John H Bushweller

List of Publications by Year
in descending order

112 papers	7,406 citations	57758 44 h-index	56724 83 g-index
118 all docs	118 docs citations	118 times ranked	7825 citing authors

#	Article	IF	Citations
1	Haploinsufficiency of CBFA2 causes familial thrombocytopenia with propensity to develop acute myelogenous leukaemia. Nature Genetics, 1999, 23, 166-175.	21.4	1,036
2	The CBFÎ² Subunit Is Essential for CBFÎ±2 (AML1) Function In Vivo. Cell, 1996, 87, 697-708.	28.9	620
3	Targeting transcription factors in cancer â€" from undruggable to reality. Nature Reviews Cancer, 2019, 19, 611-624.	28.4	515
4	Membrane structure and fusion-triggering conformational change of the fusion domain from influenza hemagglutinin. Nature Structural Biology, 2001, 8, 715-720.	9.7	406
5	Structure of outer membrane protein A transmembrane domain by NMR spectroscopy. Nature Structural Biology, 2001, 8, 334-338.	9.7	363
6	Structural and functional characterization of the mutant Escherichia coli glutaredoxin (C14.fwdarw.S) and its mixed disulfide with glutathione. Biochemistry, 1992, 31, 9288-9293.	2.5	215
7	NMR Solution Structure of the Integral Membrane Enzyme DsbB: Functional Insights into DsbB-Catalyzed Disulfide Bond Formation. Molecular Cell, 2008, 31, 896-908.	9.7	171
8	Structure of the MLL CXXC domainâ€"DNA complex and its functional role in MLL-AF9 leukemia. Nature Structural and Molecular Biology, 2010, 17, 62-68.	8.2	159
9	Site-Directed Parallel Spin-Labeling and Paramagnetic Relaxation Enhancement in Structure Determination of Membrane Proteins by Solution NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 4389-4397.	13.7	149
10	The Nuclear Magnetic Resonance Solution Structure of the Mixed Disulfide between Escherichia coli Glutaredoxin(C14S) and Glutathione. Journal of Molecular Biology, 1994, 235, 1585-1597.	4.2	134
11	The DCX-domain tandems of doublecortin and doublecortin-like kinase. Nature Structural and Molecular Biology, 2003, 10, 324-333.	8.2	122
12	The tetramer structure of the Nervy homology two domain, NHR2, is critical for AML1/ETO's activity. Cancer Cell, 2006, 9, 249-260.	16.8	121
13	Allosteric Inhibition of the Protein-Protein Interaction between the Leukemia-Associated Proteins Runx1 and CBFÎ². Chemistry and Biology, 2007, 14, 1186-1197.	6.0	114
14	NMR structure of oxidized Escherichia coli glutaredoxin: Comparison with reduced E. coli glutaredoxin and functionally related proteins. Protein Science, 1992, 1, 310-321.	7.6	111
15	Disease mutations in RUNX1 and RUNX2 create nonfunctional, dominant-negative, or hypomorphic alleles. EMBO Journal, 2007, 26, 1163-1175.	7.8	106
16	Structural Basis for Recognition of SMRT/N-CoR by the MYND Domain and Its Contribution to AML1/ETO's Activity. Cancer Cell, 2007, 11, 483-497.	16.8	106
17	A small-molecule inhibitor of the aberrant transcription factor CBFÎ²-SMMHC delays leukemia in mice. Science, 2015, 347, 779-784.	12.6	104
18	Degree of Recruitment of DOT1L to MLL-AF9 Defines Level of H3K79 Di- and Tri-methylation on Target Genes and Transformation Potential. Cell Reports, 2015, 11, 808-820.	6.4	98

