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	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
2	Principles of proteinâ€“protein recognition. Nature, 1975, 256, 705-708.	27.8	1,016
3	Interior and surface of monomeric proteins. Journal of Molecular Biology, 1987, 196, 641-656.	4.2	873
4	Conformation of amino acid side-chains in proteins. Journal of Molecular Biology, 1978, 125, 357-386.	4.2	783
5	Surface and inside volumes in globular proteins. Nature, 1979, 277, 491-492.	27.8	689
6	Surface, subunit interfaces and interior of oligomeric proteins. Journal of Molecular Biology, 1988, 204, 155-164.	4.2	643
7	Silk fibroin: Structural implications of a remarkable amino acid sequence. Proteins: Structure, Function and Bioinformatics, 2001, 44, 119-122.	2.6	606
8	CAPRI: A Critical Assessment of PRedicted Interactions. Proteins: Structure, Function and Bioinformatics, 2003, 52, 2-9.	2.6	586
9	Dissecting protein-protein recognition sites. Proteins: Structure, Function and Bioinformatics, 2002, 47, 334-343.	2.6	549
10	A Dissection of Specific and Non-specific Proteinâ€“Protein Interfaces. Journal of Molecular Biology, 2004, 336, 943-955.	4.2	426
11	Proteinâ€“protein docking benchmark version 4.0. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3111-3114.	2.6	390
12	Proteinâ€“protein interaction and quaternary structure. Quarterly Reviews of Biophysics, 2008, 41, 133-180.	5.7	354
13	The accessible surface area and stability of oligomeric proteins. Nature, 1987, 328, 834-836.	27.8	346
14	Structural Features of Proteinâˆ’Nucleic Acid Recognition Sitesâ€. Biochemistry, 1999, 38, 1999-2017.	2.5	321
15	The price of lost freedom: entropy of bimolecular complex formation. Protein Engineering, Design and Selection, 1989, 3, 1-3.	2.1	312
16	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
17	Computer analysis of protein-protein interaction. Journal of Molecular Biology, 1978, 124, 323-342.	4.2	260
18	Dissecting subunit interfaces in homodimeric proteins. Proteins: Structure, Function and Bioinformatics, 2003, 53, 708-719.	2.6	256

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19	Protein-protein interaction at crystal contacts. Proteins: Structure, Function and Bioinformatics, 1995, 23, 580-587.	2.6	255
20	Protein-protein docking benchmark 2.0: An update. Proteins: Structure, Function and Bioinformatics, 2005, 60, 214-216.	2.6	254
21	A structureâ€based benchmark for proteinâ€“protein binding affinity. Protein Science, 2011, 20, 482-491.	7.6	252
22	A protein-protein docking benchmark. Proteins: Structure, Function and Bioinformatics, 2003, 52, 88-91.	2.6	242
23	Proteinâ€“protein docking benchmark version 3.0. Proteins: Structure, Function and Bioinformatics, 2008, 73, 705-709.	2.6	224
24	Wet and dry interfaces: the role of solvent in proteinâ€“protein and proteinâ€“DNA recognition. Structure, 1999, 7, R277-R279.	3.3	199
25	Hydration of protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 60, 36-45.	2.6	194
26	Specific versus non-specific contacts in protein crystals. Nature Structural Biology, 1997, 4, 973-974.	9.7	190
27	The kinetics of protein-protein recognition. Proteins: Structure, Function and Bioinformatics, 1997, 28, 153-161.	2.6	189
28	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
29	Proteinâ€“protein docking tested in blind predictions: the CAPRI experiment. Molecular BioSystems, 2010, 6, 2351.	2.9	171
30	Elusive affinities. Proteins: Structure, Function and Bioinformatics, 1995, 21, 30-39.	2.6	162
31	Assessing predictions of protein-protein interaction: The CAPRI experiment. Protein Science, 2005, 14, 278-283.	7.6	158
32	Orthogonal packing of .beta.-pleated sheets in proteins. Biochemistry, 1982, 21, 3955-3965.	2.5	147
33	Protein-protein recognition analyzed by docking simulation. Proteins: Structure, Function and Bioinformatics, 1991, 11, 271-280.	2.6	147
34	Structural basis of macromolecular recognition. Advances in Protein Chemistry, 2002, 61, 9-73.	4.4	147
35	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
36	Role of hydrophobicity in the binding of coenzymes. Biochemistry, 1978, 17, 2943-2948.	2.5	140

