

Matthew J Cuneo

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

1,688
citations

257450

24
h-index

315739

38
g-index

59
all docs

59
docs citations

59
times ranked

2650
citing authors

#	ARTICLE	IF	CITATIONS
1	Capturing snapshots of APE1 processing DNA damage. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 924-931.	8.2	124
2	The suite of small-angle neutron scattering instruments at Oak Ridge National Laboratory. <i>Journal of Applied Crystallography</i> , 2018, 51, 242-248.	4.5	115
3	Programmable Ligand Detection System in Plants through a Synthetic Signal Transduction Pathway. <i>PLoS ONE</i> , 2011, 6, e16292.	2.5	99
4	Interplay of folded domains and the disordered low-complexity domain in mediating hnRNPA1 phase separation. <i>Nucleic Acids Research</i> , 2021, 49, 2931-2945.	14.5	81
5	Oxidation state of the XRCC1 N-terminal domain regulates DNA polymerase β binding affinity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6805-6810.	7.1	67
6	The Macromolecular Neutron Diffractometer MaNDi at the Spallation Neutron Source. <i>Journal of Applied Crystallography</i> , 2015, 48, 1302-1306.	4.5	64
7	The ubiquitin ligase adaptor SPOP in cancer. <i>FEBS Journal</i> , 2019, 286, 3946-3958.	4.7	57
8	The structural basis for partitioning of the XRCC1/DNA ligase III- β BRCT-mediated dimer complexes. <i>Nucleic Acids Research</i> , 2011, 39, 7816-7827.	14.5	56
9	Identification of cognate ligands for the <i>Escherichia coli</i> phnD protein product and engineering of a reagentless fluorescent biosensor for phosphonates. <i>Protein Science</i> , 2006, 15, 1745-1751.	7.6	53
10	Neutron and Atomic Resolution X-ray Structures of a Lytic Polysaccharide Monooxygenase Reveal Copper-Mediated Dioxygen Binding and Evidence for N-Terminal Deprotonation. <i>Biochemistry</i> , 2017, 56, 2529-2532.	2.5	53
11	Der p 5 Crystal Structure Provides Insight into the Group 5 Dust Mite Allergens. <i>Journal of Biological Chemistry</i> , 2010, 285, 25394-25401.	3.4	52
12	Structural studies of the PARP-1 BRCT domain. <i>BMC Structural Biology</i> , 2011, 11, 37.	2.3	41
13	Preventing oxidation of cellular XRCC1 affects PARP-mediated DNA damage responses. <i>DNA Repair</i> , 2013, 12, 774-785.	2.8	40
14	A low-barrier hydrogen bond mediates antibiotic resistance in a noncanonical catalytic triad. <i>Science Advances</i> , 2018, 4, eaas8667.	10.3	40
15	"To Be or Not to Be" Protonated: Atomic Details of Human Carbonic Anhydrase-Clinical Drug Complexes by Neutron Crystallography and Simulation. <i>Structure</i> , 2018, 26, 383-390.e3.	3.3	40
16	Structure-based design of robust glucose biosensors using a <i>Thermotoga maritima</i> periplasmic glucose-binding protein. <i>Protein Science</i> , 2007, 16, 2240-2250.	7.6	39
17	Orthogonal site-specific protein modification by engineering reversible thiol protection mechanisms. <i>Protein Science</i> , 2009, 14, 64-73.	7.6	39
18	The Crystal Structure of a Thermophilic Glucose Binding Protein Reveals Adaptations that Interconvert Mono and Di-saccharide Binding Sites. <i>Journal of Molecular Biology</i> , 2006, 362, 259-270.	4.2	36

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19	drtsans: The data reduction toolkit for small-angle neutron scattering at Oak Ridge National Laboratory. <i>SoftwareX</i> , 2022, 19, 101101.	2.6	32
20	Insight into the Solid Electrolyte Interphase Formation in Bis(fluorosulfonyl)Imide Based Ionic Liquid Electrolytes. <i>Advanced Functional Materials</i> , 2021, 31, 2008708.	14.9	30
21	Identification and Functional Characterization of a Novel Acetylcholine-Binding Protein from the Marine Annelid <i>Capitella teleta</i> . <i>Biochemistry</i> , 2010, 49, 2279-2287.	2.5	28
22	Structural Analysis of a Periplasmic Binding Protein in the Tripartite ATP-independent Transporter Family Reveals a Tetrameric Assembly That May Have a Role in Ligand Transport. <i>Journal of Biological Chemistry</i> , 2008, 283, 32812-32820.	3.4	27
23	Perturbation of bacteriochlorophyll molecules in Fenna-Matthews-Olson protein complexes through mutagenesis of cysteine residues. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1455-1463.	1.0	26
24	The Neutron Macromolecular Crystallography Instruments at Oak Ridge National Laboratory: Advances, Challenges, and Opportunities. <i>Crystals</i> , 2018, 8, 388.	2.2	26
25	Modulating Enzyme Activity by Altering Protein Dynamics with Solvent. <i>Biochemistry</i> , 2018, 57, 4263-4275.	2.5	26
26	Ligand-induced conformational changes in a thermophilic ribose-binding protein. <i>BMC Structural Biology</i> , 2008, 8, 50.	2.3	25
27	Selective unfolding of one Ribonuclease H domain of HIV reverse transcriptase is linked to homodimer formation. <i>Nucleic Acids Research</i> , 2014, 42, 5361-5377.	14.5	25
28	Structural Adaptations that Modulate Monosaccharide, Disaccharide, and Trisaccharide Specificities in Periplasmic Maltose-Binding Proteins. <i>Journal of Molecular Biology</i> , 2009, 389, 157-166.	4.2	24
29	Mutational and biochemical analysis of the DNA-entry nuclease EndA from <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2011, 39, 623-634.	14.5	24
30	Protein extraction into the bicontinuous microemulsion phase of a Water/SDS/pentanol/dodecane Winsor-III system: Effect on nanostructure and protein conformation. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017, 160, 144-153.	5.0	24
31	Structural Analysis of Semi-specific Oligosaccharide Recognition by a Cellulose-binding Protein of <i>Thermotoga maritima</i> Reveals Adaptations for Functional Diversification of the Oligopeptide Periplasmic Binding Protein Fold. <i>Journal of Biological Chemistry</i> , 2009, 284, 33217-33223.	3.4	22
32	Unencumbered Pol II lyase activity in nucleosome core particles. <i>Nucleic Acids Research</i> , 2017, 45, 8901-8915.	14.5	20
33	Differential Substrate Recognition by Maltose Binding Proteins Influenced by Structure and Dynamics. <i>Biochemistry</i> , 2018, 57, 5864-5876.	2.5	20
34	Low-barrier and Canonical Hydrogen Bonds Modulate Activity and Specificity of a Catalytic Triad. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 16260-16266.	13.8	20
35	Homodimerization of the p51 Subunit of HIV-1 Reverse Transcriptase. <i>Biochemistry</i> , 2010, 49, 2821-2833.	2.5	19
36	Structural characterization of the virulence factor Sda1 nuclease from <i>Streptococcus pyogenes</i> . <i>Nucleic Acids Research</i> , 2016, 44, 3946-3957.	14.5	19

