

Joel P Mackay

List of Publications by Year in descending order

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218
papers

11,227
citations

26610

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38368

95
g-index

248
all docs

248
docs citations

248
times ranked

14129
citing authors

#	ARTICLE	IF	CITATIONS
1	A NuRD for all seasons. Trends in Biochemical Sciences, 2023, 48, 11-25.	3.7	14
2	Unique protein interaction networks define the chromatin remodelling module of the NuRD complex. FEBS Journal, 2022, 289, 199-214.	2.2	13
3	Mechanism of Bloom syndrome complex assembly required for double Holliday junction dissolution and genome stability. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	12
4	RNA inhibits dMi-2/CHD4 chromatin binding and nucleosome remodeling. Cell Reports, 2022, 39, 110895.	2.9	5
5	The bromodomains of <sc>BET</sc> family proteins can recognize diacetylated histone <sc>H2A</sc>. Z. Protein Science, 2021, 30, 464-476.	3.1	8
6	BET-Family Bromodomains Can Recognize Diacetylated Sequences from Transcription Factors Using a Conserved Mechanism. Biochemistry, 2021, 60, 648-662.	1.2	7
7	Discovery of Cyclic Peptide Ligands to the SARS-CoV-2 Spike Protein Using mRNA Display. ACS Central Science, 2021, 7, 1001-1008.	5.3	47
8	Late-stage modification of peptides and proteins at cysteine with diaryliodonium salts. Chemical Science, 2021, 12, 14159-14166.	3.7	10
9	The characterization of protein interactions “ what, how and how much?. Chemical Society Reviews, 2021, 50, 12292-12307.	18.7	23
10	Purification of an insect juvenile hormone receptor complex enables insights into its post-translational phosphorylation. Journal of Biological Chemistry, 2021, 297, 101387.	1.6	14
11	A single dose, BCG-adjuvanted COVID-19 vaccine provides sterilising immunity against SARS-CoV-2 infection. Npj Vaccines, 2021, 6, 143.	2.9	47
12	Spacing Constraints of Neighboring Zinc Finger Modules within GATA2. Blood, 2021, 138, 3306-3306.	0.6	0
13	Peppy: A virtual reality environment for exploring the principles of polypeptide structure. Protein Science, 2020, 29, 157-168.	3.1	23
14	Comparative structure-function analysis of bromodomain and extraterminal motif (BET) proteins in a gene-complementation system. Journal of Biological Chemistry, 2020, 295, 1898-1914.	1.6	15
15	A heme-binding protein produced by <i>Haemophilus haemolyticus</i> inhibits non-typeable <i>Haemophilus influenzae</i>. Molecular Microbiology, 2020, 113, 381-398.	1.2	18
16	Cyclic peptides can engage a single binding pocket through highly divergent modes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26728-26738.	3.3	27
17	A Novel Purification Procedure for Active Recombinant Human DPP4 and the Inability of DPP4 to Bind SARS-CoV-2. Molecules, 2020, 25, 5392.	1.7	26
18	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. Cell Reports, 2020, 33, 108450.	2.9	37

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19	Thermostable small-molecule inhibitor of angiogenesis and vascular permeability that suppresses a pERK-FosB/β-FosB/VCAM-1 axis. <i>Science Advances</i> , 2020, 6, eaaz7815.	4.7	16
20	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
21	CHD4 slides nucleosomes by decoupling entry- and exit-side DNA translocation. <i>Nature Communications</i> , 2020, 11, 1519.	5.8	25
22	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
23	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
24	The uncharacterized bacterial protein YejG has the same architecture as domain III of elongation factor G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 699-705.	1.5	0
25	Exploring the suitability of RanBP2-type Zinc Fingers for RNA-binding protein design. <i>Scientific Reports</i> , 2019, 9, 2484.	1.6	9
26	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
27	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
28	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
29	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
30	A Transcription Factor Addiction in Leukemia Imposed by the MLL Promoter Sequence. <i>Cancer Cell</i> , 2018, 34, 970-981.e8.	7.7	53
31	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. <i>Nature Communications</i> , 2018, 9, 4300.	5.8	46
32	Expression, purification and DNA-binding properties of zinc finger domains of DOF proteins from <i>Arabidopsis thaliana</i> . <i>BioImpacts</i> , 2018, 8, 167-176.	0.7	12
33	NMR Spectroscopy in the Analysis of Protein-Protein Interactions. , 2018, , 2099-2132.		0
34	Whaddaya Know: A Guide to Uncertainty and Subjectivity in Structural Biology. <i>Trends in Biochemical Sciences</i> , 2017, 42, 155-167.	3.7	14
35	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
36	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

