

Joel Janin

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.

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	Changes in protein structure at the interface accompanying complex formation. <i>IUCrJ</i> , 2015 , 2, 643-52	4.7	14
142	Assessing Structural Predictions of Protein-Protein Recognition: The CAPRI Experiment. <i>Reviews in Computational Chemistry</i> , 2015 , 137-173		3
141	A minimal model of protein-protein binding affinities. <i>Protein Science</i> , 2014 , 23, 1813-7	6.3	21
140	The targets of CAPRI rounds 20-27. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2075-81	4.2	14
139	Reassessing buried surface areas in protein-protein complexes. <i>Protein Science</i> , 2013 , 22, 1453-7	6.3	21
138	Structural templates for modeling homodimers. <i>Protein Science</i> , 2013 , 22, 1655-63	6.3	15
137	Docking Predictions of Protein-Protein Interactions and Their Assessment: The CAPRI Experiment. <i>Focus on Structural Biology</i> , 2013 , 87-104		4
136	Protein flexibility, not disorder, is intrinsic to molecular recognition. <i>F1000 Biology Reports</i> , 2013 , 5, 2		54
135	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1980-7	4.2	78
134	Templates are available to model nearly all complexes of structurally characterized proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 9438-41	11.5	151
133	Community-wide assessment of protein-interface modeling suggests improvements to design methodology. <i>Journal of Molecular Biology</i> , 2011 , 414, 289-302	6.5	114
132	A survey of hemoglobin quaternary structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 2861-70	4.2	21
131	A structure-based benchmark for protein-protein binding affinity. <i>Protein Science</i> , 2011 , 20, 482-91	6.3	194
130	Protein-protein docking tested in blind predictions: the CAPRI experiment. <i>Molecular BioSystems</i> , 2010 , 6, 2351-62		130
129	X-ray Study of Protein-Protein Complexes and Analysis of Interfaces 2010 , 1-24		1
128	The subunit interfaces of weakly associated homodimeric proteins. <i>Journal of Molecular Biology</i> , 2010 , 398, 146-60	6.5	91
127	Human and viral nucleoside/nucleotide kinases involved in antiviral drug activation: structural and catalytic properties. <i>Antiviral Research</i> , 2010 , 86, 101-20	10.8	78

126	The targets of CAPRI Rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3067-72	4.2	25
125	Side-chain rotamer transitions at protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3219-25	4.2	15
124	Protein-protein docking benchmark version 4.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 3111-4	4.2	326
123	Analysis and prediction of protein quaternary structure. <i>Methods in Molecular Biology</i> , 2010 , 609, 349-64	1.4	20
122	Nucleoside diphosphate kinase and the activation of antiviral phosphonate analogs of nucleotides: binding mode and phosphorylation of tenofovir derivatives. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2009 , 28, 776-92	1.4	10
121	Protein-protein interaction and quaternary structure. <i>Quarterly Reviews of Biophysics</i> , 2008 , 41, 133-80	7	296
120	Dissecting protein-RNA recognition sites. <i>Nucleic Acids Research</i> , 2008 , 36, 2705-16	20.1	93
119	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. <i>Bioinformatics</i> , 2008 , 24, 652-8	7.2	72
118	Relating Macromolecular Function and Association: The Structural Basis of Protein-DNA and RNA Recognition. <i>Cellular and Molecular Bioengineering</i> , 2008 , 1, 327-338	3.9	11
117	Residue conservation in viral capsid assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 407-14	4.2	12
116	Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 705-9	4.2	191
115	Macromolecular recognition in the Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007 , 63, 1-8		83
114	The targets of CAPRI rounds 6-12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 699-703	4.2	15
113	Structural genomics: winning the second half of the game. <i>Structure</i> , 2007 , 15, 1347-9	5.2	7
112	Peptide segments in protein-protein interfaces. <i>Journal of Biosciences</i> , 2007 , 32, 101-11	2.3	31
111	A dissection of the protein-protein interfaces in icosahedral virus capsids. <i>Journal of Molecular Biology</i> , 2007 , 367, 574-90	6.5	28
110	Cloning, production, and purification of proteins for a medium-scale structural genomics project. <i>Methods in Molecular Biology</i> , 2007 , 363, 21-37	1.4	12
109	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. <i>Protein Science</i> , 2006 , 15, 1516-21	6.3	7