#	Article	IF	Citations
19	Sequence-specific1H n.m.r. assignments and determination of the three-dimensional structure of reduced escherichia coli glutaredoxin. Journal of Molecular Biology, 1991, 221, 1311-1324.	4.2	92
20	Leukemia Fusion Target AF9 Is an Intrinsically Disordered Transcriptional Regulator that Recruits Multiple Partners via Coupled Folding and Binding. Structure, 2013, 21, 176-183.	3.3	87
21	MLL protects CpG clusters from methylation within the Hoxa9 gene, maintaining transcript expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7517-7522.	7.1	86
22	The NOESY Jigsaw: Automated Protein Secondary Structure and Main-Chain Assignment from Sparse, Unassigned NMR Data. Journal of Computational Biology, 2000, 7, 537-558.	1.6	85
23	Small Molecule Inhibitor of CBFÎ²-RUNX Binding for RUNX Transcription Factor Driven Cancers. EBioMedicine, 2016, 8, 117-131.	6.1	84
24	The NMR solution structure of human glutaredoxin in the fully reduced form. Journal of Molecular Biology, 1998, 280, 687-701.	4.2	81
25	The Ig fold of the core binding factor Î± Runt domain is a member of a family of structurally and functionally related Ig-fold DNA-binding domains. Structure, 1999, 7, 1247-1256.	3.3	81
26	Charged Gels as Orienting Media for Measurement of Residual Dipolar Couplings in Soluble and Integral Membrane Proteins. Journal of the American Chemical Society, 2004, 126, 16259-16266.	13.7	81
27	Increasing the Accuracy of Solution NMR Structures of Membrane Proteins by Application of Residual Dipolar Couplings. High-Resolution Structure of Outer Membrane Protein A. Journal of the American Chemical Society, 2006, 128, 6947-6951.	13.7	75
28	RUNX1-targeted therapy for AML expressing somatic or germline mutation in RUNX1. Blood, 2019, 134, 59-73.	1.4	75
29	Application of Fragment-Based Drug Discovery to Membrane Proteins: Identification of Ligands of the Integral Membrane Enzyme DsbB. Chemistry and Biology, 2010, 17, 881-891.	6.0	70
30	Solution structure of core binding factor beta and map of the CBF alpha binding site. Nature Structural Biology, 1999, 6, 624-627.	9.7	68
31	3D 13C-15N-heteronuclear two-spin coherence spectroscopy for polypeptide backbone assignments in 13C-15N-double-labeled proteins. Journal of Biomolecular NMR, 1993, 3, 127-32.	2.8	66
32	Membrane Structures of the Hemifusion-Inducing Fusion Peptide Mutant G1S and theFusion-Blocking Mutant G1V of Influenza Virus HemagglutininSuggest a Mechanism for Pore Opening in MembraneFusion. Journal of Virology, 2005, 79, 12065-12076.	3.4	66
33	Altered affinity of CBFÎ²-SMMHC for Runx1 explains its role in leukemogenesis. Nature Structural Biology, 2002, 9, 674-679.	9.7	65
34	CBFÎ² allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium. Nature Structural and Molecular Biology, 2004, 11, 901-906.	8.2	65
35	RUNX1 is required for oncogenic Myb and Myc enhancer activity in T-cell acute lymphoblastic leukemia. Blood, 2017, 130, 1722-1733.	1.4	64
36	Biochemical and Biophysical Properties of the Core-binding Factor Î±2 (AML1) DNA-binding Domain. Journal of Biological Chemistry, 1996, 271, 26251-26260.	3.4	62

#	Article	IF	Citations
37	High resolution structure of the HDGF PWWP domain: A potential DNA binding domain. Protein Science, 2006, 15, 314-323.	7.6	62
38	Structure, dynamics and function of the outer membrane protein A (OmpA) and influenza hemagglutinin fusion domain in detergent micelles by solution NMR. FEBS Letters, 2003, 555, 139-143.	2.8	59
39	The PHD3 Domain of MLL Acts as a CYP33-Regulated Switch between MLL-Mediated Activation and Repression,. Biochemistry, 2010, 49, 6576-6586.	2.5	56
40	Energetic and Functional Contribution of Residues in the Core Binding Factor Î² (CBFÎ²) Subunit to Heterodimerization with CBFÎ±. Journal of Biological Chemistry, 2000, 275, 39579-39588.	3.4	55
41	Synthesis and evaluation of substituted 4-aryloxy- and 4-arylsulfanyl-phenyl-2-aminothiazoles as inhibitors of human breast cancer cell proliferation. Bioorganic and Medicinal Chemistry, 2004, 12, 1029-1036.	3.0	55
42	Synthesis of dimetallaazacyclobutenes via reaction of polynuclear heteroaromatic nitrogen compounds with triruthenium dodecacarbonyl: reactivity and structural elucidation. Organometallics, 1986, 5, 2193-2198.	2.3	53
43	CBFÎ² is critical for AML1-ETO and TEL-AML1 activity. Blood, 2009, 113, 3070-3079.	1.4	51
44	Biophysical characterization of interactions between the core binding factor Î± and Î² subunits and DNA. FEBS Letters, 2000, 470, 167-172.	2.8	47
45	Structural and dynamic studies of the transcription factor ERG reveal DNA binding is allosterically autoinhibited. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13374-13379.	7.1	47
46	Binding specificity and mechanistic insight into glutaredoxin-catalyzed protein disulfide reduction 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 292, 151-161.	4.2	44
47	Comparison of Backbone Dynamics of Reduced and OxidizedEscherichia coliGlutaredoxin-1 Using15N NMR Relaxation Measurementsâ€. Biochemistry, 1997, 36, 5029-5044.	2.5	42
48	Accelerated Leukemogenesis by Truncated CBFÎ²-SMMHC Defective in High-Affinity Binding with RUNX1. Cancer Cell, 2010, 17, 455-468.	16.8	39
49	RUNX proteins desensitize multiple myeloma to lenalidomide via protecting IKZFs from degradation. Leukemia, 2019, 33, 2006-2021.	7.2	36
50	Energetic Contribution of Residues in the Runx1 Runt Domain to DNA Binding. Journal of Biological Chemistry, 2003, 278, 33088-33096.	3.4	35
51	RUNX1 and RUNX2 transcription factors function in opposing roles to regulate breast cancer stem cells. Journal of Cellular Physiology, 2020, 235, 7261-7272.	4.1	34
52	Structure of the AML1-ETO eTAFH domainâ€“HEB peptide complex and its contribution to AML1-ETO activity. Blood, 2009, 113, 3558-3567.	1.4	33
53	Hepatoma Derived Growth Factor is a Nuclear Targeted Mitogen. Current Drug Targets, 2003, 4, 367-371.	2.1	32
54	Tom1 Modulates Binding of Tollip to Phosphatidylinositol 3-Phosphate via a Coupled Folding and Binding Mechanism. Structure, 2015, 23, 1910-1920.	3.3	28