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37	Neutron crystallographic studies of T4 lysozyme at cryogenic temperature. <i>Protein Science</i> , 2017, 26, 2098-2104.	7.6	19
38	De novo design of a homo-trimeric amantadine-binding protein. <i>ELife</i> , 2019, 8, .	6.0	18
39	Duplication of Genes in an ATP-binding Cassette Transport System Increases Dynamic Range While Maintaining Ligand Specificity. <i>Journal of Biological Chemistry</i> , 2014, 289, 30090-30100.	3.4	14
40	Periplasmic Binding Protein Dimer Has a Second Allosteric Event Tied to Ligand Binding. <i>Biochemistry</i> , 2017, 56, 5328-5337.	2.5	14
41	On the Case of the Misplaced Hydrogens. <i>ChemBioChem</i> , 2021, 22, 288-297.	2.6	14
42	The backbone structure of the thermophilic <i>Thermoanaerobacter tengcongensis</i> ribose binding protein is essentially identical to its mesophilic <i>E. coli</i> homolog. <i>BMC Structural Biology</i> , 2008, 8, 20.	2.3	11
43	Encoding of Promiscuity in an Aminoglycoside Acetyltransferase. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10218-10227.	6.4	11
44	Molecular details of ligand selectivity determinants in a promiscuous β -glucan periplasmic binding protein. <i>BMC Structural Biology</i> , 2013, 13, 18.	2.3	8
45	Neutron and high-resolution room-temperature X-ray data collection from crystallized lytic polysaccharide monooxygenase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1448-1452.	0.8	8
46	Dynamic nuclear polarization enhanced neutron crystallography: Amplifying hydrogen in biological crystals. <i>Methods in Enzymology</i> , 2020, 634, 153-175.	1.0	8
47	Characterization of the Redox Transition of the XRCC1 N-terminal Domain. <i>Structure</i> , 2014, 22, 1754-1763.	3.3	6
48	A nucleotide-dependent oligomerization of the <i>Escherichia coli</i> replication initiator DnaA requires residue His136 for remodeling of the chromosomal origin. <i>Nucleic Acids Research</i> , 2019, 48, 200-211.	14.5	4
49	Binding of a Soluble <i>meso</i> -Tetraarylporphyrin to Human Galectin-7 Induces Oligomerization and Modulates Its Pro-Apoptotic Activity. <i>Biochemistry</i> , 2020, 59, 4591-4600.	2.5	4
50	Low-Barrier and Canonical Hydrogen Bonds Modulate Activity and Specificity of a Catalytic Triad. <i>Angewandte Chemie</i> , 2019, 131, 16406-16412.	2.0	3
51	Neutron and X-ray analysis of the Fenna-Matthews-Olson photosynthetic antenna complex from <i>Prosthecochloris aestuarii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 171-175.	0.8	3
52	Crystallization and preliminary X-ray diffraction analysis of <i>Hypocrea jecorina</i> Cel7A in two new crystal forms. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 773-776.	0.8	2
53	“Catch and Release”: a Variation of the Archetypal Nucleotidyl Transfer Reaction. <i>ACS Catalysis</i> , 2020, 10, 3548-3555.	11.2	2
54	Oncogenic signaling of RTK fusions becomes more granular. <i>Molecular Cell</i> , 2021, 81, 2504-2506.	9.7	2

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55	Towards cryogenic neutron crystallography on the reduced form of [NiFe]-hydrogenase. Acta Crystallographica Section D: Structural Biology, 2020, 76, 946-953.	2.3	2
56	Oligomerization state and pigment binding strength of the peridininâ€Chl<i>a</i>â€Cp protein. FEBS Letters, 2015, 589, 2713-2719.	2.8	1