

Jacqueline M Matthews

List of Publications by Year in descending order

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109
papers

6,125
citations

66234

42
h-index

74018

75
g-index

113
all docs

113
docs citations

113
times ranked

9160
citing authors

#	ARTICLE	IF	CITATIONS
1	Binding and folding in transcriptional complexes. <i>Current Opinion in Structural Biology</i> , 2021, 66, 156-162.	2.6	12
2	Contrasting DNA-binding behaviour by ISL1 and LHX3 underpins differential gene targeting in neuronal cell specification. <i>Journal of Structural Biology: X</i> , 2021, 5, 100043.	0.7	1
3	The characterization of protein interactions – what, how and how much?. <i>Chemical Society Reviews</i> , 2021, 50, 12292-12307.	18.7	23
4	Mutation in a flexible linker modulates binding affinity for modular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 425-429.	1.5	2
5	Disparate binding kinetics by an intrinsically disordered domain enables temporal regulation of transcriptional complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4643-4648.	3.3	10
6	1D Self-Assembly and Ice Recrystallization Inhibition Activity of Antifreeze Glycopeptide-Functionalized Perylene Bisimides. <i>Chemistry - A European Journal</i> , 2018, 24, 7834-7839.	1.7	19
7	Interactions between LHX3- and ISL1-family LIM-homeodomain transcription factors are conserved in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017, 7, 4579.	1.6	5
8	LIM Domain Proteins – , 2017, , .		0
9	A Quantitative Fluorescence-Based Assay for Assessing LIM Domain-Peptide Interactions. <i>Angewandte Chemie</i> , 2016, 128, 13430-13433.	1.6	0
10	A Quantitative Fluorescence-Based Assay for Assessing LIM Domain-Peptide Interactions. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 13236-13239.	7.2	3
11	Discovery, characterization and <i>in vivo</i> activity of pyocin SD2, a protein antibiotic from <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2016, 473, 2345-2358.	1.7	42
12	Mechanisms of DNA-binding specificity and functional gene regulation by transcription factors. <i>Current Opinion in Structural Biology</i> , 2016, 38, 68-74.	2.6	53
13	<i>GATA</i> 1 directly mediates interactions with closely spaced pseudopalindromic but not distantly spaced double <i>GATA</i> sites on <i>DNA</i> . <i>Protein Science</i> , 2015, 24, 1649-1659.	3.1	10
14	Biochemical and biophysical characterisation of haloalkane dehalogenases <i>DmrA</i> and <i>DmrB</i> in <i>Mycobacterium</i> strain <i>JS</i> 60 and their role in growth on haloalkanes. <i>Molecular Microbiology</i> , 2015, 97, 439-453.	1.2	19
15	Protein Complex Hierarchy and Translocation Gene Products. , 2015, , 447-466.		0
16	The recently identified modifier of murine metastable epialleles, Rearranged L-Myc Fusion, is involved in maintaining epigenetic marks at CpG island shores and enhancers. <i>BMC Biology</i> , 2015, 13, 21.	1.7	16
17	Editing the genome to introduce a beneficial naturally occurring mutation associated with increased fetal globin. <i>Nature Communications</i> , 2015, 6, 7085.	5.8	94
18	<i>GATA2</i> is required for lymphatic vessel valve development and maintenance. <i>Journal of Clinical Investigation</i> , 2015, 125, 2979-2994.	3.9	177

