

# Remy Loris

## List of Publications by Year in descending order

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155  
papers

7,975  
citations

46918

47  
h-index

56606

83  
g-index

166  
all docs

166  
docs citations

166  
times ranked

8032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights into Charcotâ€“Marieâ€“Tooth diseaseâ€“linked mutations in human GDAP1. FEBS Open Bio, 2022, 12, 1306-1324.	1.0	6
2	High-affinity anti-Arc nanobodies provide tools for structural and functional studies. PLoS ONE, 2022, 17, e0269281.	1.1	5
3	Structure and substrate specificity determinants of the taurine biosynthetic enzyme cysteine sulphinic acid decarboxylase. Journal of Structural Biology, 2021, 213, 107674.	1.3	3
4	Arc selfâ€“association and formation of virusâ€“like capsids are mediated by an Nâ€“terminal helical coil motif. FEBS Journal, 2021, 288, 2930-2955.	2.2	25
5	Arabidopsis casein kinase 2 triggers stem cell exhaustion under Al toxicity and phosphate deficiency through activating the DNA damage response pathway. Plant Cell, 2021, 33, 1361-1380.	3.1	26
6	Molecular architecture of the endocytic TPLATE complex. Science Advances, 2021, 7, .	4.7	31
7	A nanobody toolbox targeting dimeric coiled-coil modules for functionalization of designed protein origami structures. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
8	Prokaryote toxinâ€“antitoxin modules: Complex regulation of an unclear function. Protein Science, 2021, 30, 1103-1113.	3.1	20
9	Alternative dimerization is required for activity and inhibition of the HEPN ribonuclease RnIA. Nucleic Acids Research, 2021, 49, 7164-7178.	6.5	6
10	Entropic pressure controls the oligomerization of the <i>Vibrio cholerae</i> ParD2 antitoxin. Acta Crystallographica Section D: Structural Biology, 2021, 77, 904-920.	1.1	5
11	The sequenceâ€“ensemble relationship in fuzzy protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
12	Nanobody-aided crystallization of the transcription regulator PaaR2 from <i>Escherichia coli</i> O157:H7. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 374-384.	0.4	2
13	Crystal and solution structure of NDRG1, a membraneâ€“binding protein linked to myelination and tumour suppression. FEBS Journal, 2021, 288, 3507-3529.	2.2	10
14	Bistable Expression of a Toxin-Antitoxin System Located in a Cryptic Prophage of Escherichia coli O157:H7. MBio, 2021, 12, e0294721.	1.8	13
15	1H, 13C, and 15N backbone and side chain chemical shift assignment of YdaS, a monomeric member of the HigA family. Biomolecular NMR Assignments, 2020, 14, 25-30.	0.4	1
16	The <i>Escherichia coli</i> RnIAâ€“RnIB toxinâ€“antitoxin complex: production, characterization and crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 31-39.	0.4	2
17	Structure of the Complete Dimeric Human GDAP1 Core Domain Provides Insights into Ligand Binding and Clustering of Disease Mutations. Frontiers in Molecular Biosciences, 2020, 7, 631232.	1.6	11
18	Crystal structure of <i>Arabidopsis thaliana</i> casein kinase 2 Î±1. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 182-191.	0.4	3

