Mark Bycroft

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89 papers	7,433 citations	41 h-index	86 g-index
90 ext. papers	7,952 ext. citations	8.2 avg, IF	5.37 L-index

#	Paper	IF	Citations
89	Transient folding intermediates characterized by protein engineering. *Nature*, **1990**, 346, 440-5	50.4	476
88	Strength and co-operativity of contributions of surface salt bridges to protein stability. *Journal of Molecular Biology*, **1990**, 216, 1031-44	6.5	382
87	The macro domain is an ADP-ribose binding module. *EMBO Journal*, **2005**, 24, 1911-20	13	380
86	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. *Biochemistry*, **1990**, 29, 9343-52	3.2	359
85	The solution structure of the S1 RNA binding domain: a member of an ancient nucleic acid-binding fold. *Cell*, **1997**, 88, 235-42	56.2	350
84	The structure of a LysM domain from E. coli membrane-bound lytic murein transglycosylase D (MltD). *Journal of Molecular Biology*, **2000**, 299, 1113-9	6.5	343
83	RNA recognition by a Staufen double-stranded RNA-binding domain. *EMBO Journal*, **2000**, 19, 997-1009	13	291
82	Aromatic-aromatic interactions and protein stability. Investigation by double-mutant cycles. *Journal of Molecular Biology*, **1991**, 218, 465-75	6.5	288
81	Molecular mechanism of the interaction between MDM2 and p53. *Journal of Molecular Biology*, **2002**, 323, 491-501	6.5	280
80	Crystal structure of a calcium-phospholipid binding domain from cytosolic phospholipase A2. *Journal of Biological Chemistry*, **1998**, 273, 1596-604	5.4	223
79	Stabilization of protein structure by interaction of alpha-helix dipole with a charged side chain. *Nature*, **1988**, 335, 740-3	50.4	216
78	Detection and characterization of a folding intermediate in barnase by NMR. *Nature*, **1990**, 346, 488-90	50.4	210
77	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. *Nature Structural and Molecular Biology*, **2010**, 17, 617-9	17.6	164
76	Surface electrostatic interactions contribute little of stability of barnase. *Journal of Molecular Biology*, **1991**, 220, 779-88	6.5	161
75	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, 7009-14	11.5	156
74	Comparative binding of p53 to its promoter and DNA recognition elements. *Journal of Molecular Biology*, **2005**, 348, 589-96	6.5	145
73	The Autophagy Receptor TAX1BP1 and the Molecular Motor Myosin VI Are Required for Clearance of Salmonella Typhimurium by Autophagy. *PLoS Pathogens*, **2015**, 11, e1005174	7.6	131

72	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, 305-21	6.5	129
71	Solution structure of the nonmethyl-CpG-binding CXXC domain of the leukaemia-associated MLL histone methyltransferase. *EMBO Journal*, **2006**, 25, 4503-12	13	127
70	The UBX domain: a widespread ubiquitin-like module. *Journal of Molecular Biology*, **2001**, 307, 17-24	6.5	119
69	Determination of the three-dimensional solution structure of barnase using nuclear magnetic resonance spectroscopy. *Biochemistry*, **1991**, 30, 8697-701	3.2	108
68	Three-dimensional solution structure and 13C assignments of barstar using nuclear magnetic resonance spectroscopy. *Biochemistry*, **1994**, 33, 8866-8877	3.2	104
67	Structure of the Jab1/MPN domain and its implications for proteasome function. *Biochemistry*, **2003**, 42, 11460-5	3.2	100
66	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, 503-11	6.5	97
65	The folding of an enzyme. V. H/2H exchange-nuclear magnetic resonance studies on the folding pathway of barnase: complementarity to and agreement with protein engineering studies. *Journal of Molecular Biology*, **1992**, 224, 837-45	6.5	90
64	The structure of a tunicate C-type lectin from Polyandrocarpa misakiensis complexed with D -galactose. *Journal of Molecular Biology*, **1999**, 290, 867-79	6.5	89
63	Structural consequences of nucleophosmin mutations in acute myeloid leukemia. *Journal of Biological Chemistry*, **2008**, 283, 23326-32	5.4	84
62	Regulation of DNA binding of p53 by its C-terminal domain. *Journal of Molecular Biology*, **2004**, 342, 801-11	6.5	84
61	The FtsK gamma domain directs oriented DNA translocation by interacting with KOPS. *Nature Structural and Molecular Biology*, **2006**, 13, 965-72	17.6	83
60	The structure of an FF domain from human HYPA/FBP11. *Journal of Molecular Biology*, **2002**, 323, 411-6	6.5	78
59	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, 53840-7	5.4	77
58	The UBAP1 subunit of ESCRT-I interacts with ubiquitin via a SOUBA domain. *Structure*, **2012**, 20, 414-28	5.2	76
57	Recruitment of TBK1 to cytosol-invading Salmonella induces WIPI2-dependent antibacterial autophagy. *EMBO Journal*, **2016**, 35, 1779-92	13	71
56	The PUB domain functions as a p97 binding module in human peptide N-glycanase. *Journal of Biological Chemistry*, **2006**, 281, 25502-8	5.4	69
55	Functional analysis of the post-transcriptional regulator RsmA reveals a novel RNA-binding site. *Journal of Molecular Biology*, **2006**, 355, 1026-36	6.5	69