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37	Location of structural domains in proteins. Biochemistry, 1981, 20, 6544-6552.	2.5	136
38	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
39	The Human nm23-H4 Gene Product Is a Mitochondrial Nucleoside Diphosphate Kinase. Journal of Biological Chemistry, 2000, 275, 14264-14272.	3.4	128
40	Protein docking algorithms: simulating molecular recognition. Current Opinion in Structural Biology, 1993, 3, 265-269.	5.7	121
41	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
42	Protein-protein recognition. Progress in Biophysics and Molecular Biology, 1995, 64, 145-166.	2.9	116
43	Packing of Î±-Helices onto Î²-Pleated sheets and the anatomy of proteins. Journal of Molecular Biology, 1980, 143, 95-128.	4.2	115
44	Three-dimensional structure of nucleoside diphosphate kinase. Journal of Bioenergetics and Biomembranes, 2000, 32, 215-225.	2.3	115
45	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
46	Dissecting proteinâ€“RNA recognition sites. Nucleic Acids Research, 2008, 36, 2705-2716.	14.5	108
47	The Subunit Interfaces of Weakly Associated Homodimeric Proteins. Journal of Molecular Biology, 2010, 398, 146-160.	4.2	107
48	Adenosine 5'-diphosphate binding and the active site of nucleoside diphosphate kinase. Biochemistry, 1994, 33, 459-467.	2.5	98
49	Macromolecular recognition in the Protein Data Bank. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1-8.	2.5	97
50	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
51	Human and viral nucleoside/nucleotide kinases involved in antiviral drug activation: Structural and catalytic properties. Antiviral Research, 2010, 86, 101-120.	4.1	96
52	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
53	Cellular Phosphorylation of Anti-HIV Nucleosides. Journal of Biological Chemistry, 1996, 271, 7887-7890.	3.4	85
54	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological proteinâ€“protein interactions. Bioinformatics, 2008, 24, 652-658.	4.1	83

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55	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
56	Crystal packing in six crystal forms of pancreatic ribonuclease. Journal of Molecular Biology, 1992, 228, 243-251.	4.2	77
57	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
58	Revisiting the Voronoi description of protein-protein interfaces. Protein Science, 2006, 15, 2082-2092.	7.6	72
59	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
60	Quantifying biological specificity: The statistical mechanics of molecular recognition. Proteins: Structure, Function and Bioinformatics, 1996, 25, 438-445.	2.6	66
61	Protein flexibility, not disorder, is intrinsic to molecular recognition. F1000 Biology Reports, 2013, 5, 2.	4.0	66
62	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
63	Domains in proteins: Definitions, location, and structural principles. Methods in Enzymology, 1985, 115, 420-430.	1.0	63
64	Catalytic Mechanism of Nucleoside Diphosphate Kinase Investigated Using Nucleotide Analogues, Viscosity Effects, and X-ray Crystallography,. Biochemistry, 1999, 38, 7265-7272.	2.5	63
65	Structural basis for activation of Î±-boranophosphate nucleotide analogues targeting drug-resistant reverse transcriptase. EMBO Journal, 2000, 19, 3520-3529.	7.8	63
66	Nucleophilic Activation by Positioning in Phosphoryl Transfer Catalyzed by Nucleoside Diphosphate Kinaseâ€,â€¡. Biochemistry, 1999, 38, 4701-4711.	2.5	62
67	Surface area of globular proteins. Journal of Molecular Biology, 1976, 105, 13-14.	4.2	61
68	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
69	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
70	Welcome to CAPRI: A Critical Assessment of PRedicted Interactions. Proteins: Structure, Function and Bioinformatics, 2002, 47, 257-257.	2.6	57
71	Pre-steady State of Reaction of Nucleoside Diphosphate Kinase with Anti-HIV Nucleotides. Journal of Biological Chemistry, 1998, 273, 11491-11497.	3.4	50
72	Refolding strategies from inclusion bodies in a structural genomics project. Journal of Structural and Functional Genomics, 2004, 5, 195-204.	1.2	49