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19	Thermodynamic Stability of the Transcription Regulator PaaR2 from Escherichia coli O157:H7. <i>Biophysical Journal</i> , 2019, 116, 1420-1431.	0.2	4
20	A dual role in regulation and toxicity for the disordered N-terminus of the toxin GraT. <i>Nature Communications</i> , 2019, 10, 972.	5.8	29
21	The quaternary structure of human tyrosine hydroxylase: effects of dystonia-associated missense variants on oligomeric state and enzyme activity. <i>Journal of Neurochemistry</i> , 2019, 148, 291-306.	2.1	20
22	Phosphorylation decelerates conformational dynamics in bacterial translation elongation factors. <i>Science Advances</i> , 2018, 4, eaap9714.	4.7	37
23	Structural Basis of Epitope Recognition by Heavy-Chain Camelid Antibodies. <i>Journal of Molecular Biology</i> , 2018, 430, 4369-4386.	2.0	101
24	Hidden States within Disordered Regions of the CcdA Antitoxin Protein. <i>Journal of the American Chemical Society</i> , 2017, 139, 2693-2701.	6.6	9
25	Ribosome-dependent <i>Vibrio cholerae</i> mRNAse HigB2 is regulated by a $\hat{\text{I}}^2$ -strand sliding mechanism. <i>Nucleic Acids Research</i> , 2017, 45, 4972-4983.	6.5	43
26	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. <i>Angewandte Chemie</i> , 2017, 129, 14686-14689.	1.6	1
27	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14494-14497.	7.2	31
28	Bivalent Llama Single-Domain Antibody Fragments against Tumor Necrosis Factor Have Picomolar Potencies due to Intramolecular Interactions. <i>Frontiers in Immunology</i> , 2017, 8, 867.	2.2	57
29	Production, biophysical characterization and crystallization of <i>Pseudomonas putida</i> GraA and its complexes with GraT and the graTA operator. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 455-462.	0.4	2
30	Molecular mechanism governing ratio-dependent transcription regulation in the ccdAB operon. <i>Nucleic Acids Research</i> , 2017, 45, 2937-2950.	6.5	29
31	Probing the Conformational Ensemble of a Bacterial Antitoxin through Molecular Dynamics Simulations and Mass Spectrometry. <i>Biophysical Journal</i> , 2016, 110, 558a.	0.2	0
32	An intrinsically disordered entropic switch determines allostery in Phd Doc regulation. <i>Nature Chemical Biology</i> , 2016, 12, 490-496.	3.9	35
33	Structural Mimicry of Receptor Interaction by Antagonistic Interleukin-6 (IL-6) Antibodies. <i>Journal of Biological Chemistry</i> , 2016, 291, 13846-13854.	1.6	24
34	Frizzled 7 and PIP2 binding by syntenin PDZ2 domain supports Frizzled 7 trafficking and signalling. <i>Nature Communications</i> , 2016, 7, 12101.	5.8	35
35	Substrate Recognition and Activity Regulation of the Escherichia coli mRNA Endonuclease MazF. <i>Journal of Biological Chemistry</i> , 2016, 291, 10950-10960.	1.6	44
36	A unique hetero-hexadecameric architecture displayed by the Escherichia coli O157 PaaA2 ParE2 antitoxin-toxin complex. <i>Journal of Molecular Biology</i> , 2016, 428, 1589-1603.	2.0	41

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37	Computational Methods to Model Persistence. <i>Methods in Molecular Biology</i> , 2016, 1333, 207-240.	0.4	4
38	Crystallization of two operator complexes from the <i>Vibrio cholerae</i> HigBA2 toxin-antitoxin module. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 226-233.	0.4	2
39	An efficient method for the purification of proteins from four distinct toxin-antitoxin modules. <i>Protein Expression and Purification</i> , 2015, 108, 30-40.	0.6	27
40	Crystallization and preliminary X-ray analysis of four cysteine proteases from <i>Ficus carica</i> latex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 459-465.	0.4	17
41	<i>Escherichia coli</i> antitoxin MazE as transcription factor: insights into MazE-DNA binding. <i>Nucleic Acids Research</i> , 2015, 43, 1241-1256.	6.5	35
42	The Intrinsically Disordered Domain of the Antitoxin Phd Chaperones the Toxin Doc against Irreversible Inactivation and Misfolding. <i>Journal of Biological Chemistry</i> , 2014, 289, 34013-34023.	1.6	10
43	A nanobody modulates the p53 transcriptional program without perturbing its functional architecture. <i>Nucleic Acids Research</i> , 2014, 42, 12928-12938.	6.5	32
44	SAXS analysis of the tRNA-modifying enzyme complex MnmE/MnmG reveals a novel interaction mode and GTP-induced oligomerization. <i>Nucleic Acids Research</i> , 2014, 42, 5978-5992.	6.5	27
45	Structural and biophysical characterization of <i>Staphylococcus aureus</i> SaMazF shows conservation of functional dynamics. <i>Nucleic Acids Research</i> , 2014, 42, 6709-6725.	6.5	33
46	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N backbone and side-chain chemical shift assignment of the toxin Doc in the unbound state. <i>Biomolecular NMR Assignments</i> , 2014, 8, 145-148.	0.4	2
47	Small-Angle X-Ray Scattering- and Nuclear Magnetic Resonance-Derived Conformational Ensemble of the Highly Flexible Antitoxin PaaA2. <i>Structure</i> , 2014, 22, 854-865.	1.6	61
48	Crystallization and preliminary X-ray analysis of two variants of the <i>Escherichia coli</i> O157 ParE2-PaaA2 toxin-antitoxin complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1284-1291.	0.4	2
49	Disorder- and Dynamics-Based Regulatory Mechanisms in Toxin-Antitoxin Modules. <i>Chemical Reviews</i> , 2014, 114, 6933-6947.	23.0	82
50	The many faces of Fic: structural and functional aspects of Fic enzymes. <i>Trends in Biochemical Sciences</i> , 2014, 39, 121-129.	3.7	62
51	Antibacterial activity of a lectin-like <i>Burkholderia cenocepacia</i> protein. <i>MicrobiologyOpen</i> , 2013, 2, 566-575.	1.2	16
52	Energetic Basis of Uncoupling Folding from Binding for an Intrinsically Disordered Protein. <i>Journal of the American Chemical Society</i> , 2013, 135, 1288-1294.	6.6	45
53	Type II Toxin-Antitoxin Loci: The phd/doc Family. , 2013, , 157-176.		1
54	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6-5-FCR3 of the <i>Plasmodium falciparum</i> VAR2CSA protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 270-274.	0.7	2

