

Mark Bycroft

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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	6.7	1
88	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, 1047-1053	6.3	10
87	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 ²	5.4 ²	14
86	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. <i>FEBS Journal</i> , 2018 , 285, 4165-4180	5.7	14
85	High-resolution NMR structures of the domains of <i>Saccharomyces cerevisiae</i> Tho1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016 , 72, 500-6	1.1	
84	Recruitment of TBK1 to cytosol-invading <i>Salmonella</i> induces WIPI2-dependent antibacterial autophagy. <i>EMBO Journal</i> , 2016 , 35, 1779-92	13	71
83	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. <i>Protein Engineering, Design and Selection</i> , 2015 , 28, 445-50	1.9	2
82	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, 1344-9	5.2	21
81	The Autophagy Receptor TAX1BP1 and the Molecular Motor Myosin VI Are Required for Clearance of <i>Salmonella</i> Typhimurium by Autophagy. <i>PLoS Pathogens</i> , 2015 , 11, e1005174	7.6	131
80	A high-resolution structure of the EF-hand domain of human polycystin-2. <i>Protein Science</i> , 2014 , 23, 1301-8	13	13
79	Structural basis for Pan3 binding to Pan2 and its function in mRNA recruitment and deadenylation. <i>EMBO Journal</i> , 2014 , 33, 1514-26	13	38
78	An integrated computational approach can classify VHL missense mutations according to risk of clear cell renal carcinoma. <i>Human Molecular Genetics</i> , 2014 , 23, 5976-88	5.6	19
77	The UBAP1 subunit of ESCRT-I interacts with ubiquitin via a SOUBA domain. <i>Structure</i> , 2012 , 20, 414-28	5.2	76
76	Structural basis of p63SAM domain mutants involved in AEC syndrome. <i>FEBS Journal</i> , 2011 , 278, 2680-8	5.7	18
75	Recognition of non-methyl histone marks. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 761-6	8.1	5
74	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	5.4	40
73	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 617-9	17.6	164

72	The structure of the FYR domain of transforming growth factor beta regulator 1. <i>Protein Science</i> , 2010 , 19, 1432-8	6.3	30
71	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, 3142-7	11.5	25
70	VHL mutations linked to type 2C von Hippel-Lindau disease cause extensive structural perturbations in pVHL. <i>Journal of Biological Chemistry</i> , 2009 , 284, 10514-22	5.4	16
69	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, 657-61	6.3	7
68	The malignant brain tumor repeats of human SCML2 bind to peptides containing monomethylated lysine. <i>Journal of Molecular Biology</i> , 2008 , 382, 1107-12	6.5	29
67	Structural consequences of nucleophosmin mutations in acute myeloid leukemia. <i>Journal of Biological Chemistry</i> , 2008 , 283, 23326-32	5.4	84
66	The solution structure of the ZnF UBP domain of USP33/VDU1. <i>Protein Science</i> , 2007 , 16, 2072-5	6.3	22
65	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, 7009-14	11.5	156
64	Solution structure of the BRK domains from CHD7. <i>Journal of Molecular Biology</i> , 2007 , 371, 1135-40	6.5	24
63	The PUB domain functions as a p97 binding module in human peptide N-glycanase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 25502-8	5.4	69
62	Solution structure of the C4 zinc finger domain of HDM2. <i>Protein Science</i> , 2006 , 15, 384-9	6.3	35
61	Functional analysis of the post-transcriptional regulator RsmA reveals a novel RNA-binding site. <i>Journal of Molecular Biology</i> , 2006 , 355, 1026-36	6.5	69
60	The FtsK gamma domain directs oriented DNA translocation by interacting with KOPS. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 965-72	17.6	83
59	Solution structure of the nonmethyl-CpG-binding CXXC domain of the leukaemia-associated MLL histone methyltransferase. <i>EMBO Journal</i> , 2006 , 25, 4503-12	13	127
58	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, 4601-11	3.2	31
57	Electrostatic interactions contribute to reduced heat capacity change of unfolding in a thermophilic ribosomal protein l30e. <i>Journal of Molecular Biology</i> , 2005 , 348, 419-31	6.5	43
56	Comparative binding of p53 to its promoter and DNA recognition elements. <i>Journal of Molecular Biology</i> , 2005 , 348, 589-96	6.5	145
55	The macro domain is an ADP-ribose binding module. <i>EMBO Journal</i> , 2005 , 24, 1911-20	13	380

