

Mark Bycroft

List of Publications by Year in descending order

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papers

8,551
citations

71004

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docs citations

90
times ranked

12603
citing authors

#	ARTICLE	IF	CITATIONS
1	SWI/SNF subunit BAF155 N-terminus structure informs the impact of cancer-associated mutations and reveals a potential drug binding site. <i>Communications Biology</i> , 2021, 4, 528.	2.0	5
2	Structure of the BRK domain of the SWI/SNF chromatin remodeling complex subunit BRG1 reveals a potential role in protein-protein interactions. <i>Protein Science</i> , 2020, 29, 1033-1039.	3.1	17
3	Crystal Structures and Nuclear Magnetic Resonance Studies of the Apo Form of the c-MYC:MAX bHLHZip Complex Reveal a Helical Basic Region in the Absence of DNA. <i>Biochemistry</i> , 2019, 58, 3144-3154.	1.2	38
4	The structure of c-MYC:MAX heterodimer provide insights into the interplay between c-MYC and the SWI/SNF chromatin remodeling complex. <i>FEBS Journal</i> , 2018, 285, 4165-4180.	2.2	22
5	Recruitment of TBK1 to cytosol-invading <i>Salmonella</i> induces WIPI2-dependent antibacterial autophagy. <i>EMBO Journal</i> , 2016, 35, 1779-1792.	3.5	107
6	High-resolution NMR structures of the domains of <i>Saccharomyces cerevisiae</i> Tho1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 500-506.	0.4	0
7	The Autophagy Receptor TAX1BP1 and the Molecular Motor Myosin VI Are Required for Clearance of <i>Salmonella Typhimurium</i> by Autophagy. <i>PLoS Pathogens</i> , 2015, 11, e1005174.	2.1	177
8	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 445-450.	1.0	4
9	The SWI/SNF Subunit INI1 Contains an N-Terminal Winged Helix DNA Binding Domain that Is a Target for Mutations in Schwannomatosis. <i>Structure</i> , 2015, 23, 1344-1349.	1.6	33
10	An integrated computational approach can classify VHL missense mutations according to risk of clear cell renal carcinoma. <i>Human Molecular Genetics</i> , 2014, 23, 5976-5988.	1.4	21
11	A high-resolution structure of the EF-hand domain of human polycystin-2. <i>Protein Science</i> , 2014, 23, 1301-1308.	3.1	26
12	Structural basis for P ^{an3} binding to P ^{an2} and its function in mRNA recruitment and deadenylation. <i>EMBO Journal</i> , 2014, 33, 1514-1526.	3.5	50
13	The UBAP1 Subunit of ESCRT-I Interacts with Ubiquitin via a SOUBA Domain. <i>Structure</i> , 2012, 20, 414-428.	1.6	88
14	Structural basis of p63 ^Δ SAM domain mutants involved in AEC syndrome. <i>FEBS Journal</i> , 2011, 278, 2680-2688.	2.2	23
15	Recognition of non-methyl histone marks. <i>Current Opinion in Structural Biology</i> , 2011, 21, 761-766.	2.6	9
16	The General Definition of the p97/Valosin-containing Protein (VCP)-interacting Motif (VIM) Delineates a New Family of p97 Cofactors. <i>Journal of Biological Chemistry</i> , 2011, 286, 38670-38678.	1.6	58
17	The structure of the FYR domain of transforming growth factor beta regulator 1. <i>Protein Science</i> , 2010, 19, 1432-1438.	3.1	33
18	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 617-619.	3.6	192

