Joel Janin

List of Publications by Citations

143 papers	16,577 citations	60 h-index	128 g-index
151 ext. papers	17,623 ext. citations	6.7 avg, IF	6.57 L-index

#	Paper	IF	Citations
143	The atomic structure of protein-protein recognition sites. *Journal of Molecular Biology*, **1999**, 285, 2177-98	6.5	1730
142	Principles of protein-protein recognition. *Nature*, **1975**, 256, 705-8	50.4	913
141	Interior and surface of monomeric proteins. *Journal of Molecular Biology*, **1987**, 196, 641-56	6.5	784
140	Conformation of amino acid side-chains in proteins. *Journal of Molecular Biology*, **1978**, 125, 357-86	6.5	705
139	Surface and inside volumes in globular proteins. *Nature*, **1979**, 277, 491-2	50.4	605
138	Surface, subunit interfaces and interior of oligomeric proteins. *Journal of Molecular Biology*, **1988**, 204, 155-64	6.5	590
137	Dissecting protein-protein recognition sites. *Proteins: Structure, Function and Bioinformatics*, **2002**, 47, 334-43	4.2	490
136	CAPRI: a Critical Assessment of PRedicted Interactions. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 2-9	4.2	487
135	Silk fibroin: structural implications of a remarkable amino acid sequence. *Proteins: Structure, Function and Bioinformatics*, **2001**, 44, 119-22	4.2	487
134	A dissection of specific and non-specific protein-protein interfaces. *Journal of Molecular Biology*, **2004**, 336, 943-55	6.5	391
133	Protein-protein docking benchmark version 4.0. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3111-4	4.2	326
132	The accessible surface area and stability of oligomeric proteins. *Nature*, **1987**, 328, 834-6	50.4	314
131	Protein-protein interaction and quaternary structure. *Quarterly Reviews of Biophysics*, **2008**, 41, 133-80	7	296
130	Structural features of protein-nucleic acid recognition sites. *Biochemistry*, **1999**, 38, 1999-2017	3.2	293
129	The price of lost freedom: entropy of bimolecular complex formation. *Protein Engineering, Design and Selection*, **1989**, 3, 1-3	1.9	288
128	Computer analysis of protein-protein interaction. *Journal of Molecular Biology*, **1978**, 124, 323-42	6.5	242
127	Structural domains in proteins and their role in the dynamics of protein function. *Progress in Biophysics and Molecular Biology*, **1983**, 42, 21-78	4.7	239

126	Dissecting subunit interfaces in homodimeric proteins. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53, 708-19	4.2	238
125	Protein-Protein Docking Benchmark 2.0: an update. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 214-6	4.2	226
124	Protein-protein interaction at crystal contacts. *Proteins: Structure, Function and Bioinformatics*, **1995** , 23, 580-7	4.2	226
123	A protein-protein docking benchmark. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 88-91	4.2	218
122	A structure-based benchmark for protein-protein binding affinity. *Protein Science*, **2011**, 20, 482-91	6.3	194
121	Protein-protein docking benchmark version 3.0. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 705-9	4.2	191
120	Specific versus non-specific contacts in protein crystals. *Nature Structural Biology*, **1997**, 4, 973-4		178
119	Wet and dry interfaces: the role of solvent in protein-protein and protein-DNA recognition. *Structure*, **1999**, 7, R277-9	5.2	177
118	The kinetics of protein-protein recognition. *Proteins: Structure, Function and Bioinformatics*, **1997**, 28, 153-61	4.2	172
117	Hydration of protein-protein interfaces. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 36-45	4.2	164
116	Elusive affinities. *Proteins: Structure, Function and Bioinformatics*, **1995**, 21, 30-9	4.2	157
115	Templates are available to model nearly all complexes of structurally characterized proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 9438-41	11.5	151
114	Assessing predictions of protein-protein interaction: the CAPRI experiment. *Protein Science*, **2005**, 14, 278-83	6.3	135
113	Orthogonal packing of beta-pleated sheets in proteins. *Biochemistry*, **1982**, 21, 3955-65	3.2	135
112	Protein-protein recognition analyzed by docking simulation. *Proteins: Structure, Function and Bioinformatics*, **1991**, 11, 271-80	4.2	134
111	Protein-protein docking tested in blind predictions: the CAPRI experiment. *Molecular BioSystems*, **2010**, 6, 2351-62		130
110	Location of structural domains in protein. *Biochemistry*, **1981**, 20, 6544-52	3.2	128
109	Structural basis of macromolecular recognition. *Advances in Protein Chemistry*, **2002**, 61, 9-73		126

