Cheryl H Arrowsmith

List of Publications by Citations

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	Histone recognition and large-scale structural analysis of the human bromodomain family. *Cell*, **2012**, 149, 214-31	56.2	1054
368	Epigenetic protein families: a new frontier for drug discovery. *Nature Reviews Drug Discovery*, **2012**, 11, 384-400	64.1	1003
367	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, 4685-90	11.5	665
366	Protein production and purification. *Nature Methods*, **2008**, 5, 135-46	21.6	655
365	The promise and peril of chemical probes. *Nature Chemical Biology*, **2015**, 11, 536-41	11.7	523
364	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	16.4	481
363	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, 15835-40	11.5	478
362	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. *Blood*, **2011**, 117, 2451-9	2.2	458
361	Ductal pancreatic cancer modeling and drug screening using human pluripotent stem cell- and patient-derived tumor organoids. *Nature Medicine*, **2015**, 21, 1364-71	50.5	403
360	A chemical probe selectively inhibits G9a and GLP methyltransferase activity in cells. *Nature Chemical Biology*, **2011**, 7, 566-74	11.7	386
359	Self-renewal as a therapeutic target in human colorectal cancer. *Nature Medicine*, **2014**, 20, 29-36	50.5	361
358	Structural basis for recognition of hemi-methylated DNA by the SRA domain of human UHRF1. *Nature*, **2008**, 455, 822-5	50.4	353
357	An orally bioavailable chemical probe of the Lysine Methyltransferases EZH2 and EZH1. *ACS Chemical Biology*, **2013**, 8, 1324-34	4.9	313
356	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, 6018-33	13	311
355	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. *Nature*, **2015**, 525, 206-11	50.4	294
354	Structure of the p53 binding domain of HAUSP/USP7 bound to Epstein-Barr nuclear antigen 1 implications for EBV-mediated immortalization. *Molecular Cell*, **2005**, 18, 25-36	17.6	264
353	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. *Nature Structural and Molecular Biology*, **2012**, 19, 1155-60	17.6	253

352	Structural proteomics of an archaeon. *Nature Structural Biology*, **2000**, 7, 903-9		247
351	Solution structure of the tetrameric minimum transforming domain of p53. *Nature Structural and Molecular Biology*, **1994**, 1, 877-90	17.6	242
350	Global analysis of protein folding using massively parallel design, synthesis, and testing. *Science*, **2017**, 357, 168-175	33.3	241
349	A small-molecule inhibitor of BCL6 kills DLBCL cells in vitro and in vivo. *Cancer Cell*, **2010**, 17, 400-11	24.3	230
348	Latent and active p53 are identical in conformation. *Nature Structural Biology*, **2001**, 8, 756-60		227
347	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, 15412-7	11.5	226
346	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. *Journal of Biological Chemistry*, **2000**, 275, 20127-35	5.4	219
345	Human HDAC7 harbors a class IIa histone deacetylase-specific zinc binding motif and cryptic deacetylase activity. *Journal of Biological Chemistry*, **2008**, 283, 11355-63	5.4	214
344	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. *Nature Communications*, **2012**, 3, 1288	17.4	209
343	Recognition and specificity determinants of the human cbx chromodomains. *Journal of Biological Chemistry*, **2011**, 286, 521-9	5.4	205
342	Molecular recognition of p53 and MDM2 by USP7/HAUSP. *Nature Structural and Molecular Biology*, **2006**, 13, 285-91	17.6	201
341	Genome-scale protein expression and structural biology of Plasmodium falciparum and related Apicomplexan organisms. *Molecular and Biochemical Parasitology*, **2007**, 151, 100-10	1.9	199
340	Genome-wide analysis of substrate specificities of the Escherichia coli haloacid dehalogenase-like phosphatase family. *Journal of Biological Chemistry*, **2006**, 281, 36149-61	5.4	198
339	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. *Nature*, **2017**, 549, 227-232	50.4	197
338	Structural biology of human H3K9 methyltransferases. *PLoS ONE*, **2010**, 5, e8570	3.7	184
337	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, 7950-3	8.3	184
336	In situ proteolysis for protein crystallization and structure determination. *Nature Methods*, **2007**, 4, 1019-21	22.6	181
335	An NMR approach to structural proteomics. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 1825-30	11.5	180

