

Remy Loris

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152
papers

6,484
citations

45
h-index

77
g-index

166
ext. papers

7,335
ext. citations

7.3
avg, IF

5.41
L-index

#	Paper	IF	Citations
152	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, 4586-91	11.5	436
151	Legume lectin structure. <i>BBA - Proteins and Proteomics</i> , 1998 , 1383, 9-36		399
150	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	5.4	307
149	<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	2.9	251
148	Toxin-antitoxin modules as bacterial metabolic stress managers. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 672-9	10.3	218
147	Allostery and intrinsic disorder mediate transcription regulation by conditional cooperativity. <i>Cell</i> , 2010 , 142, 101-11	56.2	199
146	Principles of structures of animal and plant lectins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2002 , 1572, 198-208	4	193
145	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, 1249-57		181
144	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	6.5	148
143	The Fic protein Doc uses an inverted substrate to phosphorylate and inactivate EF-Tu. <i>Nature Chemical Biology</i> , 2013 , 9, 811-7	11.7	124
142	Crystal structure of CcdB, a topoisomerase poison from <i>E. coli</i> . <i>Journal of Molecular Biology</i> , 1999 , 285, 1667-77	6.5	119
141	Rejuvenation of CcdB-poisoned gyrase by an intrinsically disordered protein domain. <i>Molecular Cell</i> , 2009 , 35, 154-63	17.6	118
140	Molecular basis of gyrase poisoning by the addiction toxin CcdB. <i>Journal of Molecular Biology</i> , 2005 , 348, 1091-102	6.5	110
139	An unusual carbohydrate binding site revealed by the structures of two <i>Maackia amurensis</i> lectins complexed with sialic acid-containing oligosaccharides. <i>Journal of Biological Chemistry</i> , 2000 , 275, 17541-8	5.4	109
138	Carbohydrate binding, quaternary structure and a novel hydrophobic binding site in two legume lectin oligomers from <i>Dolichos biflorus</i> . <i>Journal of Molecular Biology</i> , 1999 , 286, 1161-77	6.5	108
137	Structural basis of carbohydrate recognition by the lectin LecB from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2003 , 331, 861-70	6.5	103
136	Crystal structure of the intrinsically flexible addiction antidote MazE. <i>Journal of Biological Chemistry</i> , 2003 , 278, 28252-7	5.4	99

135	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, 719-32	4.1	91
134	Doc of prophage P1 is inhibited by its antitoxin partner Phd through fold complementation. <i>Journal of Biological Chemistry</i> , 2008 , 283, 30821-7	5.4	90
133	The crystallographic structure of phytohemagglutinin-L. <i>Journal of Biological Chemistry</i> , 1996 , 271, 20479-85	3.8	88
132	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> , 2003 , 49, 705-15	4.1	80
131	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6 γ -FCR3 of the <i>Plasmodium falciparum</i> VAR2CSA protein. Corrigendum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 1312-1312		78
130	H 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, 322-33	6.5	73
129	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, 112-25	6.5	69
128	Novel structures of plant lectins and their complexes with carbohydrates. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 572-7	8.1	69
127	Cancer predisposing missense and protein truncating BARD1 mutations in non-BRCA1 or BRCA2 breast cancer families. <i>Human Mutation</i> , 2010 , 31, E1175-85	4.7	67
126	Intricate interactions within the ccd plasmid addiction system. <i>Journal of Biological Chemistry</i> , 2002 , 277, 3733-42	5.4	65
125	The conserved active site proline determines the reducing power of <i>Staphylococcus aureus</i> thioredoxin. <i>Journal of Molecular Biology</i> , 2007 , 368, 800-11	6.5	62
124	The oxidase DsbA folds a protein with a nonconsecutive disulfide. <i>Journal of Biological Chemistry</i> , 2007 , 282, 31302-7	5.4	61
123	Structural basis of light chain amyloidogenicity: comparison of the thermodynamic properties, fibrillogenic potential and tertiary structural features of four V λ 6 proteins. <i>Journal of Molecular Recognition</i> , 2004 , 17, 323-31	2.6	60
122	NMR, molecular modeling, and crystallographic studies of lentil lectin-sucrose interaction. <i>Journal of Biological Chemistry</i> , 1995 , 270, 25619-28	5.4	59
121	Disorder- and dynamics-based regulatory mechanisms in toxin-antitoxin modules. <i>Chemical Reviews</i> , 2014 , 114, 6933-47	68.1	58
120	Crystal structure determination and refinement at 2.3-Å resolution of the lentil lectin. <i>Biochemistry</i> , 1993 , 32, 8772-81	3.2	58
119	A structure of the complex between concanavalin A and methyl-3,6-di-O-(α -D-mannopyranosyl)- α -D-mannopyranoside reveals two binding modes. <i>Journal of Biological Chemistry</i> , 1996 , 271, 30614-8	5.4	57
118	The structural features of concanavalin A governing non-proline peptide isomerization. <i>Journal of Biological Chemistry</i> , 2000 , 275, 19778-87	5.4	56

