

John H Bushweller

List of Publications by Year in descending order

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112
papers

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57758

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docs citations

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#	ARTICLE	IF	CITATIONS
1	The Intrinsically Disordered Proteins MLLT3 (AF9) and MLLT1 (ENL) are Multimodal Transcriptional Switches With Roles in Normal Hematopoiesis, MLL Fusion Leukemia, and Kidney Cancer. <i>Journal of Molecular Biology</i> , 2022, 434, 167117.	4.2	15
2	KIX domain determines a selective tumor-promoting role for EP300 and its vulnerability in small cell lung cancer. <i>Science Advances</i> , 2022, 8, eabl4618.	10.3	15
3	Small-Molecule Inhibitors of the MLL1 CXXC Domain, an Epigenetic Reader of DNA Methylation. <i>ACS Medicinal Chemistry Letters</i> , 2022, 13, 1363-1369.	2.8	8
4	TNF signaling regulates RUNX1 function in endothelial cells. <i>FASEB Journal</i> , 2021, 35, e21155.	0.5	28
5	An erythroid-to-myeloid cell fate conversion is elicited by LSD1 inactivation. <i>Blood</i> , 2021, 138, 1691-1704.	1.4	17
6	Targeting Runt-Related Transcription Factor 1 Prevents Pulmonary Fibrosis and Reduces Expression of Severe Acute Respiratory Syndrome Coronavirus 2 Host Mediators. <i>American Journal of Pathology</i> , 2021, 191, 1193-1208.	3.8	14
7	The CBF ² -SMMHC/NRP1 Axis Regulates FLT3 and TGF-Beta Pathways in Inv(16) Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 3314-3314.	1.4	0
8	The interaction between RUNX2 and core binding factor beta as a potential therapeutic target in canine osteosarcoma. <i>Veterinary and Comparative Oncology</i> , 2020, 18, 52-63.	1.8	5
9	Structure of the Complex of an Iminopyridinedione Protein Tyrosine Phosphatase 4A3 Phosphatase Inhibitor with Human Serum Albumin. <i>Molecular Pharmacology</i> , 2020, 98, 648-657.	2.3	7
10	BCOR Binding to MLL-AF9 Is Essential for Leukemia via Altered EYA1, SIX, and MYC Activity. <i>Blood Cancer Discovery</i> , 2020, 1, 162-177.	5.0	15
11	RUNX1 and RUNX2 transcription factors function in opposing roles to regulate breast cancer stem cells. <i>Journal of Cellular Physiology</i> , 2020, 235, 7261-7272.	4.1	34
12	Protein Disulfide Exchange by the Intramembrane Enzymes DsbB, DsbD, and CcdA. <i>Journal of Molecular Biology</i> , 2020, 432, 5091-5103.	4.2	18
13	Inhibition of the RUNX1-CBF ² transcription factor complex compromises mammary epithelial cell identity: a phenotype potentially stabilized by mitotic gene bookmarking. <i>Oncotarget</i> , 2020, 11, 2512-2530.	1.8	8
14	Targeting transcription factors in cancer from undruggable to reality. <i>Nature Reviews Cancer</i> , 2019, 19, 611-624.	28.4	515
15	RUNX1-targeted therapy for AML expressing somatic or germline mutation in RUNX1. <i>Blood</i> , 2019, 134, 59-73.	1.4	75
16	RUNX proteins desensitize multiple myeloma to lenalidomide via protecting IKZFs from degradation. <i>Leukemia</i> , 2019, 33, 2006-2021.	7.2	36
17	Solution structure and elevator mechanism of the membrane electron transporter CcdA. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 163-169.	8.2	18
18	A tool compound targeting the core binding factor Runt domain to disrupt binding to CBF ² in leukemic cells. <i>Leukemia and Lymphoma</i> , 2018, 59, 2188-2200.	1.3	11