334	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	16.4	163
333	Pharmacological targeting of the Wdr5-MLL interaction in C/EBP□N-terminal leukemia. *Nature Chemical Biology*, **2015**, 11, 571-578	11.7	159
332	L3MBTL1 recognition of mono- and dimethylated histones. *Nature Structural and Molecular Biology*, **2007**, 14, 1229-30	17.6	159
331	Protein lysine methyltransferase G9a inhibitors: design, synthesis, and structure activity relationships of 2,4-diamino-7-aminoalkoxy-quinazolines. *Journal of Medicinal Chemistry*, **2010**, 53, 5844-57	8.3	156
330	Discovery of an in vivo chemical probe of the lysine methyltransferases G9a and GLP. *Journal of Medicinal Chemistry*, **2013**, 56, 8931-42	8.3	155
329	Cruciform structures are a common DNA feature important for regulating biological processes. *BMC Molecular Biology*, **2011**, 12, 33	4.5	155
328	Structural and chemical profiling of the human cytosolic sulfotransferases. *PLoS Biology*, **2007**, 5, e97	9.7	153
327	Recognition of multivalent histone states associated with heterochromatin by UHRF1 protein. *Journal of Biological Chemistry*, **2011**, 286, 24300-11	5.4	149
326	A pulsed field gradient isotope-filtered 3D 13C HMQC-NOESY experiment for extracting intermolecular NOE contacts in molecular complexes. *FEBS Letters*, **1994**, 350, 87-90	3.8	145
325	Structural basis for molecular recognition and presentation of histone H3 by WDR5. *EMBO Journal*, **2006**, 25, 4245-52	13	143
324	Protein aggregates are recruited to aggresome by histone deacetylase 6 via unanchored ubiquitin C termini. *Journal of Biological Chemistry*, **2012**, 287, 2317-27	5.4	141
323	Characterization of segments from the central region of BRCA1: an intrinsically disordered scaffold for multiple protein-protein and protein-DNA interactions?. *Journal of Molecular Biology*, **2005**, 345, 275-87	6.5	141
322	The EED protein-protein interaction inhibitor A-395 inactivates the PRC2 complex. *Nature Chemical Biology*, **2017**, 13, 389-395	11.7	139
321	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, 871-84	3.5	137
320	Protein production: feeding the crystallographers and NMR spectroscopists. *Nature Structural Biology*, **2000**, 7 Suppl, 970-2		135
319	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. *Cancer Cell*, **2016**, 30, 891-908	24.3	135
318	A Potent, Selective, and Cell-Active Inhibitor of Human Type I Protein Arginine Methyltransferases. *ACS Chemical Biology*, **2016**, 11, 772-781	4.9	131
317	Discovery of a chemical probe for the L3MBTL3 methyllysine reader domain. *Nature Chemical Biology*, **2013**, 9, 184-91	11.7	129

316	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, 1288-98	12.6	129
315	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, 18978-83	11.5	127
314	Assignment of 15N, 13Cα, 13Cβ, and HN Resonances in an 15N,13C,2H Labeled 64 kDa Trp Repressor·Operator Complex Using Triple-Resonance NMR Spectroscopy and 2H-Decoupling. *Journal of the American Chemical Society*, **1996**, 118, 6570-6579	16.4	127
313	Protein interaction domains of the ubiquitin-specific protease, USP7/HAUSP. *Journal of Biological Chemistry*, **2003**, 278, 47753-61	5.4	125
312	p73 and p63 are homotetramers capable of weak heterotypic interactions with each other but not with p53. *Journal of Biological Chemistry*, **1999**, 274, 18709-14	5.4	123
311	Thermodynamic analysis of the structural stability of the tetrameric oligomerization domain of p53 tumor suppressor. *Biochemistry*, **1995**, 34, 5309-16	3.2	122
310	(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, 12853-8	11.5	120
309	BET bromodomain inhibition enhances T cell persistence and function in adoptive immunotherapy models. *Journal of Clinical Investigation*, **2016**, 126, 3479-94	15.9	118
308	The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. *Nature Structural Biology*, **2002**, 9, 27-31		115
307	The solution structures of the trp repressor-operator DNA complex. *Journal of Molecular Biology*, **1994**, 238, 592-614	6.5	114
306	Tandem protein interaction modules organize the ubiquitin-dependent response to DNA double-strand breaks. *Molecular Cell*, **2012**, 47, 383-95	17.6	106
305	Small-molecule ligands of methyl-lysine binding proteins. *Journal of Medicinal Chemistry*, **2011**, 54, 2504-11	8.3	106
304	Eme1 is involved in DNA damage processing and maintenance of genomic stability in mammalian cells. *EMBO Journal*, **2003**, 22, 6137-47	13	106
303	Optimization of cellular activity of G9a inhibitors 7-aminoalkoxy-quinazolines. *Journal of Medicinal Chemistry*, **2011**, 54, 6139-50	8.3	103
302	Integrating structure, bioinformatics, and enzymology to discover function: BioH, a new carboxylesterase from Escherichia coli. *Journal of Biological Chemistry*, **2003**, 278, 26039-45	5.4	103
301	WD40 repeat domain proteins: a novel target class?. *Nature Reviews Drug Discovery*, **2017**, 16, 773-786	64.1	101
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299	Sequence-specific 1H NMR assignments and secondary structure in solution of Escherichia coli trp repressor. *Biochemistry*, **1990**, 29, 6332-41	3.2	101