117	Chemical basis for the affinity maturation of a camel single domain antibody. <i>Journal of Biological Chemistry</i> , 2004 , 279, 53593-601	5.4	55
116	<i>Vibrio cholerae</i> ParE2 poisons DNA gyrase via a mechanism distinct from other gyrase inhibitors. <i>Journal of Biological Chemistry</i> , 2010 , 285, 40397-408	5.4	53
115	Structural basis of carbohydrate recognition by lectin II from <i>Ulex europaeus</i> , a protein with a promiscuous carbohydrate-binding site. <i>Journal of Molecular Biology</i> , 2000 , 301, 987-1002	6.5	53
114	Sequential structural changes upon zinc and calcium binding to metal-free concanavalin A. <i>Journal of Biological Chemistry</i> , 1996 , 271, 16144-50	5.4	52
113	Structural Basis of Epitope Recognition by Heavy-Chain Camelid Antibodies. <i>Journal of Molecular Biology</i> , 2018 , 430, 4369-4386	6.5	51
112	Crystallographic structure of metal-free concanavalin A at 2.5 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 510-24	4.2	50
111	The many faces of Fic: structural and functional aspects of Fic enzymes. <i>Trends in Biochemical Sciences</i> , 2014 , 39, 121-9	10.3	49
110	Strong in vivo maturation compensates for structurally restricted H3 loops in antibody repertoires. <i>Journal of Biological Chemistry</i> , 2005 , 280, 14114-21	5.4	48
109	The crystal structures of Man(α 1-3)Man(α 1-O)Me and Man(α 1-6)Man(α 1-O)Me in complex with concanavalin A. <i>Journal of Biological Chemistry</i> , 1999 , 274, 29188-95	5.4	48
108	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	5	46
107	Small-angle X-ray scattering- and nuclear magnetic resonance-derived conformational ensemble of the highly flexible antitoxin PaaA2. <i>Structure</i> , 2014 , 22, 854-65	5.2	44
106	Structural basis of oligomannose recognition by the <i>Pterocarpus angolensis</i> seed lectin. <i>Journal of Molecular Biology</i> , 2004 , 335, 1227-40	6.5	44
105	Isolectins I-A and I-B of <i>Griffonia (Bandeiraea) simplicifolia</i> . Crystal structure of metal-free GS I-B(4) and molecular basis for metal binding and monosaccharide specificity. <i>Journal of Biological Chemistry</i> , 2002 , 277, 6608-14	5.4	44
104	Conserved water molecules in a large family of microbial ribonucleases. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 36, 117-34	4.2	41
103	The role of weak protein-protein interactions in multivalent lectin-carbohydrate binding: crystal structure of cross-linked FRIL. <i>Journal of Molecular Biology</i> , 2000 , 299, 875-83	6.5	40
102	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	8.4	38
101	How thioredoxin can reduce a buried disulphide bond. <i>Journal of Molecular Biology</i> , 2004 , 339, 527-37	6.5	38
100	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	6.5	36