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55	A General Model for Toxin-Antitoxin Module Dynamics Can Explain Persister Cell Formation in <i>E. coli</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1003190.	1.5	54
56	Structural Determinants for Activity and Specificity of the Bacterial Toxin LlpA. <i>PLoS Pathogens</i> , 2013, 9, e1003199.	2.1	33
57	The Fic protein Doc uses an inverted substrate to phosphorylate and inactivate EF-Tu. <i>Nature Chemical Biology</i> , 2013, 9, 811-817.	3.9	159
58	Crystallization of the HigBA2 toxin-antitoxin complex from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1052-1059.	0.7	9
59	MMBL proteins: from lectin to bacteriocin. <i>Biochemical Society Transactions</i> , 2012, 40, 1553-1559.	1.6	20
60	Mutational and Structural Analysis of I - N -Carbamoylase Reveals New Insights into a Peptidase M20/M25/M40 Family Member. <i>Journal of Bacteriology</i> , 2012, 194, 5759-5768.	1.0	23
61	Plant lectin-like antibacterial proteins from phytopathogens <i>Pseudomonas syringae</i> and <i>Xanthomonas citri</i> . <i>Environmental Microbiology Reports</i> , 2012, 4, 373-380.	1.0	28
62	The ParE2-PaaA2 toxin-antitoxin complex from <i>Escherichia coli</i> O157 forms a heterodoecamer in solution and in the crystal. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 724-729.	0.7	9
63	Alternative interactions define gyrase specificity in the CcdB family. <i>Molecular Microbiology</i> , 2012, 84, 965-978.	1.2	15
64	1H, 13C, and 15N backbone and side-chain chemical shift assignment of the staphylococcal MazF mRNA interferase. <i>Biomolecular NMR Assignments</i> , 2011, 5, 157-160.	0.4	5
65	Crystallization of the <i>Staphylococcus aureus</i> MazF mRNA interferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 386-389.	0.7	5
66	Cancer predisposing missense and protein truncating <i>BARD1</i> mutations in non- <i>BRCA1</i> or <i>BRCA2</i> breast cancer families. <i>Human Mutation</i> , 2010, 31, E1175-E1185.	1.1	86
67	Purification and crystallization of Phd, the antitoxin of the <i>phd/doc</i> operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 167-171.	0.7	4
68	New toxins homologous to ParE belonging to three-component toxin-antitoxin systems in <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2010, 76, 719-732.	1.2	110
69	Structural and Thermodynamic Characterization of <i>Vibrio fischeri</i> CcdB. <i>Journal of Biological Chemistry</i> , 2010, 285, 5606-5613.	1.6	16
70	<i>Vibrio cholerae</i> ParE2 Poisons DNA Gyrase via a Mechanism Distinct from Other Gyrase Inhibitors. <i>Journal of Biological Chemistry</i> , 2010, 285, 40397-40408.	1.6	67
71	Allostery and Intrinsic Disorder Mediate Transcription Regulation by Conditional Cooperativity. <i>Cell</i> , 2010, 142, 101-111.	13.5	226
72	Sequence-specific 1H, 15N and 13C resonance assignments of the 23.7-kDa homodimeric toxin CcdB from <i>Vibrio fischeri</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 145-147.	0.4	1