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296	Small-molecule inhibition of MLL activity by disruption of its interaction with WDR5. *Biochemical Journal*, **2013**, 449, 151-9	3.8	100
295	Structural insights into aldosterone synthase substrate specificity and targeted inhibition. *Molecular Endocrinology*, **2013**, 27, 315-24		97
294	Characterization of the oligomerization defects of two p53 mutants found in families with Li-Fraumeni and Li-Fraumeni-like syndrome. *Oncogene*, **1998**, 17, 651-6	9.2	96
293	A p53 Super-tumor Suppressor Reveals a Tumor Suppressive p53-Ptpn14-Yap Axis in Pancreatic Cancer. *Cancer Cell*, **2017**, 32, 460-473.e6	24.3	93
292	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. *Cancer Cell*, **2019**, 36, 194-209.e9	24.3	92
291	Enzyme genomics: Application of general enzymatic screens to discover new enzymes. *FEMS Microbiology Reviews*, **2005**, 29, 263-79	15.1	89
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288	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. *Nature Methods*, **2015**, 12, 725-31	21.6	86
287	Accessibility of different histone H3-binding domains of UHRF1 is allosterically regulated by phosphatidylinositol 5-phosphate. *Molecular Cell*, **2014**, 54, 905-19	17.6	86
286	Structural proteomics: toward high-throughput structural biology as a tool in functional genomics. *Accounts of Chemical Research*, **2003**, 36, 183-9	24.3	84
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284	Structure of Escherichia coli ribose-5-phosphate isomerase: a ubiquitous enzyme of the pentose phosphate pathway and the Calvin cycle. *Structure*, **2003**, 11, 31-42	5.2	82
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282	A human ubiquitin conjugating enzyme (E2)-HECT E3 ligase structure-function screen. *Molecular and Cellular Proteomics*, **2012**, 11, 329-41	7.6	81
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277	Methylation-state-specific recognition of histones by the MBT repeat protein L3MBTL2. *Nucleic Acids Research*, **2009**, 37, 2204-10	20.1	77
276	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, 182-94	6.5	77
275	Trimethylation of histone H3 lysine 36 by human methyltransferase PRDM9 protein. *Journal of Biological Chemistry*, **2014**, 289, 12177-12188	5.4	76
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272	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. *Nucleic Acids Research*, **2012**, 40, 6353-66	20.1	75
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261	Study of a noncovalent trp repressor: DNA operator complex by electrospray ionization time-of-flight mass spectrometry. *Protein Science*, **1998**, 7, 1388-95	6.3	68
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254	Assay interference and off-target liabilities of reported histone acetyltransferase inhibitors. *Nature Communications*, **2017**, 8, 1527	17.4	64
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252	A SPOT on the chromatin landscape? Histone peptide arrays as a tool for epigenetic research. *Trends in Biochemical Sciences*, **2008**, 33, 305-13	10.3	63
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243	Crystal structure of Thermotoga maritima 0065, a member of the IclR transcriptional factor family. *Journal of Biological Chemistry*, **2002**, 277, 19183-90	5.4	58
242	Small-molecule ligands of methyl-lysine binding proteins: optimization of selectivity for L3MBTL3. *Journal of Medicinal Chemistry*, **2013**, 56, 7358-71	8.3	57
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238	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. *Genes and Development*, **2016**, 30, 772-85	12.6	54
237	RPRD1A and RPRD1B are human RNA polymerase II C-terminal domain scaffolds for Ser5 dephosphorylation. *Nature Structural and Molecular Biology*, **2014**, 21, 686-695	17.6	54
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