

Derek Logan

List of Publications by Year in descending order

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121
papers

5,125
citations

87888

38
h-index

98798

67
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125
all docs

125
docs citations

125
times ranked

6185
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of activin ligand traps using natural sets of type I and type II TGF β receptors. <i>IScience</i> , 2022, 25, 103590.	4.1	7
2	The engineered CD80 variant fusion therapeutic davoceticept combines checkpoint antagonism with conditional CD28 costimulation for anti-tumor immunity. <i>Nature Communications</i> , 2022, 13, 1790.	12.8	10
3	A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases. <i>Nature Communications</i> , 2022, 13, 2700.	12.8	2
4	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. <i>Nature Communications</i> , 2022, 13, .	12.8	14
5	DutaFabs are engineered therapeutic Fab fragments that can bind two targets simultaneously. <i>Nature Communications</i> , 2021, 12, 708.	12.8	15
6	Entropyâ€“Entropy Compensation between the Protein, Ligand, and Solvent Degrees of Freedom Fine-Tunes Affinity in Ligand Binding to Galectin-3C. <i>Jacs Au</i> , 2021, 1, 484-500.	7.9	17
7	Exploring ligand dynamics in protein crystal structures with ensemble refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1099-1115.	2.3	3
8	Solution Structure of the dATP-Inactivated Class I Ribonucleotide Reductase From <i>Leeuwenhoekiella blandensis</i> by SAXS and Cryo-Electron Microscopy. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 713608.	3.5	2
9	NAD ⁺ pool depletion as a signal for the Rex regulon involved in <i>Streptococcus agalactiae</i> virulence. <i>PLoS Pathogens</i> , 2021, 17, e1009791.	4.7	6
10	Exposing the distinctive modular behavior of β -strands and α -helices in folded proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28775-28783.	7.1	6
11	Interactive model building in neutron macromolecular crystallography. <i>Methods in Enzymology</i> , 2020, 634, 201-224.	1.0	5
12	Current status and future opportunities for serial crystallography at MAX IV Laboratory. <i>Journal of Synchrotron Radiation</i> , 2020, 27, 1095-1102.	2.4	7
13	FragMAX: the fragment-screening platform at the MAX IV Laboratory. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 771-777.	2.3	26
14	Are crystallographic <i>B</i> -factors suitable for calculating protein conformational entropy?. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 18149-18160.	2.8	16
15	Class Id ribonucleotide reductase utilizes a Mn ^{2(IV,III)} cofactor and undergoes large conformational changes on metal loading. <i>Journal of Biological Inorganic Chemistry</i> , 2019, 24, 863-877.	2.6	10
16	Structure and Energetics of Ligandâ€“Fluorine Interactions with Galectinâ€“3 Backbone and Sideâ€“Chain Amides: Insight into Solvation Effects and Multipolar Interactions. <i>ChemMedChem</i> , 2019, 14, 1528-1536.	3.2	24
17	Redox-induced structural changes in the di-iron and di-manganese forms of <i>Bacillus anthracis</i> ribonucleotide reductase subunit NrdF suggest a mechanism for gating of radical access. <i>Journal of Biological Inorganic Chemistry</i> , 2019, 24, 849-861.	2.6	9
18	Substituted polyfluoroaryl interactions with an arginine side chain in galectin-3 are governed by steric-, desolvation and electronic conjugation effects. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 1081-1089.	2.8	14

