

# Joel P Mackay

## List of Publications by Year in descending order

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218  
papers

11,227  
citations

26610

56  
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38368

95  
g-index

248  
all docs

248  
docs citations

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times ranked

14129  
citing authors

#	ARTICLE	IF	CITATIONS
1	Zinc fingers are sticking together. Trends in Biochemical Sciences, 1998, 23, 1-4.	3.7	426
2	Sticky fingers: zinc-fingers as protein-recognition motifs. Trends in Biochemical Sciences, 2007, 32, 63-70.	3.7	370
3	Mutations in Cardiac T-Box Factor Gene TBX20 Are Associated with Diverse Cardiac Pathologies, Including Defects of Septation and Valvulogenesis and Cardiomyopathy. American Journal of Human Genetics, 2007, 81, 280-291.	2.6	317
4	Cardiac hypertrophy and histone deacetylase-dependent transcriptional repression mediated by the atypical homeodomain protein Hop. Journal of Clinical Investigation, 2003, 112, 863-871.	3.9	289
5	Hop Is an Unusual Homeobox Gene that Modulates Cardiac Development. Cell, 2002, 110, 713-723.	13.5	256
6	Site-specific phosphorylation of tau inhibits amyloid- $\beta$ toxicity in Alzheimer's mice. Science, 2016, 354, 904-908.	6.0	241
7	Transcriptional cofactors of the FOG family interact with GATA proteins by means of multiple zinc fingers. EMBO Journal, 1999, 18, 2812-2822.	3.5	239
8	Use of Altered Specificity Mutants to Probe a Specific Protein-Protein Interaction in Differentiation. Molecular Cell, 1999, 3, 219-228.	4.5	218
9	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
10	Glycopeptide Antibiotic Activity and the Possible Role of Dimerization: A Model for Biological Signaling. Journal of the American Chemical Society, 1994, 116, 4581-4590.	6.6	210
11	Structural analysis of hydrophobins. Micron, 2008, 39, 773-784.	1.1	194
12	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E159-68.	3.3	190
13	The role of the sugar and chlorine substituents in the dimerization of vancomycin antibiotics. Journal of the American Chemical Society, 1993, 115, 232-237.	6.6	179
14	Toward an estimation of binding constants in aqueous solution: studies of associations of vancomycin group antibiotics. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 1172-1178.	3.3	162
15	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. Nucleic Acids Research, 2017, 45, 9901-9916.	6.5	160
16	Plant Homeodomain (PHD) Fingers of CHD4 Are Histone H3-binding Modules with Preference for Unmodified H3K4 and Methylated H3K9. Journal of Biological Chemistry, 2011, 286, 11779-11791.	1.6	147
17	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. Plant Cell, 2007, 19, 2898-2912.	3.1	143
18	Macromolecular NMR spectroscopy for the non-spectroscopist. FEBS Journal, 2011, 278, 687-703.	2.2	140