108	Role of hydrophobicity in the binding of coenzymes. Appendix. Translational and rotational contribution to the free energy of dissociation. *Biochemistry*, **1978**, 17, 2943-8	3.2	125
107	Protein engineering of xylose (glucose) isomerase from Actinoplanes missouriensis. 1. Crystallography and site-directed mutagenesis of metal binding sites. *Biochemistry*, **1992**, 31, 5449-58	3.2	121
106	Protein docking algorithms: simulating molecular recognition. *Current Opinion in Structural Biology*, **1993**, 3, 265-269	8.1	115
105	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. *Journal of Molecular Biology*, **2011**, 414, 289-302	6.5	114
104	The human nm23-H4 gene product is a mitochondrial nucleoside diphosphate kinase. *Journal of Biological Chemistry*, **2000**, 275, 14264-72	5.4	113
103	Three-dimensional structure of nucleoside diphosphate kinase. *Journal of Bioenergetics and Biomembranes*, **2000**, 32, 215-25	3.7	108
102	Stability and specificity of protein-protein interactions: the case of the trypsin-trypsin inhibitor complexes. *Journal of Molecular Biology*, **1976**, 100, 197-211	6.5	105
101	Packing of alpha-helices onto beta-pleated sheets and the anatomy of alpha/beta proteins. *Journal of Molecular Biology*, **1980**, 143, 95-128	6.5	104
100	Pyrophosphate-producing protein dephosphorylation by HPr kinase/phosphorylase: a relic of early life?. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 13442-7	11.5	101
99	Protein-protein recognition. *Progress in Biophysics and Molecular Biology*, **1995**, 64, 145-66	4.7	97
98	Dissecting protein-RNA recognition sites. *Nucleic Acids Research*, **2008**, 36, 2705-16	20.1	93
97	The subunit interfaces of weakly associated homodimeric proteins. *Journal of Molecular Biology*, **2010**, 398, 146-60	6.5	91
96	Adenosine 5Sdiphosphate binding and the active site of nucleoside diphosphate kinase. *Biochemistry*, **1994**, 33, 459-67	3.2	91
95	Revised structure of aspartokinase I-homoserine dehydrogenase I of Escherichia coli K12. Evidence for four identical subunits. *FEBS Journal*, **1972**, 28, 507-19		86
94	Macromolecular recognition in the Protein Data Bank. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 1-8		83
93	Human and viral nucleoside/nucleotide kinases involved in antiviral drug activation: structural and catalytic properties. *Antiviral Research*, **2010**, 86, 101-20	10.8	78
92	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1980-7	4.2	78
91	Cellular phosphorylation of anti-HIV nucleosides. Role of nucleoside diphosphate kinase. *Journal of Biological Chemistry*, **1996**, 271, 7887-90	5.4	75

