Mark Bycroft

List of Publications by Year in descending order

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#	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. Communications Biology, 2021, 4, 528.	4.4	5
2	Structure of the BRK domain of the SWI/SNF chromatin remodeling complex subunit BRG1 reveals a potential role in protein–protein interactions. Protein Science, 2020, 29, 1033-1039.	7.6	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. Biochemistry, 2019, 58, 3144-3154.	2.5	38
4	The structure of <scp>INI</scp> 1/ <scp>hSNF</scp> 5 <scp>RPT</scp> 1 and its interactions with the câ€ <scp>MYC</scp> : <scp>MAX</scp> heterodimer provide insights into the interplay between <scp>MYC</scp> and the <scp>SWI</scp> / <scp>SNF</scp> chromatin remodeling complex. FEBS Journal, 2018, 285, 4165-4180.	4.7	22
5	Recruitment of <scp>TBK</scp> 1 to cytosolâ€invading <i>Salmonella</i> induces <scp>WIPI</scp> 2â€dependent antibacterial autophagy. EMBO Journal, 2016, 35, 1779-1792.	7.8	107
6	High-resolution NMR structures of the domains ofSaccharomyces cerevisiaeTho1. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 500-506.	0.8	0
7	The Autophagy Receptor TAX1BP1 and the Molecular Motor Myosin VI Are Required for Clearance of Salmonella Typhimurium by Autophagy. PLoS Pathogens, 2015, 11, e1005174.	4.7	177
8	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. Protein Engineering, Design and Selection, 2015, 28, 445-450.	2.1	4
9	The SWI/SNF Subunit INI1 Contains an N-Terminal Winged Helix DNA Binding Domain that Is a Target for Mutations in Schwannomatosis. Structure, 2015, 23, 1344-1349.	3.3	33
10	An integrated computational approach can classify VHL missense mutations according to risk of clear cell renal carcinoma. Human Molecular Genetics, 2014, 23, 5976-5988.	2.9	21
11	A highâ€resolution structure of the EFâ€hand domain of human polycystinâ€2. Protein Science, 2014, 23, 1301-1308.	7.6	26
12	Structural basis for <scp>P</scp> an3 binding to <scp>P</scp> an2 and its function in <scp>mRNA</scp> recruitment and deadenylation. EMBO Journal, 2014, 33, 1514-1526.	7.8	50
13	The UBAP1 Subunit of ESCRT-I Interacts with Ubiquitin via a SOUBA Domain. Structure, 2012, 20, 414-428.	3.3	88
14	Structural basis of p63α SAM domain mutants involved in AEC syndrome. FEBS Journal, 2011, 278, 2680-2688.	4.7	23
15	Recognition of non-methyl histone marks. Current Opinion in Structural Biology, 2011, 21, 761-766.	5.7	9
16	The General Definition of the p97/Valosin-containing Protein (VCP)-interacting Motif (VIM) Delineates a New Family of p97 Cofactors. Journal of Biological Chemistry, 2011, 286, 38670-38678.	3.4	58
17	The structure of the FYR domain of transforming growth factor beta regulator 1. Protein Science, 2010, 19, 1432-1438.	7.6	33
18	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. Nature Structural and Molecular Biology, 2010, 17, 617-619.	8.2	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. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3142-3147.	7.1	31
20	VHL Mutations Linked to Type 2C von Hippel-Lindau Disease Cause Extensive Structural Perturbations in pVHL. Journal of Biological Chemistry, 2009, 284, 10514-10522.	3.4	20
21	Solution structure of the FCS zinc finger domain of the human polycomb group protein L(3)mbtâ€like 2. Protein Science, 2009, 18, 657-661.	7.6	10
22	The Malignant Brain Tumor Repeats of Human SCML2 Bind to Peptides Containing Monomethylated Lysine. Journal of Molecular Biology, 2008, 382, 1107-1112.	4.2	31
23	Structural Consequences of Nucleophosmin Mutations in Acute Myeloid Leukemia. Journal of Biological Chemistry, 2008, 283, 23326-23332.	3.4	107
24	Four domains of p300 each bind tightly to a sequence spanning both transactivation subdomains of p53. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7009-7014.	7.1	190
25	Solution Structure of the BRK Domains from CHD7. Journal of Molecular Biology, 2007, 371, 1135-1140.	4.2	34
26	The solution structure of the ZnF UBP domain of USP33/VDU1. Protein Science, 2007, 16, 2072-2075.	7.6	28
27	Solution structure of the C4 zinc finger domain of HDM2. Protein Science, 2006, 15, 384-389.	7.6	36
28	Functional Analysis of the Post-transcriptional Regulator RsmA Reveals a Novel RNA-binding Site. Journal of Molecular Biology, 2006, 355, 1026-1036.	4.2	87