54	Role of conformational heterogeneity in domain swapping and adapter function of the Cks proteins. <i>Journal of Biological Chemistry</i> , 2005 , 280, 30448-59	5.4	19
53	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, 53840-7	5.4	77
52	NMR structure of the alpha-hemoglobin stabilizing protein: insights into conformational heterogeneity and binding. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34963-70	5.4	47
51	The structure of the AXH domain of spinocerebellar ataxin-1. <i>Journal of Biological Chemistry</i> , 2004 , 279, 3758-65	5.4	47
50	Solution structure of the HPV-16 E2 DNA binding domain, a transcriptional regulator with a dimeric beta-barrel fold. <i>Journal of Biomolecular NMR</i> , 2004 , 30, 211-4	3	22
49	Crystallization and preliminary crystallographic analysis of a novel orange fluorescent protein from the Cnidaria tube anemone <i>Cerianthus</i> sp. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 340-1		10
48	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, 1308-10		7
47	Regulation of DNA binding of p53 by its C-terminal domain. <i>Journal of Molecular Biology</i> , 2004 , 342, 801-15	4.5	84
46	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, 46968-73	5.4	39
45	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeon <i>Thermococcus celer</i> . <i>Protein Science</i> , 2003 , 12, 1483-95	6.3	13
44	Structure of the Jab1/MPN domain and its implications for proteasome function. <i>Biochemistry</i> , 2003 , 42, 11460-5	3.2	100
43	Crystal structure of ribosomal protein L30e from the extreme thermophile <i>Thermococcus celer</i> : thermal stability and RNA binding. <i>Biochemistry</i> , 2003 , 42, 2857-65	3.2	15
42	Structural variation in PWWP domains. <i>Journal of Molecular Biology</i> , 2003 , 330, 571-6	6.5	36
41	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, 503-11	6.5	97
40	Molecular mechanism of the interaction between MDM2 and p53. <i>Journal of Molecular Biology</i> , 2002 , 323, 491-501	6.5	280
39	The structure of an FF domain from human HYPA/FBP11. <i>Journal of Molecular Biology</i> , 2002 , 323, 411-6	6.5	78
38	Structure of the C-terminal sterile alpha-motif (SAM) domain of human p73 alpha. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 545-51		27
37	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, 865-6		2

36	The UBX domain: a widespread ubiquitin-like module. <i>Journal of Molecular Biology</i> , 2001 , 307, 17-24	6.5	119
35	The ligand-binding loops in the tunicate C-type lectin TC14 are rigid. <i>Biochemistry</i> , 2001 , 40, 10966-72	3.2	17
34	Folding of a dimeric beta-barrel: residual structure in the urea denatured state of the human papillomavirus E2 DNA binding domain. <i>Protein Science</i> , 2000 , 9, 799-811	6.3	16
33	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73alpha. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 769-71		11
32	RNA recognition by a Staufien double-stranded RNA-binding domain. <i>EMBO Journal</i> , 2000 , 19, 997-1009	13	291
31	Letter to the editor: 1H, 13C and 15N NMR assignments of the C-type lectin TC14. <i>Journal of Biomolecular NMR</i> , 2000 , 18, 283-4	3	3
30	The structure of a LysM domain from E. coli membrane-bound lytic murein transglycosylase D (MltD). <i>Journal of Molecular Biology</i> , 2000 , 299, 1113-9	6.5	343
29	Biophysical characterization of elongin C from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2000 , 39, 11137-46		8
28	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, 867-79	6.5	89
27	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. <i>Journal of Molecular Biology</i> , 1999 , 291, 661-9	6.5	29
26	Characterisation of urea-denatured states of an immunoglobulin superfamily domain by heteronuclear NMR. <i>Journal of Molecular Biology</i> , 1998 , 278, 417-29	6.5	25
25	Crystal structure of a calcium-phospholipid binding domain from cytosolic phospholipase A2. <i>Journal of Biological Chemistry</i> , 1998 , 273, 1596-604	5.4	223
24	The solution structure of the S1 RNA binding domain: a member of an ancient nucleic acid-binding fold. <i>Cell</i> , 1997 , 88, 235-42	56.2	350
23	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, 624-39	6.5	54
22	Equilibrium dissociation and unfolding of the dimeric human papillomavirus strain-16 E2 DNA-binding domain. <i>Protein Science</i> , 1996 , 5, 310-9	6.3	66
21	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, 711-7	17.6	34
20	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, 305-21	6.5	129
19	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 staufien. <i>FEBS Letters</i> , 1995 , 362, 333-6	3.8	8