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37	IP ₃ -4 kinase Arg1 regulates cell wall homeostasis and surface architecture to promote <i>Cryptococcus neoformans</i> infection in a mouse model. <i>Virulence</i> , 2017, 8, 1833-1848.	1.8	12
38	dCas9-based epigenome editing suggests acquisition of histone methylation is not sufficient for target gene repression. <i>Nucleic Acids Research</i> , 2017, 45, 9901-9916.	6.5	160
39	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
40	NMR Spectroscopy in the Analysis of Protein-Protein Interactions. , 2017, , 1-34.		1
41	Architecture of the Nucleosome Remodeling and Deacetylase (NuRD) Complex. <i>FASEB Journal</i> , 2017, 31, .	0.2	0
42	The Chromatin Remodelling Protein CHD1 Contains a Previously Unrecognised C-Terminal Helical Domain. <i>Journal of Molecular Biology</i> , 2016, 428, 4298-4314.	2.0	14
43	The yeast transcription elongation factor Spt4/5 is a sequence-specific RNA binding protein. <i>Protein Science</i> , 2016, 25, 1710-1721.	3.1	11
44	The zinc fingers of YY1 bind single-stranded RNA with low sequence specificity. <i>Nucleic Acids Research</i> , 2016, 44, gkw590.	6.5	25
45	Site-specific phosphorylation of tau inhibits amyloid- β toxicity in Alzheimer's mice. <i>Science</i> , 2016, 354, 904-908.	6.0	241
46	Determinants of affinity and specificity in RNA-binding proteins. <i>Current Opinion in Structural Biology</i> , 2016, 38, 83-91.	2.6	51
47	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
48	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
49	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
50	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
51	¹ H, ¹³ C and ¹⁵ N resonance assignments of a C-terminal domain of human CHD1. <i>Biomolecular NMR Assignments</i> , 2016, 10, 31-34.	0.4	1
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	Site directed nitroxide spin labeling of oligonucleotides for NMR and EPR studies. <i>Tetrahedron</i> , 2015, 71, 813-819.	1.0	6
54	A peptide affinity reagent for isolating an intact and catalytically active multi-protein complex from mammalian cells. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 960-965.	1.4	7

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55	Homozygous Mutation of the ETS DNA-Binding Domain of FLI1 Causes a Bleeding Disorder with Giant Alpha Granules Similar to Paris-Trousseau Thrombocytopenia. <i>Blood</i> , 2015, 126, 78-78.	0.6	0
56	The Identification and Structure of an N-Terminal PR Domain Show that FOG1 Is a Member of the PRDM Family of Proteins. <i>PLoS ONE</i> , 2014, 9, e106011.	1.1	7
57	Ca ²⁺ -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
58	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
59	Structure of the Hemoglobin-IsoH 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
60	Insight into the Architecture of the NuRD Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 21844-21855.	1.6	75
61	¹ H, ¹³ C and ¹⁵ N resonance assignments of an N-terminal domain of CHD4. <i>Biomolecular NMR Assignments</i> , 2014, 8, 137-139.	0.4	1
62	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
63	Trim58 Degrades Dynein and Regulates Terminal Erythropoiesis. <i>Developmental Cell</i> , 2014, 30, 688-700.	3.1	75
64	Transcription Factor Seeks DNA Cognate Site Preferred. <i>Journal of Molecular Biology</i> , 2014, 426, 1370-1372.	2.0	0
65	Ubiquitin fusion constructs allow the expression and purification of multi-KOW domain complexes of the <i>Saccharomyces cerevisiae</i> transcription elongation factor Spt4/5. <i>Protein Expression and Purification</i> , 2014, 100, 54-60.	0.6	2
66	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
67	New Insights into the Mechanism of Dominant Anemia Caused By Zinc Finger Mutations in KLF1. <i>Blood</i> , 2014, 124, 740-740.	0.6	0
68	Is there a telltale RH fingerprint in zinc fingers that recognizes methylated CpG dinucleotides?. <i>Trends in Biochemical Sciences</i> , 2013, 38, 421-422.	3.7	2
69	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
70	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
71	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
72	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