90	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. *Bioinformatics*, **2008**, 24, 652-8	7.2	72
89	X-ray structure of a bifunctional protein kinase in complex with its protein substrate HPr. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 13437-41	11.5	69
88	Crystal packing in six crystal forms of pancreatic ribonuclease. *Journal of Molecular Biology*, **1992**, 228, 243-51	6.5	67
87	Structure of protein phosphatase methyltransferase 1 (PPM1), a leucine carboxyl methyltransferase involved in the regulation of protein phosphatase 2A activity. *Journal of Biological Chemistry*, **2004**, 279, 8351-8	5.4	65
86	Quantifying biological specificity: the statistical mechanics of molecular recognition. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 438-45	4.2	63
85	Crystal structure and functional characterization of yeast YLR011wp, an enzyme with NAD(P)H-FMN and ferric iron reductase activities. *Journal of Biological Chemistry*, **2004**, 279, 34890-7	5.4	62
84	Revisiting the Voronoi description of protein-protein interfaces. *Protein Science*, **2006**, 15, 2082-92	6.3	61
83	Structural basis for activation of alpha-boranophosphate nucleotide analogues targeting drug-resistant reverse transcriptase. *EMBO Journal*, **2000**, 19, 3520-9	13	60
82	Nucleophilic activation by positioning in phosphoryl transfer catalyzed by nucleoside diphosphate kinase. *Biochemistry*, **1999**, 38, 4701-11	3.2	60
81	Domains in proteins: definitions, location, and structural principles. *Methods in Enzymology*, **1985**, 115, 420-30	1.7	58
80	Catalytic mechanism of nucleoside diphosphate kinase investigated using nucleotide analogues, viscosity effects, and X-ray crystallography. *Biochemistry*, **1999**, 38, 7265-72	3.2	57
79	Surface area of globular proteins. *Journal of Molecular Biology*, **1976**, 105, 13-4	6.5	57
78	Crystal structure of the yeast Phox homology (PX) domain protein Grd19p complexed to phosphatidylinositol-3-phosphate. *Journal of Biological Chemistry*, **2003**, 278, 50371-6	5.4	55
77	The threonine-sensitive homoserine dehydrogenase and aspartokinase activities of Escherichia coli K 12. A study of the allosteric equilibrium. *FEBS Journal*, **1969**, 11, 520-9		54
76	Protein flexibility, not disorder, is intrinsic to molecular recognition. *F1000 Biology Reports*, **2013**, 5, 2		54
75	Welcome to CAPRI: A Critical Assessment of PRedicted Interactions. *Proteins: Structure, Function and Bioinformatics*, **2002**, 47, 257-257	4.2	52
74	Structural analysis of the 2.8 A model of Xylose isomerase from Actinoplanes missouriensis. *Proteins: Structure, Function and Bioinformatics*, **1988**, 4, 165-72	4.2	48
73	Refolding strategies from inclusion bodies in a structural genomics project. *Journal of Structural and Functional Genomics*, **2004**, 5, 195-204		47

72	Reaction pathway for the quaternary structure change in hemoglobin. *Biopolymers*, **1985**, 24, 509-26	2.2	45
71	Thermodynamics of the temperature-induced unfolding of globular proteins. *Protein Science*, **1995**, 4, 1315-24	6.3	44
70	HPr kinase/phosphorylase, the sensor enzyme of catabolite repression in Gram-positive bacteria: structural aspects of the enzyme and the complex with its protein substrate. *Journal of Bacteriology*, **2003**, 185, 4003-10	3.5	41
69	Pre-steady state of reaction of nucleoside diphosphate kinase with anti-HIV nucleotides. *Journal of Biological Chemistry*, **1998**, 273, 11491-7	5.4	41
68	Computer studies of interactions between macromolecules. *Progress in Biophysics and Molecular Biology*, **1987**, 49, 29-63	4.7	41
67	Haemoglobin: the surface buried between the alpha 1 beta 1 and alpha 2 beta 2 dimers in the deoxy and oxy structures. *Journal of Molecular Biology*, **1985**, 183, 267-70	6.5	41
66	The quaternary structure of carbonmonoxy hemoglobin ypsilanti. *Proteins: Structure, Function and Bioinformatics*, **1993**, 15, 1-4	4.2	39
65	Angstrm̈s and calories. *Structure*, **1997**, 5, 473-9	5.2	38
64	A soft, mean-field potential derived from crystal contacts for predicting protein-protein interactions. *Journal of Molecular Biology*, **1998**, 283, 1037-47	6.5	38
63	Genome-wide studies of protein-protein interaction. *Current Opinion in Structural Biology*, **2003**, 13, 383-8	8.1	37
62	Nucleoside diphosphate kinase. Investigation of the intersubunit contacts by site-directed mutagenesis and crystallography. *Journal of Biological Chemistry*, **1996**, 271, 19928-34	5.4	37
61	Thermal stability of hexameric and tetrameric nucleoside diphosphate kinases. Effect of subunit interaction. *Journal of Biological Chemistry*, **1996**, 271, 17845-51	5.4	36
60	Nucleotide binding to nucleoside diphosphate kinases: X-ray structure of human NDPK-A in complex with ADP and comparison to protein kinases. *Journal of Molecular Biology*, **2003**, 332, 915-26	6.5	33
59	3SPhosphorylated nucleotides are tight binding inhibitors of nucleoside diphosphate kinase activity. *Journal of Biological Chemistry*, **1998**, 273, 28773-8	5.4	32
58	The threonine-sensitive homoserine dehydrogenase and aspartokinase activities of Escherichia coli K 12. Relaxations of the allosteric equilibrium. *FEBS Journal*, **1969**, 11, 530-40		32
57	Peptide segments in protein-protein interfaces. *Journal of Biosciences*, **2007**, 32, 101-11	2.3	31
56	X-ray structure of Mycobacterium tuberculosis nucleoside diphosphate kinase. *Proteins: Structure, Function and Bioinformatics*, **2002**, 47, 556-7	4.2	29
55	A dissection of the protein-protein interfaces in icosahedral virus capsids. *Journal of Molecular Biology*, **2007**, 367, 574-90	6.5	28

