Joel Janin

List of Publications by Year
in descending order

144 papers	18,690 citations	17440 63 h-index	11607 135 g-index
151 all docs	151 docs citations	151 times ranked	12629 citing authors

#	Article	IF	Citations
1	Changes in protein structure at the interface accompanying complex formation. IUCrJ, 2015, 2, 643-652.	2.2	21
2	A minimal model of proteinâ€“protein binding affinities. Protein Science, 2014, 23, 1813-1817.	7.6	27
3	The targets of CAPRI rounds 20â€“27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2075-2081.	2.6	14
4	Reassessing buried surface areas in proteinâ€“protein complexes. Protein Science, 2013, 22, 1453-1457.	7.6	27
5	Structural templates for modeling homodimers. Protein Science, 2013, 22, 1655-1663.	7.6	16
6	Docking Predictions of Protein-Protein Interactions and Their Assessment: The CAPRI Experiment. Focus on Structural Biology, 2013, , 87-104.	0.1	5
7	Community-wide evaluation of methods for predicting the effect of mutations on protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1980-1987.	2.6	87
8	Protein flexibility, not disorder, is intrinsic to molecular recognition. F1000 Biology Reports, 2013, 5, 2.	4.0	66
9	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, 9438-9441.	7.1	178
10	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
11	A survey of hemoglobin quaternary structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2861-2870.	2.6	21
12	A structureâ€based benchmark for proteinâ€“protein binding affinity. Protein Science, 2011, 20, 482-491.	7.6	252
13	Human and viral nucleoside/nucleotide kinases involved in antiviral drug activation: Structural and catalytic properties. Antiviral Research, 2010, 86, 101-120.	4.1	96
14	The targets of CAPRI Rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3067-3072.	2.6	25
15	Sideâ€chain rotamer transitions at proteinâ€protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	2.6	15
16	Proteinâ€“protein docking benchmark version 4.0. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3111-3114.	2.6	390
17	Proteinâ€“protein docking tested in blind predictions: the CAPRI experiment. Molecular BioSystems, 2010, 6, 2351.	2.9	171
18	X-ray Study of Proteinâ€“Protein Complexes and Analysis of Interfaces. , 2010, , 1-24.		1

#	Article	IF	Citations
19	The Subunit Interfaces of Weakly Associated Homodimeric Proteins. Journal of Molecular Biology, 2010, 398, 146-160.	4.2	107
20	Analysis and Prediction of Protein Quaternary Structure. Methods in Molecular Biology, 2010, 609, 349-364.	0.9	22
21	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, 776-792.	1.1	18
22	Crystal structure of the YML079w protein from Saccharomyces cerevisiae reveals a new sequence family of the jelly-roll fold. Protein Science, 2009, 14, 209-215.	7.6	13
23	Relating Macromolecular Function and Association: The Structural Basis of Proteinâ€“DNA and RNA Recognition. Cellular and Molecular Bioengineering, 2008, 1, 327-338.	2.1	11
24	Residue conservation in viral capsid assembly. Proteins: Structure, Function and Bioinformatics, 2008, 71, 407-414.	2.6	14
25	Proteinâ€“protein docking benchmark version 3.0. Proteins: Structure, Function and Bioinformatics, 2008, 73, 705-709.	2.6	224
26	Proteinâ€“protein interaction and quaternary structure. Quarterly Reviews of Biophysics, 2008, 41, 133-180.	5.7	354
27	Dissecting proteinâ€“RNA recognition sites. Nucleic Acids Research, 2008, 36, 2705-2716.	14.5	108
28	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological proteinâ€“protein interactions. Bioinformatics, 2008, 24, 652-658.	4.1	83
29	A Dissection of the Proteinâ€“Protein Interfaces in Icosahedral Virus Capsids. Journal of Molecular Biology, 2007, 367, 574-590.	4.2	29
30	Macromolecular recognition in the Protein Data Bank. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1-8.	2.5	97
31	The targets of CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 699-703.	2.6	26
32	Structural Genomics: Winning the Second Half of the Game. Structure, 2007, 15, 1347-1349.	3.3	10
33	Peptide segments in protein-protein interfaces. Journal of Biosciences, 2007, 32, 101-111.	1.1	37
34	Cloning, Production, and Purification of Proteins for a Medium-Scale Structural Genomics Project. Methods in Molecular Biology, 2007, 363, 21-37.	0.9	14
35	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. Protein Science, 2006, 15, 1516-1521.	7.6	8
36	Revisiting the Voronoi description of protein-protein interfaces. Protein Science, 2006, 15, 2082-2092.	7.6	72