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73	General Strategy to Humanize a Camelid Single-domain Antibody and Identification of a Universal Humanized Nanobody Scaffold. <i>Journal of Biological Chemistry</i> , 2009, 284, 3273-3284.	1.6	441
74	Driving Forces of Gyrase Recognition by the Addiction Toxin CcdB. <i>Journal of Biological Chemistry</i> , 2009, 284, 20002-20010.	1.6	26
75	Coupling of Domain Swapping to Kinetic Stability in a Thioredoxin Mutant. <i>Journal of Molecular Biology</i> , 2009, 385, 1590-1599.	2.0	23
76	Energetics of MazG Unfolding in Correlation with Its Structural Features. <i>Journal of Molecular Biology</i> , 2009, 392, 63-74.	2.0	5
77	Rejuvenation of CcdB-Poisoned Gyrase by an Intrinsically Disordered Protein Domain. <i>Molecular Cell</i> , 2009, 35, 154-163.	4.5	153
78	A Folding Switch Regulates the Phd/doc Operon by Conditional Cooperativity. <i>Biophysical Journal</i> , 2009, 96, 68a.	0.2	0
79	Crystallization of Doc and the Phd-Doc toxin-antitoxin complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1034-1038.	0.7	9
80	Crystallization and preliminary crystallographic studies of the recombinant L-N-carbamoylase from <i>Geobacillus stearothermophilus</i> CECT43. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1135-1138.	0.7	4
81	Inhibition and Dispersion of <i>Pseudomonas aeruginosa</i> Biofilms by Glycopeptide Dendrimers Targeting the Fucose-Specific Lectin LecB. <i>Chemistry and Biology</i> , 2008, 15, 1249-1257.	6.2	211
82	Nonspecific base recognition mediated by water bridges and hydrophobic stacking in ribonuclease I from <i>Escherichia coli</i> . <i>Protein Science</i> , 2008, 17, 681-690.	3.1	10
83	Doc of Prophage P1 Is Inhibited by Its Antitoxin Partner Phd through Fold Complementation. <i>Journal of Biological Chemistry</i> , 2008, 283, 30821-30827.	1.6	103
84	The Oxidase DsbA Folds a Protein with a Nonconsecutive Disulfide. <i>Journal of Biological Chemistry</i> , 2007, 282, 31302-31307.	1.6	71
85	How a Plant Lectin Recognizes High Mannose Oligosaccharides. <i>Plant Physiology</i> , 2007, 144, 1733-1741.	2.3	19
86	The Conserved Active Site Proline Determines the Reducing Power of <i>Staphylococcus aureus</i> Thioredoxin. <i>Journal of Molecular Biology</i> , 2007, 368, 800-811.	2.0	73
87	Purification and crystallization of <i>Vibrio fischeri</i> CcdB and its complexes with fragments of gyrase and CcdA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 356-360.	0.7	5
88	Molecular basis for the preferential cleft recognition by dromedary heavy-chain antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4586-4591.	3.3	541
89	Interplay Between Ion Binding and Catalysis in the Thioredoxin-coupled Arsenate Reductase Family. <i>Journal of Molecular Biology</i> , 2006, 360, 826-838.	2.0	15
90	Interplay Between Metal Binding and cis/trans Isomerization in Legume Lectins: Structural and Thermodynamic Study of <i>P. angolensis</i> Lectin. <i>Journal of Molecular Biology</i> , 2006, 361, 153-167.	2.0	19