#	Article	IF	Citations
55	TNFâ€Î± signaling regulates RUNX1 function in endothelial cells. FASEB Journal, 2021, 35, e21155.	0.5	28
56	Functional Specificity of CpG DNA-binding CXXC Domains in Mixed Lineage Leukemia. Journal of Biological Chemistry, 2013, 288, 29901-29910.	3.4	27
57	Mutagenesis of the Runt Domain Defines Two Energetic Hot Spots for Heterodimerization with the Core Binding Factor Î² Subunit. Journal of Biological Chemistry, 2003, 278, 33097-33104.	3.4	26
58	Optimal Mutation Sites for PRE Data Collection and Membrane Protein Structure Prediction. Structure, 2011, 19, 484-495.	3.3	24
59	CBFâ€”A biophysical perspective. Seminars in Cell and Developmental Biology, 2000, 11, 377-382.	5.0	21
60	Overexpression, Purification, and Biophysical Characterization of the Heterodimerization Domain of the Core-binding Factor Î² Subunit. Journal of Biological Chemistry, 1998, 273, 2480-2487.	3.4	20
61	MQ-hCN-based pulse sequences for the measurement of 13C1'-1H1', 13C1'-15N, 1H1'-15N, 13C1'-13C2', 1H1'-13C2',13C6/8-1H6/8, 13C6/8-15N, 1H6/8-15N, 13C6-13C5, 1H6-13C5 dipolar couplings in 13C, 15N-labeled DNA (and RNA). Journal of Biomolecular NMR, 2002, 22, 9-20.	2.8	19
62	Probing the Supramodular Architecture of a Multidomain Protein: The Structure of Syntenin in Solution. Structure, 2005, 13, 319-327.	3.3	19
63	The solution structure and dynamics of the DHâ€PH module of PDZRhoGEF in isolation and in complex with nucleotideâ€free RhoA. Protein Science, 2009, 18, 2067-2079.	7.6	18
64	Structure of the AML1-ETO NHR3â€“PKA(RIIÎ±) Complex and Its Contribution to AML1-ETO Activity. Journal of Molecular Biology, 2010, 402, 560-577.	4.2	18
65	Solution structure and elevator mechanism of the membrane electron transporter CcdA. Nature Structural and Molecular Biology, 2018, 25, 163-169.	8.2	18
66	Protein Disulfide Exchange by the Intramembrane Enzymes DsbB, DsbD, and CcdA. Journal of Molecular Biology, 2020, 432, 5091-5103.	4.2	18
67	An erythroid-to-myeloid cell fate conversion is elicited by LSD1 inactivation. Blood, 2021, 138, 1691-1704.	1.4	17
68	Preparation, Characterization, and Complete Heteronuclear NMR Resonance Assignments of the Glutaredoxin (C14S)â^Ribonucleotide Reductase B1 737â^761 (C754S) Mixed Disulfideâ€. Biochemistry, 1998, 37, 5849-5857.	2.5	16
69	Structural and functional characterization of Runx1, CBFÎ², and CBFÎ²-SMMHC. Blood Cells, Molecules, and Diseases, 2003, 30, 147-156.	1.4	16
70	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. Proteins: Structure, Function and Bioinformatics, 2006, 64, 874-882.	2.6	15
71	The role of CBFÎ² in AML1-ETO's activity. Blood, 2009, 114, 2849-2850.	1.4	15
72	BCOR Binding to MLL-AF9 Is Essential for Leukemia via Altered EYA1, SIX, and MYC Activity. Blood Cancer Discovery, 2020, 1, 162-177.	5.0	15

