Christopher D Snow

List of Publications by Year
in descending order

63	4,988	159358 30	118652 62
papers	citations	h-index	g-index

64	64	64	4853
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Stabilizing DNAâ€“Protein Co-Crystals via Intra-Crystal Chemical Ligation of the DNA. Crystals, 2022, 12, 49.	1.0	4
2	Conditionally designed luminescent DNA crystals doped by Ln³⁺(Eu³⁺/Tb³⁺) complexes or fluorescent proteins with smart drug sensing property. Journal of Materials Chemistry B, 2022, 10, 6443-6452.	2.9	1
3	Lanthanide (Eu3+/Tb3+)-Loaded Î³-Cyclodextrin Nano-Aggregates for Smart Sensing of the Anticancer Drug Irinotecan. International Journal of Molecular Sciences, 2022, 23, 6597.	1.8	3
4	Smart Wearable Fluorescence Sensing of Bacterial Pathogens and Toxic Contaminants by Eu³⁺-Induced Sodium Alginate/Ag Nanoparticle Aggregates. ACS Applied Nano Materials, 2022, 5, 8393-8403.	2.4	11
5	Measuring interactions of DNA with nanoporous protein crystals by atomic force microscopy. Nanoscale, 2021, 13, 10871-10881.	2.8	6
6	Design of genetically encoded sensors to detect nucleosome ubiquitination in live cells. Journal of Cell Biology, 2021, 220, .	2.3	11
7	Histidine polypeptide-hybridized nanoscale metalâ€“organic framework to sense drug loading/release. Materials and Design, 2021, 205, 109741.	3.3	13
8	Stable Fluorescence of Eu3+ Complex Nanostructures Beneath a Protein Skin for Potential Biometric Recognition. Nanomaterials, 2021, 11, 2462.	1.9	6
9	Near infrared emitting and biocompatible Yb3+-DNA complexes with dual responses to Cu2+ and Fe3+. Optical Materials, 2020, 108, 110157.	1.7	2
10	Porous crystals as scaffolds for structural biology. Current Opinion in Structural Biology, 2020, 60, 85-92.	2.6	16
11	Drug Sensing Protein Crystals Doped with Luminescent Lanthanide Complexes. Crystal Growth and Design, 2019, 19, 5658-5664.	1.4	7
12	Porous protein crystals as scaffolds for enzyme immobilization. Biomaterials Science, 2019, 7, 1898-1904.	2.6	29
13	Advancing biomarkers for anaerobic o-xylene biodegradation via metagenomic analysis of a methanogenic consortium. Applied Microbiology and Biotechnology, 2019, 103, 4177-4192.	1.7	12
14	Protein crystal based materials for nanoscale applications in medicine and biotechnology. Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology, 2019, 11, e1547.	3.3	20
15	Enhancing the Power Conversion Efficiency for Polymer Solar Cells by Incorporating Luminescent Nanosolid Micelles as Light Converter. ACS Applied Energy Materials, 2018, 1, 1445-1454.	2.5	5
16	Characterizing the Cytocompatibility of Various Cross-Linking Chemistries for the Production of Biostable Large-Pore Protein Crystal Materials. ACS Biomaterials Science and Engineering, 2018, 4, 826-831.	2.6	18
17	Synthesis of luminescent lanthanide complexes within crosslinked protein crystal matrices. CrystEngComm, 2018, 20, 2267-2277.	1.3	7
18	Installing Guest Molecules at Specific Sites within Scaffold Protein Crystals. Bioconjugate Chemistry, 2018, 29, 17-22.	1.8	19

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19	Molecular dynamics simulations of cellulase homologs in aqueous 1-ethyl-3-methylimidazolium chloride. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1990-2002.	2.0	11
20	Programmed Assembly of Hostâ€“Guest Protein Crystals. Small, 2017, 13, 1602703.	5.2	23
21	Adsorption-Coupled Diffusion of Gold Nanoclusters within a Large-Pore Protein Crystal Scaffold. Journal of Physical Chemistry B, 2017, 121, 7652-7659.	1.2	12
22	A Structure-Based Design Protocol for Optimizing Combinatorial Protein Libraries. Methods in Molecular Biology, 2016, 1414, 99-138.	0.4	3
23	Characterization of supercharged cellulase activity and stability in ionic liquids. Journal of Molecular Catalysis B: Enzymatic, 2016, 132, 84-90.	1.8	15
24	Optimizing Shape Complementarity Scoring Parameters for Recognition of Authentic Protein Crystal Packing Arrangements. Crystal Growth and Design, 2016, 16, 5579-5583.	1.4	0
25	An Evolved Orthogonal Enzyme/Cofactor Pair. Journal of the American Chemical Society, 2016, 138, 12451-12458.	6.6	32
26	Gold nanoparticle capture within protein crystal scaffolds. Nanoscale, 2016, 8, 12693-12696.	2.8	23
27	Conservative and compensatory evolution in oxidative phosphorylation complexes of angiosperms with highly divergent rates of mitochondrial genome evolution. Evolution; International Journal of Organic Evolution, 2015, 69, 3069-3081.	1.1	68
28	Characterization of the target of ivermectin, the glutamate-gated chloride channel, fromAnopheles gambiae. Journal of Experimental Biology, 2015, 218, 1478-1486.	0.8	65
29	Discriminating between stabilizing and destabilizing protein design mutations via recombination and simulation. Protein Engineering, Design and Selection, 2015, 28, 259-267.	1.0	10
30	Methods for Library-Scale Computational Protein Design. Methods in Molecular Biology, 2014, 1216, 129-159.	0.4	3
31	Structure-guided engineering of Lactococcus lactis alcohol dehydrogenase LlAdhA for improved conversion of isobutyraldehyde to isobutanol. Journal of Biotechnology, 2013, 164, 188-195.	1.9	35
32	General approach to reversing ketol-acid reductoisomerase cofactor dependence from NADPH to NADH. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10946-10951.	3.3	102
33	Comparison of random mutagenesis and semi-rational designed libraries for improved cytochrome P450 BM3-catalyzed hydroxylation of small alkanes. Protein Engineering, Design and Selection, 2012, 25, 171-178.	1.0	79
34	A diverse set of familyÂ48 bacterial glycoside hydrolase cellulases created by structureâ€guided recombination. FEBS Journal, 2012, 279, 4453-4465.	2.2	38
35	Structure-Guided Directed Evolution of Highly Selective P450-Based Magnetic Resonance Imaging Sensors for Dopamine and Serotonin. Journal of Molecular Biology, 2012, 422, 245-262.	2.0	40
36	Engineered Bacterial Mimics of Human Drug Metabolizing Enzyme CYP2C9. ChemCatChem, 2011, 3, 1065-1071.	1.8	36