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19	Molecular basis of the interactions between the p73 N terminus and p300: Effects on transactivation and modulation by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3142-3147.	3.3	31
20	VHL Mutations Linked to Type 2C von Hippel-Lindau Disease Cause Extensive Structural Perturbations in pVHL. <i>Journal of Biological Chemistry</i> , 2009, 284, 10514-10522.	1.6	20
21	Solution structure of the FCS zinc finger domain of the human polycomb group protein L(3)mbt-like 2. <i>Protein Science</i> , 2009, 18, 657-661.	3.1	10
22	The Malignant Brain Tumor Repeats of Human SCML2 Bind to Peptides Containing Monomethylated Lysine. <i>Journal of Molecular Biology</i> , 2008, 382, 1107-1112.	2.0	31
23	Structural Consequences of Nucleophosmin Mutations in Acute Myeloid Leukemia. <i>Journal of Biological Chemistry</i> , 2008, 283, 23326-23332.	1.6	107
24	Four domains of p300 each bind tightly to a sequence spanning both transactivation subdomains of p53. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7009-7014.	3.3	190
25	Solution Structure of the BRK Domains from CHD7. <i>Journal of Molecular Biology</i> , 2007, 371, 1135-1140.	2.0	34
26	The solution structure of the ZnF UBP domain of USP33/VDU1. <i>Protein Science</i> , 2007, 16, 2072-2075.	3.1	28
27	Solution structure of the C4 zinc finger domain of HDM2. <i>Protein Science</i> , 2006, 15, 384-389.	3.1	36
28	Functional Analysis of the Post-transcriptional Regulator RsmA Reveals a Novel RNA-binding Site. <i>Journal of Molecular Biology</i> , 2006, 355, 1026-1036.	2.0	87
29	The FtsK $\hat{\text{I}}^3$ domain directs oriented DNA translocation by interacting with KOPS. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 965-972.	3.6	92
30	Solution structure of the nonmethyl-CpG-binding CXXC domain of the leukaemia-associated MLL histone methyltransferase. <i>EMBO Journal</i> , 2006, 25, 4503-4512.	3.5	146
31	The PUB Domain Functions as a p97 Binding Module in Human Peptide N-Glycanase. <i>Journal of Biological Chemistry</i> , 2006, 281, 25502-25508.	1.6	84
32	The macro domain is an ADP-ribose binding module. <i>EMBO Journal</i> , 2005, 24, 1911-1920.	3.5	439
33	Role of Conformational Heterogeneity in Domain Swapping and Adapter Function of the Cks Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 30448-30459.	1.6	23
34	Crystal Structure of a Hyperthermophilic Archaeal Acylphosphatase from <i>Pyrococcus horikoshii</i> Structural Insights into Enzymatic Catalysis, Thermostability, and Dimerization. <i>Biochemistry</i> , 2005, 44, 4601-4611.	1.2	35
35	Electrostatic Interactions Contribute to Reduced Heat Capacity Change of Unfolding in a Thermophilic Ribosomal Protein L30e. <i>Journal of Molecular Biology</i> , 2005, 348, 419-431.	2.0	44
36	Comparative Binding of p53 to its Promoter and DNA Recognition Elements. <i>Journal of Molecular Biology</i> , 2005, 348, 589-596.	2.0	167

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37	Solution Structure of the Kaposi's Sarcoma-associated Herpesvirus K3 N-terminal Domain Reveals a Novel E2-binding C4HC3-type RING Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 53840-53847.	1.6	85
38	NMR Structure of the Î±-Hemoglobin Stabilizing Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 34963-34970.	1.6	52
39	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. <i>Journal of Biological Chemistry</i> , 2004, 279, 3758-3765.	1.6	55
40	Letter to Editor: Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric Î²-barrel fold. <i>Journal of Biomolecular NMR</i> , 2004, 30, 211-214.	1.6	25
41	Crystallization and preliminary crystallographic analysis of a novel orange fluorescent protein from the Cnidarian <i>Actinopterygion</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 340-341.	2.5	11
42	Crystallization and preliminary crystallographic analysis of an acylphosphatase from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1308-1310.	2.5	7
43	Regulation of DNA Binding of p53 by its C-terminal Domain. <i>Journal of Molecular Biology</i> , 2004, 342, 801-811.	2.0	94
44	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeon <i>Thermococcus celer</i> . <i>Protein Science</i> , 2003, 12, 1483-1495.	3.1	13
45	Structure of the Jab1/MPN Domain and Its Implications for Proteasome Function. <i>Biochemistry</i> , 2003, 42, 11460-11465.	1.2	115
46	Crystal Structure of Ribosomal Protein L30e from the Extreme Thermophile <i>Thermococcus celer</i> : Thermal Stability and RNA Binding. <i>Biochemistry</i> , 2003, 42, 2857-2865.	1.2	15
47	Structural Variation in PWWP Domains. <i>Journal of Molecular Biology</i> , 2003, 330, 571-576.	2.0	38
48	The Crystal Structure of AF1521 a Protein from <i>Archaeoglobus fulgidus</i> with Homology to the Non-histone Domain of MacroH2A. <i>Journal of Molecular Biology</i> , 2003, 330, 503-511.	2.0	113
49	Crystal Structure of the Malignant Brain Tumor (MBT) Repeats in Sex Comb on Midleg-like 2 (SCML2). <i>Journal of Biological Chemistry</i> , 2003, 278, 46968-46973.	1.6	41
50	Molecular Mechanism of the Interaction between MDM2 and p53. <i>Journal of Molecular Biology</i> , 2002, 323, 491-501.	2.0	307
51	The Structure of an FF Domain from Human HYPA/FBP11. <i>Journal of Molecular Biology</i> , 2002, 323, 411-416.	2.0	82
52	The UBX domain: a widespread ubiquitin-like module. <i>Journal of Molecular Biology</i> , 2001, 307, 17-24.	2.0	130
53	The Ligand-Binding Loops in the Tunicate C-Type Lectin TC14 Are Rigid. <i>Biochemistry</i> , 2001, 40, 10966-10972.	1.2	20
54	Structure of the C-terminal sterile Î±-motif (SAM) domain of human p73. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 545-551.	2.5	28

