

Catherine L Lawson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3957313/publications.pdf>

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	The three-dimensional structure of trp repressor. <i>Nature</i> , 1985, 317, 782-786.	27.8	386
2	Critical assessment of methods of protein structure prediction (CASP)â€”Round XII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 7-15.	2.6	296
3	Catabolite activator protein: DNA binding and transcription activation. <i>Current Opinion in Structural Biology</i> , 2004, 14, 10-20.	5.7	291
4	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011, 39, D456-D464.	14.5	246
5	Structural Basis of Transcription Activation: The CAP-alpha CTD-DNA Complex. <i>Science</i> , 2002, 297, 1562-1566.	12.6	234
6	EMDataBank unified data resource for 3DEM. <i>Nucleic Acids Research</i> , 2016, 44, D396-D403.	14.5	230
7	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
8	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
9	Tandem binding in crystals of a trp repressor/operator half-site complex. <i>Nature</i> , 1993, 366, 178-182.	27.8	163
10	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
11	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
12	Flexibility of the DNA-binding domains of trp repressor. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 18-31.	2.6	142
13	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , 2007, 36, D426-D433.	14.5	136
14	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
15	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
16	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
17	Evaluation of model quality predictions in CASP9. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 91-106.	2.6	83
18	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

#	ARTICLE	IF	CITATIONS
19	Trendspotting in the Protein Data Bank. FEBS Letters, 2013, 587, 1036-1045.	2.8	74
20	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
21	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <sc>CASP</sc>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 349-369.	2.6	63
22	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	2.6	61
23	Structural identification of a key protective B-cell epitope in lyme disease antigen OspA 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 302, 1153-1164.	4.2	59
24	The structure of trp pseudorepressor at 1.65Å... shows why indole propionate acts as a trp 'inducer'. Nature, 1988, 333, 869-871.	27.8	55
25	Assessment of protein assembly prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 247-256.	2.6	54
26	Structural Conservation of Neurotropism-associated VspA within the Variable Borrelia Vsp-OspC Lipoprotein Family. Journal of Biological Chemistry, 2001, 276, 457-463.	3.4	49
27	Data management challenges in three-dimensional EM. Nature Structural and Molecular Biology, 2012, 19, 1203-1207.	8.2	49
28	A 3D cellular context for the macromolecular world. Nature Structural and Molecular Biology, 2014, 21, 841-845.	8.2	47
29	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	45
30	Indirect Readout of DNA Sequence at the Primary-kink Site in the CAP-DNA Complex: Recognition of Pyrimidine-Purine and Purine-Purine Steps. Journal of Molecular Biology, 2006, 357, 173-183.	4.2	43
31	<sc>CASP</sc>11 statistics and the prediction center evaluation system. Proteins: Structure, Function and Bioinformatics, 2016, 84, 15-19.	2.6	42
32	Signatures of Protein-DNA Recognition in Free DNA Binding Sites. Journal of Molecular Biology, 2009, 386, 1054-1065.	4.2	40
33	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. Journal of Molecular Biology, 2022, 434, 167599.	4.2	39
34	Representation of viruses in the remediated PDB archive. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 874-882.	2.5	35
35	Structural Investigation of Borrelia burgdorferi OspB, a BactericidalFab Target. Journal of Biological Chemistry, 2005, 280, 17363-17370.	3.4	30
36	Design of a data model for developing laboratory information management and analysis systems for protein production. Proteins: Structure, Function and Bioinformatics, 2004, 58, 278-284.	2.6	27

#	ARTICLE	IF	CITATIONS
37	Databases and Archiving for CryoEM. <i>Methods in Enzymology</i> , 2016, 579, 393-412.	1.0	27
38	Residual Brain Infection in Relapsingâ€Fever Borreliosis. <i>Journal of Infectious Diseases</i> , 2006, 193, 1451-1458.	4.0	26
39	Evolving data standards for cryo-EM structures. <i>Structural Dynamics</i> , 2020, 7, 014701.	2.3	26
40	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
41	The 2010 cryoâ€m modeling challenge. <i>Biopolymers</i> , 2012, 97, 651-654.	2.4	22
42	New system for archiving integrative structures. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1486-1496.	2.3	22
43	Cryoâ€electron microscopy targets in CASP13: Overview and evaluation of results. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1128-1140.	2.6	21
44	The tryptophan repressor sequence is highly conserved among the <i>Enterobacteriaceae</i> . <i>Nucleic Acids Research</i> , 1994, 22, 1821-1829.	14.5	19
45	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
46	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
47	Maltodextrin-dependent crystallization of cyclomaltodextrin glucanotransferase from <i>Bacillus circulans</i> . <i>Journal of Molecular Biology</i> , 1990, 214, 807-809.	4.2	17
48	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
49	The data universe of structural biology. <i>IUCr</i> , 2020, 7, 630-638.	2.2	16
50	Biophysical characterization of natural and mutant fluorescent proteins cloned from zooxanthellate corals. <i>FEBS Letters</i> , 2004, 570, 175-183.	2.8	15
51	Structure-Function Investigation of Vsp Serotypes of the Spirochete <i>Borrelia hermsii</i> . <i>PLoS ONE</i> , 2009, 4, e7597.	2.5	15
52	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
53	<i>E. coli</i> trp Repressor Forms a Domain-Swapped Array in Aqueous Alcohol. <i>Structure</i> , 2004, 12, 1099-1108.	3.3	13
54	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

#	ARTICLE	IF	CITATIONS
55	Chapter 4. Indirect Readout of DNA Sequence by Proteins. RSC Biomolecular Sciences, 2008, , 66-90.	0.4	12
56	Cocrystals of Escherichia coli trp Repressor Bound to an Alternative Operator DNA Sequence. Journal of Molecular Biology, 1993, 234, 496-498.	4.2	11
57	Evaluation system and web infrastructure for the second cryo-EM model challenge. Journal of Structural Biology, 2018, 204, 96-108.	2.8	11
58	Cryo-EM targets in CASP14. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1949-1958.	2.6	11
59	Structure of the Escherichia coli RNA polymerase β subunit C-terminal domain. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 806-812.	2.5	10
60	An atomic view of the L-tryptophan binding site of trp repressor. Nature Structural Biology, 1996, 3, 986-987.	9.7	8
61	Unified Data Resource for Cryo-EM. Methods in Enzymology, 2010, 483, 73-90.	1.0	7
62	Crystals of trp repressor suitable for high-resolution neutron Laue diffraction studies. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 136-138.	2.5	6
63	Anticipating innovations in structural biology. Quarterly Reviews of Biophysics, 2018, 51, e8.	5.7	6
64	Distribution of evaluation scores for the models submitted to the second cryo-EM model challenge. Data in Brief, 2018, 20, 1629-1638.	1.0	5
65	Structure of catabolite activator protein with cobalt(II) and sulfate. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 560-563.	0.8	4
66	Environment-dependent long-range structural distortion in a temperature-sensitive point mutant. Protein Science, 2012, 21, 63-74.	7.6	2
67	A structure-based method for identifying DNA-binding proteins and their sites of DNA-interaction. Journal of Structural and Functional Genomics, 2004, 5, 255-265.	1.2	1
68	Guest-protein incorporation into solvent channels of a protein host crystal (hostal). Acta Crystallographica Section D: Structural Biology, 2021, 77, 471-485.	2.3	1
69	Crystal structures of Val58Ile tryptophan repressor in a domain-swapped array in the presence and absence of L-tryptophan. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 215-225.	0.8	0
70	New online curriculum: the PDB pipeline and data archiving. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a243-a243.	0.1	0