

Catherine L Lawson

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

5,198
citations

117625

34
h-index

91884

69
g-index

75
all docs

75
docs citations

75
times ranked

5221
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
2	Evolution of standardization and dissemination of cryo-EM structures and data jointly by the community, PDB, and EMDB. <i>Journal of Biological Chemistry</i> , 2021, 296, 100560.	3.4	18
3	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	19.0	73
4	Guest-protein incorporation into solvent channels of a protein host crystal (hostal). <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 471-485.	2.3	1
5	Crystal structures of Val58Ile tryptophan repressor in a domain-swapped array in the presence and absence of L-tryptophan. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 215-225.	0.8	0
6	Cryo-EM targets in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1949-1958.	2.6	11
7	New system for archiving integrative structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1486-1496.	2.3	22
8	The RNA Polymerase $\hat{\pm}$ Subunit Recognizes the DNA Shape of the Upstream Promoter Element. <i>Biochemistry</i> , 2020, 59, 4523-4532.	2.5	12
9	Evolving data standards for cryo-EM structures. <i>Structural Dynamics</i> , 2020, 7, 014701.	2.3	26
10	The data universe of structural biology. <i>IUCr</i> , 2020, 7, 630-638.	2.2	16
11	Cryo-electron microscopy targets in CASP13: Overview and evaluation of results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1128-1140.	2.6	21
12	Assessment of protein assembly prediction in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 247-256.	2.6	54
13	Assessment of model accuracy estimations in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 345-360.	2.6	61
14	Critical assessment of methods of protein structure prediction (CASP) Round XII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 7-15.	2.6	296
15	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. <i>Data in Brief</i> , 2018, 20, 1629-1638.	1.0	5
16	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	45
17	Anticipating innovations in structural biology. <i>Quarterly Reviews of Biophysics</i> , 2018, 51, e8.	5.7	6
18	Evaluation system and web infrastructure for the second cryo-EM model challenge. <i>Journal of Structural Biology</i> , 2018, 204, 96-108.	2.8	11

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19	New online curriculum: the PDB pipeline and data archiving. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a243-a243.	0.1	0
20	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	3.3	130
21	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
22	Databases and Archiving for CryoEM. <i>Methods in Enzymology</i> , 2016, 579, 393-412.	1.0	27
23	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <sc>CASP</sc> 11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 349-369.	2.6	63
24	<sc>CASP</sc> 11 statistics and the prediction center evaluation system. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 15-19.	2.6	42
25	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
26	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
27	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	8.2	47
28	Structure of catabolite activator protein with cobalt(II) and sulfate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 560-563.	0.8	4
29	CASP prediction center infrastructure and evaluation measures in CASP10 and CASP ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 7-13.	2.6	91
30	Trendspotting in the Protein Data Bank. <i>FEBS Letters</i> , 2013, 587, 1036-1045.	2.8	74
31	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	8.2	49
32	Environmentâ€dependent longâ€range structural distortion in a temperatureâ€sensitive point mutant. <i>Protein Science</i> , 2012, 21, 63-74.	7.6	2
33	The 2010 cryoâ€m modeling challenge. <i>Biopolymers</i> , 2012, 97, 651-654.	2.4	22
34	Evaluation of model quality predictions in CASP9. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 91-106.	2.6	83
35	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011, 39, D456-D464.	14.5	246
36	Structure of the<i>Escherichia coli</i> RNA polymerase $\hat{\pm}$ subunit C-terminal domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 806-812.	2.5	10