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19	Engineering Specificity Changes on a RanBP2 Zinc Finger that Binds Single-stranded RNA. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7848-7852.	7.2	5
20	Backbone and side-chain assignments of a tethered complex between LMO4 and DEAF-1. <i>Biomolecular NMR Assignments</i> , 2014, 8, 141-144.	0.4	4
21	The Structure of an LIM-Only Protein 4 (LMO4) and Deformed Epidermal Autoregulatory Factor-1 (DEAF1) Complex Reveals a Common Mode of Binding to LMO4. <i>PLoS ONE</i> , 2014, 9, e109108.	1.1	13
22	No evidence for cumulative effects in a Dnmt3b hypomorph across multiple generations. <i>Mammalian Genome</i> , 2013, 24, 206-217.	1.0	12
23	The tandem \hat{z} -zipper: Modular binding of tandem domains and linear motifs. <i>FEBS Letters</i> , 2013, 587, 1164-1171.	1.3	21
24	New Insights into DNA Recognition by Zinc Fingers Revealed by Structural Analysis of the Oncoprotein ZNF217. <i>Journal of Biological Chemistry</i> , 2013, 288, 10616-10627.	1.6	36
25	LIM-domain-only proteins in cancer. <i>Nature Reviews Cancer</i> , 2013, 13, 111-122.	12.8	109
26	Structural Basis of the Interaction of the Breast Cancer Oncogene LMO4 with the Tumour Suppressor CtIP/RBBP8. <i>Journal of Molecular Biology</i> , 2013, 425, 1101-1110.	2.0	11
27	Synthesis of peptides and glycopeptides with polyproline II helical topology as potential antifreeze molecules. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 3569-3581.	1.4	26
28	Semiquantitative and quantitative analysis of protein-DNA interactions using steady-state measurements in surface plasmon resonance competition experiments. <i>Analytical Biochemistry</i> , 2013, 440, 178-185.	1.1	13
29	A Structural Basis for the Regulation of the LIM-Homeodomain Protein Islet 1 (Isl1) by Intra- and Intermolecular Interactions. <i>Journal of Biological Chemistry</i> , 2013, 288, 21924-21935.	1.6	21
30	A Structural Analysis of DNA Binding by Myelin Transcription Factor 1 Double Zinc Fingers. <i>Journal of Biological Chemistry</i> , 2013, 288, 35180-35191.	1.6	17
31	Analysis of disease-causing GATA1 mutations in murine gene complementation systems. <i>Blood</i> , 2013, 121, 5218-5227.	0.6	42
32	Mutations in MITF and PAX3 Cause Splashed White and Other White Spotting Phenotypes in Horses. <i>PLoS Genetics</i> , 2012, 8, e1002653.	1.5	124
33	Tropoelastin bridge region positions the cell-interactive C terminus and contributes to elastic fiber assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2878-2883.	3.3	51
34	Solution structure of a tethered Lmo2_{LIM2}/Ldb1_{LID} complex. <i>Protein Science</i> , 2012, 21, 1768-1774.	3.1	7
35	Crystallization and diffraction of an Isl1-Ldb1 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1398-1401.	0.7	1
36	Dimers, Oligomers, Everywhere. <i>Advances in Experimental Medicine and Biology</i> , 2012, 747, 1-18.	0.8	59