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19	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
20	Loss of $\alpha$ -hemoglobin-stabilizing protein impairs erythropoiesis and exacerbates $\beta$ -thalassemia. <i>Journal of Clinical Investigation</i> , 2004, 114, 1457-1466.	3.9	138
21	Dissection of the Contributions toward Dimerization of Glycopeptide Antibiotics. <i>Journal of the American Chemical Society</i> , 1994, 116, 4573-4580.	6.6	137
22	Molecular Mechanism of AHSP-Mediated Stabilization of $\alpha$ -Hemoglobin. <i>Cell</i> , 2004, 119, 629-640.	13.5	137
23	Siah ubiquitin ligase is structurally related to TRAF and modulates TNF- $\alpha$ signaling. <i>Nature Structural Biology</i> , 2002, 9, 68-75.	9.7	129
24	The C-Terminal Region of the Stalk Domain of Ubiquitous Human Kinesin Heavy Chain Contains the Binding Site for Kinesin Light Chain. <i>Biochemistry</i> , 1998, 37, 16663-16670.	1.2	122
25	The structure of versutoxin ( $\alpha$ -atractoxin-Hv1) provides insights into the binding of site 3 neurotoxins to the voltage-gated sodium channel. <i>Structure</i> , 1997, 5, 1525-1535.	1.6	115
26	Measuring protein self-association using pulsed-field-gradient NMR spectroscopy: Application to myosin light chain 2. <i>Journal of Biomolecular NMR</i> , 1995, 6, 321-8.	1.6	113
27	Self-assembly of functional, amphipathic amyloid monolayers by the fungal hydrophobin EAS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E804-11.	3.3	113
28	Binding of the CHD4 PHD2 finger to histone H3 is modulated by covalent modifications. <i>Biochemical Journal</i> , 2009, 423, 179-187.	1.7	106
29	Structural Basis and Specificity of Acetylated Transcription Factor GATA1 Recognition by BET Family Bromodomain Protein Brd3. <i>Molecular and Cellular Biology</i> , 2011, 31, 2632-2640.	1.1	106
30	Structure of oxidized $\alpha$ -haemoglobin bound to AHSP reveals a protective mechanism for haem. <i>Nature</i> , 2005, 435, 697-701.	13.7	102
31	Characterization of a Family of RanBP2-Type Zinc Fingers that Can Recognize Single-Stranded RNA. <i>Journal of Molecular Biology</i> , 2011, 407, 273-283.	2.0	99
32	Biophysical Characterization of the $\alpha$ -Globin Binding Protein $\alpha$ -Hemoglobin Stabilizing Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 40602-40609.	1.6	96
33	An erythroid chaperone that facilitates folding of $\alpha$ -globin subunits for hemoglobin synthesis. <i>Journal of Clinical Investigation</i> , 2007, 117, 1856-1865.	3.9	96
34	Bivalent recognition of nucleosomes by the tandem PHD fingers of the CHD4 ATPase is required for CHD4-mediated repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 787-792.	3.3	96
35	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
36	Protein interactions: is seeing believing?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 530-531.	3.7	89

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37	Insights into Association of the NuRD Complex with FOG-1 from the Crystal Structure of an RbAp48-FOG-1 Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 1196-1203.	1.6	89
38	Key Residues Characteristic of GATA N-fingers Are Recognized By FOG. <i>Journal of Biological Chemistry</i> , 1998, 273, 33595-33603.	1.6	83
39	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
40	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
41	Discovery and Structure of a Potent and Highly Specific Blocker of Insect Calcium Channels. <i>Journal of Biological Chemistry</i> , 2001, 276, 40306-40312.	1.6	79
42	The N-terminal Zinc Finger of the Erythroid Transcription Factor GATA-1 Binds GATC Motifs in DNA. <i>Journal of Biological Chemistry</i> , 2001, 276, 35794-35801.	1.6	78
43	The structure of an asymmetric dimer relevant to the mode of action of the glycopeptide antibiotics. <i>Structure</i> , 1994, 2, 747-754.	1.6	77
44	Evolution of Quaternary Structure in a Homotetrameric Enzyme. <i>Journal of Molecular Biology</i> , 2008, 380, 691-703.	2.0	77
45	The zinc fingers of the SR-like protein ZRANB2 are single-stranded RNA-binding domains that recognize 5' splice site-like sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5581-5586.	3.3	75
46	The structural analysis of protein-protein interactions by NMR spectroscopy. <i>Proteomics</i> , 2009, 9, 5224-5232.	1.3	75
47	Insight into the Architecture of the NuRD Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 21844-21855.	1.6	75
48	Trim58 Degrades Dynein and Regulates Terminal Erythropoiesis. <i>Developmental Cell</i> , 2014, 30, 688-700.	3.1	75
49	Nuclear Magnetic Resonance Characterization of the Jun Leucine Zipper Domain: Unusual Properties of Coiled-Coil Interfacial Polar Residues. <i>Biochemistry</i> , 1995, 34, 6164-6174.	1.2	74
50	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
51	The Cys3-Cys4 Loop of the Hydrophobin EAS Is Not Required for Rodlet Formation and Surface Activity. <i>Journal of Molecular Biology</i> , 2008, 382, 708-720.	2.0	67
52	Paris-Trousseau thrombocytopenia is phenocopied by the autosomal recessive inheritance of a DNA-binding domain mutation in FLI1. <i>Blood</i> , 2015, 126, 2027-2030.	0.6	65
53	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
54	Autonomous folding of a peptide corresponding to the N-terminal hairpin from ubiquitin. <i>Protein Science</i> , 1999, 8, 1320-1331.	3.1	62