54	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strain-16 E2 DNA-binding domain. *Protein Science*, **1996**, 5, 310-9	6.3	66
53	Amperometric enzyme electrodes. *Journal of Electroanalytical Chemistry and Interfacial Electrochemistry*, **1987**, 218, 119-126		55
52	Structure and stability of an immunoglobulin superfamily domain from twitchin, a muscle protein of the nematode Caenorhabditis elegans. *Journal of Molecular Biology*, **1996**, 264, 624-39	6.5	54
51	NMR structure of the alpha-hemoglobin stabilizing protein: insights into conformational heterogeneity and binding. *Journal of Biological Chemistry*, **2004**, 279, 34963-70	5.4	47
50	The structure of the AXH domain of spinocerebellar ataxin-1. *Journal of Biological Chemistry*, **2004**, 279, 3758-65	5.4	47
49	Electrostatic interactions contribute to reduced heat capacity change of unfolding in a thermophilic ribosomal protein l30e. *Journal of Molecular Biology*, **2005**, 348, 419-31	6.5	43
48	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	5.4	40
47	Crystal structure of the malignant brain tumor (MBT) repeats in Sex Comb on Midleg-like 2 (SCML2). *Journal of Biological Chemistry*, **2003**, 278, 46968-73	5.4	39
46	Structural basis for Pan3 binding to Pan2 and its function in mRNA recruitment and deadenylation. *EMBO Journal*, **2014**, 33, 1514-26	13	38
45	Structural variation in PWWP domains. *Journal of Molecular Biology*, **2003**, 330, 571-6	6.5	36
44	Solution structure of the C4 zinc finger domain of HDM2. *Protein Science*, **2006**, 15, 384-9	6.3	35
43	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, 711-7	17.6	34
42	Identification of the barstar binding site of barnase by NMR spectroscopy and hydrogen-deuterium exchange. *FEBS Letters*, **1993**, 331, 165-72	3.8	34
41	Sequential assignment of the 1H nuclear magnetic resonance spectrum of barnase. *Biochemistry*, **1990**, 29, 7425-32	3.2	34
40	Crystal structure of a hyperthermophilic archaeal acylphosphatase from Pyrococcus horikoshii--structural insights into enzymatic catalysis, thermostability, and dimerization. *Biochemistry*, **2005**, 44, 4601-11	3.2	31
39	The structure of the FYR domain of transforming growth factor beta regulator 1. *Protein Science*, **2010**, 19, 1432-8	6.3	30
38	The malignant brain tumor repeats of human SCML2 bind to peptides containing monomethylated lysine. *Journal of Molecular Biology*, **2008**, 382, 1107-12	6.5	29
37	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. *Journal of Molecular Biology*, **1999**, 291, 661-9	6.5	29