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37	Unified Data Resource for Cryo-EM. <i>Methods in Enzymology</i> , 2010, 483, 73-90.	1.0	7
38	Structure-Function Investigation of Vsp Serotypes of the Spirochete <i>Borrelia hermsii</i> . <i>PLoS ONE</i> , 2009, 4, e7597.	2.5	15
39	Three-dimensional EM structure of an intact activator-dependent transcription initiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19830-19835.	7.1	76
40	Signatures of Protein-DNA Recognition in Free DNA Binding Sites. <i>Journal of Molecular Biology</i> , 2009, 386, 1054-1065.	4.2	40
41	Representation of viruses in the remediated PDB archive. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 874-882.	2.5	35
42	Chapter 4. Indirect Readout of DNA Sequence by Proteins. <i>RSC Biomolecular Sciences</i> , 2008, , 66-90.	0.4	12
43	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , 2007, 36, D426-D433.	14.5	136
44	Indirect Readout of DNA Sequence at the Primary-kink Site in the CAP-DNA Complex: Recognition of Pyrimidine-Purine and Purine-Purine Steps. <i>Journal of Molecular Biology</i> , 2006, 357, 173-183.	4.2	43
45	Residual Brain Infection in Relapsing-Fever Borreliosis. <i>Journal of Infectious Diseases</i> , 2006, 193, 1451-1458.	4.0	26
46	Crystal Structure of Neurotropism-Associated Variable Surface Protein 1 (Vsp1) of <i>Borrelia turicatae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4522-4530.	2.2	19
47	Structural Investigation of <i>Borrelia burgdorferi</i> OspB, a BactericidalFab Target. <i>Journal of Biological Chemistry</i> , 2005, 280, 17363-17370.	3.4	30
48	<i>E. coli</i> trp Repressor Forms a Domain-Swapped Array in Aqueous Alcohol. <i>Structure</i> , 2004, 12, 1099-1108.	3.3	13
49	Catabolite activator protein: DNA binding and transcription activation. <i>Current Opinion in Structural Biology</i> , 2004, 14, 10-20.	5.7	291
50	A structure-based method for identifying DNA-binding proteins and their sites of DNA-interaction. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 255-265.	1.2	1
51	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	2.6	27
52	Biophysical characterization of natural and mutant fluorescent proteins cloned from zooxanthellate corals. <i>FEBS Letters</i> , 2004, 570, 175-183.	2.8	15
53	Crystals of trp repressor suitable for high-resolution neutron Laue diffraction studies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 136-138.	2.5	6
54	Structural Basis of Transcription Activation: The CAP-alpha CTD-DNA Complex. <i>Science</i> , 2002, 297, 1562-1566.	12.6	234

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55	Approaches toward the Directed Design of a Vaccine against <i>Borrelia burgdorferi</i> . <i>Journal of Infectious Diseases</i> , 2002, 185, S46-S51.	4.0	22
56	Structural Conservation of Neurotropism-associated VspA within the Variable <i>Borrelia</i> Vsp-OspC Lipoprotein Family. <i>Journal of Biological Chemistry</i> , 2001, 276, 457-463.	3.4	49
57	Structural identification of a key protective B-cell epitope in lyme disease antigen OspA 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 302, 1153-1164.	4.2	59
58	Model for lentivirus capsid core assembly based on crystal dimers of EIAV p26. <i>Journal of Molecular Biology</i> , 1999, 286, 83-93.	4.2	107
59	An atomic view of the L-tryptophan binding site of trp repressor. <i>Nature Structural Biology</i> , 1996, 3, 986-987.	9.7	8
60	Site-Directed Mutations in Tyrosine 195 of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251 Affect Activity and Product Specificity. <i>Biochemistry</i> , 1995, 34, 3368-3376.	2.5	146
61	Crystallization and Preliminary X-Ray Analysis of <i>Borrelia burgdorferi</i> Outer Surface Protein A (OspA) Complexed with a Murine Monoclonal Antibody Fab Fragment. <i>Journal of Structural Biology</i> , 1995, 115, 335-337.	2.8	16
62	Nucleotide Sequence and X-ray Structure of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251 in a Maltose-dependent Crystal Form. <i>Journal of Molecular Biology</i> , 1994, 236, 590-600.	4.2	228
63	The tryptophan repressor sequence is highly conserved among the <i>Enterobacteriaceae</i> . <i>Nucleic Acids Research</i> , 1994, 22, 1821-1829.	14.5	19
64	Tandem binding in crystals of a trp repressor/operator half-site complex. <i>Nature</i> , 1993, 366, 178-182.	27.8	163
65	Cocrystals of <i>Escherichia coli</i> trp Repressor Bound to an Alternative Operator DNA Sequence. <i>Journal of Molecular Biology</i> , 1993, 234, 496-498.	4.2	11
66	Maltodextrin-dependent crystallization of cyclomaltodextrin gluconotransferase from <i>Bacillus circulans</i> . <i>Journal of Molecular Biology</i> , 1990, 214, 807-809.	4.2	17
67	Use of electron microscopy in the examination of lattice defects in crystals of alcohol oxidase. <i>FEBS Letters</i> , 1989, 244, 213-216.	2.8	14
68	Flexibility of the DNA-binding domains of trp repressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 18-31.	2.6	142
69	The structure of trp pseudorepressor at 1.65Å... shows why indole propionate acts as a trp 'inducer'. <i>Nature</i> , 1988, 333, 869-871.	27.8	55
70	The three-dimensional structure of trp repressor. <i>Nature</i> , 1985, 317, 782-786.	27.8	386