

# Remy Loris

## List of Publications by Year in descending order

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155  
papers

7,975  
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46918

47  
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56606

83  
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166  
all docs

166  
docs citations

166  
times ranked

8032  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis for the preferential cleft recognition by dromedary heavy-chain antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4586-4591.	3.3	541
2	Legume lectin structure. BBA - Proteins and Proteomics, 1998, 1383, 9-36.	2.1	455
3	General Strategy to Humanize a Camelid Single-domain Antibody and Identification of a Universal Humanized Nanobody Scaffold. Journal of Biological Chemistry, 2009, 284, 3273-3284.	1.6	441
4	Pseudomonas aeruginosa lectin LecB is located in the outer membrane and is involved in biofilm formation. Microbiology (United Kingdom), 2005, 151, 1313-1323.	0.7	303
5	Principles of structures of animal and plant lectins. Biochimica Et Biophysica Acta - General Subjects, 2002, 1572, 198-208.	1.1	230
6	Toxin-antitoxin modules as bacterial metabolic stress managers. Trends in Biochemical Sciences, 2005, 30, 672-679.	3.7	230
7	Allostery and Intrinsic Disorder Mediate Transcription Regulation by Conditional Cooperativity. Cell, 2010, 142, 101-111.	13.5	226
8	Inhibition and Dispersion of Pseudomonas aeruginosa Biofilms by Glycopeptide Dendrimers Targeting the Fucose-Specific Lectin LecB. Chemistry and Biology, 2008, 15, 1249-1257.	6.2	211
9	Identification of a Universal VHH Framework to Graft Non-canonical Antigen-binding Loops of Camel Single-domain Antibodies. Journal of Molecular Biology, 2005, 352, 597-607.	2.0	194
10	The Fic protein Doc uses an inverted substrate to phosphorylate and inactivate EF-Tu. Nature Chemical Biology, 2013, 9, 811-817.	3.9	159
11	Crystal structure of CcdB, a topoisomerase poison from E. coli 1 Edited by T. Richmond. Journal of Molecular Biology, 1999, 285, 1667-1677.	2.0	158
12	Rejuvenation of CcdB-Poisoned Gyrase by an Intrinsically Disordered Protein Domain. Molecular Cell, 2009, 35, 154-163.	4.5	153
13	Molecular Basis of Gyrase Poisoning by the Addiction Toxin CcdB. Journal of Molecular Biology, 2005, 348, 1091-1102.	2.0	130
14	An Unusual Carbohydrate Binding Site Revealed by the Structures of Two Maackia amurensis Lectins Complexed with Sialic Acid-containing Oligosaccharides. Journal of Biological Chemistry, 2000, 275, 17541-17548.	1.6	125
15	Carbohydrate binding, quaternary structure and a novel hydrophobic binding site in two legume lectin oligomers from Dolichos biflorus 1 Edited by R. Huber. Journal of Molecular Biology, 1999, 286, 1161-1177.	2.0	121
16	Structural Basis of Carbohydrate Recognition by the Lectin LecB from Pseudomonas aeruginosa. Journal of Molecular Biology, 2003, 331, 861-870.	2.0	117
17	New toxins homologous to ParE belonging to three-component toxin-antitoxin systems in Escherichia coli O157:H7. Molecular Microbiology, 2010, 76, 719-732.	1.2	110
18	Crystal Structure of the Intrinsically Flexible Addiction Antidote MazE. Journal of Biological Chemistry, 2003, 278, 28252-28257.	1.6	109