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37	Polarizable protein packing. Journal of Computational Chemistry, 2011, 32, 1334-1344.	1.5	3
38	Engineered ketol-acid reductoisomerase and alcohol dehydrogenase enable anaerobic 2-methylpropan-1-ol production at theoretical yield in Escherichia coli. Metabolic Engineering, 2011, 13, 345-352.	3.6	257
39	Combinatorial Alanine Substitution Enables Rapid Optimization of Cytochrome P450_{BM3} for Selective Hydroxylation of Large Substrates. ChemBioChem, 2010, 11, 2502-2505.	1.3	100
40	Efficient screening of fungal cellobiohydrolase class I enzymes for thermostabilizing sequence blocks by SCHEMA structure-guided recombination. Protein Engineering, Design and Selection, 2010, 23, 871-880.	1.0	92
41	Non-Bulk-Like Solvent Behavior in the Ribosome Exit Tunnel. PLoS Computational Biology, 2010, 6, e1000963.	1.5	36
42	A family of thermostable fungal cellulases created by structure-guided recombination. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5610-5615.	3.3	244
43	SCHEMA Recombination of a Fungal Cellulase Uncovers a Single Mutation That Contributes Markedly to Stability. Journal of Biological Chemistry, 2009, 284, 26229-26233.	1.6	108
44	SHARPENâ€"Systematic Hierarchical Algorithms for Rotamers and Proteins on an Extended Network. Journal of Computational Chemistry, 2009, 30, 999-1005.	1.5	13
45	Evolutionary History of a Specialized P450 Propane Monooxygenase. Journal of Molecular Biology, 2008, 383, 1069-1080.	2.0	185
46	Hunting for predictive computational drug-discovery models. Expert Review of Anti-Infective Therapy, 2008, 6, 291-293.	2.0	1
47	Side-chain recognition and gating in the ribosome exit tunnel. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16549-16554.	3.3	83
48	Chapter 8. Computer Simulations of Protein Folding. RSC Biomolecular Sciences, 2008, , 161-187.	0.4	3
49	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. Nature Biotechnology, 2007, 25, 1051-1056.	9.4	144
50	Electric Fields at the Active Site of an Enzyme: Direct Comparison of Experiment with Theory. Science, 2006, 313, 200-204.	6.0	296
51	Kinetic Definition of Protein Folding Transition State Ensembles and Reaction Coordinates. Biophysical Journal, 2006, 91, 14-24.	0.2	33
52	How Well Can Simulation Predict Protein Folding Kinetics and Thermodynamics?. Annual Review of Biophysics and Biomolecular Structure, 2005, 34, 43-69.	18.3	225
53	Dimerization of the p53 Oligomerization Domain: Identification of a Folding Nucleus by Molecular Dynamics Simulations. Journal of Molecular Biology, 2005, 345, 869-878.	2.0	36
54	Direct calculation of the binding free energies of FKBP ligands. Journal of Chemical Physics, 2005, 123, 084108.	1.2	179

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55	An Integrated Approach to Analyzing Activation Profiles in Immune Cells by Combining Cytomic and Proteomic Techniques of Cell Analysis/Sorting and Protein Fractionation.. Blood, 2005, 106, 3934-3934.	0.6	0
56	Using path sampling to build better Markovian state models: Predicting the folding rate and mechanism of a tryptophan zipper beta hairpin. Journal of Chemical Physics, 2004, 121, 415.	1.2	245
57	Trp zipper folding kinetics by molecular dynamics and temperature-jump spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4077-4082.	3.3	185
58	Atomistic protein folding simulations on the submillisecond time scale using worldwide distributed computing. Biopolymers, 2003, 68, 91-109.	1.2	346
59	Surface Salt Bridges, Double-Mutant Cycles, and Protein Stability:Â an Experimental and Computational Analysis of the Interaction of the Asp 23 Side Chain with the N-Terminus of the N-Terminal Domain of the Ribosomal Protein L9â€. Biochemistry, 2003, 42, 7050-7060.	1.2	72
60	The Trp Cage:Â Folding Kinetics and Unfolded State Topology via Molecular Dynamics Simulations. Journal of the American Chemical Society, 2002, 124, 14548-14549.	6.6	234
61	Native-like Mean Structure in the Unfolded Ensemble of Small Proteins. Journal of Molecular Biology, 2002, 323, 153-164.	2.0	168
62	Simulation of Folding of a Small Alpha-helical Protein in Atomistic Detail using Worldwide-distributed Computing. Journal of Molecular Biology, 2002, 323, 927-937.	2.0	266
63	Absolute comparison of simulated and experimental protein-folding dynamics. Nature, 2002, 420, 102-106.	13.7	646