

Stephen A Wells

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

1,725
citations

304368

22
h-index

288905

40
g-index

57
all docs

57
docs citations

57
times ranked

2044
citing authors

#	ARTICLE	IF	CITATIONS
1	The flexibility window in zeolites. <i>Nature Materials</i> , 2006, 5, 962-965.	13.3	177
2	Constrained geometric simulation of diffusive motion in proteins. <i>Physical Biology</i> , 2005, 2, S127-S136.	0.8	166
3	Negative Thermal Expansion in ZrW ₂ O ₈ : Mechanisms, Rigid Unit Modes, and Neutron Total Scattering. <i>Physical Review Letters</i> , 2005, 95, 255501.	2.9	164
4	Formation of a metallic glass by thermal decomposition of Fe(CO) ₅ . <i>Physical Review Letters</i> , 1985, 55, 410-413.	2.9	139
5	Fitting Low-Resolution Cryo-EM Maps of Proteins Using Constrained Geometric Simulations. <i>Biophysical Journal</i> , 2008, 94, 1613-1621.	0.2	70
6	“Something in the way she moves”: The functional significance of flexibility in the multiple roles of protein disulfide isomerase (PDI). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1383-1394.	1.1	58
7	Exploring the Energy Landscapes of Protein Folding Simulations with Bayesian Computation. <i>Biophysical Journal</i> , 2012, 102, 878-886.	0.2	51
8	Finding best-fit polyhedral rotations with geometric algebra. <i>Journal of Physics Condensed Matter</i> , 2002, 14, 4567-4584.	0.7	45
9	Real-space rigid-unit-mode analysis of dynamic disorder in quartz, cristobalite and amorphous silica. <i>Journal of Physics Condensed Matter</i> , 2002, 14, 4645-4657.	0.7	43
10	Reverse Monte Carlo with geometric analysis “RMC+GA”. <i>Journal of Applied Crystallography</i> , 2004, 37, 536-544.	1.9	40
11	A complete thermodynamic analysis of enzyme turnover links the free energy landscape to enzyme catalysis. <i>FEBS Journal</i> , 2017, 284, 2829-2842.	2.2	39
12	Total scattering and reverse Monte Carlo study of the 105 K displacive phase transition in strontium titanate. <i>Journal of Physics Condensed Matter</i> , 2005, 17, S111-S124.	0.7	38
13	Li ⁺ ion motion in quartz and Î ² -eucryptite studied by dielectric spectroscopy and atomistic simulations. <i>Journal of Physics Condensed Matter</i> , 2004, 16, 8173-8189.	0.7	36
14	Protein flexibility is key to cisplatin crosslinking in calmodulin. <i>Protein Science</i> , 2012, 21, 1269-1279.	3.1	36
15	Thermal stability, storage and release of proteins with tailored fit in silica. <i>Scientific Reports</i> , 2017, 7, 46568.	1.6	36
16	Docking of Photosystem I Subunit C Using a Constrained Geometric Simulation. <i>Journal of the American Chemical Society</i> , 2006, 128, 8803-8812.	6.6	32
17	Flexibility windows and compression of monoclinic and orthorhombic silicalites. <i>Physical Review B</i> , 2012, 85, .	1.1	28
18	Structures of mesophilic and extremophilic citrate synthases reveal rigidity and flexibility for function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2657-2670.	1.5	28