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19	Small molecule inhibition of the CBF $\hat{1}$ ² /RUNX interaction decreases ovarian cancer growth and migration through alterations in genes related to epithelial-to-mesenchymal transition. <i>Gynecologic Oncology</i> , 2018, 149, 350-360.	1.4	14
20	Direct Binding of BCOR, but Not CBX8, to MLL-AF9 Is Essential for MLL-AF9 Leukemia Via Regulation of the EYA1/SIX1 Gene Network. <i>Blood</i> , 2018, 132, 1316-1316.	1.4	2
21	Structure and Biophysics of CBF $\hat{1}$ ² /RUNX and Its Translocation Products. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 21-31.	1.6	10
22	Molecular Basis and Targeted Inhibition of CBF $\hat{1}$ ² -SMMHC Acute Myeloid Leukemia. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 229-244.	1.6	3
23	RUNX1 is required for oncogenic Myb and Myc enhancer activity in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2017, 130, 1722-1733.	1.4	64
24	Bacillus anthracis Peptidoglycan Integrity Is Disrupted by the Chemokine CXCL10 through the FtsE/X Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 740.	3.5	12
25	CBF $\hat{1}$ ² -SMMHC Inhibition Disrupts Enhancer Chromatin Dynamics and Represses MYC Transcriptional Program in Inv(16) Leukemia. <i>Blood</i> , 2017, 130, 784-784.	1.4	0
26	Small Molecule Inhibitor of CBF $\hat{1}$ ² -RUNX Binding for RUNX Transcription Factor Driven Cancers. <i>EBioMedicine</i> , 2016, 8, 117-131.	6.1	84
27	A small-molecule inhibitor of the aberrant transcription factor CBF $\hat{1}$ ² -SMMHC delays leukemia in mice. <i>Science</i> , 2015, 347, 779-784.	12.6	104
28	Tom1 Modulates Binding of Tollip to Phosphatidylinositol 3-Phosphate via a Coupled Folding and Binding Mechanism. <i>Structure</i> , 2015, 23, 1910-1920.	3.3	28
29	Degree of Recruitment of DOT1L to MLL-AF9 Defines Level of H3K79 Di- and Tri-methylation on Target Genes and Transformation Potential. <i>Cell Reports</i> , 2015, 11, 808-820.	6.4	98
30	Importance of a specific amino acid pairing for murine MLL leukemias driven by MLLT1/3 or AFF1/4. <i>Leukemia Research</i> , 2014, 38, 1309-1315.	0.8	5
31	Selective Inhibition of the Leukemia Fusion Protein CBF $\hat{1}$ ² -SMMHC By Small Molecule AI-10-49 in the Treatment of Inv(16) AML. <i>Blood</i> , 2014, 124, 390-390.	1.4	0
32	Leukemia Fusion Target AF9 Is an Intrinsically Disordered Transcriptional Regulator that Recruits Multiple Partners via Coupled Folding and Binding. <i>Structure</i> , 2013, 21, 176-183.	3.3	87
33	Functional Specificity of CpG DNA-binding CXXC Domains in Mixed Lineage Leukemia. <i>Journal of Biological Chemistry</i> , 2013, 288, 29901-29910.	3.4	27
34	Structural and dynamic studies of the transcription factor ERG reveal DNA binding is allosterically autoinhibited. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13374-13379.	7.1	47
35	Structural and Functional Studies Of The Intrinsically Disordered Protein AF9 In MLL-AF9 Leukemia. <i>Blood</i> , 2013, 122, 3762-3762.	1.4	0
36	A Small Molecule Inhibitor of the CBF $\hat{1}$ ² -SMMHC/RUNX Interaction Attenuates Inv(16) Leukemia in Vivo. <i>Blood</i> , 2012, 120, 286-286.	1.4	1