18	Three-dimensional solution structure and ^{13}C assignments of barstar using nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1994 , 33, 8866-8877	3.2	104
17	Structure and dynamics of barnase complexed with $3\text{H}\text{GMP}$ studied by NMR spectroscopy. <i>Biochemistry</i> , 1993 , 32, 10975-87	3.2	22
16	Identification of the barstar binding site of barnase by NMR spectroscopy and hydrogen-deuterium exchange. <i>FEBS Letters</i> , 1993 , 331, 165-72	3.8	34
15	Assignment of the backbone ^1H and ^{15}N NMR resonances and secondary structure characterization of barstar. <i>FEBS Letters</i> , 1993 , 332, 81-7	3.8	17
14	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. <i>Journal of Molecular Biology</i> , 1992 , 224, 837-45	6.5	90
13	Determination of the three-dimensional solution structure of barnase using nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1991 , 30, 8697-701	3.2	108
12	Characterization of phosphate binding in the active site of barnase by site-directed mutagenesis and NMR. <i>Biochemistry</i> , 1991 , 30, 11348-56	3.2	26
11	Aromatic-aromatic interactions and protein stability. Investigation by double-mutant cycles. <i>Journal of Molecular Biology</i> , 1991 , 218, 465-75	6.5	288
10	Surface electrostatic interactions contribute little of stability of barnase. <i>Journal of Molecular Biology</i> , 1991 , 220, 779-88	6.5	161
9	Physical-organic molecular biology: pathway and stability of protein folding. <i>Pure and Applied Chemistry</i> , 1991 , 63, 187-194	2.1	6
8	Transient folding intermediates characterized by protein engineering. <i>Nature</i> , 1990 , 346, 440-5	50.4	476
7	Detection and characterization of a folding intermediate in barnase by NMR. <i>Nature</i> , 1990 , 346, 488-90	50.4	210
6	Sequential assignment of the ^1H nuclear magnetic resonance spectrum of barnase. <i>Biochemistry</i> , 1990 , 29, 7425-32	3.2	34
5	Strength and co-operativity of contributions of surface salt bridges to protein stability. <i>Journal of Molecular Biology</i> , 1990 , 216, 1031-44	6.5	382
4	Estimating the contribution of engineered surface electrostatic interactions to protein stability by using double-mutant cycles. <i>Biochemistry</i> , 1990 , 29, 9343-52	3.2	359
3	Stabilization of protein structure by interaction of alpha-helix dipole with a charged side chain. <i>Nature</i> , 1988 , 335, 740-3	50.4	216
2	Assignment of histidine resonances in the ^1H NMR (500 MHz) spectrum of subtilisin BPN U using site-directed mutagenesis. <i>Biochemistry</i> , 1988 , 27, 7390-4	3.2	16
1	Amperometric enzyme electrodes. <i>Journal of Electroanalytical Chemistry and Interfacial Electrochemistry</i> , 1987 , 218, 119-126		55