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73	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
74	Î±-Hemoglobin-stabilizing Protein (AHSP) Perturbs the Proximal Heme Pocket of Oxy-Î±-hemoglobin and Weakens the Iron-Oxygen Bond*. <i>Journal of Biological Chemistry</i> , 2013, 288, 19986-20001.	1.6	12
75	Analysis of disease-causing GATA1 mutations in murine gene complementation systems. <i>Blood</i> , 2013, 121, 5218-5227.	0.6	42
76	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
77	The Detection and Quantitation of Protein Oligomerization. <i>Advances in Experimental Medicine and Biology</i> , 2012, 747, 19-41.	0.8	42
78	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
79	Solution structure of a tethered Lmo2_{LIM2}/Ldb1_{LID} complex. <i>Protein Science</i> , 2012, 21, 1768-1774.	3.1	7
80	Bivalent Recognition of a Single Nucleosome by the Tandem PHD Fingers of CHD4 is Required for CHD4-Mediated Repression. <i>Biophysical Journal</i> , 2012, 102, 480a.	0.2	0
81	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
82	Synthesis of the Bacteriocin Glycopeptide Sublancin 168 and <i>S</i>-Glycosylated Variants. <i>Organic Letters</i> , 2012, 14, 1910-1913.	2.4	41
83	Determination of ribonuclease sequence-specificity using Pentaproboscopes and mass spectrometry. <i>Rna</i> , 2012, 18, 1267-1278.	1.6	39
84	Modular Assembly of RanBP2â€¢Type Zinc Finger Domains to Target Singleâ€¢Stranded RNA. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5371-5375.	7.2	7
85	A rapid method for assessing the RNA-binding potential of a protein. <i>Nucleic Acids Research</i> , 2012, 40, e105-e105.	6.5	29
86	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
87	Backbone and sidechain ¹ H, ¹³ C and ¹⁵ N chemical shift assignments of the hydrophobin DewA from <i>Aspergillus nidulans</i> . <i>Biomolecular NMR Assignments</i> , 2012, 6, 83-86.	0.4	5
88	Two-timing zinc finger transcription factors liaising with RNA. <i>Trends in Biochemical Sciences</i> , 2012, 37, 199-205.	3.7	45
89	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
90	Dissecting the Molecular Pathways That Underlie Disease-Causing GATA1 Mutations. <i>Blood</i> , 2012, 120, 3439-3439.	0.6	0

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91	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
92	The Structure of a Truncated Phosphoribosylanthranilate Isomerase Suggests a Unified Model for Evolution of the (β) ₈ Barrel Fold. <i>Journal of Molecular Biology</i> , 2011, 408, 291-303.	2.0	17
93	Macromolecular NMR spectroscopy for the non- ϵ spectroscopist. <i>FEBS Journal</i> , 2011, 278, 687-703.	2.2	140
94	Macromolecular NMR spectroscopy for the non- ϵ spectroscopist: beyond macromolecular solution structure determination. <i>FEBS Journal</i> , 2011, 278, 704-715.	2.2	53
95	The prospects for designer single-stranded RNA-binding proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 256-261.	3.6	59
96	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
97	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
98	Plant Homeodomain (PHD) Fingers of CHD4 Are Histone H3-binding Modules with Preference for Unmodified H3K4 and Methylated H3K9. <i>Journal of Biological Chemistry</i> , 2011, 286, 11779-11791.	1.6	147
99	Bromodomain protein Brd3 associates with acetylated GATA1 to promote its chromatin occupancy at erythroid target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E159-68.	3.3	190
100	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
101	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
102	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
103	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
104	AHSP (α -haemoglobin-stabilizing protein) stabilizes apo- α -haemoglobin in a partially folded state. <i>Biochemical Journal</i> , 2010, 432, 275-282.	1.7	14
105	¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of the N-terminal domain of the histidine kinase inhibitor Kipl from <i>Bacillus subtilis</i> . <i>Biomolecular NMR Assignments</i> , 2010, 4, 167-169.	0.4	1
106	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
107	Two-state conformational equilibrium in the Par4 leucine zipper domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2433-2449.	1.5	9
108	Beyond DNA: Zinc Finger Domains as RNA-Binding Modules. <i>Methods in Molecular Biology</i> , 2010, 649, 479-491.	0.4	48