99	Energetic basis of uncoupling folding from binding for an intrinsically disordered protein. <i>Journal of the American Chemical Society</i> , 2013 , 135, 1288-94	16.4	35
98	The monosaccharide binding site of lentil lectin: an X-ray and molecular modelling study. <i>Glycoconjugate Journal</i> , 1994 , 11, 507-17	3	34
97	Structural determinants for activity and specificity of the bacterial toxin LlpA. <i>PLoS Pathogens</i> , 2013 , 9, e1003199	7.6	30
96	Crystal structure of Pterocarpus angolensis lectin in complex with glucose, sucrose, and turanose. <i>Journal of Biological Chemistry</i> , 2003 , 278, 16297-303	5.4	30
95	Recognition of the intrinsically flexible addiction antidote MazE by a dromedary single domain antibody fragment. Structure, thermodynamics of binding, stability, and influence on interactions with DNA. <i>Journal of Biological Chemistry</i> , 2003 , 278, 14101-11	5.4	30
94	Analysis of a water mediated protein-protein interactions within RNase T1. <i>Biochemistry</i> , 2000 , 39, 6586-93	3.2	30
93	Substrate Recognition and Activity Regulation of the Escherichia coli mRNA Endonuclease MazF. <i>Journal of Biological Chemistry</i> , 2016 , 291, 10950-60	5.4	28
92	Dissection of the structural and functional role of a conserved hydration site in RNase T1. <i>Protein Science</i> , 1999 , 8, 722-30	6.3	28
91	Structural and biophysical characterization of Staphylococcus aureus SaMazF shows conservation of functional dynamics. <i>Nucleic Acids Research</i> , 2014 , 42, 6709-25	20.1	27
90	Structural analysis of two crystal forms of lentil lectin at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 20, 330-46	4.2	27
89	Escherichia coli antitoxin MazE as transcription factor: insights into MazE-DNA binding. <i>Nucleic Acids Research</i> , 2015 , 43, 1241-56	20.1	26
88	Hydrolysis of a slow cyclic thiophosphate substrate of RNase T1 analyzed by time-resolved crystallography. <i>Nature Structural Biology</i> , 1998 , 5, 280-3		26
87	Ribosome-dependent Vibrio cholerae mRNAse HigB2 is regulated by a β-strand sliding mechanism. <i>Nucleic Acids Research</i> , 2017 , 45, 4972-4983	20.1	25
86	Driving forces of gyrase recognition by the addiction toxin CcdB. <i>Journal of Biological Chemistry</i> , 2009 , 284, 20002-10	5.4	25
85	Crystal structure of arcelin-5, a lectin-like defense protein from Phaseolus vulgaris. <i>Journal of Biological Chemistry</i> , 1996 , 271, 32796-802	5.4	25
84	An intrinsically disordered entropic switch determines allostery in Phd-Doc regulation. <i>Nature Chemical Biology</i> , 2016 , 12, 490-6	11.7	25
83	Frizzled 7 and PIP2 binding by syntenin PDZ2 domain supports Frizzled 7 trafficking and signalling. <i>Nature Communications</i> , 2016 , 7, 12101	17.4	24
82	Plant lectin-like antibacterial proteins from phytopathogens Pseudomonas syringae and Xanthomonas citri. <i>Environmental Microbiology Reports</i> , 2012 , 4, 373-80	3.7	24

81	A nanobody modulates the p53 transcriptional program without perturbing its functional architecture. <i>Nucleic Acids Research</i> , 2014 , 42, 12928-38	20.1	24
80	Energetics of structural transitions of the addiction antitoxin MazE: is a programmed bacterial cell death dependent on the intrinsically flexible nature of the antitoxins?. <i>Journal of Biological Chemistry</i> , 2005 , 280, 17397-407	5.4	22
79	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, 5978-92	20.1	21
78	A unique hetero-hexadecameric architecture displayed by the Escherichia coli O157 PaaA2-ParE2 antitoxin-toxin complex. <i>Journal of Molecular Biology</i> , 2016 , 428, 1589-603	6.5	20
77	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 14494-14497	16.4	20
76	Crystallization of CcdB in complex with a GyrA fragment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1132-4		20
75	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, 1012-5		20
74	Phosphorylation decelerates conformational dynamics in bacterial translation elongation factors. <i>Science Advances</i> , 2018 , 4, eaap9714	14.3	19
73	Structural Mimicry of Receptor Interaction by Antagonistic Interleukin-6 (IL-6) Antibodies. <i>Journal of Biological Chemistry</i> , 2016 , 291, 13846-54	5.4	19
72	A dual role in regulation and toxicity for the disordered N-terminus of the toxin GraT. <i>Nature Communications</i> , 2019 , 10, 972	17.4	19
71	MMBL proteins: from lectin to bacteriocin. <i>Biochemical Society Transactions</i> , 2012 , 40, 1553-9	5.1	18
70	Interplay between metal binding and cis/trans isomerization in legume lectins: structural and thermodynamic study of P. angolensis lectin. <i>Journal of Molecular Biology</i> , 2006 , 361, 153-67	6.5	17
69	A nucleophile activation dyad in ribonucleases. A combined X-ray crystallographic/ab initio quantum chemical study. <i>Journal of Biological Chemistry</i> , 2002 , 277, 36770-4	5.4	17
68	Molecular mechanism governing ratio-dependent transcription regulation in the ccdAB operon. <i>Nucleic Acids Research</i> , 2017 , 45, 2937-2950	20.1	16
67	Coupling of domain swapping to kinetic stability in a thioredoxin mutant. <i>Journal of Molecular Biology</i> , 2009 , 385, 1590-9	6.5	16
66	How a plant lectin recognizes high mannose oligosaccharides. <i>Plant Physiology</i> , 2007 , 144, 1733-41	6.6	16
65	Structural Features of the Legume Lectins.. <i>Trends in Glycoscience and Glycotechnology</i> , 1998 , 10, 349-360.1		16
64	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, 513-5	6.5	16

