</i> , <b>2001</b> , 19, 191-203	3	3
54	Latent and active p53 are identical in conformation. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 756-60		227
53	The weak interdomain coupling observed in the 70 kDa subunit of human replication protein A is unaffected by ssDNA binding. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 3270-6	20.1	38
52	Structure and functionality of a designed p53 dimer. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 605-17	6.5	65
51	The solution structure of bacteriophage lambda protein W, a small morphogenetic protein possessing a novel fold. <i>Journal of Molecular Biology</i> , <b>2001</b> , 308, 9-14	6.5	36
50	Solution structure and dynamics of yeast elongin C in complex with a von Hippel-Lindau peptide. <i>Journal of Molecular Biology</i> , <b>2001</b> , 312, 177-86	6.5	25
49	Protein production: feeding the crystallographers and NMR spectroscopists. <i>Nature Structural Biology</i> , <b>2000</b> , 7 Suppl, 970-2		135
48	Structural proteomics of an archaeon. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 903-9		247
47	Structural proteomics: prospects for high throughput sample preparation. <i>Progress in Biophysics and Molecular Biology</i> , <b>2000</b> , 73, 339-45	4.7	73

46	Assignment of <sup>1</sup> H(N), <sup>15</sup> N, <sup>13</sup> C(alpha), <sup>13</sup> CO and <sup>13</sup> C(beta) resonances in a 67 kDa p53 dimer using 4D-TROSY NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , <b>2000</b> , 18, 173-6	3	27
45	NMR structure determination and structure-based functional characterization of conserved hypothetical protein MTH1175 from <i>Methanobacterium thermoautotrophicum</i> . <i>Journal of Structural and Functional Genomics</i> , <b>2000</b> , 1, 15-25		22
44	DNA binding specificity studies of four ETS proteins support an indirect read-out mechanism of protein-DNA recognition. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 28363-70	5.4	82
43	Placental transforming growth factor-beta is a downstream mediator of the growth arrest and apoptotic response of tumor cells to DNA damage and p53 overexpression. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 20127-35	5.4	219
42	Crystal structure of dTDP-4-keto-6-deoxy-D-hexulose 3,5-epimerase from <i>Methanobacterium thermoautotrophicum</i> complexed with dTDP. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 24608-12	5.4	48
41	Structure of a conserved domain common to the transcription factors TFIIS, elongin A, and CRSP70. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 31266-8	5.4	48
40	Elongin from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 11174-80	5.4	17
39	Structure-based functional classification of hypothetical protein MTH538 from <i>Methanobacterium thermoautotrophicum</i> . <i>Journal of Molecular Biology</i> , <b>2000</b> , 302, 189-203	6.5	26
38	p73 and p63 are homotetramers capable of weak heterotypic interactions with each other but not with p53. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 18709-14	5.4	123
37	Subunit-specific backbone NMR assignments of a 64 kDa trp repressor/DNA complex: a role for N-terminal residues in tandem binding. <i>Journal of Biomolecular NMR</i> , <b>1998</b> , 11, 307-18	3	19
36	Characterization of the oligomerization defects of two p53 mutants found in families with Li-Fraumeni and Li-Fraumeni-like syndrome. <i>Oncogene</i> , <b>1998</b> , 17, 651-6	9.2	96
35	NMR of large (s> 25 kDa) proteins and protein complexes. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , <b>1998</b> , 32, 277-286	10.4	22
34	Study of a noncovalent trp repressor: DNA operator complex by electrospray ionization time-of-flight mass spectrometry. <i>Protein Science</i> , <b>1998</b> , 7, 1388-95	6.3	68
33	New perceptions of transcription factor properties from NMR. <i>Biochemistry and Cell Biology</i> , <b>1998</b> , 76, 368-378	3.6	6
32	Quantitative hydroxyl radical footprinting reveals cooperative interactions between DNA-binding subdomains of PU.1 and IRF4. <i>Biochemistry</i> , <b>1998</b> , 37, 9802-11	3.2	21
31	Hydroxyl radical footprinting of DNA complexes of the ets domain of PU.1 and its comparison to the crystal structure. <i>Biochemistry</i> , <b>1998</b> , 37, 5129-35	3.2	14
30	Cooperative interaction between the DNA-binding domains of PU.1 and IRF4. <i>Journal of Molecular Biology</i> , <b>1998</b> , 279, 1075-83	6.5	32
29	Yeast transcript elongation factor (TFIIS), structure and function. I: NMR structural analysis of the minimal transcriptionally active region. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 22589-94	5.4	42