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55	Structural basis for the recognition of Idb1 by the N-terminal LIM domains of LMO2 and LMO4. <i>EMBO Journal</i> , 2003, 22, 2224-2233.	3.5	62
56	CHD4 Is a Peripheral Component of the Nucleosome Remodeling and Deacetylase Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 15853-15866.	1.6	62
57	A class of zinc fingers involved in protein-protein interactions. <i>FEBS Journal</i> , 2000, 267, 1030-1038.	0.2	59
58	Probing Site Specificity of DNA Binding Metallointercalators by NMR Spectroscopy and Molecular Modeling. <i>Biochemistry</i> , 2001, 40, 4867-4878.	1.2	59
59	The prospects for designer single-stranded RNA-binding proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 256-261.	3.6	59
60	Structural and functional analysis of the Josephin domain of the polyglutamine protein ataxin-3. <i>Biochemical and Biophysical Research Communications</i> , 2004, 322, 387-394.	1.0	58
61	Structure of the Hemoglobin-IsdH Complex Reveals the Molecular Basis of Iron Capture by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6728-6738.	1.6	58
62	Engineering a Protein Scaffold from a PHD Finger. <i>Structure</i> , 2003, 11, 803-813.	1.6	56
63	Interactions of the Antitumor Agent Molybdocene Dichloride with Oligonucleotides. <i>Inorganic Chemistry</i> , 1998, 37, 2432-2437.	1.9	53
64	Molecular Analysis of the Interaction between the Hematopoietic Master Transcription Factors GATA-1 and PU.1. <i>Journal of Biological Chemistry</i> , 2006, 281, 28296-28306.	1.6	53
65	Macromolecular NMR spectroscopy for the non-spectroscopist: beyond macromolecular solution structure determination. <i>FEBS Journal</i> , 2011, 278, 704-715.	2.2	53
66	A Transcription Factor Addiction in Leukemia Imposed by the MLL Promoter Sequence. <i>Cancer Cell</i> , 2018, 34, 970-981.e8.	7.7	53
67	Backbone Dynamics of the c-Jun Leucine Zipper: <sup>15</sup> N NMR Relaxation Studies. <i>Biochemistry</i> , 1996, 35, 4867-4877.	1.2	52
68	Determinants of affinity and specificity in RNA-binding proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 83-91.	2.6	51
69	Refinement of the subunit interaction network within the nucleosome remodelling and deacetylase (NuRD) complex. <i>FEBS Journal</i> , 2017, 284, 4216-4232.	2.2	51
70	The solution structure of the N-terminal zinc finger of GATA-1 reveals a specific binding face for the transcriptional co-factor FOG. <i>Journal of Biomolecular NMR</i> , 1999, 13, 249-262.	1.6	50
71	Structural Basis for Hemoglobin Capture by <i>Staphylococcus aureus</i> Cell-surface Protein, IsdH. <i>Journal of Biological Chemistry</i> , 2011, 286, 38439-38447.	1.6	50
72	The N-terminal Region of Chromodomain Helicase DNA-binding Protein 4 (CHD4) Is Essential for Activity and Contains a High Mobility Group (HMG) Box-like-domain That Can Bind Poly(ADP-ribose). <i>Journal of Biological Chemistry</i> , 2016, 291, 924-938.	1.6	49