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19	The Crystallographic Structure of Phytohemagglutinin-L. <i>Journal of Biological Chemistry</i> , 1996, 271, 20479-20485.	1.6	106
20	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
21	Structural Basis of Epitope Recognition by Heavy-Chain Camelid Antibodies. <i>Journal of Molecular Biology</i> , 2018, 430, 4369-4386.	2.0	101
22	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
23	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
24	1H NMR Study of the Solution Structure of Ac-AMP2, a Sugar Binding Antimicrobial Protein Isolated from <i>Amaranthus caudatus</i> . <i>Journal of Molecular Biology</i> , 1996, 258, 322-333.	2.0	87
25	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
26	Disorder- and Dynamics-Based Regulatory Mechanisms in Toxin Antitoxin Modules. <i>Chemical Reviews</i> , 2014, 114, 6933-6947.	23.0	82
27	Novel structures of plant lectins and their complexes with carbohydrates. <i>Current Opinion in Structural Biology</i> , 1999, 9, 572-577.	2.6	73
28	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four $\beta$ 6 proteins. <i>Journal of Molecular Recognition</i> , 2004, 17, 323-331.	1.1	73
29	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
30	The Oxidase DsbA Folds a Protein with a Nonconsecutive Disulfide. <i>Journal of Biological Chemistry</i> , 2007, 282, 31302-31307.	1.6	71
31	Intricate Interactions within the <i>ccd</i> Plasmid Addiction System. <i>Journal of Biological Chemistry</i> , 2002, 277, 3733-3742.	1.6	69
32	NMR, Molecular Modeling, and Crystallographic Studies of Lentil Lectin-Sucrose Interaction. <i>Journal of Biological Chemistry</i> , 1995, 270, 25619-25628.	1.6	68
33	The Structural Features of Concanavalin A Governing Non-proline Peptide Isomerization. <i>Journal of Biological Chemistry</i> , 2000, 275, 19778-19787.	1.6	67
34	<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
35	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
36	A Structure of the Complex between Concanavalin A and Methyl-3,6-di-O-( $\beta$ -D-mannopyranosyl)- $\beta$ -D-mannopyranoside Reveals Two Binding Modes. <i>Journal of Biological Chemistry</i> , 1996, 271, 30614-30618.	1.6	65

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37	Crystal structure determination and refinement at 2.3-Å resolution of the lentil lectin. <i>Biochemistry</i> , 1993, 32, 8772-8781.	1.2	64
38	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
39	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
40	Sequential Structural Changes upon Zinc and Calcium Binding to Metal-free Concanavalin A. <i>Journal of Biological Chemistry</i> , 1996, 271, 16144-16150.	1.6	60
41	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
42	The Crystal Structures of $\text{Man}(\alpha 1\text{-}3)\text{Man}(\alpha 1\text{-}6)\text{Me}$ and $\text{Man}(\alpha 1\text{-}6)\text{Man}(\alpha 1\text{-}3)\text{Me}$ in Complex with Concanavalin A. <i>Journal of Biological Chemistry</i> , 1999, 274, 29188-29195.	1.6	58
43	Crystallographic structure of metal-free concanavalin A at 2.5 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 510-524.	1.5	57
44	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
45	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
46	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
47	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
48	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
49	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
50	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
51	Substrate Recognition and Activity Regulation of the <i>Escherichia coli</i> mRNA Endonuclease MazF. <i>Journal of Biological Chemistry</i> , 2016, 291, 10950-10960.	1.6	44
52	Ribosome-dependent <i>Vibrio cholerae</i> mRNAase HgB2 is regulated by a $\beta$ -strand sliding mechanism. <i>Nucleic Acids Research</i> , 2017, 45, 4972-4983.	6.5	43
53	Conserved water molecules in a large family of microbial ribonucleases. , 1999, 36, 117-134.		42
54	The role of weak protein-protein interactions in multivalent lectin-carbohydrate binding: crystal structure of cross-linked FRIL 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 299, 875-883.	2.0	42

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55	How Thioredoxin can Reduce a Buried Disulphide Bond. <i>Journal of Molecular Biology</i> , 2004, 339, 527-537.	2.0	41
56	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
57	The monosaccharide binding site of lentil lectin: an X-ray and molecular modelling study. <i>Glycoconjugate Journal</i> , 1994, 11, 507-517.	1.4	39
58	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
59	Phosphorylation decelerates conformational dynamics in bacterial translation elongation factors. <i>Science Advances</i> , 2018, 4, eaap9714.	4.7	37
60	Escherichia coli antitoxin MazE as transcription factor: insights into MazE-DNA binding. <i>Nucleic Acids Research</i> , 2015, 43, 1241-1256.	6.5	35
61	An intrinsically disordered entropic switch determines allostery in Phd-Doc regulation. <i>Nature Chemical Biology</i> , 2016, 12, 490-496.	3.9	35
62	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
63	Analysis of a Water Mediated Protein-Protein Interactions within RNase T1. <i>Biochemistry</i> , 2000, 39, 6586-6593.	1.2	33
64	Structural Determinants for Activity and Specificity of the Bacterial Toxin LlpA. <i>PLoS Pathogens</i> , 2013, 9, e1003199.	2.1	33
65	Structural and biophysical characterization of Staphylococcus aureus SaMazF shows conservation of functional dynamics. <i>Nucleic Acids Research</i> , 2014, 42, 6709-6725.	6.5	33
66	Crystal Structure of Arcelin-5, a Lectin-like Defense Protein from <i>Phaseolus vulgaris</i> . <i>Journal of Biological Chemistry</i> , 1996, 271, 32796-32802.	1.6	32
67	A nanobody modulates the p53 transcriptional program without perturbing its functional architecture. <i>Nucleic Acids Research</i> , 2014, 42, 12928-12938.	6.5	32
68	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
69	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
70	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
71	Molecular architecture of the endocytic TPLATE complex. <i>Science Advances</i> , 2021, 7, .	4.7	31
72	Structural analysis of two crystal forms of lentil lectin at 1.8 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 330-346.	1.5	30

