

# Joel Janin

## List of Publications by Year in descending order

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144  
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18,690  
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21215

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g-index

151  
all docs

151  
docs citations

151  
times ranked

14389  
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in protein structure at the interface accompanying complex formation. IUCr, 2015, 2, 643-652.	1.0	21
2	A minimal model of protein-protein binding affinities. Protein Science, 2014, 23, 1813-1817.	3.1	27
3	The targets of CAPRI rounds 20-27. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2075-2081.	1.5	14
4	Reassessing buried surface areas in protein-protein complexes. Protein Science, 2013, 22, 1453-1457.	3.1	27
5	Structural templates for modeling homodimers. Protein Science, 2013, 22, 1655-1663.	3.1	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.	1.5	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.	3.3	178
10	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
11	A survey of hemoglobin quaternary structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2861-2870.	1.5	21
12	A structure-based benchmark for protein-protein binding affinity. Protein Science, 2011, 20, 482-491.	3.1	252
13	Human and viral nucleoside/nucleotide kinases involved in antiviral drug activation: Structural and catalytic properties. Antiviral Research, 2010, 86, 101-120.	1.9	96
14	The targets of CAPRI Rounds 13-19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3067-3072.	1.5	25
15	Side-chain rotamer transitions at protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	1.5	15
16	Protein-protein docking benchmark version 4.0. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3111-3114.	1.5	390
17	Protein-protein docking tested in blind predictions: the CAPRI experiment. Molecular BioSystems, 2010, 6, 2351.	2.9	171
18	X-ray Study of Protein-Protein Complexes and Analysis of Interfaces. , 2010, , 1-24.		1

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19	The Subunit Interfaces of Weakly Associated Homodimeric Proteins. <i>Journal of Molecular Biology</i> , 2010, 398, 146-160.	2.0	107
20	Analysis and Prediction of Protein Quaternary Structure. <i>Methods in Molecular Biology</i> , 2010, 609, 349-364.	0.4	22
21	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, 776-792.	0.4	18
22	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> , 2009, 14, 209-215.	3.1	13
23	Relating Macromolecular Function and Association: The Structural Basis of Protein-DNA and RNA Recognition. <i>Cellular and Molecular Bioengineering</i> , 2008, 1, 327-338.	1.0	11
24	Residue conservation in viral capsid assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 407-414.	1.5	14
25	Protein-protein docking benchmark version 3.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 705-709.	1.5	224
26	Protein-protein interaction and quaternary structure. <i>Quarterly Reviews of Biophysics</i> , 2008, 41, 133-180.	2.4	354
27	Dissecting protein-RNA recognition sites. <i>Nucleic Acids Research</i> , 2008, 36, 2705-2716.	6.5	108
28	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. <i>Bioinformatics</i> , 2008, 24, 652-658.	1.8	83
29	A Dissection of the Protein-Protein Interfaces in Icosahedral Virus Capsids. <i>Journal of Molecular Biology</i> , 2007, 367, 574-590.	2.0	29
30	Macromolecular recognition in the Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1-8.	2.5	97
31	The targets of CAPRI rounds 6-12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 699-703.	1.5	26
32	Structural Genomics: Winning the Second Half of the Game. <i>Structure</i> , 2007, 15, 1347-1349.	1.6	10
33	Peptide segments in protein-protein interfaces. <i>Journal of Biosciences</i> , 2007, 32, 101-111.	0.5	37
34	Cloning, Production, and Purification of Proteins for a Medium-Scale Structural Genomics Project. <i>Methods in Molecular Biology</i> , 2007, 363, 21-37.	0.4	14
35	Crystal structure of the yeast His6 enzyme suggests a reaction mechanism. <i>Protein Science</i> , 2006, 15, 1516-1521.	3.1	8
36	Revisiting the Voronoi description of protein-protein interfaces. <i>Protein Science</i> , 2006, 15, 2082-2092.	3.1	72