28	Yeast transcript elongation factor (TFIIS), structure and function. II: RNA polymerase binding, transcript cleavage, and read-through. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 22595-605	5.4	63
27	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 NOESY. <i>Biochemistry</i> , <b>1997</b> , 36, 5293-9	3.2	20
26	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. <i>EMBO Journal</i> , <b>1997</b> , 16, 6018-33	13	311
25	Assignment of $^{15}\text{N}$ , $^{13}\text{C}$ and $^1\text{H}$ Resonances in an $^{15}\text{N}$ , $^{13}\text{C}$ , $^2\text{H}$ Labeled 64 kDa Trp Repressor-DNA Complex Using Triple-Resonance NMR Spectroscopy and $^2\text{H}$ -Decoupling. <i>Journal of the American Chemical Society</i> , <b>1996</b> , 118, 6570-6579	16.4	127
24	Thermodynamic analysis of the structural stability of the tetrameric oligomerization domain of p53 tumor suppressor. <i>Biochemistry</i> , <b>1995</b> , 34, 5309-16	3.2	122
23	Secretion and circular dichroism analysis of the C-terminal signal peptides of HlyA and LktA. <i>Biochemistry</i> , <b>1995</b> , 34, 4193-201	3.2	48
22	Structural analysis and comparison of the C-terminal transport signal domains of hemolysin A and leukotoxin A. <i>FEBS Letters</i> , <b>1995</b> , 366, 1-5	3.8	20
21	Toward the solution structure of large (>30 kDa) proteins and macromolecular complexes. <i>Techniques in Protein Chemistry</i> , <b>1995</b> , 6, 503-510		1
20	Solution structure of the tetrameric minimum transforming domain of p53. <i>Nature Structural and Molecular Biology</i> , <b>1994</b> , 1, 877-90	17.6	242
19	The solution structures of the trp repressor-operator DNA complex. <i>Journal of Molecular Biology</i> , <b>1994</b> , 238, 592-614	6.5	114
18	A pulsed field gradient isotope-filtered 3D $^{13}\text{C}$ HMQC-NOESY experiment for extracting intermolecular NOE contacts in molecular complexes. <i>FEBS Letters</i> , <b>1994</b> , 350, 87-90	3.8	145
17	An HNCA Pulse Scheme for the Backbone Assignment of $^{15}\text{N}$ , $^{13}\text{C}$ , $^2\text{H}$ -Labeled Proteins: Application to a 37-kDa Trp Repressor-DNA Complex. <i>Journal of the American Chemical Society</i> , <b>1994</b> , 116, 6464-6465	16.4	163
16	A Suite of Triple Resonance NMR Experiments for the Backbone Assignment of $^{15}\text{N}$ , $^{13}\text{C}$ , $^2\text{H}$ Labeled Proteins with High Sensitivity. <i>Journal of the American Chemical Society</i> , <b>1994</b> , 116, 11655-11666	16.4	481
15	The effect of selective deuteration on magnetization transfer in larger proteins. <i>Journal of Biomolecular NMR</i> , <b>1992</b> , 2, 183-94	3	35
14	The solution structures of Escherichia coli trp repressor and trp aporepressor at an intermediate resolution. <i>FEBS Journal</i> , <b>1991</b> , 202, 53-66		54
13	Segmental differences in the stability of the trp-repressor peptide backbone. <i>Journal of Biomolecular NMR</i> , <b>1991</b> , 1, 349-61	3	34
12	Determination of Large Protein Structures from NMR Data: Definition of the Solution Structure of the TRP Repressor <b>1991</b> , 363-374		1
11	The use of selective deuteration for the sequence specific $^1\text{H}$ NMR assignment of larger proteins. <i>Makromolekulare Chemie Macromolecular Symposia</i> , <b>1990</b> , 34, 33-46		4

10	Sequence-specific <sup>1</sup> H NMR assignments and secondary structure in solution of Escherichia coli trp repressor. <i>Biochemistry</i> , <b>1990</b> , 29, 6332-41	3.2	101
9	NMR studies of the Escherichia coli trp aporepressor. Sequence-specific assignment of the aromatic proton resonances. <i>FEBS Journal</i> , <b>1989</b> , 183, 545-53		14
8	NMR assignments for the amino-terminal residues of trp repressor and their role in DNA binding. <i>Biochemistry</i> , <b>1989</b> , 28, 3875-9	3.2	28
7	A correlation between .beta.-hydrogen isotope effects on carbon-13 NMR chemical shifts in unsaturated systems and the strength of hyperconjugative interactions. <i>Journal of the American Chemical Society</i> , <b>1986</b> , 108, 7918-7920	16.4	20
6	Tritium isotope effects on carbon-13 NMR chemical shifts. <i>Journal of the American Chemical Society</i> , <b>1986</b> , 108, 1356-1357	16.4	10
5	Design and characterisation of mutant and wild-type huntingtin proteins produced from a toolkit of scalable eukaryotic expression systems		1
4	A semi-automated organoid screening method demonstrates epigenetic control of intestinal epithelial differentiation		2
3	Discovery of Small-Molecule Antagonists of the PWWP Domain of NSD2		1
2	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress responses		2
1	Pharmacological targeting of a PWWP domain demonstrates cooperative control of NSD2 localization		1