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37	Synthesis of the Bacteriocin Glycopeptide Sublancin 168 and <i>l</i> -Glycosylated Variants. <i>Organic Letters</i> , 2012, 14, 1910-1913.	2.4	41
38	Contribution of DEAF1 Structural Domains to the Interaction with the Breast Cancer Oncogene LMO4. <i>PLoS ONE</i> , 2012, 7, e39218.	1.1	21
39	Total Synthesis of Homogeneous Antifreeze Glycopeptides and Glycoproteins. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 3606-3610.	7.2	106
40	Modular Assembly of RanBP2-Type Zinc Finger Domains to Target Single-Stranded RNA. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5371-5375.	7.2	7
41	¹ H, ¹⁵ N and ¹³ C assignments of an intramolecular LMO4-LIM1/CtIP complex. <i>Biomolecular NMR Assignments</i> , 2012, 6, 31-34.	0.4	3
42	Solution Structure of the LIM-Homeodomain Transcription Factor Complex Lhx3/Ldb1 and the Effects of a Pituitary Mutation on Key Lhx3 Interactions. <i>PLoS ONE</i> , 2012, 7, e40719.	1.1	7
43	Protein-protein interactions: Analysis of a false positive GST pulldown result. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2365-2371.	1.5	17
44	Structural basis of simultaneous recruitment of the transcriptional regulators LMO2 and FOG1/ZFPM1 by the transcription factor GATA1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14443-14448.	3.3	42
45	Structural Basis for Partial Redundancy in a Class of Transcription Factors, the LIM Homeodomain Proteins, in Neural Cell Type Specification. <i>Journal of Biological Chemistry</i> , 2011, 286, 42971-42980.	1.6	35
46	¹ H, ¹⁵ N and ¹³ C assignments of an intramolecular Lmo2-LIM2/Ldb1-LID complex. <i>Biomolecular NMR Assignments</i> , 2010, 4, 203-206.	0.4	5
47	LIM Domain Binding Proteins 1 and 2 Have Different Oligomeric States. <i>Journal of Molecular Biology</i> , 2010, 399, 133-144.	2.0	38
48	Structural Analysis of MED-1 Reveals Unexpected Diversity in the Mechanism of DNA Recognition by GATA-type Zinc Finger Domains. <i>Journal of Biological Chemistry</i> , 2009, 284, 5827-5835.	1.6	22
49	Crystallization and diffraction of an Lhx4-Isl2 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 151-153.	0.7	5
50	It Takes Two to Tango: The Structure and Function of LIM, RING, PHD and MYND Domains. <i>Current Pharmaceutical Design</i> , 2009, 15, 3681-3696.	0.9	80
51	The Importance of pH in Regulating the Function of the <i>Fasciola hepatica</i> Cathepsin L1 Cysteine Protease. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e369.	1.3	69
52	Assembly of the oncogenic DNA-binding complex LMO2-Ldb1-TAL1-E12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1461-1474.	1.5	26
53	Implementing the LIM code: the structural basis for cell type-specific assembly of LIM-homeodomain complexes. <i>EMBO Journal</i> , 2008, 27, 2018-2029.	3.5	68
54	Designed metal-binding sites in biomolecular and bioinorganic interactions. <i>Current Opinion in Structural Biology</i> , 2008, 18, 484-490.	2.6	28

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55	Response to Chatr-aryamontri et al.: Protein interactions: to believe or not to believe?. Trends in Biochemical Sciences, 2008, 33, 242-243.	3.7	17
56	ATP Binding Equilibria of the Na ⁺ ,K ⁺ -ATPase. Biochemistry, 2008, 47, 13103-13114.	1.2	14
57	Structural and Biophysical Analysis of the DNA Binding Properties of Myelin Transcription Factor 1. Journal of Biological Chemistry, 2008, 283, 5158-5167.	1.6	27
58	Competition between LIM-binding domains. Biochemical Society Transactions, 2008, 36, 1393-1397.	1.6	33
59	Dimerization of CtIP may stabilize in vivo interactions with the Retinoblastoma-pocket domain. Biochemical and Biophysical Research Communications, 2007, 354, 197-202.	1.0	6
60	Grb7 SH2 domain structure and interactions with a cyclic peptide inhibitor of cancer cell migration and proliferation. BMC Structural Biology, 2007, 7, 58.	2.3	47
61	Modifiers of epigenetic reprogramming show paternal effects in the mouse. Nature Genetics, 2007, 39, 614-622.	9.4	154
62	Protein interactions: is seeing believing?. Trends in Biochemical Sciences, 2007, 32, 530-531.	3.7	89
63	Disparate thermodynamics governing T cell receptor-MHC-I interactions implicate extrinsic factors in guiding MHC restriction. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6641-6646.	3.3	52
64	Identification of the Key LMO2-binding Determinants on Ldb1. Journal of Molecular Biology, 2006, 359, 66-75.	2.0	31
65	Stabilization of a binary protein complex by intein-mediated cyclization. Protein Science, 2006, 15, 2612-2618.	3.1	29
66	Structural basis for rodlet assembly in fungal hydrophobins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3621-3626.	3.3	218
67	Mutation of a Critical Arginine in the GTP-binding Site of Transglutaminase 2 Disinhibits Intracellular Cross-linking Activity. Journal of Biological Chemistry, 2006, 281, 12603-12609.	1.6	70
68	Mechanism of allosteric regulation of transglutaminase 2 by GTP. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19683-19688.	3.3	136
69	Assessment of the Robustness of a Serendipitous Zinc Binding Fold: Mutagenesis and Protein Grafting. Structure, 2005, 13, 257-266.	1.6	9
70	Protein-protein interactions in human disease. Current Opinion in Structural Biology, 2005, 15, 441-446.	2.6	310
71	¹ H, ¹⁵ N and ¹³ C Assignments of an Intramolecular Lhx3:ldb1 Complex. Journal of Biomolecular NMR, 2005, 33, 198-198.	1.6	7
72	A Complex Mechanism Determines Polarity of DNA Replication Fork Arrest by the Replication Terminator Complex of Bacillus subtilis. Journal of Biological Chemistry, 2005, 280, 13105-13113.	1.6	11