108	Revisiting the Voronoi description of protein-protein interfaces. <i>Protein Science</i> , 2006 , 15, 2082-92	6.3	61
107	Crystal structure of the YML079w protein from <i>Saccharomyces cerevisiae</i> reveals a new sequence family of the jelly-roll fold. <i>Protein Science</i> , 2005 , 14, 209-15	6.3	9
106	Assessing predictions of protein-protein interaction: the CAPRI experiment. <i>Protein Science</i> , 2005 , 14, 278-83	6.3	135
105	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. <i>Protein Science</i> , 2005 , 14, 1350-6	6.3	18
104	Crystal structure of yeast YER010Cp, a knotable member of the RraA protein family. <i>Protein Science</i> , 2005 , 14, 2751-8	6.3	4
103	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 664-70		13
102	Hydration of protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 36-45	4.2	164
101	The targets of CAPRI rounds 3-5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 170-5	4.2	22
100	Protein-Protein Docking Benchmark 2.0: an update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 214-6	4.2	226
99	A docking analysis of the statistical physics of protein-protein recognition. <i>Physical Biology</i> , 2005 , 2, S17-23		14
98	Crystal structure of the bifunctional chorismate synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004 , 279, 619-25	5.4	22
97	Crystal structure of yeast allantoicase reveals a repeated jelly roll motif. <i>Journal of Biological Chemistry</i> , 2004 , 279, 23447-52	5.4	19
96	Structure of protein phosphatase methyltransferase 1 (PPM1), a leucine carboxyl methyltransferase involved in the regulation of protein phosphatase 2A activity. <i>Journal of Biological Chemistry</i> , 2004 , 279, 8351-8	5.4	65
95	Crystal structure and functional characterization of yeast YLR011wp, an enzyme with NAD(P)H-FMN and ferric iron reductase activities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34890-7	5.4	62
94	Crystal structure of the YDR533c <i>S. cerevisiae</i> protein, a class II member of the Hsp31 family. <i>Structure</i> , 2004 , 12, 839-47	5.2	28
93	Refolding strategies from inclusion bodies in a structural genomics project. <i>Journal of Structural and Functional Genomics</i> , 2004 , 5, 195-204		47
92	Crystal structure of the YGR205w protein from <i>Saccharomyces cerevisiae</i> : close structural resemblance to <i>E. coli</i> pantothenate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 776-83	4.2	12
91	The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004 , 86, 617-23	4.6	17

90	A dissection of specific and non-specific protein-protein interfaces. <i>Journal of Molecular Biology</i> , 2004 , 336, 943-55	6.5	391
89	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. <i>Journal of Bacteriology</i> , 2003 , 185, 4003-10	3.5	41
88	Genome-wide studies of protein-protein interaction. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 383-8.1		37
87	A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003 , 10, 4-8	2.4	17
86	CAPRI: a Critical Assessment of PRedicted Interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 2-9	4.2	487
85	A protein-protein docking benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 88-91	4.2	218
84	Dissecting subunit interfaces in homodimeric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 708-19	4.2	238
83	Nucleotide binding to nucleoside diphosphate kinases: X-ray structure of human NDPK-A in complex with ADP and comparison to protein kinases. <i>Journal of Molecular Biology</i> , 2003 , 332, 915-26	6.5	33
82	The 62-kb upstream region of Bombyx mori fibroin heavy chain gene is clustered of repetitive elements and candidate matrix association regions. <i>Gene</i> , 2003 , 312, 189-95	3.8	11
81	Structural analysis of the activation of ribavirin analogs by NDP kinase: comparison with other ribavirin targets. <i>Molecular Pharmacology</i> , 2003 , 63, 538-46	4.3	24
80	Crystal structure of the yeast Phox homology (PX) domain protein Grd19p complexed to phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003 , 278, 50371-6	5.4	55
79	Dissecting protein-protein recognition sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 334-43	4.2	490
78	Welcome to CAPRI: A Critical Assessment of PRedicted Interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 257-257	4.2	52
77	X-ray structure of Mycobacterium tuberculosis nucleoside diphosphate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 556-7	4.2	29
76	Improving nucleoside diphosphate kinase for antiviral nucleotide analogs activation. <i>Journal of Biological Chemistry</i> , 2002 , 277, 39953-9	5.4	23
75	X-ray structure of a bifunctional protein kinase in complex with its protein substrate HPr. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13437-41	11.5	69
74	Pyrophosphate-producing protein dephosphorylation by HPr kinase/phosphorylase: a relic of early life?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 13442-7	11.5	101
73	Protein modules and protein-protein interaction. Introduction. <i>Advances in Protein Chemistry</i> , 2002 , 61, 1-8		27