54	Crystal structure of the YDR533c S. cerevisiae protein, a class II member of the Hsp31 family. *Structure*, **2004**, 12, 839-47	5.2	28
53	Rigid-body docking with mutant constraints of influenza hemagglutinin with antibody HC19. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 8-18	4.2	28
52	Protein modules and protein-protein interaction. Introduction. *Advances in Protein Chemistry*, **2002**, 61, 1-8		27
51	The targets of CAPRI Rounds 13-19. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3067-72	4.2	25
50	Chemical rescue of phosphoryl transfer in a cavity mutant: a cautionary tale for site-directed mutagenesis. *Biochemistry*, **2001**, 40, 403-13	3.2	25
49	Structural analysis of the activation of ribavirin analogs by NDP kinase: comparison with other ribavirin targets. *Molecular Pharmacology*, **2003**, 63, 538-46	4.3	24
48	Improving nucleoside diphosphate kinase for antiviral nucleotide analogs activation. *Journal of Biological Chemistry*, **2002**, 277, 39953-9	5.4	23
47	Crystal structure of the bifunctional chorismate synthase from Saccharomyces cerevisiae. *Journal of Biological Chemistry*, **2004**, 279, 619-25	5.4	22
46	The targets of CAPRI rounds 3-5. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 170-5	4.2	22
45	A minimal model of protein-protein binding affinities. *Protein Science*, **2014**, 23, 1813-7	6.3	21
44	Reassessing buried surface areas in protein-protein complexes. *Protein Science*, **2013**, 22, 1453-7	6.3	21
43	A survey of hemoglobin quaternary structures. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 2861-70	4.2	21
42	Analysis and prediction of protein quaternary structure. *Methods in Molecular Biology*, **2010**, 609, 349-64	1.4	20
41	Crystal structure of yeast allantoicase reveals a repeated jelly roll motif. *Journal of Biological Chemistry*, **2004**, 279, 23447-52	5.4	19
40	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. *Protein Science* , **2005**, 14, 1350-6	6.3	18
39	A structural genomics initiative on yeast proteins. *Journal of Synchrotron Radiation*, **2003**, 10, 4-8	2.4	17
38	The Paris-Sud yeast structural genomics pilot-project: from structure to function. *Biochimie*, **2004**, 86, 617-23	4.6	17
37	Structural templates for modeling homodimers. *Protein Science*, **2013**, 22, 1655-63	6.3	15