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19	GASP: software for geometric simulations of flexibility in polyhedral and molecular framework structures. <i>Molecular Simulation</i> , 2015, 41, 1409-1421.	0.9	27
20	Tetrahedral Distortion and Energetic Packing Penalty in Zeolite Frameworks: A Linked Phenomena?. <i>Journal of Physical Chemistry B</i> , 2005, 109, 14783-14785.	1.2	26
21	In Silico and Structural Analyses Demonstrate That Intrinsic Protein Motions Guide T Cell Receptor Complementarity Determining Region Loop Flexibility. <i>Frontiers in Immunology</i> , 2018, 9, 674.	2.2	26
22	Structure and Function in Homodimeric Enzymes: Simulations of Cooperative and Independent Functional Motions. <i>PLoS ONE</i> , 2015, 10, e0133372.	1.1	24
23	The flexibility and dynamics of protein disulfide isomerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1776-1785.	1.5	24
24	TCR-induced alteration of primary MHC peptide anchor residue. <i>European Journal of Immunology</i> , 2019, 49, 1052-1066.	1.6	23
25	Structural evolution of zeolite levynite under hydrostatic and non-hydrostatic pressure: geometric modelling. <i>Physics and Chemistry of Minerals</i> , 2006, 33, 243-255.	0.3	22
26	The origin of the compressibility anomaly in amorphous silica: a molecular dynamics study. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 275210.	0.7	22
27	Compression behaviour and flexibility window of the analcime-like feldspathoids: experimental and theoretical findings. <i>European Journal of Mineralogy</i> , 2009, 21, 571-580.	0.4	22
28	The ALS Nutrition/NIPPV Study: Design, feasibility, and initial results. <i>Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders</i> , 2011, 12, 17-25.	2.3	19
29	Ionic diffusion in quartz studied by transport measurements, SIMS and atomistic simulations. <i>Journal of Physics Condensed Matter</i> , 2005, 17, 1099-1112.	0.7	18
30	Template-Based Geometric Simulation of Flexible Frameworks. <i>Materials</i> , 2012, 5, 415-431.	1.3	17
31	High-resolution NMR studies of structure and dynamics of human ERp27 indicate extensive interdomain flexibility. <i>Biochemical Journal</i> , 2013, 450, 321-332.	1.7	14
32	MODELLING CHARGE TRANSPORT IN DNA USING TRANSFER MATRICES WITH DIAGONAL TERMS. <i>International Journal of Modern Physics B</i> , 2009, 23, 4138-4149.	1.0	13
33	Flexibility windows in faujasite with explicit water and methanol extra-framework content. <i>Dalton Transactions</i> , 2015, 44, 5978-5984.	1.6	13
34	Pressure-induced symmetry changes in body-centred cubic zeolites. <i>Royal Society Open Science</i> , 2019, 6, 182158.	1.1	13
35	Monoclonal antibody stability can be usefully monitored using the excitation-energy-dependent fluorescence edge-shift. <i>Biochemical Journal</i> , 2020, 477, 3599-3612.	1.7	13
36	Intrinsic flexibility of porous materials; theory, modelling and the flexibility window of the EMT zeolite framework. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2015, 71, 641-647.	0.5	12

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37	Exposing the Interplay Between Enzyme Turnover, Protein Dynamics, and the Membrane Environment in Monoamine Oxidase B. <i>Biochemistry</i> , 2019, 58, 2362-2372.	1.2	12
38	Salt bridge impact on global rigidity and thermostability in thermophilic citrate synthase. <i>Physical Biology</i> , 2020, 17, 016002.	0.8	11
39	Cation substitution and strain screening in framework structures: The role of rigid unit modes. <i>Chemical Geology</i> , 2006, 225, 213-221.	1.4	10
40	Charge transport in cancer-related genes and early carcinogenesis. <i>Computer Physics Communications</i> , 2011, 182, 36-38.	3.0	10
41	Structure and <i>in silico</i> simulations of a cold-active esterase reveals its prime cold-adaptation mechanism. <i>Open Biology</i> , 2021, 11, 210182.	1.5	10
42	Evidence of Correlated Static Disorder in the Fenna-Matthews-Olson Complex. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 2350-2356.	2.1	9
43	Defining the flexibility window in ordered aluminosilicate zeolites. <i>Royal Society Open Science</i> , 2017, 4, 170757.	1.1	9
44	The steric influence of extra-framework cations on framework flexibility: an LTA case study. <i>Zeitschrift Fur Kristallographie - Crystalline Materials</i> , 2019, 234, 461-468.	0.4	9
45	Framework flexibility and rational design of new zeolites for catalysis. <i>Applied Petrochemical Research</i> , 2012, 2, 69-72.	1.3	8
46	Structure and function of <i>L</i> -threonine-3-dehydrogenase from the parasitic protozoan <i>Trypanosoma brucei</i> revealed by X-ray crystallography and geometric simulations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 861-876.	1.1	8
47	Early stages of phase selection in MOF formation observed in molecular Monte Carlo simulations. <i>RSC Advances</i> , 2019, 9, 14382-14390.	1.7	8
48	Intrinsic Flexibility of the EMT Zeolite Framework under Pressure. <i>Molecules</i> , 2019, 24, 641.	1.7	8
49	Mechanism of CO ₂ capture in nanostructured sodium amide encapsulated in porous silica. <i>Surface and Coatings Technology</i> , 2018, 350, 227-233.	2.2	7
50	Cisplatin uptake and release in pH sensitive zeolitic imidazole frameworks. <i>Journal of Chemical Physics</i> , 2021, 154, 244703.	1.2	7
51	Determining the structure of zeolite frameworks at high pressures. <i>CrystEngComm</i> , 2021, 23, 5615-5623.	1.3	6
52	Geometric Simulation of Flexible Motion in Proteins. <i>Methods in Molecular Biology</i> , 2014, 1084, 173-192.	0.4	5
53	Characterization of Folding Cores in the Cyclophilin A-Cyclosporin A Complex. <i>Biophysical Journal</i> , 2015, 108, 1739-1746.	0.2	4
54	Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. <i>Water Research</i> , 2022, 217, 118415.	5.3	3

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55	Using geometric simulation software â€˜GASPâ€™™ to model conformational flexibility in a family of zinc metalâ€“organic frameworks. <i>New Journal of Chemistry</i> , 2021, 45, 8728-8737.	1.4	2