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	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
2	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
3	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
4	Oxygen binding constants for human hemoglobin tetramers. Biochemistry, 1987, 26, 3995-4002.	2.5	78
5	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
6	Allosteric interpretation of the oxygen-binding reaction of human hemoglobin tetramers. Biochemistry, 1987, 26, 4003-4008.	2.5	60
7	Normal mode analysis as a prerequisite for drug design: Application to matrix metalloproteinases inhibitors. FEBS Letters, 2006, 580, 5130-5136.	2.8	58
8	Kinetics of pore-mediated release of marker molecules from liposomes or cells. Biophysical Chemistry, 1992, 42, 291-296.	2.8	56
9	New Insights into the Allosteric Mechanism of Human Hemoglobin from Molecular Dynamics Simulations. Biophysical Journal, 2002, 82, 3224-3245.	0.5	50
10	Odorant Binding and Conformational Dynamics in the Odorant-binding Protein. Journal of Biological Chemistry, 2006, 281, 29929-29937.	3.4	46
11	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
12	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
13	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
14	Nested allosteric interaction in tarantula hemocyanin revealed through the binding of oxygen and carbon monoxide. Biochemistry, 1988, 27, 6901-6908.	2.5	38
15	Quantitative analysis of linkage in macromolecules when one ligand is present in limited total quantity. Biochemistry, 1988, 27, 6829-6835.	2.5	34
16	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
17	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
18	Reassessing buried surface areas in proteinâ€"protein complexes. Protein Science, 2013, 22, 1453-1457.	7.6	27

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19	Finding and visualizing nucleic acid base stacking. Journal of Molecular Graphics, 1996, 14, 6-11.	1.1	26
20	Allosteric formulation of thermal transitions in macromolecules, including effects of ligand binding and oligomerization. Biopolymers, 1989, 28, 1705-1729.	2.4	24
21	Changes in protein structure at the interface accompanying complex formation. IUCrJ, 2015, 2, 643-652.	2.2	21
22	Carbon dioxide and oxygen linkage in human hemoglobin tetramers. Journal of Molecular Biology, 1987, 196, 927-934.	4.2	20
23	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
24	A hierarchical ?nesting? approach to describe the stability of alpha helices with side-chain interactions. Biopolymers, 1990, 30, 335-347.	2.4	19
25	Binding of oxygen and carbon monoxide to the hemocyanin from the spiny lobster. Journal of Molecular Biology, 1989, 207, 829-832.	4.2	17
26	Linkage of organic phosphates to oxygen binding in human hemoglobin at high concentrations. Biochemistry, 1988, 27, 6835-6843.	2.5	16
27	Analysis and parameter resolution in highly cooperative systems. Biophysical Chemistry, 1988, 30, 133-141.	2.8	15
28	Sideâ€chain rotamer transitions at proteinâ€protein interfaces. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3219-3225.	2.6	15
29	Mobility and Core-Protein Binding Patterns of Disordered C-Terminal Tails in Î²-Tubulin Isotypes. Biochemistry, 2017, 56, 1746-1756.	2.5	15
30	Conformational ensembles and sampled energy landscapes: Analysis and comparison. Journal of Computational Chemistry, 2015, 36, 1213-1231.	3.3	14
31	An Integrative Approach to the Study of Filamentous Oligomeric Assemblies, with Application to RecA. PLoS ONE, 2015, 10, e0116414.	2.5	14
32	Disulfide Bond Substitution by Directed Evolution in an Engineered Binding Protein. ChemBioChem, 2009, 10, 1349-1359.	2.6	13
33	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
34	New twists on an old story: hemoglobin. Trends in Biochemical Sciences, 1988, 13, 465-467.	7.5	11
35	Estimating friction coefficients of mixed globular/chain molecules, such as protein/DNA complexes. Biophysical Journal, 1995, 69, 840-848.	0.5	8
36	Integrating Three Views of Arf1 Activation Dynamics. Journal of Molecular Biology, 2004, 337, 969-983.	4.2	8

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37	Role of Nucleic Acid Binding in Sir3p-Dependent Interactions with Chromatin Fibers. Biochemistry, 2009, 48, 276-288.	2.5	8
38	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
39	Analysis of zeros of binding polynomials for tetrameric hemoglobins. Biophysical Chemistry, 1986, 24, 295-309.	2.8	6
40	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
41	Building Biological Relevance Into Integrative Modelling of Macromolecular Assemblies. Frontiers in Molecular Biosciences, 2022, 9, 826136.	3.5	2
42	Gasâ€solution microcalorimeter for determining heat binding curves. Review of Scientific Instruments, 1987, 58, 632-638.	1.3	1
43	Differential Core Histone Binding Behavior. Cell Biochemistry and Biophysics, 2002, 37, 01-14.	1.8	1
44	Modeling Perturbations in Protein Filaments at the Micro and Meso Scale using NAMD and PTools/Heligeom. Bio-protocol, 2021, 11, e4097.	0.4	1