29	The FtsK Î ³ domain directs oriented DNA translocation by interacting with KOPS. Nature Structural and Molecular Biology, 2006, 13, 965-972.	8.2	92
30	Solution structure of the nonmethyl-CpG-binding CXXC domain of the leukaemia-associated MLL histone methyltransferase. EMBO Journal, 2006, 25, 4503-4512.	7.8	146
31	The PUB Domain Functions as a p97 Binding Module in Human Peptide N-Glycanase. Journal of Biological Chemistry, 2006, 281, 25502-25508.	3.4	84
32	The macro domain is an ADP-ribose binding module. EMBO Journal, 2005, 24, 1911-1920.	7.8	439
33	Role of Conformational Heterogeneity in Domain Swapping and Adapter Function of the Cks Proteins. Journal of Biological Chemistry, 2005, 280, 30448-30459.	3.4	23
34	Crystal Structure of a Hyperthermophilic Archaeal Acylphosphatase fromPyrococcus horikoshiiStructural Insights into Enzymatic Catalysis, Thermostability, and Dimerizationâ€,‡. Biochemistry, 2005, 44, 4601-4611.	2.5	35
35	Electrostatic Interactions Contribute to Reduced Heat Capacity Change of Unfolding in a Thermophilic Ribosomal Protein L30e. Journal of Molecular Biology, 2005, 348, 419-431.	4.2	44
36	Comparative Binding of p53 to its Promoter and DNA Recognition Elements. Journal of Molecular Biology, 2005, 348, 589-596.	4.2	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. Journal of Biological Chemistry, 2004, 279, 53840-53847.	3.4	85
38	NMR Structure of the α-Hemoglobin Stabilizing Protein. Journal of Biological Chemistry, 2004, 279, 34963-34970.	3.4	52
39	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. Journal of Biological Chemistry, 2004, 279, 3758-3765.	3.4	55
40	Letter to Editor: Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric β-barrel fold. Journal of Biomolecular NMR, 2004, 30, 211-214.	2.8	25
41	Crystallization and preliminary crystallographic analysis of a novel orange fluorescent protein from theCnidariatube anemoneCerianthussp Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 340-341.	2.5	11
42	Crystallization and preliminary crystallographic analysis of an acylphosphatase from the hyperthermophilic archaeonPyrococcus horikoshii. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1308-1310.	2.5	7
43	Regulation of DNA Binding of p53 by its C-terminal Domain. Journal of Molecular Biology, 2004, 342, 801-811.	4.2	94
44	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeonThermococcus celer. Protein Science, 2003, 12, 1483-1495.	7.6	13
45	Structure of the Jab1/MPN Domain and Its Implications for Proteasome Function. Biochemistry, 2003, 42, 11460-11465.	2.5	115
46	Crystal Structure of Ribosomal Protein L30e from the Extreme ThermophileThermococcus celer:Â Thermal Stability and RNA Bindingâ€,‡. Biochemistry, 2003, 42, 2857-2865.	2.5	15
47	Structural Variation in PWWP Domains. Journal of Molecular Biology, 2003, 330, 571-576.	4.2	38
48	The Crystal Structure of AF1521 a Protein from Archaeoglobus fulgidus with Homology to the Non-histone Domain of MacroH2A. Journal of Molecular Biology, 2003, 330, 503-511.	4.2	113
49	Crystal Structure of the Malignant Brain Tumor (MBT) Repeats in Sex Comb on Midleg-like 2 (SCML2). Journal of Biological Chemistry, 2003, 278, 46968-46973.	3.4	41
50	Molecular Mechanism of the Interaction between MDM2 and p53. Journal of Molecular Biology, 2002, 323, 491-501.	4.2	307
51	The Structure of an FF Domain from Human HYPA/FBP11. Journal of Molecular Biology, 2002, 323, 411-416.	4.2	82
52	The UBX domain: a widespread ubiquitin-like module. Journal of Molecular Biology, 2001, 307, 17-24.	4.2	130
53	The Ligand-Binding Loops in the Tunicate C-Type Lectin TC14 Are Rigid. Biochemistry, 2001, 40, 10966-10972.	2.5	20
54	Structure of the C-terminal sterile α-motif (SAM) domain of human p73α. Acta Crystallographica Section D: Biological Crystallography, 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 archaeonThermococcus celer. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 865-866.	2.5	2
56	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73α. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 769-771.	2.5	11
57	RNA recognition by a Staufen double-stranded RNA-binding domain. EMBO Journal, 2000, 19, 997-1009.	7.8	331
58	Letter to the editor: 1H, 13C and 15N NMR assignments of the C-type lectin TC14. Journal of Biomolecular NMR, 2000, 18, 283-284.	2.8	3
59	The structure of a LysM domain from E. coli membrane-bound lytic murein transglycosylase D (MltD) 1 1Edited by P. E. Wight. Journal of Molecular Biology, 2000, 299, 1113-1119.	4.2	402
