

Christopher D Snow

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

4,988
citations

159358

30
h-index

118652

62
g-index

64
all docs

64
docs citations

64
times ranked

4853
citing authors

#	ARTICLE	IF	CITATIONS
1	Absolute comparison of simulated and experimental protein-folding dynamics. <i>Nature</i> , 2002, 420, 102-106.	13.7	646
2	Atomistic protein folding simulations on the submillisecond time scale using worldwide distributed computing. <i>Biopolymers</i> , 2003, 68, 91-109.	1.2	346
3	Electric Fields at the Active Site of an Enzyme: Direct Comparison of Experiment with Theory. <i>Science</i> , 2006, 313, 200-204.	6.0	296
4	Simulation of Folding of a Small Alpha-helical Protein in Atomistic Detail using Worldwide-distributed Computing. <i>Journal of Molecular Biology</i> , 2002, 323, 927-937.	2.0	266
5	Engineered ketol-acid reductoisomerase and alcohol dehydrogenase enable anaerobic 2-methylpropan-1-ol production at theoretical yield in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2011, 13, 345-352.	3.6	257
6	Using path sampling to build better Markovian state models: Predicting the folding rate and mechanism of a tryptophan zipper beta hairpin. <i>Journal of Chemical Physics</i> , 2004, 121, 415.	1.2	245
7	A family of thermostable fungal cellulases created by structure-guided recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5610-5615.	3.3	244
8	The Trp Cage: Folding Kinetics and Unfolded State Topology via Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2002, 124, 14548-14549.	6.6	234
9	How Well Can Simulation Predict Protein Folding Kinetics and Thermodynamics?. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2005, 34, 43-69.	18.3	225
10	Trp zipper folding kinetics by molecular dynamics and temperature-jump spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4077-4082.	3.3	185
11	Evolutionary History of a Specialized P450 Propane Monooxygenase. <i>Journal of Molecular Biology</i> , 2008, 383, 1069-1080.	2.0	185
12	Direct calculation of the binding free energies of FKBP ligands. <i>Journal of Chemical Physics</i> , 2005, 123, 084108.	1.2	179
13	Native-like Mean Structure in the Unfolded Ensemble of Small Proteins. <i>Journal of Molecular Biology</i> , 2002, 323, 153-164.	2.0	168
14	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. <i>Nature Biotechnology</i> , 2007, 25, 1051-1056.	9.4	144
15	SCHEMA Recombination of a Fungal Cellulase Uncovers a Single Mutation That Contributes Markedly to Stability. <i>Journal of Biological Chemistry</i> , 2009, 284, 26229-26233.	1.6	108
16	General approach to reversing ketol-acid reductoisomerase cofactor dependence from NADPH to NADH. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10946-10951.	3.3	102
17	Combinatorial Alanine Substitution Enables Rapid Optimization of Cytochrome P450 _{BM3} for Selective Hydroxylation of Large Substrates. <i>ChemBioChem</i> , 2010, 11, 2502-2505.	1.3	100
18	Efficient screening of fungal cellobiohydrolase class I enzymes for thermostabilizing sequence blocks by SCHEMA structure-guided recombination. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 871-880.	1.0	92

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19	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
20	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
21	Surface Salt Bridges, Double-Mutant Cycles, and Protein Stability: 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 L9. Biochemistry, 2003, 42, 7050-7060.	1.2	72
22	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
23	Characterization of the target of ivermectin, the glutamate-gated chloride channel, from <i>Anopheles gambiae</i> . Journal of Experimental Biology, 2015, 218, 1478-1486.	0.8	65
24	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
25	A diverse set of family 48 bacterial glycoside hydrolase cellulases created by structure-guided recombination. FEBS Journal, 2012, 279, 4453-4465.	2.2	38
26	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
27	Non-Bulk-Like Solvent Behavior in the Ribosome Exit Tunnel. PLoS Computational Biology, 2010, 6, e1000963.	1.5	36
28	Engineered Bacterial Mimics of Human Drug Metabolizing Enzyme CYP2C9. ChemCatChem, 2011, 3, 1065-1071.	1.8	36
29	Structure-guided engineering of Lactococcus lactis alcohol dehydrogenase LIAdhA for improved conversion of isobutyraldehyde to isobutanol. Journal of Biotechnology, 2013, 164, 188-195.	1.9	35
30	Kinetic Definition of Protein Folding Transition State Ensembles and Reaction Coordinates. Biophysical Journal, 2006, 91, 14-24.	0.2	33
31	An Evolved Orthogonal Enzyme/Cofactor Pair. Journal of the American Chemical Society, 2016, 138, 12451-12458.	6.6	32
32	Porous protein crystals as scaffolds for enzyme immobilization. Biomaterials Science, 2019, 7, 1898-1904.	2.6	29
33	Gold nanoparticle capture within protein crystal scaffolds. Nanoscale, 2016, 8, 12693-12696.	2.8	23
34	Programmed Assembly of Host-Guest Protein Crystals. Small, 2017, 13, 1602703.	5.2	23
35	Protein crystal based materials for nanoscale applications in medicine and biotechnology. Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology, 2019, 11, e1547.	3.3	20
36	Installing Guest Molecules at Specific Sites within Scaffold Protein Crystals. Bioconjugate Chemistry, 2018, 29, 17-22.	1.8	19