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73	Thermodynamics of the temperatureâ€induced unfolding of globular proteins. Protein Science, 1995, 4, 1315-1324.	7.6	48
74	Reaction pathway for the quaternary structure change in hemoglobin. Biopolymers, 1985, 24, 509-526.	2.4	46
75	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
76	Computer studies of interactions between macromolecules. Progress in Biophysics and Molecular Biology, 1987, 49, 29-63.	2.9	45
77	Nucleoside Diphosphate Kinase. Journal of Biological Chemistry, 1996, 271, 19928-19934.	3.4	45
78	Ã…ngstrÃ¶ms and calories. Structure, 1997, 5, 473-479.	3.3	45
79	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
80	For Guldberg and Waage, with love and cratic entropy. Proteins: Structure, Function and Bioinformatics, 1996, 24, i-ii.	2.6	42
81	The quaternary structure of carbonmonoxy hemoglobin ypsilanti. Proteins: Structure, Function and Bioinformatics, 1993, 15, 1-4.	2.6	40
82	Thermal Stability of Hexameric and Tetrameric Nucleoside Diphosphate Kinases. Journal of Biological Chemistry, 1996, 271, 17845-17851.	3.4	40
83	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
84	Genome-wide studies of proteinâ€“protein interaction. Current Opinion in Structural Biology, 2003, 13, 383-388.	5.7	39
85	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
86	Peptide segments in protein-protein interfaces. Journal of Biosciences, 2007, 32, 101-111.	1.1	37
87	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
88	3â€²-Phosphorylated Nucleotides Are Tight Binding Inhibitors of Nucleoside Diphosphate Kinase Activity. Journal of Biological Chemistry, 1998, 273, 28773-28778.	3.4	35
89	X-ray structure ofMycobacterium tuberculosis nucleoside diphosphate kinase. Proteins: Structure, Function and Bioinformatics, 2002, 47, 556-557.	2.6	33
90	Rigid-body docking with mutant constraints of influenza hemagglutinin with antibody HC19. Proteins: Structure, Function and Bioinformatics, 1994, 18, 8-18.	2.6	32

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91	Introduction. Advances in Protein Chemistry, 2002, 61, 1-8.	4.4	31
92	Crystal Structure of the YDR533c S. cerevisiae Protein, a Class II Member of the Hsp31 Family. Structure, 2004, 12, 839-847.	3.3	31
93	Crystal Structure of the Bifunctional Chorismate Synthase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 619-625.	3.4	29
94	A Dissection of the Proteinâ€“Protein Interfaces in Icosahedral Virus Capsids. Journal of Molecular Biology, 2007, 367, 574-590.	4.2	29
95	Improving Nucleoside Diphosphate Kinase for Antiviral Nucleotide Analogs Activation. Journal of Biological Chemistry, 2002, 277, 39953-39959.	3.4	28
96	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
97	Reassessing buried surface areas in proteinâ€“protein complexes. Protein Science, 2013, 22, 1453-1457.	7.6	27
98	A minimal model of proteinâ€“protein binding affinities. Protein Science, 2014, 23, 1813-1817.	7.6	27
99	The targets of CAPRI rounds 6â€“12. Proteins: Structure, Function and Bioinformatics, 2007, 69, 699-703.	2.6	26
100	The targets of CAPRI Rounds 13â€“19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3067-3072.	2.6	25
101	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
102	Crystal Structure of Yeast Allantoicase Reveals a Repeated Jelly Roll Motif. Journal of Biological Chemistry, 2004, 279, 23447-23452.	3.4	23
103	The targets of CAPRI rounds 3-5. Proteins: Structure, Function and Bioinformatics, 2005, 60, 170-175.	2.6	23
104	Analysis and Prediction of Protein Quaternary Structure. Methods in Molecular Biology, 2010, 609, 349-364.	0.9	22
105	A survey of hemoglobin quaternary structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2861-2870.	2.6	21
106	Changes in protein structure at the interface accompanying complex formation. IUCrJ, 2015, 2, 643-652.	2.2	21
107	A structural genomics initiative on yeast proteins. Journal of Synchrotron Radiation, 2003, 10, 4-8.	2.4	20
108	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. Protein Science, 2005, 14, 1350-1356.	7.6	20