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37	Assessing predictions of protein-protein interaction: The CAPRI experiment. <i>Protein Science</i> , 2005, 14, 278-283.	3.1	158
38	Crystal structure of yeast YHR049W/FSH1, a member of the serine hydrolase family. <i>Protein Science</i> , 2005, 14, 1350-1356.	3.1	20
39	Crystal structure of yeast YER010Cp, aknotable member of the RraA protein family. <i>Protein Science</i> , 2005, 14, 2751-2758.	3.1	5
40	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, 664-670.	2.5	14
41	Hydration of protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 36-45.	1.5	194
42	Sailing the route from Gaeta, Italy, to CAPRI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 149-149.	1.5	5
43	The targets of CAPRI rounds 3-5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 170-175.	1.5	23
44	Protein-protein docking benchmark 2.0: An update. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 214-216.	1.5	254
45	A docking analysis of the statistical physics of protein-protein recognition. <i>Physical Biology</i> , 2005, 2, S17-S23.	0.8	14
46	Crystal Structure of the Bifunctional Chorismate Synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 619-625.	1.6	29
47	Crystal Structure of Yeast Allantoicase Reveals a Repeated Jelly Roll Motif. <i>Journal of Biological Chemistry</i> , 2004, 279, 23447-23452.	1.6	23
48	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, 8351-8358.	1.6	82
49	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, 34890-34897.	1.6	71
50	Crystal Structure of the YDR533c <i>S. cerevisiae</i> Protein, a Class II Member of the Hsp31 Family. <i>Structure</i> , 2004, 12, 839-847.	1.6	31
51	Refolding strategies from inclusion bodies in a structural genomics project. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 195-204.	1.2	49
52	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, 776-783.	1.5	17
53	The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004, 86, 617-623.	1.3	18
54	A Dissection of Specific and Non-specific Protein-Protein Interfaces. <i>Journal of Molecular Biology</i> , 2004, 336, 943-955.	2.0	426

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55	Genome-wide studies of protein-protein interaction. <i>Current Opinion in Structural Biology</i> , 2003, 13, 383-388.	2.6	39
56	A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 4-8.	1.0	20
57	CAPRI: A Critical Assessment of PRedicted Interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 2-9.	1.5	586
58	A protein-protein docking benchmark. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 88-91.	1.5	242
59	Dissecting subunit interfaces in homodimeric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 708-719.	1.5	256
60	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, 915-926.	2.0	36
61	The 62-kb upstream region of <i>Bombyx mori</i> fibroin heavy chain gene is clustered of repetitive elements and candidate matrix association regions. <i>Gene</i> , 2003, 312, 189-195.	1.0	11
62	Structural Analysis of the Activation of Ribavirin Analogs by NDP Kinase: Comparison with Other Ribavirin Targets. <i>Molecular Pharmacology</i> , 2003, 63, 538-546.	1.0	24
63	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003, 278, 50371-50376.	1.6	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. <i>Journal of Bacteriology</i> , 2003, 185, 4003-4010.	1.0	45
65	Improving Nucleoside Diphosphate Kinase for Antiviral Nucleotide Analogs Activation. <i>Journal of Biological Chemistry</i> , 2002, 277, 39953-39959.	1.6	28
66	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, 13437-13441.	3.3	73
67	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, 13442-13447.	3.3	112
68	Introduction. <i>Advances in Protein Chemistry</i> , 2002, 61, 1-8.	4.4	31
69	Nucleoside-Diphosphate Kinase: Structural and Kinetic Analysis of Reaction Pathway and Phosphohistidine Intermediate. <i>Methods in Enzymology</i> , 2002, 354, 118-134.	0.4	16
70	Structural basis of macromolecular recognition. <i>Advances in Protein Chemistry</i> , 2002, 61, 9-73.	4.4	147
71	Dissecting protein-protein recognition sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 334-343.	1.5	549
72	Welcome to CAPRI: A Critical Assessment of PRedicted Interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 257-257.	1.5	57

