Matthew J Cuneo

List of Publications by Year
in descending order

56	1,688	257450	315739
papers	citations	24 h-index	38 g-index

59	59	59	2650
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	drtsans: The data reduction toolkit for small-angle neutron scattering at Oak Ridge National Laboratory. SoftwareX, 2022, 19, 101101.	2.6	32
2	On the Case of the Misplaced Hydrogens. ChemBioChem, 2021, 22, 288-297.	2.6	14
3	Insight into the Solid Electrolyte Interphase Formation in Bis(fluorosulfonyl)Imide Based Ionic Liquid Electrolytes. Advanced Functional Materials, 2021, 31, 2008708.	14.9	30
4	Interplay of folded domains and the disordered low-complexity domain in mediating hnRNPA1 phase separation. Nucleic Acids Research, 2021, 49, 2931-2945.	14.5	81
5	Oncogenic signaling of RTK fusions becomes more granular. Molecular Cell, 2021, 81, 2504-2506.	9.7	2
6	Binding of a Soluble meso-Tetraarylporphyrin to Human Galectin-7 Induces Oligomerization and Modulates Its Pro-Apoptotic Activity. Biochemistry, 2020, 59, 4591-4600.	2.5	4
7	Dynamic nuclear polarization enhanced neutron crystallography: Amplifying hydrogen in biological crystals. Methods in Enzymology, 2020, 634, 153-175.	1.0	8
8	â€œCatch and Releaseâ€: a Variation of the Archetypal Nucleotidyl Transfer Reaction. ACS Catalysis, 2020, 10, 3548-3555.	11.2	2
9	Towards cryogenic neutron crystallography on the reduced form of [NiFe]-hydrogenase. Acta Crystallographica Section D: Structural Biology, 2020, 76, 946-953.	2.3	2
10	Lowâ€Barrier and Canonical Hydrogen Bonds Modulate Activity and Specificity of a Catalytic Triad. Angewandte Chemie, 2019, 131, 16406-16412.	2.0	3
11	Lowâ€Barrier and Canonical Hydrogen Bonds Modulate Activity and Specificity of a Catalytic Triad. Angewandte Chemie - International Edition, 2019, 58, 16260-16266.	13.8	20
12	A nucleotide-dependent oligomerization of the Escherichia coli replication initiator DnaA requires residue His136 for remodeling of the chromosomal origin. Nucleic Acids Research, 2019, 48, 200-211.	14.5	4
13	The ubiquitin ligase adaptor SPOP in cancer. FEBS Journal, 2019, 286, 3946-3958.	4.7	57
14	Neutron and X-ray analysis of the Fennaâ€“Matthewsâ€“Olson photosynthetic antenna complex from Prosthecochloris aestuarii. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 171-175.	0.8	3
15	De novo design of a homo-trimeric amantadine-binding protein. ELife, 2019, 8, .	6.0	18
16	The suite of small-angle neutron scattering instruments at Oak Ridge National Laboratory. Journal of Applied Crystallography, 2018, 51, 242-248.	4.5	115
17	A low-barrier hydrogen bond mediates antibiotic resistance in a noncanonical catalytic triad. Science Advances, 2018, 4, eaas8667.	10.3	40
18	"To Be or Not to Be" Protonated: Atomic Details of Human Carbonic Anhydrase-Clinical Drug Complexes by Neutron Crystallography and Simulation. Structure, 2018, 26, 383-390.e3.	3.3	40

#	Article	IF	Citations
19	The Neutron Macromolecular Crystallography Instruments at Oak Ridge National Laboratory: Advances, Challenges, and Opportunities. Crystals, 2018, 8, 388.	2.2	26
20	Encoding of Promiscuity in an Aminoglycoside Acetyltransferase. Journal of Medicinal Chemistry, 2018, 61, 10218-10227.	6.4	11
21	Differential Substrate Recognition by Maltose Binding Proteins Influenced by Structure and Dynamics. Biochemistry, 2018, 57, 5864-5876.	2.5	20
22	Modulating Enzyme Activity by Altering Protein Dynamics with Solvent. Biochemistry, 2018, 57, 4263-4275.	2.5	26
23	Neutron and Atomic Resolution X-ray Structures of a Lytic Polysaccharide Monooxygenase Reveal Copper-Mediated Dioxygen Binding and Evidence for N-Terminal Deprotonation. Biochemistry, 2017, 56, 2529-2532.	2.5	53
24	Protein extraction into the bicontinuous microemulsion phase of a Water/SDS/pentanol/dodecane winsor-III system: Effect on nanostructure and protein conformation. Colloids and Surfaces B: Biointerfaces, 2017, 160, 144-153.	5.0	24
25	Periplasmic Binding Protein Dimer Has a Second Allosteric Event Tied to Ligand Binding. Biochemistry, 2017, 56, 5328-5337.	2.5	14
26	Neutron crystallographic studies of T4 lysozyme at cryogenic temperature. Protein Science, 2017, 26, 2098-2104.	7.6	19
27	Unencumbered Pol Î² lyase activity in nucleosome core particles. Nucleic Acids Research, 2017, 45, 8901-8915.	14.5	20
28	Perturbation of bacteriochlorophyll molecules in Fennaâ€“Matthewsâ€“Olson protein complexes through mutagenesis of cysteine residues. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 1455-1463.	1.0	26
29	Structural characterization of the virulence factor Sda1 nuclease fromStreptococcus pyogenes. Nucleic Acids Research, 2016, 44, 3946-3957.	14.5	19
30	Oligomerization state and pigment binding strength of the peridininâ€Chlaâ€protein. FEBS Letters, 2015, 589, 2713-2719.	2.8	1
31	Neutron and high-resolution room-temperature X-ray data collection from crystallized lytic polysaccharide monooxygenase. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1448-1452.	0.8	8
32	Capturing snapshots of APE1 processing DNA damage. Nature Structural and Molecular Biology, 2015, 22, 924-931.	8.2	124
33	The Macromolecular Neutron Diffractometer MaNDi at the Spallation Neutron Source. Journal of Applied Crystallography, 2015, 48, 1302-1306.	4.5	64
34	Duplication of Genes in an ATP-binding Cassette Transport System Increases Dynamic Range While Maintaining Ligand Specificity. Journal of Biological Chemistry, 2014, 289, 30090-30100.	3.4	14
35	Characterization of the Redox Transition of the XRCC1 N-terminal Domain. Structure, 2014, 22, 1754-1763.	3.3	6
36	Selective unfolding of one Ribonuclease H domain of HIV reverse transcriptase is linked to homodimer formation. Nucleic Acids Research, 2014, 42, 5361-5377.	14.5	25