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109	The zinc fingers of the SR-like protein ZRANB2 are single-stranded RNA-binding domains that recognize 5' splice site-like sequences. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5581-5586.	3.3	75
110	A cis-Proline in α -Hemoglobin Stabilizing Protein Directs the Structural Reorganization of α -Hemoglobin. Journal of Biological Chemistry, 2009, 284, 29462-29469.	1.6	19
111	Structural Analysis of MED-1 Reveals Unexpected Diversity in the Mechanism of DNA Recognition by GATA-type Zinc Finger Domains. Journal of Biological Chemistry, 2009, 284, 5827-5835.	1.6	22
112	The structural analysis of protein-protein interactions by NMR spectroscopy. Proteomics, 2009, 9, 5224-5232.	1.3	75
113	Conformational Stability and DNA Binding Specificity of the Cardiac T-Box Transcription Factor Tbx20. Journal of Molecular Biology, 2009, 389, 606-618.	2.0	22
114	A mass spectrometric investigation of the ability of metal complexes to modulate transcription factor activity. Chemical Communications, 2009, , 5546.	2.2	14
115	Binding of the CHD4 PHD2 finger to histone H3 is modulated by covalent modifications. Biochemical Journal, 2009, 423, 179-187.	1.7	106
116	It Takes Two to Tango: The Structure and Function of LIM, RING, PHD and MYND Domains. Current Pharmaceutical Design, 2009, 15, 3681-3696.	0.9	80
117	Structural analysis of hydrophobins. Micron, 2008, 39, 773-784.	1.1	194
118	Crystallization of a ZRANB2-RNA complex. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1175-1177.	0.7	5
119	NMR spectroscopy as a tool for the rapid assessment of the conformation of GST-fusion proteins. Protein Science, 2008, 17, 1630-1635.	3.1	8
120	Implementing the LIM code: the structural basis for cell type-specific assembly of LIM-homeodomain complexes. EMBO Journal, 2008, 27, 2018-2029.	3.5	68
121	Designed metal-binding sites in biomolecular and bioinorganic interactions. Current Opinion in Structural Biology, 2008, 18, 484-490.	2.6	28
122	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
123	Evolution of Quaternary Structure in a Homotetrameric Enzyme. Journal of Molecular Biology, 2008, 380, 691-703.	2.0	77
124	The Cys3-Cys4 Loop of the Hydrophobin EAS Is Not Required for Rodlet Formation and Surface Activity. Journal of Molecular Biology, 2008, 382, 708-720.	2.0	67
125	Escherichia coli Glucuronylsynthase: An Engineered Enzyme for the Synthesis of β -Glucuronides. Organic Letters, 2008, 10, 1585-1588.	2.4	32
126	Structure and Inhibition of Orotidine 5'-Monophosphate Decarboxylase from <i>Plasmodium falciparum</i> . Biochemistry, 2008, 47, 3842-3854.	1.2	21

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127	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
128	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. <i>Plant Cell</i> , 2007, 19, 2898-2912.	3.1	143
129	An erythroid chaperone that facilitates folding of β -globin subunits for hemoglobin synthesis. <i>Journal of Clinical Investigation</i> , 2007, 117, 1856-1865.	3.9	96
130	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
131	Mutations in Cardiac T-Box Factor Gene TBX20 Are Associated with Diverse Cardiac Pathologies, Including Defects of Septation and Valvulogenesis and Cardiomyopathy. <i>American Journal of Human Genetics</i> , 2007, 81, 280-291.	2.6	317
132	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
133	Sticky fingers: zinc-fingers as protein-recognition motifs. <i>Trends in Biochemical Sciences</i> , 2007, 32, 63-70.	3.7	370
134	Protein interactions: is seeing believing?. <i>Trends in Biochemical Sciences</i> , 2007, 32, 530-531.	3.7	89
135	Analysis of the Structure and Function of the Transcriptional Coregulator HOP. <i>Biochemistry</i> , 2006, 45, 10584-10590.	1.2	30
136	GATA-1: One protein, many partners. <i>International Journal of Biochemistry and Cell Biology</i> , 2006, 38, 6-11.	1.2	44
137	Identification of the Key LMO2-binding Determinants on Ldb1. <i>Journal of Molecular Biology</i> , 2006, 359, 66-75.	2.0	31
138	A Novel Haem-binding Interface in the 22 kDa Haem-binding Protein p22HBP. <i>Journal of Molecular Biology</i> , 2006, 362, 287-297.	2.0	8
139	Zinc fingers are known as domains for binding DNA and RNA. Do they also mediate protein-protein interactions?. <i>IUBMB Life</i> , 2006, 58, 731-733.	1.5	4
140	Structural basis for rodlet assembly in fungal hydrophobins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3621-3626.	3.3	218
141	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
142	Role of Alpha Hemoglobin-Stabilizing Protein in Normal Erythropoiesis and β -Thalassemia. <i>Annals of the New York Academy of Sciences</i> , 2005, 1054, 103-117.	1.8	41
143	Structure of oxidized β -haemoglobin bound to AHSP reveals a protective mechanism for haem. <i>Nature</i> , 2005, 435, 697-701.	13.7	102
144	Assessment of the Robustness of a Serendipitous Zinc Binding Fold: Mutagenesis and Protein Grafting. <i>Structure</i> , 2005, 13, 257-266.	1.6	9

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145	Grb7-SH2 domain dimerisation is affected by a single point mutation. <i>European Biophysics Journal</i> , 2005, 34, 454-460.	1.2	29
146	¹ H, ¹⁵ N and ¹³ C Assignments of an Intramolecular Lhx3:ldb1 Complex. <i>Journal of Biomolecular NMR</i> , 2005, 33, 198-198.	1.6	7
147	A Complex Mechanism Determines Polarity of DNA Replication Fork Arrest by the Replication Terminator Complex of <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 13105-13113.	1.6	11
148	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
149	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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