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73	X-ray structure of <i>Mycobacterium tuberculosis</i> nucleoside diphosphate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 556-557.	1.5	33
74	ACTIVATION OF ANTI-REVERSE TRANSCRIPTASE NUCLEOTIDE ANALOGS BY NUCLEOSIDE DIPHOSPHATE KINASE: IMPROVEMENT BY Î±-BORANOPHOSPHATE SUBSTITUTION. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2001, 20, 297-306.	0.4	14
75	Chemical Rescue of Phosphoryl Transfer in a Cavity Mutant: A Cautionary Tale for Site-Directed Mutagenesis. <i>Biochemistry</i> , 2001, 40, 403-413.	1.2	27
76	Binding of Nucleotides to Nucleoside Diphosphate Kinase: A Calorimetric Study. <i>Biochemistry</i> , 2001, 40, 4583-4589.	1.2	15
77	Mechanism of phosphoryl transfer by nucleoside diphosphate kinase. <i>FEBS Journal</i> , 2001, 268, 1964-1971.	0.2	17
78	Silk fibroin: Structural implications of a remarkable amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 119-122.	1.5	606
79	Three-dimensional structure of nucleoside diphosphate kinase. <i>Journal of Bioenergetics and Biomembranes</i> , 2000, 32, 215-225.	1.0	115
80	Structural basis for activation of Î±-boranophosphate nucleotide analogues targeting drug-resistant reverse transcriptase. <i>EMBO Journal</i> , 2000, 19, 3520-3529.	3.5	63
81	The Human nm23-H4 Gene Product Is a Mitochondrial Nucleoside Diphosphate Kinase. <i>Journal of Biological Chemistry</i> , 2000, 275, 14264-14272.	1.6	128
82	Wet and dry interfaces: the role of solvent in protein-DNA recognition. <i>Structure</i> , 1999, 7, R277-R279.	1.6	199
83	p55-hGRF, a short natural form of the Ras-GDP exchange factor. High yield production and characterization. <i>FEBS Journal</i> , 1999, 263, 806-816.	0.2	2
84	Structural Features of Protein-Nucleic Acid Recognition Sites. <i>Biochemistry</i> , 1999, 38, 1999-2017.	1.2	321
85	Phosphorylation of Anti-HIV Nucleoside Analogs by Nucleoside Diphosphate Kinase. <i>Nucleosides &amp; Nucleotides</i> , 1999, 18, 829-830.	0.5	2
86	Catalytic Mechanism of Nucleoside Diphosphate Kinase Investigated Using Nucleotide Analogues, Viscosity Effects, and X-ray Crystallography. <i>Biochemistry</i> , 1999, 38, 7265-7272.	1.2	63
87	Nucleophilic Activation by Positioning in Phosphoryl Transfer Catalyzed by Nucleoside Diphosphate Kinase. <i>Biochemistry</i> , 1999, 38, 4701-4711.	1.2	62
88	The atomic structure of protein-protein recognition sites 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 2177-2198.	2.0	1,886
89	A soft, mean-field potential derived from crystal contacts for predicting protein-protein interactions. <i>Journal of Molecular Biology</i> , 1998, 283, 1037-1047.	2.0	40
90	Pre-steady State of Reaction of Nucleoside Diphosphate Kinase with Anti-HIV Nucleotides. <i>Journal of Biological Chemistry</i> , 1998, 273, 11491-11497.	1.6	50

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91	3â€²-Phosphorylated Nucleotides Are Tight Binding Inhibitors of Nucleoside Diphosphate Kinase Activity. Journal of Biological Chemistry, 1998, 273, 28773-28778.	1.6	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.	13.7	13
94	Ã…ngstrÃ¶ms and calories. Structure, 1997, 5, 473-479.	1.6	45
95	The kinetics of protein-protein recognition. , 1997, 28, 153-161.		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.	1.5	1
98	For Guldberg and Waage, with love and cratic entropy. Proteins: Structure, Function and Bioinformatics, 1996, 24, i-ii.	1.5	42
99	Nucleoside Diphosphate Kinase. Journal of Biological Chemistry, 1996, 271, 19928-19934.	1.6	45
100	Cellular Phosphorylation of Anti-HIV Nucleosides. Journal of Biological Chemistry, 1996, 271, 7887-7890.	1.6	85
101	Thermal Stability of Hexameric and Tetrameric Nucleoside Diphosphate Kinases. Journal of Biological Chemistry, 1996, 271, 17845-17851.	1.6	40
102	Quantifying biological specificity: The statistical mechanics of molecular recognition. Proteins: Structure, Function and Bioinformatics, 1996, 25, 438-445.	1.5	66
103	Protein-protein recognition. Progress in Biophysics and Molecular Biology, 1995, 64, 145-166.	1.4	116
104	Elusive affinities. Proteins: Structure, Function and Bioinformatics, 1995, 21, 30-39.	1.5	162
105	Protein-protein interaction at crystal contacts. Proteins: Structure, Function and Bioinformatics, 1995, 23, 580-587.	1.5	255
106	Thermodynamics of the temperatureâ€”induced unfolding of globular proteins. Protein Science, 1995, 4, 1315-1324.	3.1	48
107	Proteins with a ring. Structure, 1994, 2, 571-573.	1.6	4
108	Rigid-body docking with mutant constraints of influenza hemagglutinin with antibody HC19. Proteins: Structure, Function and Bioinformatics, 1994, 18, 8-18.	1.5	32