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37	Optimal Mutation Sites for PRE Data Collection and Membrane Protein Structure Prediction. <i>Structure</i> , 2011, 19, 484-495.	3.3	24
38	The Role of the Intrinsically Disordered and Multifunctional AF9 C-Terminal Domain in MLL-AF9 Leukemia. <i>Blood</i> , 2011, 118, 3464-3464.	1.4	0
39	Accelerated Leukemogenesis by Truncated CBF $\hat{2}$ -SMMHC Defective in High-Affinity Binding with RUNX1. <i>Cancer Cell</i> , 2010, 17, 455-468.	16.8	39
40	Application of Fragment-Based Drug Discovery to Membrane Proteins: Identification of Ligands of the Integral Membrane Enzyme DsbB. <i>Chemistry and Biology</i> , 2010, 17, 881-891.	6.0	70
41	Structure of the MLL CXXC domain-DNA complex and its functional role in MLL-AF9 leukemia. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 62-68.	8.2	159
42	The PHD3 Domain of MLL Acts as a CYP33-Regulated Switch between MLL-Mediated Activation and Repression. <i>Biochemistry</i> , 2010, 49, 6576-6586.	2.5	56
43	Structure of the AML1-ETO NHR3-PKA(RII \pm) Complex and Its Contribution to AML1-ETO Activity. <i>Journal of Molecular Biology</i> , 2010, 402, 560-577.	4.2	18
44	DNMT1 Cxxc Domain Can Functionally Substitute In An MLL Fusion Protein. <i>Blood</i> , 2010, 116, 4193-4193.	1.4	0
45	The solution structure and dynamics of the DH-EPH module of PDZRhoGEF in isolation and in complex with nucleotide-free RhoA. <i>Protein Science</i> , 2009, 18, 2067-2079.	7.6	18
46	CBF $\hat{2}$ is critical for AML1-ETO and TEL-AML1 activity. <i>Blood</i> , 2009, 113, 3070-3079.	1.4	51
47	Structure of the AML1-ETO eTAFH domain-HEB peptide complex and its contribution to AML1-ETO activity. <i>Blood</i> , 2009, 113, 3558-3567.	1.4	33
48	The role of CBF $\hat{2}$ in AML1-ETO's activity. <i>Blood</i> , 2009, 114, 2849-2850.	1.4	15
49	Structural Basis for MLL Cxxc Domain Protection against CpG DNA Methylation and the Essential Role of This Function in MLL-AF9 Leukemia. <i>Blood</i> , 2009, 114, 763-763.	1.4	0
50	NMR Solution Structure of the Integral Membrane Enzyme DsbB: Functional Insights into DsbB-Catalyzed Disulfide Bond Formation. <i>Molecular Cell</i> , 2008, 31, 896-908.	9.7	171
51	MLL protects CpG clusters from methylation within the Hoxa9 gene, maintaining transcript expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7517-7522.	7.1	86
52	Allosteric Inhibition of the Protein-Protein Interaction between the Leukemia-Associated Proteins Runx1 and CBF $\hat{2}$. <i>Chemistry and Biology</i> , 2007, 14, 1186-1197.	6.0	114
53	Disease mutations in RUNX1 and RUNX2 create nonfunctional, dominant-negative, or hypomorphic alleles. <i>EMBO Journal</i> , 2007, 26, 1163-1175.	7.8	106
54	Structural Basis for Recognition of SMRT/N-CoR by the MYND Domain and Its Contribution to AML1/ETO's Activity. <i>Cancer Cell</i> , 2007, 11, 483-497.	16.8	106

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55	Development of Small Molecule Inhibitors of the AML1-ETO and CBF $\hat{\nu}$ 2-SMMHC Oncoproteins.. Blood, 2007, 110, 1591-1591.	1.4	1
56	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
57	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
58	A Mutation in the S-switch Region of the Runt Domain Alters the Dynamics of an Allosteric Network Responsible for CBF $\hat{\nu}$ 2 Regulation. Journal of Molecular Biology, 2006, 364, 1073-1083.	4.2	12
59	The DC-module of doublecortin: Dynamics, domain boundaries, and functional implications. Proteins: Structure, Function and Bioinformatics, 2006, 64, 874-882.	2.6	15
60	High resolution structure of the HDGF PWWP domain: A potential DNA binding domain. Protein Science, 2006, 15, 314-323.	7.6	62
61	The tetramer structure of the Neryv homology two domain, NHR2, is critical for AML1/ETO's activity. Cancer Cell, 2006, 9, 249-260.	16.8	121
62	Probing the Supramodular Architecture of a Multidomain Protein: The Structure of Syntenin in Solution. Structure, 2005, 13, 319-327.	3.3	19
63	Membrane Structures of the Hemifusion-Inducing Fusion Peptide Mutant G1S and the Fusion-Blocking Mutant G1V of Influenza Virus Hemagglutinin Suggest a Mechanism for Pore Opening in Membrane Fusion. Journal of Virology, 2005, 79, 12065-12076.	3.4	66
64	Development of Small Molecule Inhibitor of the AML1-ETO Oncoprotein.. Blood, 2005, 106, 1515-1515.	1.4	0
65	The CBF $\hat{\nu}$ 2-SMMHC Oncoprotein Inhibits Binding of the Runx1 Runt Domain to DNA.. Blood, 2005, 106, 2709-2709.	1.4	0
66	Development of Small Molecule Inhibitors of the CBF $\hat{\nu}$ 2-SMMHC Oncoprotein.. Blood, 2005, 106, 3359-3359.	1.4	0
67	Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO.. Blood, 2005, 106, 2854-2854.	1.4	9
68	CBF $\hat{\nu}$ 2 allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium. Nature Structural and Molecular Biology, 2004, 11, 901-906.	8.2	65
69	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
70	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
71	Structural and Functional Characterization of the NHR2 and Runt Domains of AML1/ETO.. Blood, 2004, 104, 482-482.	1.4	1
72	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