72	Nucleoside-diphosphate kinase: structural and kinetic analysis of reaction pathway and phosphohistidine intermediate. <i>Methods in Enzymology</i> , 2002 , 354, 118-34	1.7	13
71	Structural basis of macromolecular recognition. <i>Advances in Protein Chemistry</i> , 2002 , 61, 9-73		126
70	Mechanism of phosphoryl transfer by nucleoside diphosphate kinase pH dependence and role of the active site Lys16 and Tyr56 residues. <i>FEBS Journal</i> , 2001 , 268, 1964-71		13
69	Silk fibroin: structural implications of a remarkable amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 44, 119-22	4.2	487
68	Activation of anti-reverse transcriptase nucleotide analogs by nucleoside diphosphate kinase: improvement by alpha-boranophosphate substitution. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2001 , 20, 297-306	1.4	14
67	Chemical rescue of phosphoryl transfer in a cavity mutant: a cautionary tale for site-directed mutagenesis. <i>Biochemistry</i> , 2001 , 40, 403-13	3.2	25
66	Binding of nucleotides to nucleoside diphosphate kinase: a calorimetric study. <i>Biochemistry</i> , 2001 , 40, 4583-9	3.2	12
65	Three-dimensional structure of nucleoside diphosphate kinase. <i>Journal of Bioenergetics and Biomembranes</i> , 2000 , 32, 215-25	3.7	108
64	Structural basis for activation of alpha-boranophosphate nucleotide analogues targeting drug-resistant reverse transcriptase. <i>EMBO Journal</i> , 2000 , 19, 3520-9	13	60
63	The human nm23-H4 gene product is a mitochondrial nucleoside diphosphate kinase. <i>Journal of Biological Chemistry</i> , 2000 , 275, 14264-72	5.4	113
62	Wet and dry interfaces: the role of solvent in protein-protein and protein-DNA recognition. <i>Structure</i> , 1999 , 7, R277-9	5.2	177
61	p55-hGRF, a short natural form of the Ras-GDP exchange factor high yield production and characterization. <i>FEBS Journal</i> , 1999 , 263, 806-16		1
60	Structural features of protein-nucleic acid recognition sites. <i>Biochemistry</i> , 1999 , 38, 1999-2017	3.2	293
59	Phosphorylation of anti-HIV nucleoside analogs by nucleoside diphosphate kinase. <i>Nucleosides & Nucleotides</i> , 1999 , 18, 829-30		2
58	Catalytic mechanism of nucleoside diphosphate kinase investigated using nucleotide analogues, viscosity effects, and X-ray crystallography. <i>Biochemistry</i> , 1999 , 38, 7265-72	3.2	57
57	Nucleophilic activation by positioning in phosphoryl transfer catalyzed by nucleoside diphosphate kinase. <i>Biochemistry</i> , 1999 , 38, 4701-11	3.2	60
56	The atomic structure of protein-protein recognition sites. <i>Journal of Molecular Biology</i> , 1999 , 285, 2177-98	3.5	1730
55	A soft, mean-field potential derived from crystal contacts for predicting protein-protein interactions. <i>Journal of Molecular Biology</i> , 1998 , 283, 1037-47	6.5	38