36	Side-chain rotamer transitions at protein-protein interfaces. *Proteins: Structure, Function and Bioinformatics*, **2010**, 78, 3219-25	4.2	15
35	The targets of CAPRI rounds 6-12. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 699-703	4.2	15
34	Changes in protein structure at the interface accompanying complex formation. *IUCrJ*, **2015**, 2, 643-52	4.7	14
33	The targets of CAPRI rounds 20-27. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 2075-81	4.2	14
32	A docking analysis of the statistical physics of protein-protein recognition. *Physical Biology*, **2005**, 2, S17-23	3	14
31	Activation of anti-reverse transcriptase nucleotide analogs by nucleoside diphosphate kinase: improvement by alpha-boranophosphate substitution. *Nucleosides, Nucleotides and Nucleic Acids*, **2001**, 20, 297-306	1.4	14
30	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. *Acta Crystallographica Section D: Biological Crystallography*, **2005**, 61, 664-70		13
29	Mechanism of phosphoryl transfer by nucleoside diphosphate kinase pH dependence and role of the active site Lys16 and Tyr56 residues. *FEBS Journal*, **2001**, 268, 1964-71		13
28	Nucleoside-diphosphate kinase: structural and kinetic analysis of reaction pathway and phosphohistidine intermediate. *Methods in Enzymology*, **2002**, 354, 118-34	1.7	13
27	A polymerase I palm in adenylyl cyclase?. *Nature*, **1997**, 388, 34-34	50.4	12
26	Residue conservation in viral capsid assembly. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 407-14	4.2	12
25	Crystal structure of the YGR205w protein from Saccharomyces cerevisiae: close structural resemblance to E. coli pantothenate kinase. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 776-83	4.2	12
24	Binding of nucleotides to nucleoside diphosphate kinase: a calorimetric study. *Biochemistry*, **2001**, 40, 4583-9	3.2	12
23	Shared structural motif in proteins. *Nature*, **1993**, 365, 21	50.4	12
22	Cloning, production, and purification of proteins for a medium-scale structural genomics project. *Methods in Molecular Biology*, **2007**, 363, 21-37	1.4	12
21	Relating Macromolecular Function and Association: The Structural Basis of Protein–DNA and RNA Recognition. *Cellular and Molecular Bioengineering*, **2008**, 1, 327-338	3.9	11
20	The 62-kb upstream region of Bombyx mori fibroin heavy chain gene is clustered of repetitive elements and candidate matrix association regions. *Gene*, **2003**, 312, 189-95	3.8	11
19	Crystallization and preliminary X-ray diffraction studies of nucleoside diphosphate kinase from Dictyostelium discoideum. *Journal of Molecular Biology*, **1991**, 217, 239-40	6.5	11

18	Nucleoside diphosphate kinase and the activation of antiviral phosphonate analogs of nucleotides: binding mode and phosphorylation of tenofovir derivatives. *Nucleosides, Nucleotides and Nucleic Acids*, **2009**, 28, 776-92	1.4	10
17	Crystal structure of the YML079w protein from Saccharomyces cerevisiae reveals a new sequence family of the jelly-roll fold. *Protein Science*, **2005**, 14, 209-15	6.3	9
16	Structural genomics: winning the second half of the game. *Structure*, **2007**, 15, 1347-9	5.2	7
15	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. *Protein Science*, **2006**, 15, 1516-21	6.3	7
14	Mechanism of the nucleoside diphosphate kinase reaction: X-ray structure of the phosphohistidine intermediate. *Techniques in Protein Chemistry*, **1996**, 7, 209-217		6
13	Docking Predictions of Protein-Protein Interactions and Their Assessment: The CAPRI Experiment. *Focus on Structural Biology*, **2013**, 87-104		4
12	Crystal structure of yeast YER010Cp, a knotable member of the RraA protein family. *Protein Science* , **2005**, 14, 2751-8	6.3	4
11	Assessing Structural Predictions of Protein□Protein Recognition: The CAPRI Experiment. *Reviews in Computational Chemistry*, **2015**, 137-173		3
10	Proteins with a ring. *Structure*, **1994**, 2, 571-3	5.2	3
9	Structure and stability of proteins: The role of solvent. *Colloids and Surfaces*, **1984**, 10, 1-7		3
8	Crystallization of E. coli aspartokinase I-homoserine dehydrogenase I. *FEBS Letters*, **1974**, 45, 318-9	3.8	3
7	Phosphorylation of anti-HIV nucleoside analogs by nucleoside diphosphate kinase. *Nucleosides & Nucleotides*, **1999**, 18, 829-30		2
6	Protein-protein interaction: an analysis by computer simulation. *Novartis Foundation Symposium*, **1991**, 161, 237-49; discussion 250-2		2
5	X-ray Study of Protein□Protein Complexes and Analysis of Interfaces **2010**, 1-24		1
4	p55-hGRF, a short natural form of the Ras-GDP exchange factor high yield production and characterization. *FEBS Journal*, **1999**, 263, 806-16		1
3	Quantifying biological specificity: The statistical mechanics of molecular recognition. *Proteins: Structure, Function and Bioinformatics*, **1996**, 25, 438-445	4.2	1
2	Principles of Protein □Protein Recognition in Protease-Inhibitor and Antigen-Antibody Complexes **1993**, 103-114		
1	Protein-Protein Recognition: An Analysis by Docking Simulation. *NATO ASI Series Series B: Physics*, **1994**, 331-337		