#	Article	IF	Citations
37	Assessing predictions of protein-protein interaction: The CAPRI experiment. Protein Science, 2005, 14, 278-283.	7.6	158
38	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. Protein Science, 2005, 14, 1350-1356.	7.6	20
39	Crystal structure of yeast YER010Cp, aknotable member of the RraA protein family. Protein Science, 2005, 14, 2751-2758.	7.6	5
40	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, 664-670.	2.5	14
41	Hydration of protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 60, 36-45.	2.6	194
42	Sailing the route from Gaeta, Italy, to CAPRI. Proteins: Structure, Function and Bioinformatics, 2005, 60, 149-149.	2.6	5
43	The targets of CAPRI rounds 3-5. Proteins: Structure, Function and Bioinformatics, 2005, 60, 170-175.	2.6	23
44	Protein-protein docking benchmark 2.0: An update. Proteins: Structure, Function and Bioinformatics, 2005, 60, 214-216.	2.6	254
45	A docking analysis of the statistical physics of proteinâ€“protein recognition. Physical Biology, 2005, 2, S17-S23.	1.8	14
46	Crystal Structure of the Bifunctional Chorismate Synthase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 619-625.	3.4	29
47	Crystal Structure of Yeast Allantoicase Reveals a Repeated Jelly Roll Motif. Journal of Biological Chemistry, 2004, 279, 23447-23452.	3.4	23
48	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, 8351-8358.	3.4	82
49	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, 34890-34897.	3.4	71
50	Crystal Structure of the YDR533c S. cerevisiae Protein, a Class II Member of the Hsp31 Family. Structure, 2004, 12, 839-847.	3.3	31
51	Refolding strategies from inclusion bodies in a structural genomics project. Journal of Structural and Functional Genomics, 2004, 5, 195-204.	1.2	49
52	Crystal structure of the YGR205w protein from Saccharomyces cerevisiae : Close structural resemblance to E. coli pantothenate kinase. Proteins: Structure, Function and Bioinformatics, 2004, 54, 776-783.	2.6	17
53	The Paris-Sud yeast structural genomics pilot-project: from structure to function. Biochimie, 2004, 86, 617-623.	2.6	18
54	A Dissection of Specific and Non-specific Proteinâ€“Protein Interfaces. Journal of Molecular Biology, 2004, 336, 943-955.	4.2	426

#	Article	IF	Citations
55	Genome-wide studies of proteinâ€“protein interaction. Current Opinion in Structural Biology, 2003, 13, 383-388.	5.7	39
56	A structural genomics initiative on yeast proteins. Journal of Synchrotron Radiation, 2003, 10, 4-8.	2.4	20
57	CAPRI: A Critical Assessment of PRedicted Interactions. Proteins: Structure, Function and Bioinformatics, 2003, 52, 2-9.	2.6	586
58	A protein-protein docking benchmark. Proteins: Structure, Function and Bioinformatics, 2003, 52, 88-91.	2.6	242
59	Dissecting subunit interfaces in homodimeric proteins. Proteins: Structure, Function and Bioinformatics, 2003, 53, 708-719.	2.6	256
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, 915-926.	4.2	36
61	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, 189-195.	2.2	11
62	Structural Analysis of the Activation of Ribavirin Analogs by NDP Kinase: Comparison with Other Ribavirin Targets. Molecular Pharmacology, 2003, 63, 538-546.	2.3	24
63	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. Journal of Biological Chemistry, 2003, 278, 50371-50376.	3.4	64
64	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, 4003-4010.	2.2	45
65	Improving Nucleoside Diphosphate Kinase for Antiviral Nucleotide Analogs Activation. Journal of Biological Chemistry, 2002, 277, 39953-39959.	3.4	28
66	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, 13437-13441.	7.1	73
67	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, 13442-13447.	7.1	112
68	Introduction. Advances in Protein Chemistry, 2002, 61, 1-8.	4.4	31
69	Nucleoside-Diphosphate Kinase: Structural and Kinetic Analysis of Reaction Pathway and Phosphohistidine Intermediate. Methods in Enzymology, 2002, 354, 118-134.	1.0	16
70	Structural basis of macromolecular recognition. Advances in Protein Chemistry, 2002, 61, 9-73.	4.4	147
71	Dissecting protein-protein recognition sites. Proteins: Structure, Function and Bioinformatics, 2002, 47, 334-343.	2.6	549
72	Welcome to CAPRI: A Critical Assessment of PRedicted Interactions. Proteins: Structure, Function and Bioinformatics, 2002, 47, 257-257.	2.6	57