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73	Assignment of ^1H , ^{13}C and ^{15}N resonances of the N-terminal microtubule-binding domain of human doublecortin. <i>Journal of Biomolecular NMR</i> , 2003, 25, 81-82.	2.8	2
74	The DCX-domain tandems of doublecortin and doublecortin-like kinase. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 324-333.	8.2	122
75	Structure, dynamics and function of the outer membrane protein A (OmpA) and influenza hemagglutinin fusion domain in detergent micelles by solution NMR. <i>FEBS Letters</i> , 2003, 555, 139-143.	2.8	59
76	Structural and functional characterization of Runx1, CBF $\hat{1}^2$, and CBF $\hat{1}^2$ -SMMHC. <i>Blood Cells, Molecules, and Diseases</i> , 2003, 30, 147-156.	1.4	16
77	Energetic Contribution of Residues in the Runx1 Runt Domain to DNA Binding. <i>Journal of Biological Chemistry</i> , 2003, 278, 33088-33096.	3.4	35
78	Mutagenesis of the Runt Domain Defines Two Energetic Hot Spots for Heterodimerization with the Core Binding Factor $\hat{1}^2$ Subunit. <i>Journal of Biological Chemistry</i> , 2003, 278, 33097-33104.	3.4	26
79	Hepatoma Derived Growth Factor is a Nuclear Targeted Mitogen. <i>Current Drug Targets</i> , 2003, 4, 367-371.	2.1	32
80	Altered affinity of CBF $\hat{1}^2$ -SMMHC for Runx1 explains its role in leukemogenesis. <i>Nature Structural Biology</i> , 2002, 9, 674-679.	9.7	65
81	MQ-hCN-based pulse sequences for the measurement of $^{13}\text{C}1'-^{1}\text{H}1'$, $^{13}\text{C}1'-^{15}\text{N}$, $^{1}\text{H}1'-^{15}\text{N}$, $^{13}\text{C}1'-^{13}\text{C}2'$, $^{1}\text{H}1'-^{13}\text{C}2'$, $^{13}\text{C}6/8-^{1}\text{H}6/8$, $^{13}\text{C}6/8-^{15}\text{N}$, $^{1}\text{H}6/8-^{15}\text{N}$, $^{13}\text{C}6-^{13}\text{C}5$, $^{1}\text{H}6-^{13}\text{C}5$ dipolar couplings in ^{13}C , ^{15}N -labeled DNA (and RNA). <i>Journal of Biomolecular NMR</i> , 2002, 22, 9-20.		19
82	An Optimized PCR-Based Procedure for Production of $^{13}\text{C}/^{15}\text{N}$ -Labeled DNA. <i>Biochemical and Biophysical Research Communications</i> , 2001, 284, 295-300.	2.1	11
83	Structure of outer membrane protein A transmembrane domain by NMR spectroscopy. <i>Nature Structural Biology</i> , 2001, 8, 334-338.	9.7	363
84	Membrane structure and fusion-triggering conformational change of the fusion domain from influenza hemagglutinin. <i>Nature Structural Biology</i> , 2001, 8, 715-720.	9.7	406
85	The NOESY Jigsaw: Automated Protein Secondary Structure and Main-Chain Assignment from Sparse, Unassigned NMR Data. <i>Journal of Computational Biology</i> , 2000, 7, 537-558.	1.6	85
86	Energetic and Functional Contribution of Residues in the Core Binding Factor $\hat{1}^2$ (CBF $\hat{1}^2$) Subunit to Heterodimerization with CBF $\hat{1}^1$. <i>Journal of Biological Chemistry</i> , 2000, 275, 39579-39588.	3.4	55
87	CBF $\hat{1}^1$ A biophysical perspective. <i>Seminars in Cell and Developmental Biology</i> , 2000, 11, 377-382.	5.0	21
88	Biophysical characterization of interactions between the core binding factor $\hat{1}^1$ and $\hat{1}^2$ subunits and DNA. <i>FEBS Letters</i> , 2000, 470, 167-172.	2.8	47
89	Solution structure of core binding factor beta and map of the CBF alpha binding site. <i>Nature Structural Biology</i> , 1999, 6, 624-627.	9.7	68
90	Haploinsufficiency of CBFA2 causes familial thrombocytopenia with propensity to develop acute myelogenous leukaemia. <i>Nature Genetics</i> , 1999, 23, 166-175.	21.4	1,036