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55	Crystallization and preliminary crystallographic studies of a ribosomal protein L30e from the hyperthermophilic archaeon <i>Thermococcus celer</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 865-866.	2.5	2
56	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73 Δ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 769-771.	2.5	11
57	RNA recognition by a Staufen double-stranded RNA-binding domain. <i>EMBO Journal</i> , 2000, 19, 997-1009.	3.5	331
58	Letter to the editor: 1H, 13C and 15N NMR assignments of the C-type lectin TC14. <i>Journal of Biomolecular NMR</i> , 2000, 18, 283-284.	1.6	3
59	The structure of a LysM domain from <i>E. coli</i> membrane-bound lytic murein transglycosylase D (MltD) 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 299, 1113-1119.	2.0	402
60	Biophysical Characterization of Elongin C from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2000, 39, 11137-11146.	1.2	10
61	Folding of a dimeric β -barrel: Residual structure in the urea denatured state of the human papillomavirus E2 DNA binding domain. <i>Protein Science</i> , 2000, 9, 799-811.	3.1	16
62	The structure of a tunicate C-type lectin from <i>Polyandrocarpa misakiensis</i> complexed with d-galactose. <i>Journal of Molecular Biology</i> , 1999, 290, 867-879.	2.0	94
63	NMR structure of the N-terminal domain of <i>Saccharomyces cerevisiae</i> RNase HI reveals a fold with a strong resemblance to the N-terminal domain of ribosomal protein L9 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 291, 661-669.	2.0	30
64	Characterisation of urea-denatured states of an immunoglobulin superfamily domain by heteronuclear NMR 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 278, 417-429.	2.0	29
65	Crystal Structure of a Calcium-Phospholipid Binding Domain from Cytosolic Phospholipase A2. <i>Journal of Biological Chemistry</i> , 1998, 273, 1596-1604.	1.6	256
66	The Solution Structure of the S1 RNA Binding Domain: A Member of an Ancient Nucleic Acid-binding Fold. <i>Cell</i> , 1997, 88, 235-242.	13.5	391
67	Structure and Stability of an Immunoglobulin Superfamily Domain from Twitchin, a Muscle Protein of the Nematode <i>Caenorhabditis elegans</i> . <i>Journal of Molecular Biology</i> , 1996, 264, 624-639.	2.0	59
68	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strain Δ 16 E2 DNA-binding domain. <i>Protein Science</i> , 1996, 5, 310-319.	3.1	77
69	The dimeric DNA binding domain of the human papillomavirus E2 protein folds through a monomeric intermediate which cannot be native-like. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 711-717.	3.6	35
70	A Comparison of the pH, Urea, and Temperature-denatured States of Barnase by Heteronuclear NMR: Implications for the Initiation of Protein Folding. <i>Journal of Molecular Biology</i> , 1995, 254, 305-321.	2.0	134
71	Assignment of the backbone 1H, 15N, 13C NMR resonances and secondary structure of a double-stranded RNA binding domain from the <i>Drosophila</i> protein staufen. <i>FEBS Letters</i> , 1995, 362, 333-336.	1.3	9
72	Three-dimensional solution structure and 13C assignments of barstar using nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1994, 33, 8866-8877.	1.2	110

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73	Identification of the barstar binding site of barnase by NMR spectroscopy and hydrogen-deuterium exchange. FEBS Letters, 1993, 331, 165-172.	1.3	38
74	Assignment of the backbone ¹ H and ¹⁵ N NMR resonances and secondary structure characterization of barstar. FEBS Letters, 1993, 332, 81-87.	1.3	20
75	Structure and dynamics of barnase complexed with 3'-GMP studied by NMR spectroscopy. Biochemistry, 1993, 32, 10975-10987.	1.2	25
76	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 837-845.	2.0	100
77	Determination of the three-dimensional solution structure of barnase using nuclear magnetic resonance spectroscopy. Biochemistry, 1991, 30, 8697-8701.	1.2	125
78	Characterization of phosphate binding in the active site of barnase by site-directed mutagenesis and NMR. Biochemistry, 1991, 30, 11348-11356.	1.2	33
79	Aromatic-aromatic interactions and protein stability. Journal of Molecular Biology, 1991, 218, 465-475.	2.0	315
80	Surface electrostatic interactions contribute little to stability of barnase. Journal of Molecular Biology, 1991, 220, 779-788.	2.0	176
81	Physical-organic molecular biology: pathway and stability of protein folding. Pure and Applied Chemistry, 1991, 63, 187-194.	0.9	7
82	Transient folding intermediates characterized by protein engineering. Nature, 1990, 346, 440-445.	13.7	501
83	Detection and characterization of a folding intermediate in barnase by NMR. Nature, 1990, 346, 488-490.	13.7	241
84	Sequential assignment of the proton nuclear magnetic resonance spectrum of barnase. Biochemistry, 1990, 29, 7425-7432.	1.2	39
85	Strength and co-operativity of contributions of surface salt bridges to protein stability. Journal of Molecular Biology, 1990, 216, 1031-1044.	2.0	410
86	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. Biochemistry, 1990, 29, 9343-9352.	1.2	390
87	Stabilization of protein structure by interaction of α -helix dipole with a charged side chain. Nature, 1988, 335, 740-743.	13.7	239
88	Assignment of histidine resonances in the proton NMR (500 MHz) spectrum of subtilisin BPN' using site-directed mutagenesis. Biochemistry, 1988, 27, 7390-7394.	1.2	16
89	Amperometric enzyme electrodes. Journal of Electroanalytical Chemistry and Interfacial Electrochemistry, 1987, 218, 119-126.	0.3	64