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73	Zinc fingers as protein recognition motifs: Structural basis for the GATA-1/Friend of GATA interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 583-588.	3.3	89
74	Stabilization of Native Protein Fold by Intein-Mediated Covalent Cyclization. <i>Journal of Molecular Biology</i> , 2005, 346, 1095-1108.	2.0	42
75	TC-1 Is a Novel Tumorigenic and Natively Disordered Protein Associated with Thyroid Cancer. <i>Cancer Research</i> , 2004, 64, 2766-2773.	0.4	64
76	Dimerization of CtIP, a BRCA1- and CtBP-interacting Protein, Is Mediated by an N-terminal Coiled-coil Motif. <i>Journal of Biological Chemistry</i> , 2004, 279, 26932-26938.	1.6	46
77	A Classic Zinc Finger from Friend of GATA Mediates an Interaction with the Coiled-coil of Transforming Acidic Coiled-coil 3. <i>Journal of Biological Chemistry</i> , 2004, 279, 39789-39797.	1.6	28
78	Tandem LIM domains provide synergistic binding in the LMO4:Ldb1 complex. <i>EMBO Journal</i> , 2004, 23, 3589-3598.	3.5	84
79	The power of two: protein dimerization in biology. <i>Trends in Biochemical Sciences</i> , 2004, 29, 618-625.	3.7	491
80	Structural Studies on a Protein-Binding Zinc-Finger Domain of Eos Reveal Both Similarities and Differences to Classical Zinc Fingers. <i>Biochemistry</i> , 2004, 43, 13318-13327.	1.2	11
81	Structural basis for the recognition of Ldb1 by the N-terminal LIM domains of LMO2 and LMO4. <i>EMBO Journal</i> , 2003, 22, 2224-2233.	3.5	62
82	Engineering a Protein Scaffold from a PHD Finger. <i>Structure</i> , 2003, 11, 803-813.	1.6	56
83	Crystallization of FLINC4, an intramolecular LMO4-Ldb1 complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1484-1486.	2.5	10
84	LIM domain-binding protein 1: a multifunctional cofactor that interacts with diverse proteins. <i>EMBO Reports</i> , 2003, 4, 1132-1137.	2.0	146
85	The LIM Protein FHL3 Binds Basic Krüppel-like Factor/Krüppel-like Factor 3 and Its Co-repressor C-terminal-binding Protein 2. <i>Journal of Biological Chemistry</i> , 2003, 278, 12786-12795.	1.6	55
86	CCHX Zinc Finger Derivatives Retain the Ability to Bind Zn(II) and Mediate Protein-DNA Interactions. <i>Journal of Biological Chemistry</i> , 2003, 278, 28011-28018.	1.6	46
87	Recombinant CLIC1 (NCC27) Assembles in Lipid Bilayers via a pH-dependent Two-state Process to Form Chloride Ion Channels with Identical Characteristics to Those Observed in Chinese Hamster Ovary Cells Expressing CLIC1. <i>Journal of Biological Chemistry</i> , 2002, 277, 26003-26011.	1.6	110
88	Characterization of the Conserved Interaction between GATA and FOG Family Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 35720-35729.	1.6	24
89	A New Zinc Binding Fold Underlines the Versatility of Zinc Binding Modules in Protein Evolution. <i>Structure</i> , 2002, 10, 639-648.	1.6	21
90	Letter to the Editor: (1)H, (15)N and (13)C assignments of FLIN4, an intramolecular LMO4:Ldb1 complex. <i>Journal of Biomolecular NMR</i> , 2002, 23, 165-166.	1.6	4