60	Biophysical Characterization of Elongin C from Saccharomyces cerevisiae. Biochemistry, 2000, 39, 11137-11146.	2.5	10
61	Folding of a dimeric βâ€barrel: Residual structure in the urea denatured state of the human papillomavirus E2 DNA binding domain. Protein Science, 2000, 9, 799-811.	7.6	16
62	The structure of a tunicate C-type lectin from polyandrocarpa misakiensis complexed with d-galactose. Journal of Molecular Biology, 1999, 290, 867-879.	4.2	94
63	NMR structure of the N-terminal domain of Saccharomyces cerevisiae RNase HI reveals a fold with a strong resemblance to the N-terminal domain of ribosomal protein L9 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 291, 661-669.	4.2	30
64	Characterisation of urea-denatured states of an immunoglobulin superfamily domain by heteronuclear NMR 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 278, 417-429.	4.2	29
65	Crystal Structure of a Calcium-Phospholipid Binding Domain from Cytosolic Phospholipase A2. Journal of Biological Chemistry, 1998, 273, 1596-1604.	3.4	256
66	The Solution Structure of the S1 RNA Binding Domain: A Member of an Ancient Nucleic Acid–Binding Fold. Cell, 1997, 88, 235-242.	28.9	391
67	Structure and Stability of an Immunoglobulin Superfamily Domain from Twitchin, a Muscle Protein of the NematodeCaenorhabditis elegans. Journal of Molecular Biology, 1996, 264, 624-639.	4.2	59
68	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strainâ€16 E2 DNAâ€binding domain. Protein Science, 1996, 5, 310-319.	7.6	77
69	The dimeric DNA binding domain of the human papillomavirus E2 protein folds through a monomeric intermediate which cannot be native-like. Nature Structural and Molecular Biology, 1996, 3, 711-717.	8.2	35
70	A Comparison of the pH, Urea, and Temperature-denatured States of Barnase by Heteronuclear NMR: Implications for the Initiation of Protein Folding. Journal of Molecular Biology, 1995, 254, 305-321.	4.2	134
71	Assignment of the backbone1H,15N,13C NMR resonances and secondary structure of a double-stranded RNA binding domain from theDrosophilaprotein staufen. FEBS Letters, 1995, 362, 333-336.	2.8	9
72	Three-dimensional solution structure and 13C assignments of barstar using nuclear magnetic resonance spectroscopy. Biochemistry, 1994, 33, 8866-8877.	2.5	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.	2.8	38
74	Assignment of the backbone1H and15N NMR resonances and secondary structure characterization of barstar. FEBS Letters, 1993, 332, 81-87.	2.8	20
75	Structure and dynamics of barnase complexed with 3'-GMP studied by NMR spectroscopy. Biochemistry, 1993, 32, 10975-10987.	2.5	25
76	The folding of an enzyme. Journal of Molecular Biology, 1992, 224, 837-845.	4.2	100
77	Determination of the three-dimensional solution structure of barnase using nuclear magnetic resonance spectroscopy. Biochemistry, 1991, 30, 8697-8701.	2.5	125
78	Characterization of phosphate binding in the active site of barnase by site-directed mutagenesis and NMR. Biochemistry, 1991, 30, 11348-11356.	2.5	33
79	Aromatic-aromatic interactions and protein stability. Journal of Molecular Biology, 1991, 218, 465-475.	4.2	315
80	Surface electrostatic interactions contribute little to stability of barnase. Journal of Molecular Biology, 1991, 220, 779-788.	4.2	176
81	Physical-organic molecular biology: pathway and stability of protein folding. Pure and Applied Chemistry, 1991, 63, 187-194.	1.9	7
82	Transient folding intermediates characterized by protein engineering. Nature, 1990, 346, 440-445.	27.8	501
83	Detection and characterization of a folding intermediate in barnase by NMR. Nature, 1990, 346, 488-490.	27.8	241
84	Sequential assignment of the proton nuclear magnetic resonance spectrum of barnase. Biochemistry, 1990, 29, 7425-7432.	2.5	39
85	Strength and co-operativity of contributions of surface salt bridges to protein stability. Journal of Molecular Biology, 1990, 216, 1031-1044.	4.2	410
86	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. Biochemistry, 1990, 29, 9343-9352.	2.5	390
87	Stabilization of protein structure by interaction of α-helix dipole with a charged side chain. Nature, 1988, 335, 740-743.	27.8	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.	2.5	16
89	Amperometric enzyme electrodes. Journal of Electroanalytical Chemistry and Interfacial Electrochemistry, 1987, 218, 119-126.	0.1	64