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37	Characterizing the Cytocompatibility of Various Cross-Linking Chemistries for the Production of Biostable Large-Pore Protein Crystal Materials. <i>ACS Biomaterials Science and Engineering</i> , 2018, 4, 826-831.	2.6	18
38	Porous crystals as scaffolds for structural biology. <i>Current Opinion in Structural Biology</i> , 2020, 60, 85-92.	2.6	16
39	Characterization of supercharged cellulase activity and stability in ionic liquids. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2016, 132, 84-90.	1.8	15
40	SHARPEN—Systematic Hierarchical Algorithms for Rotamers and Proteins on an Extended Network. <i>Journal of Computational Chemistry</i> , 2009, 30, 999-1005.	1.5	13
41	Histidine polypeptide-hybridized nanoscale metal-organic framework to sense drug loading/release. <i>Materials and Design</i> , 2021, 205, 109741.	3.3	13
42	Adsorption-Coupled Diffusion of Gold Nanoclusters within a Large-Pore Protein Crystal Scaffold. <i>Journal of Physical Chemistry B</i> , 2017, 121, 7652-7659.	1.2	12
43	Advancing biomarkers for anaerobic o-xylene biodegradation via metagenomic analysis of a methanogenic consortium. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4177-4192.	1.7	12
44	Molecular dynamics simulations of cellulase homologs in aqueous 1-ethyl-3-methylimidazolium chloride. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 1990-2002.	2.0	11
45	Design of genetically encoded sensors to detect nucleosome ubiquitination in live cells. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	11
46	Smart Wearable Fluorescence Sensing of Bacterial Pathogens and Toxic Contaminants by Eu ³⁺ -Induced Sodium Alginate/Ag Nanoparticle Aggregates. <i>ACS Applied Nano Materials</i> , 2022, 5, 8393-8403.	2.4	11
47	Discriminating between stabilizing and destabilizing protein design mutations via recombination and simulation. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 259-267.	1.0	10
48	Synthesis of luminescent lanthanide complexes within crosslinked protein crystal matrices. <i>CrystEngComm</i> , 2018, 20, 2267-2277.	1.3	7
49	Drug Sensing Protein Crystals Doped with Luminescent Lanthanide Complexes. <i>Crystal Growth and Design</i> , 2019, 19, 5658-5664.	1.4	7
50	Measuring interactions of DNA with nanoporous protein crystals by atomic force microscopy. <i>Nanoscale</i> , 2021, 13, 10871-10881.	2.8	6
51	Stable Fluorescence of Eu ³⁺ Complex Nanostructures Beneath a Protein Skin for Potential Biometric Recognition. <i>Nanomaterials</i> , 2021, 11, 2462.	1.9	6
52	Enhancing the Power Conversion Efficiency for Polymer Solar Cells by Incorporating Luminescent Nanosolid Micelles as Light Converter. <i>ACS Applied Energy Materials</i> , 2018, 1, 1445-1454.	2.5	5
53	Stabilizing DNA-Protein Co-Crystals via Intra-Crystal Chemical Ligation of the DNA. <i>Crystals</i> , 2022, 12, 49.	1.0	4
54	Polarizable protein packing. <i>Journal of Computational Chemistry</i> , 2011, 32, 1334-1344.	1.5	3

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55	A Structure-Based Design Protocol for Optimizing Combinatorial Protein Libraries. <i>Methods in Molecular Biology</i> , 2016, 1414, 99-138.	0.4	3
56	Methods for Library-Scale Computational Protein Design. <i>Methods in Molecular Biology</i> , 2014, 1216, 129-159.	0.4	3
57	Chapter 8. Computer Simulations of Protein Folding. <i>RSC Biomolecular Sciences</i> , 2008, , 161-187.	0.4	3
58	Lanthanide (Eu ³⁺ /Tb ³⁺)-Loaded β -Cyclodextrin Nano-Aggregates for Smart Sensing of the Anticancer Drug Irinotecan. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6597.	1.8	3
59	Near infrared emitting and biocompatible Yb ³⁺ -DNA complexes with dual responses to Cu ²⁺ and Fe ³⁺ . <i>Optical Materials</i> , 2020, 108, 110157.	1.7	2
60	Hunting for predictive computational drug-discovery models. <i>Expert Review of Anti-Infective Therapy</i> , 2008, 6, 291-293.	2.0	1
61	Conditionally designed luminescent DNA crystals doped by Ln ³⁺ (Eu ³⁺ /Tb ³⁺) complexes or fluorescent proteins with smart drug sensing property. <i>Journal of Materials Chemistry B</i> , 2022, 10, 6443-6452.	2.9	1
62	Optimizing Shape Complementarity Scoring Parameters for Recognition of Authentic Protein Crystal Packing Arrangements. <i>Crystal Growth and Design</i> , 2016, 16, 5579-5583.	1.4	0
63	An Integrated Approach to Analyzing Activation Profiles in Immune Cells by Combining Cytomic and Proteomic Techniques of Cell Analysis/Sorting and Protein Fractionation.. <i>Blood</i> , 2005, 106, 3934-3934.	0.6	0