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19	Structural Basis for YjbH Adaptor-Mediated Recognition of Transcription Factor Spx. <i>Structure</i> , 2019, 27, 923-936.e6.	3.3	16
20	A surface-exposed GH26 β -mannanase from <i>Bacteroides ovatus</i> : Structure, role, and phylogenetic analysis of BoMan26B. <i>Journal of Biological Chemistry</i> , 2019, 294, 9100-9117.	3.4	19
21	MM-131, a bispecific anti-Met/EpCAM mAb, inhibits HGF-dependent and HGF-independent Met signaling through concurrent binding to EpCAM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7533-7542.	7.1	26
22	Structure-based design and in vivo anti-arthritic activity evaluation of a potent dipeptidyl cyclopropyl nitrile inhibitor of cathepsin C. <i>Biochemical Pharmacology</i> , 2019, 164, 349-367.	4.4	21
23	Discovery of three novel sesquiterpene synthases from <i>Streptomyces chartreusis</i> NRRL 3882 and crystal structure of an α -eudesmol synthase. <i>Journal of Biotechnology</i> , 2019, 297, 71-77.	3.8	6
24	Insight into the dimer dissociation process of the <i>Chromobacterium violaceum</i> (S)-selective amine transaminase. <i>Scientific Reports</i> , 2019, 9, 16946.	3.3	8
25	3-Substituted 1-Naphthamidomethyl-C-galactosyls Interact with Two Unique Sub-Sites for High-Affinity and High-Selectivity Inhibition of Galectin-3. <i>Molecules</i> , 2019, 24, 4554.	3.8	5
26	Interplay between Conformational Entropy and Solvation Entropy in Protein-Ligand Binding. <i>Journal of the American Chemical Society</i> , 2019, 141, 2012-2026.	13.7	89
27	Refinement of protein structures using a combination of quantum-mechanical calculations with neutron and X-ray crystallographic data. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 368-380.	2.3	13
28	Hunting down hydrogen: applying neutron macromolecular crystallography to galectins. <i>Biochemist</i> , 2019, 41, 20-23.	0.5	0
29	FragMAX – the new fragment screening facility of the MAX-IV Laboratory. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2019, 75, e38-e38.	0.1	0
30	Elucidation of Hydrogen Bonding Patterns in Ligand-Free, Lactose- and Glycerol-Bound Galectin-3C by Neutron Crystallography to Guide Drug Design. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4412-4420.	6.4	32
31	Structural and Biophysical Characterization of Human EXTL3: Domain Organization, Glycosylation, and Solution Structure. <i>Biochemistry</i> , 2018, 57, 1166-1177.	2.5	7
32	Synthesis of branched and linear 1,4-linked galactan oligosaccharides. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 1157-1162.	2.8	5
33	Systematic Tuning of Fluoro-galectin-3 Interactions Provides Thiodigalactoside Derivatives with Single-Digit nM Affinity and High Selectivity. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 1164-1175.	6.4	76
34	Monosaccharide Derivatives with Low Nanomolar Lectin Affinity and High Selectivity Based on Combined Fluorine-Amide, Phenyl-Arginine, Sulfur-I, and Halogen Bond Interactions. <i>ChemMedChem</i> , 2018, 13, 133-137.	3.2	75
35	Designing interactions by control of protein-ligand complex conformation: tuning arginine-arene interaction geometry for enhanced electrostatic protein-ligand interactions. <i>Chemical Science</i> , 2018, 9, 1014-1021.	7.4	15
36	The Cost of Long Catalytic Loops in Folding and Stability of the ALS-Associated Protein SOD1. <i>Journal of the American Chemical Society</i> , 2018, 140, 16570-16579.	13.7	11

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37	Transaminase-catalyzed Racemization with Potential for Dynamic Kinetic Resolutions. <i>ChemCatChem</i> , 2018, 10, 5012-5018.	3.7	9
38	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. <i>ELife</i> , 2018, 7, .	6.0	40
39	Structural characterization of a novel amino acid decarboxylase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a427-a427.	0.1	0
40	Quantum refinement of X-ray and neutron protein crystal structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e175-e175.	0.1	0
41	Galectin-3: studying role of fluorine interaction to achieve high affinity and selectivity. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, e198-e198.	0.1	0
42	Galactomannan Catabolism Conferred by a Polysaccharide Utilization Locus of <i>Bacteroides ovatus</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 229-243.	3.4	91
43	Crystal structure of β -glucosidase 1A from <i>Thermotoga neapolitana</i> and comparison of active site mutants for hydrolysis of flavonoid glucosides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 872-884.	2.6	7
44	Three-dimensional structures and functional studies of two GH43 arabinofuranosidases from <i>Weissella</i> sp. strain 142 and <i>Lactobacillus Brevis</i> . <i>FEBS Journal</i> , 2017, 284, 2019-2036.	4.7	16
45	Crystal structure of human chondroadherin: solving a difficult molecular-replacement problem using <i>de novo</i> models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 53-63.	2.3	9
46	Cover Image, Volume 85, Issue 5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C4-C4.	2.6	0
47	Cover Image, Volume 85, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, C4.	2.6	0
48	A De Novo Designed Coiled-Coil Peptide with a Reversible pH-Induced Oligomerization Switch. <i>Structure</i> , 2016, 24, 946-955.	3.3	36
49	Structural Mechanism of Allosteric Activity Regulation in a Ribonucleotide Reductase with Double ATP Cones. <i>Structure</i> , 2016, 24, 906-917.	3.3	28
50	Context matters: The importance of dimerization-induced conformation of the LukGH leukocidin of <i>Staphylococcus aureus</i> for the generation of neutralizing antibodies. <i>MAbs</i> , 2016, 8, 1347-1360.	5.2	44
51	Perdeuteration, crystallization, data collection and comparison of five neutron diffraction data sets of complexes of human galectin-3C. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1194-1202.	2.3	15
52	Tricking a Protein To Swap Strands. <i>Journal of the American Chemical Society</i> , 2016, 138, 15571-15579.	18.7	6
53	Cancer Differentiating Agent Hexamethylene Bisacetamide Inhibits BET Bromodomain Proteins. <i>Cancer Research</i> , 2016, 76, 2376-2383.	0.9	15
54	What can we learn about nucleotide metabolism from a thermophilic anaerobic ribonucleotide reductase?. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s231-s232.	0.1	0