63	The contribution of metal ions to the conformational stability of ribonuclease T1: crystal versus solution. <i>FEBS Journal</i> , 2001 , 268, 3993-4000		15
62	Structural and thermodynamic characterization of <i>Vibrio fischeri</i> CcdB. <i>Journal of Biological Chemistry</i> , 2010 , 285, 5606-13	5.4	14
61	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, 1569-76		14
60	A catalytic function for the structurally conserved residue Phe 100 of ribonuclease T1. <i>Protein Science</i> , 1996 , 5, 1523-30	6.3	14
59	Antibacterial activity of a lectin-like <i>Burkholderia cenocepacia</i> protein. <i>MicrobiologyOpen</i> , 2013 , 2, 566-75	5.4	13
58	Interplay between ion binding and catalysis in the thioredoxin-coupled arsenate reductase family. <i>Journal of Molecular Biology</i> , 2006 , 360, 826-38	6.5	13
57	Overexpression, purification and crystallization of bacteriocin LlpA from <i>Pseudomonas</i> sp. BW11M1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1922-4		13
56	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, 459-65	1.1	12
55	Structural basis for the recognition of complex-type biantennary oligosaccharides by <i>Pterocarpus angolensis</i> lectin. <i>FEBS Journal</i> , 2006 , 273, 2407-20	5.7	12
54	Alternative interactions define gyrase specificity in the CcdB family. <i>Molecular Microbiology</i> , 2012 , 84, 965-78	4.1	11
53	An efficient method for the purification of proteins from four distinct toxin-antitoxin modules. <i>Protein Expression and Purification</i> , 2015 , 108, 30-40	2	11
52	Molecular architecture of the endocytic TPLATE complex. <i>Science Advances</i> , 2021 , 7,	14.3	11
51	Mutational and structural analysis of L-N-carbamoylase reveals new insights into a peptidase M20/M25/M40 family member. <i>Journal of Bacteriology</i> , 2012 , 194, 5759-68	3.5	10
50	Impact of natural variation in bacterial F17G adhesins on crystallization behaviour. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1149-59		10
49	Nonspecific base recognition mediated by water bridges and hydrophobic stacking in ribonuclease I from <i>Escherichia coli</i> . <i>Protein Science</i> , 2008 , 17, 681-90	6.3	9
48	Untangle, a tool for filtering overlapping diffraction patterns from multicrystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 983-4		9
47	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, 1180-4		9
46	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	6	9

45	Crystallization of Doc and the Phd-Doc toxin-antitoxin complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 1034-8		8
44	Two crystal forms of the lentil lectin diffract to high resolution. <i>Journal of Molecular Biology</i> , 1992 , 223, 579-81	6.5	8
43	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	5.7	8
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, 34013-23	5.4	7
41	Purification, crystallization, and preliminary X-ray studies on the rhizome lectin from stinging nettle and its complex with NNW"-triacetylchitotriose. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 205-8	4.2	7
40	Arabidopsis 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	11.6	7
39	Hidden States within Disordered Regions of the CcdA Antitoxin Protein. <i>Journal of the American Chemical Society</i> , 2017 , 139, 2693-2701	16.4	6
38	The ParE2-PaaA2 toxin-antitoxin complex from Escherichia coli O157 forms a heterodoecamer in solution and in the crystal. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 724-9		6
37	Structural basis of carbohydrate recognition by a Man(alpha1-2)Man-specific lectin from Bowringia milbraedii. <i>Glycobiology</i> , 2006 , 16, 635-40	5.8	6
36	Crystallization of the HigBA2 toxin-antitoxin complex from Vibrio cholerae. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 1052-9		6
35	¹ H, ¹³ C, and ¹⁵ N backbone and side-chain chemical shift assignment of the staphylococcal MazF mRNA interferase. <i>Biomolecular NMR Assignments</i> , 2011 , 5, 157-60	0.7	5
34	Purification and crystallization of Vibrio fischeri CcdB and its complexes with fragments of gyrase and CcdA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 356-60		5
33	Crystal and solution structure of NDRG1, a membrane-binding protein linked to myelination and tumour suppression. <i>FEBS Journal</i> , 2021 , 288, 3507-3529	5.7	5
32	Energetics of MazG unfolding in correlation with its structural features. <i>Journal of Molecular Biology</i> , 2009 , 392, 63-74	6.5	4
31	Crystallization and preliminary crystallographic studies of the recombinant L-N-carbamoylase from Geobacillus stearothermophilus CECT43. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 1135-8		4
30	Combining site-specific mutagenesis and seeding as a strategy to crystallize difficult proteins: the case of Staphylococcus aureus thioredoxin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 1255-8		4
29	Crystallization and crystal manipulation of the Pterocarpus angolensis seed lectin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 685-9		4
28	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, 949-52		4