54	Pre-steady state of reaction of nucleoside diphosphate kinase with anti-HIV nucleotides. <i>Journal of Biological Chemistry</i> , 1998 , 273, 11491-7	5-4	41
53	3SPosphorylated nucleotides are tight binding inhibitors of nucleoside diphosphate kinase activity. <i>Journal of Biological Chemistry</i> , 1998 , 273, 28773-8	5-4	32
52	Specific versus non-specific contacts in protein crystals. <i>Nature Structural Biology</i> , 1997 , 4, 973-4		178
51	A polymerase I palm in adenylyl cyclase?. <i>Nature</i> , 1997 , 388, 34-34	50.4	12
50	Angströms and calories. <i>Structure</i> , 1997 , 5, 473-9	5.2	38
49	The kinetics of protein-protein recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 28, 153-61	4.2	172
48	Mechanism of the nucleoside diphosphate kinase reaction: X-ray structure of the phosphohistidine intermediate. <i>Techniques in Protein Chemistry</i> , 1996 , 7, 209-217		6
47	Quantifying biological specificity: The statistical mechanics of molecular recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 438-445	4.2	1
46	Nucleoside diphosphate kinase. Investigation of the intersubunit contacts by site-directed mutagenesis and crystallography. <i>Journal of Biological Chemistry</i> , 1996 , 271, 19928-34	5-4	37
45	Cellular phosphorylation of anti-HIV nucleosides. Role of nucleoside diphosphate kinase. <i>Journal of Biological Chemistry</i> , 1996 , 271, 7887-90	5-4	75
44	Thermal stability of hexameric and tetrameric nucleoside diphosphate kinases. Effect of subunit interaction. <i>Journal of Biological Chemistry</i> , 1996 , 271, 17845-51	5-4	36
43	Quantifying biological specificity: the statistical mechanics of molecular recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 438-45	4.2	63
42	Elusive affinities. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 21, 30-9	4.2	157
41	Protein-protein interaction at crystal contacts. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 580-7	4.2	226
40	Thermodynamics of the temperature-induced unfolding of globular proteins. <i>Protein Science</i> , 1995 , 4, 1315-24	6.3	44
39	Protein-protein recognition. <i>Progress in Biophysics and Molecular Biology</i> , 1995 , 64, 145-66	4.7	97
38	Proteins with a ring. <i>Structure</i> , 1994 , 2, 571-3	5.2	3
37	Rigid-body docking with mutant constraints of influenza hemagglutinin with antibody HC19. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 18, 8-18	4.2	28

36	Adenosine 5Sdiphosphate binding and the active site of nucleoside diphosphate kinase. <i>Biochemistry</i> , 1994 , 33, 459-67	3.2	91
35	Protein-Protein Recognition: An Analysis by Docking Simulation. <i>NATO ASI Series Series B: Physics</i> , 1994 , 331-337		
34	Protein docking algorithms: simulating molecular recognition. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 265-269	8.1	115
33	The quaternary structure of carbonmonoxy hemoglobin ypsilanti. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 1-4	4.2	39
32	Shared structural motif in proteins. <i>Nature</i> , 1993 , 365, 21	50.4	12
31	Principles of Protein [Protein Recognition in Protease-Inhibitor and Antigen-Antibody Complexes 1993 , 103-114		
30	Protein engineering of xylose (glucose) isomerase from <i>Actinoplanes missouriensis</i> . 1. Crystallography and site-directed mutagenesis of metal binding sites. <i>Biochemistry</i> , 1992 , 31, 5449-58	3.2	121
29	Crystal packing in six crystal forms of pancreatic ribonuclease. <i>Journal of Molecular Biology</i> , 1992 , 228, 243-51	6.5	67
28	Protein-protein recognition analyzed by docking simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991 , 11, 271-80	4.2	134
27	Crystallization and preliminary X-ray diffraction studies of nucleoside diphosphate kinase from <i>Dictyostelium discoideum</i> . <i>Journal of Molecular Biology</i> , 1991 , 217, 239-40	6.5	11
26	Protein-protein interaction: an analysis by computer simulation. <i>Novartis Foundation Symposium</i> , 1991 , 161, 237-49; discussion 250-2		2
25	The price of lost freedom: entropy of bimolecular complex formation. <i>Protein Engineering, Design and Selection</i> , 1989 , 3, 1-3	1.9	288
24	Structural analysis of the 2.8 A model of Xylose isomerase from <i>Actinoplanes missouriensis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1988 , 4, 165-72	4.2	48
23	Surface, subunit interfaces and interior of oligomeric proteins. <i>Journal of Molecular Biology</i> , 1988 , 204, 155-64	6.5	590
22	Interior and surface of monomeric proteins. <i>Journal of Molecular Biology</i> , 1987 , 196, 641-56	6.5	784
21	Computer studies of interactions between macromolecules. <i>Progress in Biophysics and Molecular Biology</i> , 1987 , 49, 29-63	4.7	41
20	The accessible surface area and stability of oligomeric proteins. <i>Nature</i> , 1987 , 328, 834-6	50.4	314
19	Reaction pathway for the quaternary structure change in hemoglobin. <i>Biopolymers</i> , 1985 , 24, 509-26	2.2	45