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91	Combining site-specific mutagenesis and seeding as a strategy to crystallize 'difficult' proteins: the case of <i>Staphylococcus aureus</i> thioredoxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1255-1258.	0.7	6
92	Structural basis for the recognition of complex-type biantennary oligosaccharides by <i>Pterocarpus angolensis</i> lectin. <i>FEBS Journal</i> , 2006, 273, 2407-2420.	2.2	13
93	Structural basis of carbohydrate recognition by a Man( $\alpha$ 1-2)Man-specific lectin from <i>Bowringia milbraedii</i> . <i>Glycobiology</i> , 2006, 16, 635-640.	1.3	7
94	Toxin-antitoxin modules as bacterial metabolic stress managers. <i>Trends in Biochemical Sciences</i> , 2005, 30, 672-679.	3.7	230
95	Crystallization and crystal manipulation of the <i>Pterocarpus angolensis</i> seed lectin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 685-689.	2.5	5
96	Impact of natural variation in bacterial F17G adhesins on crystallization behaviour. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1149-1159.	2.5	10
97	Crystallization and preliminary X-ray analysis of the Man( $\alpha$ 1-2)Man-specific lectin from <i>Bowringia milbraedii</i> in complex with its carbohydrate ligand. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 931-934.	0.7	1
98	Crystallization of the C-terminal domain of the addiction antidote CcdA in complex with its toxin CcdB. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 949-952.	0.7	4
99	Strong in Vivo Maturation Compensates for Structurally Restricted H3 Loops in Antibody Repertoires. <i>Journal of Biological Chemistry</i> , 2005, 280, 14114-14121.	1.6	52
100	Energetics of Structural Transitions of the Addiction Antitoxin MazE. <i>Journal of Biological Chemistry</i> , 2005, 280, 17397-17407.	1.6	23
101	Molecular Basis of Gyrase Poisoning by the Addiction Toxin CcdB. <i>Journal of Molecular Biology</i> , 2005, 348, 1091-1102.	2.0	130
102	Antigen Binding and Solubility Effects upon the Veneering of a Camel VHH in Framework-2 to Mimic a VH. <i>Journal of Molecular Biology</i> , 2005, 350, 112-125.	2.0	90
103	Identification of a Universal VHH Framework to Graft Non-canonical Antigen-binding Loops of Camel Single-domain Antibodies. <i>Journal of Molecular Biology</i> , 2005, 352, 597-607.	2.0	194
104	<i>Pseudomonas aeruginosa</i> lectin LecB is located in the outer membrane and is involved in biofilm formation. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1313-1323.	0.7	303
105	Chemical Basis for the Affinity Maturation of a Camel Single Domain Antibody. <i>Journal of Biological Chemistry</i> , 2004, 279, 53593-53601.	1.6	66
106	Untangle, a tool for filtering overlapping diffraction patterns from multicrystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 983-984.	2.5	9
107	The structure of a triple mutant of p1258 arsenate reductase from <i>Staphylococcus aureus</i> and its 5-thio-2-nitrobenzoic acid adduct. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1180-1184.	2.5	10
108	Crystallization of CcdB in complex with a GyrA fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1132-1134.	2.5	20