#	Article	IF	Citations
73	X-ray structure ofMycobacterium tuberculosis nucleoside diphosphate kinase. Proteins: Structure, Function and Bioinformatics, 2002, 47, 556-557.	2.6	33
74	ACTIVATION OF ANTI-REVERSE TRANSCRIPTASE NUCLEOTIDE ANALOGS BY NUCLEOSIDE DIPHOSPHATE KINASE: IMPROVEMENT BY Î±-BORANOPHOSPHATE SUBSTITUTION. Nucleosides, Nucleotides and Nucleic Acids, 2001, 20, 297-306.	1.1	14
75	Chemical Rescue of Phosphoryl Transfer in a Cavity Mutant:Â A Cautionary Tale for Site-Directed Mutagenesisâ€,â€¡. Biochemistry, 2001, 40, 403-413.	2.5	27
76	Binding of Nucleotides to Nucleoside Diphosphate Kinase:Â A Calorimetric Studyâ€¡. Biochemistry, 2001, 40, 4583-4589.	2.5	15
77	Mechanism of phosphoryl transfer by nucleoside diphosphate kinase. FEBS Journal, 2001, 268, 1964-1971.	0.2	17
78	Silk fibroin: Structural implications of a remarkable amino acid sequence. Proteins: Structure, Function and Bioinformatics, 2001, 44, 119-122.	2.6	606
79	Three-dimensional structure of nucleoside diphosphate kinase. Journal of Bioenergetics and Biomembranes, 2000, 32, 215-225.	2.3	115
80	Structural basis for activation of Î±-boranophosphate nucleotide analogues targeting drug-resistant reverse transcriptase. EMBO Journal, 2000, 19, 3520-3529.	7.8	63
81	The Human nm23-H4 Gene Product Is a Mitochondrial Nucleoside Diphosphate Kinase. Journal of Biological Chemistry, 2000, 275, 14264-14272.	3.4	128
82	Wet and dry interfaces: the role of solvent in proteinâ€“protein and proteinâ€“DNA recognition. Structure, 1999, 7, R277-R279.	3.3	199
83	p55-hGRF, a short natural form of the Ras-GDP exchange factor. High yield production and characterization. FEBS Journal, 1999, 263, 806-816.	0.2	2
84	Structural Features of Proteinâ˜'Nucleic Acid Recognition Sitesâ€. Biochemistry, 1999, 38, 1999-2017.	2.5	321
85	Phosphorylation of Anti-HIV Nucleoside Analogs by Nucleoside Diphosphate Kinase. Nucleosides & Nucleotides, 1999, 18, 829-830.	0.5	2
86	Catalytic Mechanism of Nucleoside Diphosphate Kinase Investigated Using Nucleotide Analogues, Viscosity Effects, and X-ray Crystallography,. Biochemistry, 1999, 38, 7265-7272.	2.5	63
87	Nucleophilic Activation by Positioning in Phosphoryl Transfer Catalyzed by Nucleoside Diphosphate Kinaseâ€,â€¡. Biochemistry, 1999, 38, 4701-4711.	2.5	62
88	The atomic structure of protein-protein recognition sites 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1999, 285, 2177-2198.	4.2	1,886
89	A soft, mean-field potential derived from crystal contacts for predicting protein-protein interactions. Journal of Molecular Biology, 1998, 283, 1037-1047.	4.2	40
90	Pre-steady State of Reaction of Nucleoside Diphosphate Kinase with Anti-HIV Nucleotides. Journal of Biological Chemistry, 1998, 273, 11491-11497.	3.4	50