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109	Adenosine 5'-diphosphate binding and the active site of nucleoside diphosphate kinase. <i>Biochemistry</i> , 1994, 33, 459-467.	1.2	98
110	Protein-Protein Recognition: An Analysis by Docking Simulation. <i>NATO ASI Series Series B: Physics</i> , 1994, , 331-337.	0.2	0
111	The quaternary structure of carbonmonoxy hemoglobin ypsilanti. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 1-4.	1.5	40
112	Shared structural motif in proteins. <i>Nature</i> , 1993, 365, 21-21.	13.7	13
113	Protein docking algorithms: simulating molecular recognition. <i>Current Opinion in Structural Biology</i> , 1993, 3, 265-269.	2.6	121
114	Principles of Protein " Protein Recognition in Protease-Inhibitor and Antigen-Antibody Complexes. , 1993, , 103-114.		0
115	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, 5449-5458.	1.2	143
116	Crystal packing in six crystal forms of pancreatic ribonuclease. <i>Journal of Molecular Biology</i> , 1992, 228, 243-251.	2.0	77
117	Crystallization and preliminary X-ray diffraction studies of nucleoside diphosphate kinase from <i>Dictyostelium discoideum</i> . <i>Journal of Molecular Biology</i> , 1991, 217, 239-240.	2.0	12
118	Protein-protein recognition analyzed by docking simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 11, 271-280.	1.5	147
119	Protein-Protein Interaction: An Analysis by Computer Simulation. <i>Novartis Foundation Symposium</i> , 1991, 161, 237-259.	1.2	2
120	The price of lost freedom: entropy of bimolecular complex formation. <i>Protein Engineering, Design and Selection</i> , 1989, 3, 1-3.	1.0	312
121	Structural analysis of the 2.8 Å... model of xylose isomerase from <i>Actinoplanes missouriensis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 165-172.	1.5	57
122	Surface, subunit interfaces and interior of oligomeric proteins. <i>Journal of Molecular Biology</i> , 1988, 204, 155-164.	2.0	643
123	Interior and surface of monomeric proteins. <i>Journal of Molecular Biology</i> , 1987, 196, 641-656.	2.0	873
124	Computer studies of interactions between macromolecules. <i>Progress in Biophysics and Molecular Biology</i> , 1987, 49, 29-63.	1.4	45
125	The accessible surface area and stability of oligomeric proteins. <i>Nature</i> , 1987, 328, 834-836.	13.7	346
126	Reaction pathway for the quaternary structure change in hemoglobin. <i>Biopolymers</i> , 1985, 24, 509-526.	1.2	46



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127	Domains in proteins: Definitions, location, and structural principles. <i>Methods in Enzymology</i> , 1985, 115, 420-430.	0.4	63
128	Haemoglobin: The surface buried between the $\hat{1}\hat{1}^2$ and $\hat{1}\hat{2}^2$ dimers in the deoxy and oxy structures. <i>Journal of Molecular Biology</i> , 1985, 183, 267-270.	2.0	46
129	Structure and stability of proteins: The role of solvent. <i>Colloids and Surfaces</i> , 1984, 10, 1-7.	0.9	6
130	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.	1.4	267
131	Orthogonal packing of $\beta$ -pleated sheets in proteins. <i>Biochemistry</i> , 1982, 21, 3955-3965.	1.2	147
132	Location of structural domains in proteins. <i>Biochemistry</i> , 1981, 20, 6544-6552.	1.2	136
133	Packing of $\alpha$ -Helices onto $\beta$ -Pleated sheets and the anatomy of proteins. <i>Journal of Molecular Biology</i> , 1980, 143, 95-128.	2.0	115
134	Surface and inside volumes in globular proteins. <i>Nature</i> , 1979, 277, 491-492.	13.7	689
135	Role of hydrophobicity in the binding of coenzymes. <i>Biochemistry</i> , 1978, 17, 2943-2948.	1.2	140
136	Computer analysis of protein-protein interaction. <i>Journal of Molecular Biology</i> , 1978, 124, 323-342.	2.0	260
137	Conformation of amino acid side-chains in proteins. <i>Journal of Molecular Biology</i> , 1978, 125, 357-386.	2.0	783
138	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.	2.0	117
139	Surface area of globular proteins. <i>Journal of Molecular Biology</i> , 1976, 105, 13-14.	2.0	61
140	Principles of protein-protein recognition. <i>Nature</i> , 1975, 256, 705-708.	13.7	1,016
141	Crystallization of <i>E. coli</i> aspartokinase I - homoserine dehydrogenase I. <i>FEBS Letters</i> , 1974, 45, 318-319.	1.3	4
142	Revised Structure of Aspartokinase I-Homoserine Dehydrogenase I of <i>Escherichia coli</i> K12. Evidence for Four Identical Subunits. <i>FEBS Journal</i> , 1972, 28, 507-519.	0.2	96
143	The Threonine-Sensitive Homoserine Dehydrogenase and Aspartokinase Activities of <i>Escherichia coli</i> K12. A Study of the Allosteric Equilibrium. <i>FEBS Journal</i> , 1969, 11, 520-529.	0.2	60
144	The Threonine-Sensitive Homoserine Dehydrogenase and Aspartokinase Activities of <i>Escherichia coli</i> K12. Relaxations of the Allosteric Equilibrium. <i>FEBS Journal</i> , 1969, 11, 530-540.	0.2	37