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109	Overexpression, purification and crystallization of bacteriocin LlpA from <i>Pseudomonas</i> sp. BW11M1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1922-1924.	2.5	13
110	The fimbrial adhesin F17-G of enterotoxigenic <i>Escherichia coli</i> has an immunoglobulin-like lectin domain that binds N-acetylglucosamine. <i>Molecular Microbiology</i> , 2004, 49, 705-715.	1.2	89
111	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four V <sub>L</sub> 6 proteins. <i>Journal of Molecular Recognition</i> , 2004, 17, 323-331.	1.1	73
112	Structural Basis of Oligomannose Recognition by the <i>Pterocarpus angolensis</i> Seed Lectin. <i>Journal of Molecular Biology</i> , 2004, 335, 1227-1240.	2.0	48
113	How Thioredoxin can Reduce a Buried Disulphide Bond. <i>Journal of Molecular Biology</i> , 2004, 339, 527-537.	2.0	41
114	Solving the phase problem for carbohydrate-binding proteins using selenium derivatives of their ligands: a case study involving the bacterial F17-G adhesin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1012-1015.	2.5	21
115	Structural Basis of Carbohydrate Recognition by the Lectin LecB from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2003, 331, 861-870.	2.0	117
116	Recognition of the Intrinsically Flexible Addiction Antidote MazE by a Dromedary Single Domain Antibody Fragment. <i>Journal of Biological Chemistry</i> , 2003, 278, 14101-14111.	1.6	31
117	Crystal Structure of <i>Pterocarpus angolensis</i> Lectin in Complex with Glucose, Sucrose, and Turanose. <i>Journal of Biological Chemistry</i> , 2003, 278, 16297-16303.	1.6	50
118	Crystal Structure of the Intrinsically Flexible Addiction Antidote MazE. <i>Journal of Biological Chemistry</i> , 2003, 278, 28252-28257.	1.6	109
119	Isolectins I-A and I-B of <i>Griffonia (Bandeiraea) simplicifolia</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 6608-6614.	1.6	51
120	A Nucleophile Activation Dyad in Ribonucleases. <i>Journal of Biological Chemistry</i> , 2002, 277, 36770-36774.	1.6	19
121	Intricate Interactions within the ccd Plasmid Addiction System. <i>Journal of Biological Chemistry</i> , 2002, 277, 3733-3742.	1.6	69
122	Principles of structures of animal and plant lectins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2002, 1572, 198-208.	1.1	230
123	Weak protein-protein interactions in lectins: the crystal structure of a vegetative lectin from the legume <i>Dolichos biflorus</i> . <i>Journal of Molecular Biology</i> , 2001, 309, 193-201.	2.0	37
124	The contribution of metal ions to the conformational stability of ribonuclease T1. <i>FEBS Journal</i> , 2001, 268, 3993-4000.	0.2	15
125	Zinc/calcium- and cadmium/cadmium-substituted concanavalin A: interplay of metal binding, pH and molecular packing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1569-1576.	2.5	18
126	The Structural Features of Concanavalin A Governing Non-proline Peptide Isomerization. <i>Journal of Biological Chemistry</i> , 2000, 275, 19778-19787.	1.6	67



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127	An Unusual Carbohydrate Binding Site Revealed by the Structures of Two Maackia amurensis Lectins Complexed with Sialic Acid-containing Oligosaccharides. <i>Journal of Biological Chemistry</i> , 2000, 275, 17541-17548.	1.6	125
128	The role of weak protein-protein interactions in multivalent lectin-carbohydrate binding: crystal structure of cross-linked FRIL 1 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 875-883.	2.0	42
129	Structural basis of carbohydrate recognition by lectin II from <i>Ulex europaeus</i> , a protein with a promiscuous carbohydrate-binding site 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 301, 987-1002.	2.0	59
130	Analysis of a Water Mediated Protein-Protein Interactions within RNase T1. <i>Biochemistry</i> , 2000, 39, 6586-6593.	1.2	33
131	The Crystal Structures of $\text{Man}(\alpha 1 \rightarrow 3)\text{Man}(\alpha 1 \rightarrow \text{O})\text{Me}$ and $\text{Man}(\alpha 1 \rightarrow 6)\text{Man}(\alpha 1 \rightarrow \text{O})\text{Me}$ in Complex with Concanavalin A. <i>Journal of Biological Chemistry</i> , 1999, 274, 29188-29195.	1.6	58
132	Novel structures of plant lectins and their complexes with carbohydrates. <i>Current Opinion in Structural Biology</i> , 1999, 9, 572-577.	2.6	73
133	Conserved water molecules in a large family of microbial ribonucleases. , 1999, 36, 117-134.		42
134	Crystal structure of CcdB, a topoisomerase poison from <i>E. coli</i> 1 Edited by T. Richmond. <i>Journal of Molecular Biology</i> , 1999, 285, 1667-1677.	2.0	158
135	Carbohydrate binding, quaternary structure and a novel hydrophobic binding site in two legume lectin oligomers from <i>Dolichos biflorus</i> 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 286, 1161-1177.	2.0	121
136	Dissection of the structural and functional role of a conserved hydration site in RNase T1. <i>Protein Science</i> , 1999, 8, 722-730.	3.1	31
137	Hydrolysis of a slow cyclic thiophosphate substrate of RNase T1 analyzed by time-resolved crystallography. <i>Nature Structural Biology</i> , 1998, 5, 280-283.	9.7	29
138	Legume lectin structure. <i>BBA - Proteins and Proteomics</i> , 1998, 1383, 9-36.	2.1	455
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