#	Article	IF	Citations
91	3â€²-Phosphorylated Nucleotides Are Tight Binding Inhibitors of Nucleoside Diphosphate Kinase Activity. Journal of Biological Chemistry, 1998, 273, 28773-28778.	3.4	35
92	Specific versus non-specific contacts in protein crystals. Nature Structural Biology, 1997, 4, 973-974.	9.7	190
93	A polymerase I palm in adenylyl cyclase?. Nature, 1997, 388, 34-34.	27.8	13
94	Ã…ngstrÃ¶ms and calories. Structure, 1997, 5, 473-479.	3.3	45
95	The kinetics of protein-protein recognition. Proteins: Structure, Function and Bioinformatics, 1997, 28, 153-161.	2.6	189
96	Mechanism of the nucleoside diphosphate kinase reaction: X-ray structure of the phosphohistidine intermediate. Techniques in Protein Chemistry, 1996, 7, 209-217.	0.3	6
97	Quantifying biological specificity: The statistical mechanics of molecular recognition. Proteins: Structure, Function and Bioinformatics, 1996, 25, 438-445.	2.6	1
98	For Guldberg and Waage, with love and cratic entropy. Proteins: Structure, Function and Bioinformatics, 1996, 24, i-ii.	2.6	42
99	Nucleoside Diphosphate Kinase. Journal of Biological Chemistry, 1996, 271, 19928-19934.	3.4	45
100	Cellular Phosphorylation of Anti-HIV Nucleosides. Journal of Biological Chemistry, 1996, 271, 7887-7890.	3.4	85
101	Thermal Stability of Hexameric and Tetrameric Nucleoside Diphosphate Kinases. Journal of Biological Chemistry, 1996, 271, 17845-17851.	3.4	40
102	Quantifying biological specificity: The statistical mechanics of molecular recognition. Proteins: Structure, Function and Bioinformatics, 1996, 25, 438-445.	2.6	66
103	Protein-protein recognition. Progress in Biophysics and Molecular Biology, 1995, 64, 145-166.	2.9	116
104	Elusive affinities. Proteins: Structure, Function and Bioinformatics, 1995, 21, 30-39.	2.6	162
105	Protein-protein interaction at crystal contacts. Proteins: Structure, Function and Bioinformatics, 1995, 23, 580-587.	2.6	255
106	Thermodynamics of the temperatureâ€induced unfolding of globular proteins. Protein Science, 1995, 4, 1315-1324.	7.6	48
107	Proteins with a ring. Structure, 1994, 2, 571-573.	3.3	4
108	Rigid-body docking with mutant constraints of influenza hemagglutinin with antibody HC19. Proteins: Structure, Function and Bioinformatics, 1994, 18, 8-18.	2.6	32