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55	The macromolecular crystallography beamlines BioMAX and MicroMAX at the MAX IV laboratory. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s190-s190.	0.1	0
56	Structure-Function Analysis of Heterodimer Formation, Oligomerization, and Receptor Binding of the <i>Staphylococcus aureus</i> Bi-component Toxin LukGH. <i>Journal of Biological Chemistry</i> , 2015, 290, 142-156.	3.4	54
57	The Origin and Evolution of Ribonucleotide Reduction. <i>Life</i> , 2015, 5, 604-636.	2.4	74
58	Status of the crystallography beamlines at the MAX IV Laboratory. <i>European Physical Journal Plus</i> , 2015, 130, 1.	2.6	2
59	Structural Aspects of N-Glycosylations and the C-terminal Region in Human Glypican-1. <i>Journal of Biological Chemistry</i> , 2015, 290, 22991-23008.	3.4	20
60	Neutron Crystallographic Studies Reveal Hydrogen Bond and Water-Mediated Interactions between a Carbohydrate-Binding Module and Its Bound Carbohydrate Ligand. <i>Biochemistry</i> , 2015, 54, 6435-6438.	2.5	14
61	Thermodynamics of protein destabilization in live cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12402-12407.	7.1	187
62	Crystallization, neutron data collection, initial structure refinement and analysis of a xyloglucan heptamer bound to an engineered carbohydrate-binding module from xylanase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1072-1077.	0.8	3
63	The Crystal Structure of <i>Thermotoga maritima</i> Class III Ribonucleotide Reductase Lacks a Radical Cysteine Pre-Positioned in the Active Site. <i>PLoS ONE</i> , 2015, 10, e0128199.	2.5	10
64	An <i>Aspergillus nidulans</i> Î ² -mannanase with high transglycosylation capacity revealed through comparative studies within glycosidase family 5. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 10091-10104.	3.6	42
65	Carbohydrate binding module recognition of xyloglucan defined by polar contacts with branching xyloses and C-H...O interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3466-3475.	2.6	13
66	Improving the diffraction of glypican-1 crystals by controlled dehydration. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C321-C321.	0.1	0
67	The first ribonucleotide reductase without an activating radical cysteine. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1053-C1053.	0.1	0
68	Improvements in the order, isotropy and electron density of glypican-1 crystals by controlled dehydration. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2524-2533.	2.5	11
69	The macromolecular crystallography beamline I911-3 at the MAX IV laboratory. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 648-653.	2.4	42
70	Global structural motions from the strain of a single hydrogen bond. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3829-3834.	7.1	39
71	BioMAX: The Future Macromolecular Crystallography Beamline at MAX IV. <i>Journal of Physics: Conference Series</i> , 2013, 425, 072012.	0.4	7
72	BioMAX: the first MX beamline at MAX IV. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2013, 69, s400-s400.	0.3	0