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109	The Paris-Sud yeast structural genomics pilot-project: from structure to function. Biochimie, 2004, 86, 617-623.	2.6	18
110	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
111	Mechanism of phosphoryl transfer by nucleoside diphosphate kinase. FEBS Journal, 2001, 268, 1964-1971.	0.2	17
112	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
113	Nucleoside-Diphosphate Kinase: Structural and Kinetic Analysis of Reaction Pathway and Phosphohistidine Intermediate. Methods in Enzymology, 2002, 354, 118-134.	1.0	16
114	Structural templates for modeling homodimers. Protein Science, 2013, 22, 1655-1663.	7.6	16
115	Binding of Nucleotides to Nucleoside Diphosphate Kinase:Â A Calorimetric Studyâ€¡. Biochemistry, 2001, 40, 4583-4589.	2.5	15
116	Sideâ€chain rotamer transitions at proteinâ€protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	2.6	15
117	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
118	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
119	A docking analysis of the statistical physics of proteinâ€“protein recognition. Physical Biology, 2005, 2, S17-S23.	1.8	14
120	Residue conservation in viral capsid assembly. Proteins: Structure, Function and Bioinformatics, 2008, 71, 407-414.	2.6	14
121	The targets of CAPRI rounds 20â€“27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2075-2081.	2.6	14
122	Cloning, Production, and Purification of Proteins for a Medium-Scale Structural Genomics Project. Methods in Molecular Biology, 2007, 363, 21-37.	0.9	14
123	Shared structural motif in proteins. Nature, 1993, 365, 21-21.	27.8	13
124	A polymerase I palm in adenylyl cyclase?. Nature, 1997, 388, 34-34.	27.8	13
125	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
126	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

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127	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
128	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
129	Structural Genomics: Winning the Second Half of the Game. Structure, 2007, 15, 1347-1349.	3.3	10
130	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. Protein Science, 2006, 15, 1516-1521.	7.6	8
131	Structure and stability of proteins: The role of solvent. Colloids and Surfaces, 1984, 10, 1-7.	0.9	6
132	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
133	Crystal structure of yeast YER010Cp, aknotable member of the RraA protein family. Protein Science, 2005, 14, 2751-2758.	7.6	5
134	Sailing the route from Gaeta, Italy, to CAPRI. Proteins: Structure, Function and Bioinformatics, 2005, 60, 149-149.	2.6	5
135	Docking Predictions of Protein-Protein Interactions and Their Assessment: The CAPRI Experiment. Focus on Structural Biology, 2013, , 87-104.	0.1	5
136	Crystallization of E. coli aspartokinase I - homoserine dehydrogenase I. FEBS Letters, 1974, 45, 318-319.	2.8	4
137	Proteins with a ring. Structure, 1994, 2, 571-573.	3.3	4
138	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
139	Phosphorylation of Anti-HIV Nucleoside Analogs by Nucleoside Diphosphate Kinase. Nucleosides & Nucleotides, 1999, 18, 829-830.	0.5	2
140	Proteinâ€Protein Interaction: An Analysis by Computer Simulation. Novartis Foundation Symposium, 1991, 161, 237-259.	1.1	2
141	Quantifying biological specificity: The statistical mechanics of molecular recognition. Proteins: Structure, Function and Bioinformatics, 1996, 25, 438-445.	2.6	1
142	X-ray Study of Proteinâ€“Protein Complexes and Analysis of Interfaces. , 2010, , 1-24.		1
143	Principles of Protein â€” Protein Recognition in Protease-Inhibitor and Antigen-Antibody Complexes. , 1993, , 103-114.		0
144	Protein-Protein Recognition: An Analysis by Docking Simulation. NATO ASI Series Series B: Physics, 1994, , 331-337.	0.2	0