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91	Zinc Fingers–Folds for Many Occasions. <i>IUBMB Life</i> , 2002, 54, 351-355.	1.5	274
92	¹ H, ¹⁵ N and ¹³ C assignments of FLIN2, an intramolecular LMO2:ldb1 complex. <i>Journal of Biomolecular NMR</i> , 2001, 21, 385-386.	1.6	4
93	The Hydrophobin EAS Is Largely Unstructured in Solution and Functions by Forming Amyloid-Like Structures. <i>Structure</i> , 2001, 9, 83-91.	1.6	139
94	Design, production and characterization of FLIN2 and FLIN4: the engineering of intramolecular ldb1:LMO complexes. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 493-499.	1.0	31
95	A class of zinc fingers involved in protein-protein interactions. <i>FEBS Journal</i> , 2000, 267, 1030-1038.	0.2	59
96	The Core of the Respiratory Syncytial Virus Fusion Protein Is a Trimeric Coiled Coil. <i>Journal of Virology</i> , 2000, 74, 5911-5920.	1.5	80
97	The Single Mutation Phe173 → Ala Induces a Molten Globule-like State in Murine Interleukin-6. <i>Biochemistry</i> , 2000, 39, 1942-1950.	1.2	17
98	Physicochemical Characterization of an Antagonistic Human Interleukin-6 Dimer. <i>Biochemistry</i> , 1998, 37, 10671-10680.	1.2	10
99	Roles of Histidine 31 and Tryptophan 34 in the Structure, Self-Association, and Folding of Murine Interleukin-6. <i>Biochemistry</i> , 1997, 36, 6187-6196.	1.2	22
100	Disruption of the Disulfide Bonds of Recombinant Murine Interleukin-6 Induces Formation of a Partially Unfolded State. <i>Biochemistry</i> , 1997, 36, 2380-2389.	1.2	20
101	Interleukin-6: Structure–function relationships. <i>Protein Science</i> , 1997, 6, 929-955.	3.1	347
102	The association of unfolding intermediates during the equilibrium unfolding of recombinant murine interleukin-6. <i>Techniques in Protein Chemistry</i> , 1996, , 449-457.	0.3	1
103	Influence of Interleukin-6 (IL-6) Dimerization on Formation of the High Affinity Hexameric IL-6 Receptor Complex. <i>Journal of Biological Chemistry</i> , 1996, 271, 20138-20144.	1.6	55
104	Equilibrium Denaturation of Recombinant Murine Interleukin-6: Effect of pH, Denaturants, and Salt on Formation of Folding Intermediates. <i>Biochemistry</i> , 1995, 34, 11652-11659.	1.2	18
105	Exploring the energy surface of protein folding by structure-reactivity relationships and engineered proteins: Observation of Hammond behavior for the gross structure of the transition state and anti-Hammond behavior for structural elements for unfolding/folding of barnase. <i>Biochemistry</i> , 1995, 34, 6805-6814.	1.2	141
106	Extrapolation to water of kinetic and equilibrium data for the unfolding of barnase in urea solutions. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1089-1095.	1.0	71
107	Single versus parallel pathways of protein folding and fractional formation of structure in the transition state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10426-10429.	3.3	186
108	±-Helix stability in proteins. <i>Journal of Molecular Biology</i> , 1992, 227, 560-568.	2.0	230

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109	The pathway of arginine catabolism in <i>Giardia intestinalis</i> . <i>Molecular and Biochemical Parasitology</i> , 1992, 51, 29-36.	0.5	86