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73	Trimming Down a Protein Structure to Its Bare Foldons. <i>Journal of Biological Chemistry</i> , 2012, 287, 2731-2738.	3.4	23
74	Crystal Structure of N-Glycosylated Human Glypican-1 Core Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 14040-14051.	3.4	54
75	Structural basis for carbohydrate-binding specificity—A comparative assessment of two engineered carbohydrate-binding modules. <i>Glycobiology</i> , 2012, 22, 948-961.	2.5	35
76	DNA building blocks: keeping control of manufacture. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2012, 47, 50-63.	5.2	212
77	The Carbohydrate-Binding Site in Galectin-3 Is Preorganized To Recognize a Sugarlike Framework of Oxygens: Ultra-High-Resolution Structures and Water Dynamics. <i>Biochemistry</i> , 2012, 51, 296-306.	2.5	137
78	Crystal structures of the <i>Chromobacterium violaceum</i> transaminase reveal major structural rearrangements upon binding of coenzyme PLP. <i>FEBS Journal</i> , 2012, 279, 779-792.	4.7	108
79	The Cassiopeia suite of beamlines at the MAX IV laboratory. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, s147-s147.	0.3	0
80	BioMAX, a multipurpose high-throughput crystallography beamline at MAX IV. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, s147-s147.	0.3	0
81	Small-angle X-ray Scattering Study of a Rex Family Repressor: Conformational Response to NADH and NAD ⁺ Binding in Solution. <i>Journal of Molecular Biology</i> , 2011, 408, 670-683.	4.2	23
82	Closing the circle on ribonucleotide reductases. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 251-253.	8.2	14
83	Implications of the Inability of <i>Listeria monocytogenes</i> EGD-e To Grow Anaerobically Due to a Deletion in the Class III NrdD Ribonucleotide Reductase for Its Use as a Model Laboratory Strain. <i>Journal of Bacteriology</i> , 2011, 193, 2931-2940.	2.2	9
84	High-resolution crystal structures of the flavoprotein NrdI in oxidized and reduced states—an unusual flavodoxin. <i>FEBS Journal</i> , 2010, 277, 4265-4277.	4.7	33
85	Structural Basis for Adenosylcobalamin Activation in AdoCbl-Dependent Ribonucleotide Reductases. <i>ACS Chemical Biology</i> , 2010, 5, 933-942.	3.4	42
86	Folding Catalysis by Transient Coordination of Zn ²⁺ to the Cu Ligands of the ALS-Associated Enzyme Cu/Zn Superoxide Dismutase 1. <i>Journal of the American Chemical Society</i> , 2010, 132, 13495-13504.	13.7	81
87	Structural and Functional Analyses of Î ² -Glucosidase 3B from <i>Thermotoga neapolitana</i> : A Thermostable Three-Domain Representative of Glycoside Hydrolase 3. <i>Journal of Molecular Biology</i> , 2010, 397, 724-739.	4.2	117
88	Phosphorylation of hormone-sensitive lipase by protein kinase A <i>in vitro</i> promotes an increase in its hydrophobic surface area. <i>FEBS Journal</i> , 2009, 276, 4752-4762.	4.7	43
89	Functional features cause misfolding of the ALS-provoking enzyme SOD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9667-9672.	7.1	89
90	Purification, crystallization and preliminary X-ray diffraction analysis of human chondroadherin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 516-519.	0.7	1