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73	Involvement of the N-finger in the Self-association of GATA-1. <i>Journal of Biological Chemistry</i> , 1998, 273, 30560-30567.	1.6	48
74	Beyond DNA: Zinc Finger Domains as RNA-Binding Modules. <i>Methods in Molecular Biology</i> , 2010, 649, 479-491.	0.4	48
75	Grb7 SH2 domain structure and interactions with a cyclic peptide inhibitor of cancer cell migration and proliferation. <i>BMC Structural Biology</i> , 2007, 7, 58.	2.3	47
76	Discovery of Cyclic Peptide Ligands to the SARS-CoV-2 Spike Protein Using mRNA Display. <i>ACS Central Science</i> , 2021, 7, 1001-1008.	5.3	47
77	A single dose, BCG-adjuvanted COVID-19 vaccine provides sterilising immunity against SARS-CoV-2 infection. <i>Npj Vaccines</i> , 2021, 6, 143.	2.9	47
78	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
79	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. <i>Nature Communications</i> , 2018, 9, 4300.	5.8	46
80	Two-timing zinc finger transcription factors liaising with RNA. <i>Trends in Biochemical Sciences</i> , 2012, 37, 199-205.	3.7	45
81	GATA-1: One protein, many partners. <i>International Journal of Biochemistry and Cell Biology</i> , 2006, 38, 6-11.	1.2	44
82	The <i>Bacillus subtilis</i> cell division proteins FtsL and DivIC are intrinsically unstable and do not interact with one another in the absence of other septasomal components. <i>Molecular Microbiology</i> , 2002, 44, 663-674.	1.2	42
83	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
84	The Detection and Quantitation of Protein Oligomerization. <i>Advances in Experimental Medicine and Biology</i> , 2012, 747, 19-41.	0.8	42
85	Analysis of disease-causing GATA1 mutations in murine gene complementation systems. <i>Blood</i> , 2013, 121, 5218-5227.	0.6	42
86	The Transactivation Domain within Cysteine/Histidine-rich Region 1 of CBP Comprises Two Novel Zinc-binding Modules. <i>Journal of Biological Chemistry</i> , 2000, 275, 15128-15134.	1.6	41
87	Role of Alpha Hemoglobin-Stabilizing Protein in Normal Erythropoiesis and $\beta^2$ -Thalassemia. <i>Annals of the New York Academy of Sciences</i> , 2005, 1054, 103-117.	1.8	41
88	Synthesis of the Bacteriocin Glycopeptide Sublancin 168 and <i>S</i> -Glycosylated Variants. <i>Organic Letters</i> , 2012, 14, 1910-1913.	2.4	41
89	The dimerization and topological specificity functions of MinE reside in a structurally autonomous C-terminal domain. <i>Molecular Microbiology</i> , 1999, 31, 1161-1169.	1.2	40
90	Solution Structures of Two CCHC Zinc Fingers from the FOG Family Protein U-Shaped that Mediate Protein-Protein Interactions. <i>Structure</i> , 2000, 8, 1157-1166.	1.6	39