#	Article	IF	Citations
37	Crystallization and preliminary X-ray diffraction analysis ofHypocrea jecorinaCel7A in two new crystal forms. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 773-776.	0.8	2
38	Preventing oxidation of cellular XRCC1 affects PARP-mediated DNA damage responses. DNA Repair, 2013, 12, 774-785.	2.8	40
39	Molecular details of ligand selectivity determinants in a promiscuous Î²-glucan periplasmic binding protein. BMC Structural Biology, 2013, 13, 18.	2.3	8
40	Structural studies of the PARP-1 BRCT domain. BMC Structural Biology, 2011, 11, 37.	2.3	41
41	Mutational and biochemical analysis of the DNA-entry nuclease EndA from Streptococcus pneumoniae. Nucleic Acids Research, 2011, 39, 623-634.	14.5	24
42	The structural basis for partitioning of the XRCC1/DNA ligase III-Î± BRCT-mediated dimer complexes. Nucleic Acids Research, 2011, 39, 7816-7827.	14.5	56
43	Programmable Ligand Detection System in Plants through a Synthetic Signal Transduction Pathway. PLoS ONE, 2011, 6, e16292.	2.5	99
44	Der p 5 Crystal Structure Provides Insight into the Group 5 Dust Mite Allergens. Journal of Biological Chemistry, 2010, 285, 25394-25401.	3.4	52
45	Oxidation state of the XRCC1 N-terminal domain regulates DNA polymerase Î² binding affinity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6805-6810.	7.1	67
46	Identification and Functional Characterization of a Novel Acetylcholine-Binding Protein from the Marine Annelid Capitella teleta. Biochemistry, 2010, 49, 2279-2287.	2.5	28
47	Homodimerization of the p51 Subunit of HIV-1 Reverse Transcriptase. Biochemistry, 2010, 49, 2821-2833.	2.5	19
48	Structural Analysis of Semi-specific Oligosaccharide Recognition by a Cellulose-binding Protein of Thermotoga maritima Reveals Adaptations for Functional Diversification of the Oligopeptide Periplasmic Binding Protein Fold. Journal of Biological Chemistry, 2009, 284, 33217-33223.	3.4	22
49	Orthogonal site-specific protein modification by engineering reversible thiol protection mechanisms. Protein Science, 2009, 14, 64-73.	7.6	39
50	Structural Adaptations that Modulate Monosaccharide, Disaccharide, and Trisaccharide Specificities in Periplasmic Maltose-Binding Proteins. Journal of Molecular Biology, 2009, 389, 157-166.	4.2	24
51	The backbone structure of the thermophilic Thermoanaerobacter tengcongensis ribose binding protein is essentially identical to its mesophilic E. coli homolog. BMC Structural Biology, 2008, 8, 20.	2.3	11
52	Ligand-induced conformational changes in a thermophilic ribose-binding protein. BMC Structural Biology, 2008, 8, 50.	2.3	25
53	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. Journal of Biological Chemistry, 2008, 283, 32812-32820.	3.4	27
54	Structureâ€based design of robust glucose biosensors using a Thermotoga maritima periplasmic glucoseâ€binding protein. Protein Science, 2007, 16, 2240-2250.	7.6	39

#	Article	IF	Citations
55	The Crystal Structure of a Thermophilic Glucose Binding Protein Reveals Adaptations that Interconvert Mono and Di-saccharide Binding Sites. Journal of Molecular Biology, 2006, 362, 259-270.	4.2	36
56	Identification of cognate ligands for theEscherichia coli phnDprotein product and engineering of a reagentless fluorescent biosensor for phosphonates. Protein Science, 2006, 15, 1745-1751.	7.6	53