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91	Structure and functional properties of the <i>Bacillus subtilis</i> transcriptional repressor Rex. <i>Molecular Microbiology</i> , 2008, 69, 466-478.	2.5	134
92	Ser649 and Ser650 Are the Major Determinants of Protein Kinase A-Mediated Activation of Human Hormone-Sensitive Lipase against Lipid Substrates. <i>PLoS ONE</i> , 2008, 3, e3756.	2.5	49
93	Folding of S6 Structures with Divergent Amino Acid Composition: Pathway Flexibility Within Partly Overlapping Foldons. <i>Journal of Molecular Biology</i> , 2007, 365, 237-248.	4.2	30
94	The Coupling between Disulphide Status, Metallation and Dimer Interface Strength in Cu/Zn Superoxide Dismutase. <i>Journal of Molecular Biology</i> , 2007, 365, 333-342.	4.2	93
95	Expression, purification, crystallization and preliminary X-ray diffraction analysis of <i>Thermotoga neapolitana</i> β -glucosidase B. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 802-806.	0.7	7
96	Modern mRNA Proofreading and Repair: Clues that the Last Universal Common Ancestor Possessed an RNA Genome?. <i>Molecular Biology and Evolution</i> , 2005, 22, 1444-1455.	8.9	74
97	A New Tyrosyl Radical on Phe208 as Ligand to the Diron Center in <i>Escherichia coli</i> Ribonucleotide Reductase, Mutant R2-Y122H. <i>Journal of Biological Chemistry</i> , 2005, 280, 11233-11246.	3.4	13
98	Structural Insights into Fusidic Acid Resistance and Sensitivity in EF-G. <i>Journal of Molecular Biology</i> , 2005, 348, 939-949.	4.2	56
99	Crystal structure of a mutant elongation factor G trapped with a GTP analogue. <i>FEBS Letters</i> , 2005, 579, 4492-4497.	2.8	64
100	The New Macromolecular Crystallography Stations At MAX-lab: The MAD Station. <i>AIP Conference Proceedings</i> , 2004, , .	0.4	10
101	Structural mechanism of allosteric substrate specificity regulation in a ribonucleotide reductase. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1142-1149.	8.2	81
102	Structural Basis for Interactions between Tenascins and Lectican C-Type Lectin Domains. <i>Structure</i> , 2004, 12, 1495-1506.	3.3	113
103	A metal-binding site in the catalytic subunit of anaerobic ribonucleotide reductase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3826-3831.	7.1	29
104	Deoxyribonucleotide synthesis in anaerobic microorganisms: The class III ribonucleotide reductase. <i>Progress in Molecular Biology and Translational Science</i> , 2002, 72, 95-127.	1.9	47
105	The Evolution of the Ribonucleotide Reductases: Much Ado About Oxygen. <i>Journal of Molecular Evolution</i> , 2002, 55, 180-196.	1.8	55
106	Structure and function of the radical enzyme ribonucleotide reductase. <i>Progress in Biophysics and Molecular Biology</i> , 2001, 77, 177-268.	2.9	280
107	Structural Basis for Allosteric Substrate Specificity Regulation in Anaerobic Ribonucleotide Reductases. <i>Structure</i> , 2001, 9, 739-750.	3.3	51
108	A Glycyl Radical Site in the Crystal Structure of a Class III Ribonucleotide Reductase. <i>Science</i> , 1999, 283, 1499-1504.	12.6	188

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109	Crystal Structures of Two Self-Hydroxylating Ribonucleotide Reductase Protein R2 Mutants:Â Structural Basis for the Oxygen-Insertion Step of Hydroxylation Reactions Catalyzed by Diiron Proteinsâ€–. <i>Biochemistry</i> , 1998, 37, 10798-10807.	2.5	50
110	Glycyl-tRNA synthetase from <i>Thermus thermophilus</i> . Wide structural divergence with other prokaryotic glycyl-tRNA synthetases and functional inter-relation with prokaryotic and eukaryotic glycylation systems. <i>FEBS Journal</i> , 1998, 251, 744-757.	0.2	29
111	Kinetics of Transient Radicals in <i>Escherichia coli</i> Ribonucleotide Reductase. <i>Journal of Biological Chemistry</i> , 1997, 272, 10414-10421.	3.4	29
112	Crystal structure of reduced protein R2 of ribonucleotide reductase: the structural basis for oxygen activation at a dinuclear iron site. <i>Structure</i> , 1996, 4, 1053-1064.	3.3	277
113	Virus Crystallography. , 1996, 56, 319-364.		2
114	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. <i>Structure</i> , 1995, 3, 571-580.	3.3	77
115	Crystal structure of glycyl-tRNA synthetase from <i>Thermus thermophilus</i> .. <i>EMBO Journal</i> , 1995, 14, 4156-4167.	7.8	119
116	Crystal structure of glycyl-tRNA synthetase from <i>Thermus thermophilus</i> . <i>EMBO Journal</i> , 1995, 14, 4156-67.	7.8	39
117	Crystallisation of the Glycyl-tRNA Synthetase from <i>Thermus thermophilus</i> and Initial Crystallographic Data. <i>Journal of Molecular Biology</i> , 1994, 241, 732-735.	4.2	12
118	Structure of a major immunogenic site on foot-and-mouth disease virus. <i>Nature</i> , 1993, 362, 566-568.	27.8	360
119	Structural and kinetic features of crystal growth inhibition: adipic acid growing in the presence of n-alkanoic acids. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1992, 88, 3461.	1.7	42
120	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1992, 228, 1263-1268.	4.2	23
121	Structural and serological evidence for a novel mechanism of antigenic variation in foot-and-mouth disease virus. <i>Nature</i> , 1990, 347, 569-572.	27.8	216