Charles H Robert

List of Publications by Year
in descending order

44 papers	1,467 citations	361413 20 h-index	315739 38 g-index
44 all docs	44 docs citations	44 times ranked	1651 citing authors

#	Article	IF	Citations
1	Building Biological Relevance Into Integrative Modelling of Macromolecular Assemblies. Frontiers in Molecular Biosciences, 2022, 9, 826136.	3.5	2
2	Modeling Perturbations in Protein Filaments at the Micro and Meso Scale using NAMD and PTools/Heligeom. Bio-protocol, 2021, 11, e4097.	0.4	1
3	Mobility and Core-Protein Binding Patterns of Disordered C-Terminal Tails in Î²-Tubulin Isotypes. Biochemistry, 2017, 56, 1746-1756.	2.5	15
4	Hybridizing rapidly exploring random trees and basin hopping yields an improved exploration of energy landscapes. Journal of Computational Chemistry, 2016, 37, 739-752.	3.3	12
5	Investigating the Structural Variability and Binding Modes of the Glioma Targeting NFL-TBS.40â€“63 Peptide on Tubulin. Biochemistry, 2015, 54, 3660-3669.	2.5	8
6	Conformational ensembles and sampled energy landscapes: Analysis and comparison. Journal of Computational Chemistry, 2015, 36, 1213-1231.	3.3	14
7	Changes in protein structure at the interface accompanying complex formation. IUCrJ, 2015, 2, 643-652.	2.2	21
8	An Integrative Approach to the Study of Filamentous Oligomeric Assemblies, with Application to RecA. PLoS ONE, 2015, 10, e0116414.	2.5	14
9	Reassessing buried surface areas in proteinâ€“protein complexes. Protein Science, 2013, 22, 1453-1457.	7.6	27
10	Free Energy Profiles along Consensus Normal Modes Provide Insight into HIV-1 Protease Flap Opening. Journal of Chemical Theory and Computation, 2011, 7, 2348-2352.	5.3	32
11	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
12	How does heparin prevent the pH inactivation of cathepsin B? Allosteric mechanism elucidated by docking and molecular dynamics. BMC Genomics, 2010, 11, S5.	2.8	44
13	Sideâ€chain rotamer transitions at proteinâ€protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	2.6	15
14	A Computational Study of a Recreated G Protein-GEF Reaction Intermediate Competent for Nucleotide Exchange: Fate of the Mg Ion. PLoS ONE, 2010, 5, e9142.	2.5	3
15	Consensus modes, a robust description of protein collective motions from multiple-minima normal mode analysisâ€”application to the HIV-1 protease. Physical Chemistry Chemical Physics, 2010, 12, 2850.	2.8	31
16	Disulfide Bond Substitution by Directed Evolution in an Engineered Binding Protein. ChemBioChem, 2009, 10, 1349-1359.	2.6	13
17	Role of Nucleic Acid Binding in Sir3p-Dependent Interactions with Chromatin Fibers. Biochemistry, 2009, 48, 276-288.	2.5	8
18	Odorant Binding and Conformational Dynamics in the Odorant-binding Protein. Journal of Biological Chemistry, 2006, 281, 29929-29937.	3.4	46

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19	Normal mode analysis as a prerequisite for drug design: Application to matrix metalloproteinases inhibitors. FEBS Letters, 2006, 580, 5130-5136.	2.8	58
20	Integrating Three Views of Arf1 Activation Dynamics. Journal of Molecular Biology, 2004, 337, 969-983.	4.2	8
21	New Insights into the Allosteric Mechanism of Human Hemoglobin from Molecular Dynamics Simulations. Biophysical Journal, 2002, 82, 3224-3245.	0.5	50
22	Differential Core Histone Binding Behavior. Cell Biochemistry and Biophysics, 2002, 37, 01-14.	1.8	1
23	A soft, mean-field potential derived from crystal contacts for predicting protein-protein interactions. Journal of Molecular Biology, 1998, 283, 1037-1047.	4.2	40
24	Finding and visualizing nucleic acid base stacking. Journal of Molecular Graphics, 1996, 14, 6-11.	1.1	26
25	Significance of bound water to local chain conformations in protein crystals.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 7600-7604.	7.1	20
26	Estimating friction coefficients of mixed globular/chain molecules, such as protein/DNA complexes. Biophysical Journal, 1995, 69, 840-848.	0.5	8
27	Three-dimensional structure of extended chromatin fibers as revealed by tapping-mode scanning force microscopy.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 11621-11625.	7.1	226
28	Kinetics of pore-mediated release of marker molecules from liposomes or cells. Biophysical Chemistry, 1992, 42, 291-296.	2.8	56
29	A combined study of aggregation, membrane affinity and pore activity of natural and modified melittin. Biochimica Et Biophysica Acta - Biomembranes, 1991, 1069, 77-86.	2.6	43
30	A hierarchical ?nesting? approach to describe the stability of alpha helices with side-chain interactions. Biopolymers, 1990, 30, 335-347.	2.4	19
31	Pore formation kinetics in membranes, determined from the release of marker molecules out of liposomes or cells. Biophysical Journal, 1990, 58, 577-583.	0.5	84
32	Allosteric formulation of thermal transitions in macromolecules, including effects of ligand binding and oligomerization. Biopolymers, 1989, 28, 1705-1729.	2.4	24
33	Binding of oxygen and carbon monoxide to the hemocyanin from the spiny lobster. Journal of Molecular Biology, 1989, 207, 829-832.	4.2	17
34	Analysis and parameter resolution in highly cooperative systems. Biophysical Chemistry, 1988, 30, 133-141.	2.8	15
35	Quantitative analysis of linkage in macromolecules when one ligand is present in limited total quantity. Biochemistry, 1988, 27, 6829-6835.	2.5	34
36	Linkage of organic phosphates to oxygen binding in human hemoglobin at high concentrations. Biochemistry, 1988, 27, 6835-6843.	2.5	16

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37	Nested allosteric interaction in tarantula hemocyanin revealed through the binding of oxygen and carbon monoxide. Biochemistry, 1988, 27, 6901-6908.	2.5	38
38	New twists on an old story: hemoglobin. Trends in Biochemical Sciences, 1988, 13, 465-467.	7.5	11
39	Gasâ€solution microcalorimeter for determining heat binding curves. Review of Scientific Instruments, 1987, 58, 632-638.	1.3	1
40	Nesting: hierarchies of allosteric interactions.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 1891-1895.	7.1	71
41	Carbon dioxide and oxygen linkage in human hemoglobin tetramers. Journal of Molecular Biology, 1987, 196, 927-934.	4.2	20
42	Allosteric interpretation of the oxygen-binding reaction of human hemoglobin tetramers. Biochemistry, 1987, 26, 4003-4008.	2.5	60
43	Oxygen binding constants for human hemoglobin tetramers. Biochemistry, 1987, 26, 3995-4002.	2.5	78
44	Analysis of zeros of binding polynomials for tetrameric hemoglobins. Biophysical Chemistry, 1986, 24, 295-309.	2.8	6