18	Domains in proteins: definitions, location, and structural principles. <i>Methods in Enzymology</i> , 1985 , 115, 420-30	1.7	58
17	Haemoglobin: the surface buried between the alpha 1 beta 1 and alpha 2 beta 2 dimers in the deoxy and oxy structures. <i>Journal of Molecular Biology</i> , 1985 , 183, 267-70	6.5	41
16	Structure and stability of proteins: The role of solvent. <i>Colloids and Surfaces</i> , 1984 , 10, 1-7		3
15	Structural domains in proteins and their role in the dynamics of protein function. <i>Progress in Biophysics and Molecular Biology</i> , 1983 , 42, 21-78	4.7	239
14	Orthogonal packing of beta-pleated sheets in proteins. <i>Biochemistry</i> , 1982 , 21, 3955-65	3.2	135
13	Location of structural domains in protein. <i>Biochemistry</i> , 1981 , 20, 6544-52	3.2	128
12	Packing of alpha-helices onto beta-pleated sheets and the anatomy of alpha/beta proteins. <i>Journal of Molecular Biology</i> , 1980 , 143, 95-128	6.5	104
11	Surface and inside volumes in globular proteins. <i>Nature</i> , 1979 , 277, 491-2	50.4	605
10	Role of hydrophobicity in the binding of coenzymes. Appendix. Translational and rotational contribution to the free energy of dissociation. <i>Biochemistry</i> , 1978 , 17, 2943-8	3.2	125
9	Computer analysis of protein-protein interaction. <i>Journal of Molecular Biology</i> , 1978 , 124, 323-42	6.5	242
8	Conformation of amino acid side-chains in proteins. <i>Journal of Molecular Biology</i> , 1978 , 125, 357-86	6.5	705
7	Stability and specificity of protein-protein interactions: the case of the trypsin-trypsin inhibitor complexes. <i>Journal of Molecular Biology</i> , 1976 , 100, 197-211	6.5	105
6	Surface area of globular proteins. <i>Journal of Molecular Biology</i> , 1976 , 105, 13-4	6.5	57
5	Principles of protein-protein recognition. <i>Nature</i> , 1975 , 256, 705-8	50.4	913
4	Crystallization of E. coli aspartokinase I-homoserine dehydrogenase I. <i>FEBS Letters</i> , 1974 , 45, 318-9	3.8	3
3	Revised structure of aspartokinase I-homoserine dehydrogenase I of Escherichia coli K12. Evidence for four identical subunits. <i>FEBS Journal</i> , 1972 , 28, 507-19		86
2	The threonine-sensitive homoserine dehydrogenase and aspartokinase activities of Escherichia coli K 12. A study of the allosteric equilibrium. <i>FEBS Journal</i> , 1969 , 11, 520-9		54
1	The threonine-sensitive homoserine dehydrogenase and aspartokinase activities of Escherichia coli K 12. Relaxations of the allosteric equilibrium. <i>FEBS Journal</i> , 1969 , 11, 530-40		32