#	Article	IF	Citations
73	The Intrinsically Disordered Proteins MLLT3 (AF9) and MLLT1 (ENL) â€“ Multimodal Transcriptional Switches With Roles in Normal Hematopoiesis, MLL Fusion Leukemia, and Kidney Cancer. Journal of Molecular Biology, 2022, 434, 167117.	4.2	15
74	KIX domain determines a selective tumor-promoting role for EP300 and its vulnerability in small cell lung cancer. Science Advances, 2022, 8, eabl4618.	10.3	15
75	A PCR-based method for uniform 13 C/15 N labeling of long DNA oligomers. FEBS Letters, 1998, 436, 372-376.	2.8	14
76	Small molecule inhibition of the CBFÎ²/RUNX interaction decreases ovarian cancer growth and migration through alterations in genes related to epithelial-to-mesenchymal transition. Gynecologic Oncology, 2018, 149, 350-360.	1.4	14
77	Targeting Runt-Related Transcription Factor 1 Prevents Pulmonary Fibrosis and Reduces Expression of Severe Acute Respiratory Syndrome Coronavirus 2 Host Mediators. American Journal of Pathology, 2021, 191, 1193-1208.	3.8	14
78	Complete ¹H, ¹³C, and ¹⁵N NMR resonance assignments and secondary structure of human glutaredoxin in the fully reduced form. Protein Science, 1997, 6, 383-390.	7.6	12
79	A Mutation in the S-switch Region of the Runt Domain Alters the Dynamics of an Allosteric Network Responsible for CBFÎ² Regulation. Journal of Molecular Biology, 2006, 364, 1073-1083.	4.2	12
80	Bacillus anthracis Peptidoglycan Integrity Is Disrupted by the Chemokine CXCL10 through the FtsE/X Complex. Frontiers in Microbiology, 2017, 8, 740.	3.5	12
81	Sulfoxide analogs of dihydro- and tetrahydroprephenate as inhibitors of prephenate dehydratase. Journal of Organic Chemistry, 1989, 54, 2404-2409.	3.2	11
82	An Optimized PCR-Based Procedure for Production of 13C/15N-Labeled DNA. Biochemical and Biophysical Research Communications, 2001, 284, 295-300.	2.1	11
83	A tool compound targeting the core binding factor Runt domain to disrupt binding to CBFÎ² in leukemic cells. Leukemia and Lymphoma, 2018, 59, 2188-2200.	1.3	11
84	Stereodynamics of 9,11-Diphenyl-10-azatetracyclo[6.3.0.0.4,110.5,9]undecanes. Highly Restricted Nitrogen Inversion and Isolated Phenyl Rotation. X-ray Crystallographic, Dynamic NMR, and Molecular Mechanics Studies. Journal of Organic Chemistry, 1996, 61, 4319-4327.	3.2	10
85	Structure and Biophysics of CBFÎ²/RUNX and Its Translocation Products. Advances in Experimental Medicine and Biology, 2017, 962, 21-31.	1.6	10
86	Synthesis ofCis- andTrans-1-methylcyclohexane-1,4-diols and Their 4-Hemisuccinate Esters. Synthetic Communications, 1989, 19, 745-754.	2.1	9
87	Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO.. Blood, 2005, 106, 2854-2854.	1.4	9
88	Complete heteronuclear NMR resonance assignments and secondary structure of core binding factor beta (1-141). Journal of Biomolecular NMR, 1998, 12, 459-460.	2.8	8
89	Inhibition of the RUNX1-CBFÎ² transcription factor complex compromises mammary epithelial cell identity: a phenotype potentially stabilized by mitotic gene bookmarking. Oncotarget, 2020, 11, 2512-2530.	1.8	8
90	Small-Molecule Inhibitors of the MLL1 CXXC Domain, an Epigenetic Reader of DNA Methylation. ACS Medicinal Chemistry Letters, 2022, 13, 1363-1369.	2.8	8