27	Prokaryote toxin-antitoxin modules: Complex regulation of an unclear function. <i>Protein Science</i> , 2021 , 30, 1103-1113	6.3	4
26	Thermodynamic Stability of the Transcription Regulator PaaR2 from Escherichia coli O157:H7. <i>Biophysical Journal</i> , 2019 , 116, 1420-1431	2.9	3
25	Crystallization of the Staphylococcus aureus MazF mRNA interferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 386-9		3
24	Purification and crystallization of Phd, the antitoxin of the phd/doc operon. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 167-71		3
23	Computational Methods to Model Persistence. <i>Methods in Molecular Biology</i> , 2016 , 1333, 207-40	1.4	2
22	The Escherichia coli RnlA-RnlB toxin-antitoxin complex: production, characterization and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020 , 76, 31-39	1.1	2
21	Production, biophysical characterization and crystallization of Pseudomonas putida GraA and its complexes with GraT and the graTA operator. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017 , 73, 455-462	1.1	2
20	¹ H, ¹³ C, and ¹⁵ N backbone and side-chain chemical shift assignment of the toxin Doc in the unbound state. <i>Biomolecular NMR Assignments</i> , 2014 , 8, 145-8	0.7	2
19	Production, crystallization and X-ray diffraction analysis of two nanobodies against the Duffy binding-like (DBL) domain DBL6?-FCR3 of the Plasmodium falciparum VAR2CSA protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 270-4		2
18	Crystallization of two related lectins from the legume plant Dolichos biflorus. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1446-9		2
17	Molecular determinants of Arc oligomerization and formation of virus-like capsids		2
16	Crystallization and preliminary X-ray analysis of two variants of the Escherichia coli O157 ParE2-PaaA2 toxin-antitoxin complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1284-91	1.1	1
15	Type II Toxin-Antitoxin Loci: The phd/doc Family 2013 , 157-176		1
14	The Thermodynamic Basis of the Fuzzy Interaction of an Intrinsically Disordered Protein. <i>Angewandte Chemie</i> , 2017 , 129, 14686-14689	3.6	1
13	Crystallization of two operator complexes from the Vibrio cholerae HigBA2 toxin-antitoxin module. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 226-33	1.1	1
12	Sequence-specific ¹ H, ¹⁵ N and ¹³ C resonance assignments of the 23.7-kDa homodimeric toxin CcdB from Vibrio fischeri. <i>Biomolecular NMR Assignments</i> , 2009 , 3, 145-7	0.7	1
11	Crystallization and preliminary X-ray analysis of the Man(alpha1-2)Man-specific lectin from Bowringia mildbraedii in complex with its carbohydrate ligand. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 931-4		1
10	High-affinity nanobodies as tools for structural and functional studies on mammalian Arc		1

9	Crystal structure of Arabidopsis thaliana casein kinase 2 β . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020 , 76, 182-191	1.1	1
8	Bistable Expression of a Toxin-Antitoxin System Located in a Cryptic Prophage of Escherichia coli O157:H7. <i>MBio</i> , 2021 , e0294721	7.8	1
7	Alternative dimerization is required for activity and inhibition of the HEPN ribonuclease RnIA. <i>Nucleic Acids Research</i> , 2021 , 49, 7164-7178	20.1	1
6	Entropic pressure controls the oligomerization of the Vibrio cholerae ParD2 antitoxin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 904-920	5.5	1
5	H, C, and N backbone and side chain chemical shift assignment of YdaS, a monomeric member of the HigA family. <i>Biomolecular NMR Assignments</i> , 2020 , 14, 25-30	0.7	1
4	Structure and substrate specificity determinants of the taurine biosynthetic enzyme cysteine sulphinic acid decarboxylase. <i>Journal of Structural Biology</i> , 2021 , 213, 107674	3.4	1
3	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	5.6	1
2	Structural Features of Lectins and Their Binding Sites413-431		
1	Nanobody-aided crystallization of the transcription regulator PaaR2 from Escherichia coli O157:H7. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 374-384	1.1	