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91	The Solution Structure and Intramolecular Associations of the Tec Kinase Src Homology 3 Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 755-762.	1.6	39
92	Determination of ribonuclease sequence-specificity using Pentaprobates and mass spectrometry. <i>Rna</i> , 2012, 18, 1267-1278.	1.6	39
93	The BRD3 ET domain recognizes a short peptide motif through a mechanism that is conserved across chromatin remodelers and transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2018, 293, 7160-7175.	1.6	39
94	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. <i>Cell Reports</i> , 2020, 33, 108450.	2.9	37
95	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
96	Arabinosylation Modulates the Growth-Regulating Activity of the Peptide Hormone CLE40a from Soybean. <i>Cell Chemical Biology</i> , 2017, 24, 1347-1355.e7.	2.5	35
97	The Structure of the Zinc Finger Domain from Human Splicing Factor ZNF265 Fold. <i>Journal of Biological Chemistry</i> , 2003, 278, 22805-22811.	1.6	34
98	The MTA1 subunit of the nucleosome remodeling and deacetylase complex can recruit two copies of RBBP4/7. <i>Protein Science</i> , 2016, 25, 1472-1482.	3.1	33
99	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. <i>Nucleic Acids Research</i> , 2017, 45, 1130-1143.	6.5	33
100	Development of a Sensitive Peptide-Based Immunoassay: Application to Detection of the Jun and Fos Oncoproteins. <i>Biochemistry</i> , 1996, 35, 9069-9075.	1.2	32
101	Crystal and Solution Structures of a Superantigen from <i>Yersinia pseudotuberculosis</i> Reveal a Jelly-Roll Fold. <i>Structure</i> , 2004, 12, 145-156.	1.6	32
102	<i>Escherichia coli</i> Glucuronylsynthase: An Engineered Enzyme for the Synthesis of $\beta$ -Glucuronides. <i>Organic Letters</i> , 2008, 10, 1585-1588.	2.4	32
103	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
104	Identification of the Key LMO2-binding Determinants on Ldb1. <i>Journal of Molecular Biology</i> , 2006, 359, 66-75.	2.0	31
105	Analysis of the Structure and Function of the Transcriptional Coregulator HOP. <i>Biochemistry</i> , 2006, 45, 10584-10590.	1.2	30
106	Effects of Calcium Binding and the Hypertrophic Cardiomyopathy A8V Mutation on the Dynamic Equilibrium between Closed and Open Conformations of the Regulatory N-Domain of Isolated Cardiac Troponin C. <i>Biochemistry</i> , 2013, 52, 1950-1962.	1.2	30
107	Grb7-SH2 domain dimerisation is affected by a single point mutation. <i>European Biophysics Journal</i> , 2005, 34, 454-460.	1.2	29
108	A rapid method for assessing the RNA-binding potential of a protein. <i>Nucleic Acids Research</i> , 2012, 40, e105-e105.	6.5	29

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109	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
110	Designed metal-binding sites in biomolecular and bioinorganic interactions. <i>Current Opinion in Structural Biology</i> , 2008, 18, 484-490.	2.6	28
111	Type I Shorthorn Sculpin Antifreeze Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 24073-24080.	1.6	27
112	CSL: A notch above the rest. <i>International Journal of Biochemistry and Cell Biology</i> , 2005, 37, 2472-2477.	1.2	27
113	Structural and Biophysical Analysis of the DNA Binding Properties of Myelin Transcription Factor 1. <i>Journal of Biological Chemistry</i> , 2008, 283, 5158-5167.	1.6	27
114	Cyclic peptides can engage a single binding pocket through highly divergent modes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26728-26738.	3.3	27
115	Ikars: a key regulator of haematopoiesis. <i>International Journal of Biochemistry and Cell Biology</i> , 2002, 34, 1304-1307.	1.2	26
116	Solution structure of a hydrophobic analogue of the winter flounder antifreeze protein. <i>FEBS Journal</i> , 2002, 269, 1259-1266.	0.2	26
117	A Novel Purification Procedure for Active Recombinant Human DPP4 and the Inability of DPP4 to Bind SARS-CoV-2. <i>Molecules</i> , 2020, 25, 5392.	1.7	26
118	Semisynthesis of an evasin from tick saliva reveals a critical role of tyrosine sulfation for chemokine binding and inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12657-12664.	3.3	26
119	The zinc fingers of YY1 bind single-stranded RNA with low sequence specificity. <i>Nucleic Acids Research</i> , 2016, 44, gkw590.	6.5	25
120	CHD4 slides nucleosomes by decoupling entry- and exit-side DNA translocation. <i>Nature Communications</i> , 2020, 11, 1519.	5.8	25
121	Characterization of the Conserved Interaction between GATA and FOG Family Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 35720-35729.	1.6	24
122	Pentaprobe: a comprehensive sequence for the one-step detection of DNA-binding activities. <i>Nucleic Acids Research</i> , 2003, 31, 124e-124.	6.5	24
123	Crystal structure of the <i>Melampsora lini</i> effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. <i>Molecular Plant Pathology</i> , 2018, 19, 1196-1209.	2.0	24
124	Measuring macromolecular diffusion using heteronuclear multiple-quantum pulsed-field-gradient NMR. <i>Journal of Biomolecular NMR</i> , 1997, 10, 1-8.	1.6	23
125	The Multi-zinc Finger Protein ZNF217 Contacts DNA through a Two-finger Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 38190-38201.	1.6	23
126	Peppy: A virtual reality environment for exploring the principles of polypeptide structure. <i>Protein Science</i> , 2020, 29, 157-168.	3.1	23