36	Structure of the C-terminal sterile alpha-motif (SAM) domain of human p73 alpha. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 545-51		27
35	Characterization of phosphate binding in the active site of barnase by site-directed mutagenesis and NMR. *Biochemistry*, **1991**, 30, 11348-56	3.2	26
34	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, 3142-7	11.5	25
33	Characterisation of urea-denatured states of an immunoglobulin superfamily domain by heteronuclear NMR. *Journal of Molecular Biology*, **1998**, 278, 417-29	6.5	25
32	Solution structure of the BRK domains from CHD7. *Journal of Molecular Biology*, **2007**, 371, 1135-40	6.5	24
31	The solution structure of the ZnF UBP domain of USP33/VDU1. *Protein Science*, **2007**, 16, 2072-5	6.3	22
30	Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric beta-barrel fold. *Journal of Biomolecular NMR*, **2004**, 30, 211-4	3	22
29	Structure and dynamics of barnase complexed with 3'GMP studied by NMR spectroscopy. *Biochemistry*, **1993**, 32, 10975-87	3.2	22
28	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, 1344-9	5.2	21
27	An integrated computational approach can classify VHL missense mutations according to risk of clear cell renal carcinoma. *Human Molecular Genetics*, **2014**, 23, 5976-88	5.6	19
26	Role of conformational heterogeneity in domain swapping and adapter function of the Cks proteins. *Journal of Biological Chemistry*, **2005**, 280, 30448-59	5.4	19
25	Structural basis of p63 SAM domain mutants involved in AEC syndrome. *FEBS Journal*, **2011**, 278, 2680-8	5.7	18
24	The ligand-binding loops in the tunicate C-type lectin TC14 are rigid. *Biochemistry*, **2001**, 40, 10966-72	3.2	17
23	Assignment of the backbone 1H and 15N NMR resonances and secondary structure characterization of barstar. *FEBS Letters*, **1993**, 332, 81-7	3.8	17
22	VHL mutations linked to type 2C von Hippel-Lindau disease cause extensive structural perturbations in pVHL. *Journal of Biological Chemistry*, **2009**, 284, 10514-22	5.4	16
21	Folding of a dimeric beta-barrel: residual structure in the urea denatured state of the human papillomavirus E2 DNA binding domain. *Protein Science*, **2000**, 9, 799-811	6.3	16
20	Assignment of histidine resonances in the 1H NMR (500 MHz) spectrum of subtilisin BPN using site-directed mutagenesis. *Biochemistry*, **1988**, 27, 7390-4	3.2	16
19	Crystal structure of ribosomal protein L30e from the extreme thermophile Thermococcus celer: thermal stability and RNA binding. *Biochemistry*, **2003**, 42, 2857-65	3.2	15

18	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	3.2	14
17	The structure of INI1/hSNF5 RPT1 and its interactions with the c-MYC:MAX heterodimer provide insights into the interplay between MYC and the SWI/SNF chromatin remodeling complex. *FEBS Journal*, **2018**, 285, 4165-4180	5.7	14
16	A high-resolution structure of the EF-hand domain of human polycystin-2. *Protein Science*, **2014**, 23, 1301-8	6.9	13
15	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeon Thermococcus celer. *Protein Science*, **2003**, 12, 1483-95	6.3	13
14	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73alpha. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 769-71		11
13	Crystallization and preliminary crystallographic analysis of a novel orange fluorescent protein from the Cnidaria tube anemone Cerianthus sp. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 340-1		10
12	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, 1047-1053	6.3	10
11	Biophysical characterization of elongin C from Saccharomyces cerevisiae. *Biochemistry*, **2000**, 39, 11137-46	3.2	8
10	Assignment of the backbone 1H,15N,13C NMR resonances and secondary structure of a double-stranded RNA binding domain from the Drosophila protein staufen. *FEBS Letters*, **1995**, 362, 333-6	3.8	8
9	Solution structure of the FCS zinc finger domain of the human polycomb group protein L(3)mbt-like 2. *Protein Science*, **2009**, 18, 657-61	6.3	7
8	Crystallization and preliminary crystallographic analysis of an acylphosphatase from the hyperthermophilic archaeon Pyrococcus horikoshii. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 1308-10		7
7	Physical-organic molecular biology: pathway and stability of protein folding. *Pure and Applied Chemistry*, **1991**, 63, 187-194	2.1	6
6	Recognition of non-methyl histone marks. *Current Opinion in Structural Biology*, **2011**, 21, 761-6	8.1	5
5	Letter to the editor: 1H, 13C and 15N NMR assignments of the C-type lectin TC14. *Journal of Biomolecular NMR*, **2000**, 18, 283-4	3	3
4	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. *Protein Engineering, Design and Selection*, **2015**, 28, 445-50	1.9	2
3	Crystallization and preliminary crystallographic studies of a ribosomal protein L30e from the hyperthermophilic archaeon Thermococcus celer. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 865-6		2
2	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	6.7	1
1	High-resolution NMR structures of the domains of Saccharomyces cerevisiae Tho1. *Acta Crystallographica Section F, Structural Biology Communications*, **2016**, 72, 500-6	1.1	