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73	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
74	Molecular mechanism governing ratio-dependent transcription regulation in the <i>ccdAB</i> operon. <i>Nucleic Acids Research</i> , 2017, 45, 2937-2950.	6.5	29
75	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
76	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
77	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
78	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
79	Driving Forces of Gyrase Recognition by the Addiction Toxin CcdB. <i>Journal of Biological Chemistry</i> , 2009, 284, 20002-20010.	1.6	26
80	<i>Arabidopsis</i> casein kinase 2 triggers stem cell exhaustion under Al toxicity and phosphate deficiency through activating the DNA damage response pathway. <i>Plant Cell</i> , 2021, 33, 1361-1380.	3.1	26
81	Arc self-association and formation of virus-like capsids are mediated by an N-terminal helical coil motif. <i>FEBS Journal</i> , 2021, 288, 2930-2955.	2.2	25
82	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
83	Energetics of Structural Transitions of the Addiction Antitoxin MazE. <i>Journal of Biological Chemistry</i> , 2005, 280, 17397-17407.	1.6	23
84	Coupling of Domain Swapping to Kinetic Stability in a Thioredoxin Mutant. <i>Journal of Molecular Biology</i> , 2009, 385, 1590-1599.	2.0	23
85	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
86	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
87	Crystallization of CcdB in complex with a GyrA fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1132-1134.	2.5	20
88	MMBL proteins: from lectin to bacteriocin. <i>Biochemical Society Transactions</i> , 2012, 40, 1553-1559.	1.6	20
89	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
90	Prokaryote toxin-antitoxin modules: Complex regulation of an unclear function. <i>Protein Science</i> , 2021, 30, 1103-1113.	3.1	20

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91	A Nucleophile Activation Dyad in Ribonucleases. <i>Journal of Biological Chemistry</i> , 2002, 277, 36770-36774.	1.6	19
92	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
93	How a Plant Lectin Recognizes High Mannose Oligosaccharides. <i>Plant Physiology</i> , 2007, 144, 1733-1741.	2.3	19
94	Structural Features of the Legume Lectins.. <i>Trends in Glycoscience and Glycotechnology</i> , 1998, 10, 349-360.	0.0	18
95	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
96	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
97	Purification, Circular Dichroism Analysis, Crystallization and Preliminary X-ray Diffraction Analysis of the F Plasmid CcdB Killer Protein. <i>Journal of Molecular Biology</i> , 1993, 231, 513-515.	2.0	16
98	Structural and Thermodynamic Characterization of <i>Vibrio fischeri</i> CcdB. <i>Journal of Biological Chemistry</i> , 2010, 285, 5606-5613.	1.6	16
99	Antibacterial activity of a lectin-like <i>Burkholderia cenocepacia</i> protein. <i>MicrobiologyOpen</i> , 2013, 2, 566-575.	1.2	16
100	The contribution of metal ions to the conformational stability of ribonuclease T1. <i>FEBS Journal</i> , 2001, 268, 3993-4000.	0.2	15
101	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
102	Alternative interactions define gyrase specificity in the CcdB family. <i>Molecular Microbiology</i> , 2012, 84, 965-978.	1.2	15
103	A catalytic function for the structurally conserved residue Phe 100 of ribonuclease T <sub>1</sub> . <i>Protein Science</i> , 1996, 5, 1523-1530.	3.1	14
104	A nanobody toolbox targeting dimeric coiled-coil modules for functionalization of designed protein origami structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
105	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
106	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
107	Bistable Expression of a Toxin-Antitoxin System Located in a Cryptic Prophage of <i>Escherichia coli</i> O157:H7. <i>MBio</i> , 2021, 12, e0294721.	1.8	13
108	The sequence-ensemble relationship in fuzzy protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12