#	Article	IF	Citations
91	Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. Molecular Pharmacology, 2020, 98, 648-657.	2.3	7
92	Biosynthetic 15N and 13C isotope labelling of glutathione in the mixed disulfide with Escherichia coli glutaredoxin documented by sequence-specific NMR assignments. FEBS Journal, 1993, 218, 327-334.	0.2	6
93	1H, 13C and 15N NMR resonance assignments of vaccinia glutaredoxin-1 in the fully reduced form. , 1998, 12, 353-355.		5
94	Importance of a specific amino acid pairing for murine MLL leukemias driven by MLLT1/3 or AFF1/4. Leukemia Research, 2014, 38, 1309-1315.	0.8	5
95	The interaction between RUNX2 and core binding factor beta as a potential therapeutic target in canine osteosarcoma. Veterinary and Comparative Oncology, 2020, 18, 52-63.	1.8	5
96	Molecular Basis and Targeted Inhibition of CBFÎ²-SMMHC Acute Myeloid Leukemia. Advances in Experimental Medicine and Biology, 2017, 962, 229-244.	1.6	3
97	Assignment of 1H, 13C and 15N resonances of the N-terminal microtubule-binding domain of human doublecortin. Journal of Biomolecular NMR, 2003, 25, 81-82.	2.8	2
98	Direct Binding of BCOR, but Not CBX8, to MLL-AF9 Is Essential for MLL-AF9 Leukemia Via Regulation of the EYA1/SIX1 Gene Network. Blood, 2018, 132, 1316-1316.	1.4	2
99	A Small Molecule Inhibitor of the CBFÎ²-SMMHC/RUNX Interaction Attenuates Inv(16) Leukemia in Vivo. Blood, 2012, 120, 286-286.	1.4	1
100	Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO.. Blood, 2004, 104, 482-482.	1.4	1
101	Biochemical and In Vivo Characterization of Amino Acid Substitutions in the Runx1 (AML1) Runt Domain Found in FPD/AML, AML M0, and Cleidocranial Dysplasia (CCD) Patients.. Blood, 2004, 104, 464-464.	1.4	1
102	Development of Small Molecule Inhibitors of the AML1-ETO and CBFÎ²-SMMHC Oncoproteins.. Blood, 2007, 110, 1591-1591.	1.4	1
103	Development of Small Molecule Inhibitor of the AML1-ETO Oncoprotein.. Blood, 2005, 106, 1515-1515.	1.4	0
104	The CBFb-SMMHC Oncoprotein Inhibits Binding of the Runx1 Runt Domain to DNA.. Blood, 2005, 106, 2709-2709.	1.4	0
105	Development of Small Molecule Inhibitors of the CBFÎ²-SMMHC Oncoprotein.. Blood, 2005, 106, 3359-3359.	1.4	0
106	Structural Basis for MLL Cxxc Domain Protection against CpG DNA Methylation and the Essential Role of This Function in MLL-AF9 Leukemia.. Blood, 2009, 114, 763-763.	1.4	0
107	DNMT1 Cxxc Domain Can Functionally Substitute In An MLL Fusion Protein. Blood, 2010, 116, 4193-4193.	1.4	0
108	The Role of the Intrinsically Disordered and Multifunctional AF9 C-Terminal Domain in MLL-AF9 Leukemia,. Blood, 2011, 118, 3464-3464.	1.4	0

#	Article	IF	Citations
109	Structural and Functional Studies Of The Intrinsically Disordered Protein AF9 In MLL-AF9 Leukemia. Blood, 2013, 122, 3762-3762.	1.4	0
110	Selective Inhibition of the Leukemia Fusion Protein CBFÎ²-SMMHC By Small Molecule AI-10-49 in the Treatment of Inv(16) AML. Blood, 2014, 124, 390-390.	1.4	0
111	CBFÎ²-SMMHC Inhibition Disrupts Enhancer Chromatin Dynamics and Represses MYC Transcriptional Program in Inv(16) Leukemia. Blood, 2017, 130, 784-784.	1.4	0
112	The CBFÎ²-SMMHC/NRP1 Axis Regulates FLT3 and TGF-Beta Pathways in Inv(16) Acute Myeloid Leukemia. Blood, 2021, 138, 3314-3314.	1.4	0