#	Article	IF	Citations
109	Adenosine 5'-diphosphate binding and the active site of nucleoside diphosphate kinase. Biochemistry, 1994, 33, 459-467.	2.5	98
110	Protein-Protein Recognition: An Analysis by Docking Simulation. NATO ASI Series Series B: Physics, 1994, , 331-337.	0.2	0
111	The quaternary structure of carbonmonoxy hemoglobin ypsilanti. Proteins: Structure, Function and Bioinformatics, 1993, 15, 1-4.	2.6	40
112	Shared structural motif in proteins. Nature, 1993, 365, 21-21.	27.8	13
113	Protein docking algorithms: simulating molecular recognition. Current Opinion in Structural Biology, 1993, 3, 265-269.	5.7	121
114	Principles of Protein â€" Protein Recognition in Protease-Inhibitor and Antigen-Antibody Complexes. , 1993, , 103-114.		0
115	Protein engineering of xylose (glucose) isomerase from Actinoplanes missouriensis. 1. Crystallography and site-directed mutagenesis of metal binding sites. Biochemistry, 1992, 31, 5449-5458.	2.5	143
116	Crystal packing in six crystal forms of pancreatic ribonuclease. Journal of Molecular Biology, 1992, 228, 243-251.	4.2	77
117	Crystallization and preliminary X-ray diffraction studies of nucleoside diphosphate kinase from Dictyostelium discoideum. Journal of Molecular Biology, 1991, 217, 239-240.	4.2	12
118	Protein-protein recognition analyzed by docking simulation. Proteins: Structure, Function and Bioinformatics, 1991, 11, 271-280.	2.6	147
119	Proteinâ€Protein Interaction: An Analysis by Computer Simulation. Novartis Foundation Symposium, 1991, 161, 237-259.	1.1	2
120	The price of lost freedom: entropy of bimolecular complex formation. Protein Engineering, Design and Selection, 1989, 3, 1-3.	2.1	312
121	Structural analysis of the 2.8 Ã... model of xylose isomerase fromActinoplanes missouriensis. Proteins: Structure, Function and Bioinformatics, 1988, 4, 165-172.	2.6	57
122	Surface, subunit interfaces and interior of oligomeric proteins. Journal of Molecular Biology, 1988, 204, 155-164.	4.2	643
123	Interior and surface of monomeric proteins. Journal of Molecular Biology, 1987, 196, 641-656.	4.2	873
124	Computer studies of interactions between macromolecules. Progress in Biophysics and Molecular Biology, 1987, 49, 29-63.	2.9	45
125	The accessible surface area and stability of oligomeric proteins. Nature, 1987, 328, 834-836.	27.8	346
126	Reaction pathway for the quaternary structure change in hemoglobin. Biopolymers, 1985, 24, 509-526.	2.4	46

#	Article	IF	Citations
127	Domains in proteins: Definitions, location, and structural principles. Methods in Enzymology, 1985, 115, 420-430.	1.0	63
128	Haemoglobin: The surface buried between the Î±1Î²1 and Î±2Î²2 dimers in the deoxy and oxy structures. Journal of Molecular Biology, 1985, 183, 267-270.	4.2	46
129	Structure and stability of proteins: The role of solvent. Colloids and Surfaces, 1984, 10, 1-7.	0.9	6
130	Structural domains in proteins and their role in the dynamics of protein function. Progress in Biophysics and Molecular Biology, 1983, 42, 21-78.	2.9	267
131	Orthogonal packing of .beta.-pleated sheets in proteins. Biochemistry, 1982, 21, 3955-3965.	2.5	147
132	Location of structural domains in proteins. Biochemistry, 1981, 20, 6544-6552.	2.5	136
133	Packing of Î±-Helices onto Î²-Pleated sheets and the anatomy of proteins. Journal of Molecular Biology, 1980, 143, 95-128.	4.2	115
134	Surface and inside volumes in globular proteins. Nature, 1979, 277, 491-492.	27.8	689
135	Role of hydrophobicity in the binding of coenzymes. Biochemistry, 1978, 17, 2943-2948.	2.5	140
136	Computer analysis of protein-protein interaction. Journal of Molecular Biology, 1978, 124, 323-342.	4.2	260
137	Conformation of amino acid side-chains in proteins. Journal of Molecular Biology, 1978, 125, 357-386.	4.2	783
138	Stability and specificity of protein-protein interactions: The case of the trypsin-trypsin inhibitor complexes. Journal of Molecular Biology, 1976, 100, 197-211.	4.2	117
139	Surface area of globular proteins. Journal of Molecular Biology, 1976, 105, 13-14.	4.2	61
140	Principles of proteinâ€“protein recognition. Nature, 1975, 256, 705-708.	27.8	1,016
141	Crystallization of E. coli aspartokinase I - homoserine dehydrogenase I. FEBS Letters, 1974, 45, 318-319.	2.8	4
142	Revised Structure of Aspartokinase I-Homoserine Dehydrogenase I of Escherichia coli K12. Evidence for Four Identical Subunits. FEBS Journal, 1972, 28, 507-519.	0.2	96
143	The Threonine-Sensitive Homoserine Dehydrogenase and Aspartokinase Activities of Escherichia coli K 12. A Study of the Allosteric Equilibrium. FEBS Journal, 1969, 11, 520-529.	0.2	60
144	The Threonine-Sensitive Homoserine Dehydrogenase and Aspartokinase Activities of Escherichia coli K 12. Relaxations of the Allosteric Equilibrium. FEBS Journal, 1969, 11, 530-540.	0.2	37