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127	The characterization of protein interactions “ what, how and how much?. <i>Chemical Society Reviews</i> , 2021, 50, 12292-12307.	18.7	23
128	Solution Structure of a Recombinant Type I Sculpin Antifreeze Protein,. <i>Biochemistry</i> , 2005, 44, 1980-1988.	1.2	22
129	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
130	Conformational Stability and DNA Binding Specificity of the Cardiac T-Box Transcription Factor Tbx20. <i>Journal of Molecular Biology</i> , 2009, 389, 606-618.	2.0	22
131	The stoichiometry and interactome of the Nucleosome Remodeling and Deacetylase (NuRD) complex are conserved across multiple cell lines. <i>FEBS Journal</i> , 2019, 286, 2043-2061.	2.2	22
132	GATAD2B-associated neurodevelopmental disorder (GAND): clinical and molecular insights into a NuRD-related disorder. <i>Genetics in Medicine</i> , 2020, 22, 878-888.	1.1	22
133	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
134	Structure and Inhibition of Orotidine 5- $\alpha$ -Monophosphate Decarboxylase from <i>Plasmodium falciparum</i> . <i>Biochemistry</i> , 2008, 47, 3842-3854.	1.2	21
135	The NuRD complex and macrocephaly associated neurodevelopmental disorders. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2019, 181, 548-556.	0.7	21
136	The Binding of Syndapin SH3 Domain to Dynamin Proline-rich Domain Involves Short and Long Distance Elements. <i>Journal of Biological Chemistry</i> , 2016, 291, 9411-9424.	1.6	20
137	Receptor homodimerization plays a critical role in a novel dominant negative P2RY12 variant identified in a family with severe bleeding. <i>Journal of Thrombosis and Haemostasis</i> , 2018, 16, 44-53.	1.9	20
138	A cis-Proline in $\beta$ -Hemoglobin Stabilizing Protein Directs the Structural Reorganization of $\beta$ -Hemoglobin. <i>Journal of Biological Chemistry</i> , 2009, 284, 29462-29469.	1.6	19
139	A heme-binding protein produced by <i>Haemophilus haemolyticus</i> inhibits non-typeable <i>Haemophilus influenzae</i> . <i>Molecular Microbiology</i> , 2020, 113, 381-398.	1.2	18
140	Response to Chatr-aryamontri et al.: Protein interactions: to believe or not to believe?. <i>Trends in Biochemical Sciences</i> , 2008, 33, 242-243.	3.7	17
141	The Structure of a Truncated Phosphoribosylanthranilate Isomerase Suggests a Unified Model for Evolution of the $(\beta)_8$ Barrel Fold. <i>Journal of Molecular Biology</i> , 2011, 408, 291-303.	2.0	17
142	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
143	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
144	The hydrophobic domain 26 of human tropoelastin is unstructured in solution. <i>Journal of Structural Biology</i> , 2005, 150, 154-162.	1.3	16

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145	Solution Structure of the THAP Domain from <i>Caenorhabditis elegans</i> C-terminal Binding Protein (CtBP). <i>Journal of Molecular Biology</i> , 2007, 366, 382-390.	2.0	16
146	Thermostable small-molecule inhibitor of angiogenesis and vascular permeability that suppresses a pERK-FosB/Î”FosBâ€”VCAM-1 axis. <i>Science Advances</i> , 2020, 6, eaaz7815.	4.7	16
147	Interdomain orientation of cardiac Troponin C characterized by paramagnetic relaxation enhancement NMR reveals a compact state. <i>Protein Science</i> , 2012, 21, 1376-1387.	3.1	15
148	Ca <sup>2+</sup> -Induced PRE-NMR Changes in the Troponin Complex Reveal the Possessive Nature of the Cardiac Isoform for Its Regulatory Switch. <i>PLoS ONE</i> , 2014, 9, e112976.	1.1	15
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