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91	The Ig fold of the core binding factor β Runt domain is a member of a family of structurally and functionally related Ig-fold DNA-binding domains. <i>Structure</i> , 1999, 7, 1247-1256.	3.3	81
92	Binding specificity and mechanistic insight into glutaredoxin-catalyzed protein disulfide reduction 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 292, 151-161.	4.2	44
93	^1H , ^{13}C and ^{15}N NMR resonance assignments of vaccinia glutaredoxin-1 in the fully reduced form. , 1998, 12, 353-355.		5
94	Complete heteronuclear NMR resonance assignments and secondary structure of core binding factor beta (1-141). <i>Journal of Biomolecular NMR</i> , 1998, 12, 459-460.	2.8	8
95	A PCR-based method for uniform $^{13}\text{C}/^{15}\text{N}$ labeling of long DNA oligomers. <i>FEBS Letters</i> , 1998, 436, 372-376.	2.8	14
96	Preparation, Characterization, and Complete Heteronuclear NMR Resonance Assignments of the Glutaredoxin (C14S) β Ribonucleotide Reductase B1 737 β 761 (C754S) Mixed Disulfide β . <i>Biochemistry</i> , 1998, 37, 5849-5857.	2.5	16
97	The NMR solution structure of human glutaredoxin in the fully reduced form. <i>Journal of Molecular Biology</i> , 1998, 280, 687-701.	4.2	81
98	Overexpression, Purification, and Biophysical Characterization of the Heterodimerization Domain of the Core-binding Factor β Subunit. <i>Journal of Biological Chemistry</i> , 1998, 273, 2480-2487.	3.4	20
99	Comparison of Backbone Dynamics of Reduced and Oxidized <i>Escherichia coli</i> Glutaredoxin-1 Using ^{15}N NMR Relaxation Measurements β . <i>Biochemistry</i> , 1997, 36, 5029-5044.	2.5	42
100	Complete ^1H , ^{13}C , and ^{15}N NMR resonance assignments and secondary structure of human glutaredoxin in the fully reduced form. <i>Protein Science</i> , 1997, 6, 383-390.	7.6	12
101	The CBF β Subunit Is Essential for CBF β 2 (AML1) Function In Vivo. <i>Cell</i> , 1996, 87, 697-708.	28.9	620
102	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. <i>Journal of Organic Chemistry</i> , 1996, 61, 4319-4327.	3.2	10
103	Biochemical and Biophysical Properties of the Core-binding Factor β 2 (AML1) DNA-binding Domain. <i>Journal of Biological Chemistry</i> , 1996, 271, 26251-26260.	3.4	62
104	The Nuclear Magnetic Resonance Solution Structure of the Mixed Disulfide between <i>Escherichia coli</i> Glutaredoxin(C14S) and Glutathione. <i>Journal of Molecular Biology</i> , 1994, 235, 1585-1597.	4.2	134
105	3D ^{13}C - ^{15}N -heteronuclear two-spin coherence spectroscopy for polypeptide backbone assignments in ^{13}C - ^{15}N -double-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1993, 3, 127-32.	2.8	66
106	Biosynthetic ^{15}N and ^{13}C isotope labelling of glutathione in the mixed disulfide with <i>Escherichia coli</i> glutaredoxin documented by sequence-specific NMR assignments. <i>FEBS Journal</i> , 1993, 218, 327-334.	0.2	6
107	NMR structure of oxidized <i>Escherichia coli</i> glutaredoxin: Comparison with reduced <i>E. coli</i> glutaredoxin and functionally related proteins. <i>Protein Science</i> , 1992, 1, 310-321.	7.6	111
108	Structural and functional characterization of the mutant <i>Escherichia coli</i> glutaredoxin (C14.fwdarw.S) and its mixed disulfide with glutathione. <i>Biochemistry</i> , 1992, 31, 9288-9293.	2.5	215

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109	Sequence-specific ¹ H n.m.r. assignments and determination of the three-dimensional structure of reduced escherichia coli glutaredoxin. <i>Journal of Molecular Biology</i> , 1991, 221, 1311-1324.	4.2	92
110	Synthesis of <i>Cis</i> - and <i>Trans</i> -1-methylcyclohexane-1,4-diols and Their 4-Hemisuccinate Esters. <i>Synthetic Communications</i> , 1989, 19, 745-754.	2.1	9
111	Sulfoxide analogs of dihydro- and tetrahydroprephenate as inhibitors of prephenate dehydratase. <i>Journal of Organic Chemistry</i> , 1989, 54, 2404-2409.	3.2	11
112	Synthesis of dimetallaazacyclobutenes via reaction of polynuclear heteroaromatic nitrogen compounds with triruthenium dodecacarbonyl: reactivity and structural elucidation. <i>Organometallics</i> , 1986, 5, 2193-2198.	2.3	53