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109	Structure of the Complete Dimeric Human GDAP1 Core Domain Provides Insights into Ligand Binding and Clustering of Disease Mutations. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 631232.	1.6	11
110	The structure of a triple mutant of pI258 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
111	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
112	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
113	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
114	Crystal and solution structure of NDRG1, a membrane-binding protein linked to myelination and tumour suppression. <i>FEBS Journal</i> , 2021, 288, 3507-3529.	2.2	10
115	Two crystal forms of the lentil lectin diffract to high resolution. <i>Journal of Molecular Biology</i> , 1992, 223, 579-581.	2.0	9
116	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
117	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
118	The ParE-PaaA2 toxin-antitoxin complex from <i>Escherichia coli</i> O157 forms a heterododecamer in solution and in the crystal. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 724-729.	0.7	9
119	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
120	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
121	Purification, crystallization, and preliminary X-ray studies on the rhizome lectin from stinging nettle and its complex with N <sup>2</sup> -triacetylchitotriose. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 205-208.	1.5	7
122	Structural basis of carbohydrate recognition by a Man(1-2)Man-specific lectin from <i>Bowringia milbraedii</i> . <i>Glycobiology</i> , 2006, 16, 635-640.	1.3	7
123	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
124	Alternative dimerization is required for activity and inhibition of the HEPN ribonuclease RnIA. <i>Nucleic Acids Research</i> , 2021, 49, 7164-7178.	6.5	6
125	Structural insights into Charcot-Marie-Tooth disease-linked mutations in human GDAP1. <i>FEBS Open Bio</i> , 2022, 12, 1306-1324.	1.0	6
126	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



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127	Purification and crystallization of <i>Vibrio fischeri</i> CcdB and its complexes with fragments of gyrase and CcdA. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 356-360.	0.7	5
128	Energetics of MazG Unfolding in Correlation with Its Structural Features. Journal of Molecular Biology, 2009, 392, 63-74.	2.0	5
129	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N backbone and side-chain chemical shift assignment of the staphylococcal MazF mRNA interferase. Biomolecular NMR Assignments, 2011, 5, 157-160.	0.4	5
130	Crystallization of the <i>Staphylococcus aureus</i> MazF mRNA interferase. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 386-389.	0.7	5
131	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
132	High-affinity anti-Arc nanobodies provide tools for structural and functional studies. PLoS ONE, 2022, 17, e0269281.	1.1	5
133	Crystallization of the C-terminal domain of the addiction antidote CcdA in complex with its toxin CcdB. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 949-952.	0.7	4
134	Crystallization and preliminary crystallographic studies of the recombinant L-N-carbamoylase from <i>Geobacillus stearothermophilus</i> CECT43. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 1135-1138.	0.7	4
135	Purification and crystallization of Phd, the antitoxin of the <i>phd/doc</i> operon. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 167-171.	0.7	4
136	Computational Methods to Model Persistence. Methods in Molecular Biology, 2016, 1333, 207-240.	0.4	4
137	Thermodynamic Stability of the Transcription Regulator PaaR2 from <i>Escherichia coli</i> O157:H7. Biophysical Journal, 2019, 116, 1420-1431.	0.2	4
138	Crystallization of two related lectins from the legume plant <i>Dolichos biflorus</i> . Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1446-1449.	2.5	3
139	Structure and substrate specificity determinants of the taurine biosynthetic enzyme cysteine sulphinic acid decarboxylase. Journal of Structural Biology, 2021, 213, 107674.	1.3	3
140	Crystal structure of <i>Arabidopsis thaliana</i> casein kinase 2 $\hat{1}\pm 1$ . Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 182-191.	0.4	3
141	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6 $\hat{S}$ -FCR3 of the <i>Plasmodium falciparum</i> VAR2CSA protein. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 270-274.	0.7	2
142	<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. Biomolecular NMR Assignments, 2014, 8, 145-148.	0.4	2
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