

Carol A Rohl

List of Publications by Year in descending order

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35
papers

7,482
citations

186265

28
h-index

361022

35
g-index

35
all docs

35
docs citations

35
times ranked

11175
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein Structure Prediction Using Rosetta. <i>Methods in Enzymology</i> , 2004, 383, 66-93.	1.0	1,445
2	Protein-Protein Docking with Simultaneous Optimization of Rigid-body Displacement and Side-chain Conformations. <i>Journal of Molecular Biology</i> , 2003, 331, 281-299.	4.2	1,017
3	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	5.6	872
4	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012, 22, 1173-1183.	5.5	557
5	Modeling structurally variable regions in homologous proteins with rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 656-677.	2.6	292
6	Automated prediction of CASP-5 structures using the Robetta server. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 524-533.	2.6	261
7	Helix propagation and α propensities of the amino acids measured in alanine-based peptides in 40 volume percent trifluoroethanol. <i>Protein Science</i> , 1996, 5, 2623-2637.	7.6	256
8	Rosetta in CASP4: Progress in ab initio protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 119-126.	2.6	242
9	De Novo Prediction of Three-dimensional Structures for Major Protein Families. <i>Journal of Molecular Biology</i> , 2002, 322, 65-78.	4.2	237
10	De Novo Determination of Protein Backbone Structure from Residual Dipolar Couplings Using Rosetta. <i>Journal of the American Chemical Society</i> , 2002, 124, 2723-2729.	13.7	177
11	Rosetta predictions in CASP5: Successes, failures, and prospects for complete automation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 457-468.	2.6	162
12	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009, 6, 647-649.	19.0	160
13	Comparison of NH Exchange and Circular Dichroism as Techniques for Measuring the Parameters of the Helix-Coil Transition in Peptides. <i>Biochemistry</i> , 1997, 36, 8435-8442.	2.5	159
14	An improved protein decoy set for testing energy functions for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 76-87.	2.6	150
15	Physically realistic homology models built with ROSETTA can be more accurate than their templates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5361-5366.	7.1	149
16	Definition, conservation and epigenetics of housekeeping and tissue-enriched genes. <i>BMC Genomics</i> , 2009, 10, 269.	2.8	134
17	Solution Structure of the Sodium Channel Inactivation Gate. <i>Biochemistry</i> , 1999, 38, 855-861.	2.5	130
18	Kinetics of amide proton exchange in helical peptides of varying chain lengths. Interpretation by the Lifson-Roig equation. <i>Biochemistry</i> , 1992, 31, 1263-1269.	2.5	125

#	ARTICLE	IF	CITATIONS
19	Prediction of CASP6 structures using automated rosetta protocols. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 157-166.	2.6	124
20	Nonlinear partial differential equations and applications: Circular dichroism spectra of short, fixed-nucleus alanine helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15416-15421.	7.1	119
21	[1] Deciphering rules of helix stability in peptides. <i>Methods in Enzymology</i> , 1998, 295, 1-26.	1.0	115
22	Digital Genome-Wide ncRNA Expression, Including SnoRNAs, across 11 Human Tissues Using PolyA-Neutral Amplification. <i>PLoS ONE</i> , 2010, 5, e11779.	2.5	108
23	Exchange Kinetics of Individual Amide Protons in ¹⁵ N-Labeled Helical Peptides Measured by Isotope-Edited NMR. <i>Biochemistry</i> , 1994, 33, 7760-7767.	2.5	99
24	Addition of side chain interactions to modified Lifson-Roig helix-coil theory: Application to energetics of Phenylalanine-Methionine interactions. <i>Protein Science</i> , 1995, 4, 2383-2391.	7.6	96
25	Models for the 3 ₁₀ -helix/coil, π -helix/coil, and \pm 3 ₁₀ -helix/coil transitions in isolated peptides. <i>Protein Science</i> , 1996, 5, 1687-1696.	7.6	79
26	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <i>BMC Genomics</i> , 2010, 11, 244.	2.8	45
27	Rapid knot detection and application to protein structure prediction. <i>Bioinformatics</i> , 2006, 22, e252-e259.	4.1	36
28	Exact solutions for chemical bond orientations from residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2002, 22, 137-151.	2.8	31
29	Protein Structure Estimation from Minimal Restraints Using Rosetta. <i>Methods in Enzymology</i> , 2005, 394, 244-260.	1.0	29
30	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. <i>BMC Genomics</i> , 2010, 11, 473.	2.8	29
31	Crystal structure and electrical properties of (BEDT-TTF) ₂ Cp(CN) ₅ ·(solvent) _x . <i>Synthetic Metals</i> , 1989, 33, 1-9.	3.9	16
32	Knowledge based identification of essential signaling from genome-scale siRNA experiments. <i>BMC Systems Biology</i> , 2009, 3, 80.	3.0	12
33	Pokefind: a novel topological filter for use with protein structure prediction. <i>Bioinformatics</i> , 2009, 25, i281-i288.	4.1	11
34	Cataloging the Relationships Between Proteins: A Review of Interaction Databases. <i>Molecular Biotechnology</i> , 2006, 34, 69-94.	2.4	6
35	BEDT-TTF Salts with Square-Planar Gold(III) Complex Anions: $\hat{\Gamma}^2$ -(ET) ₂ AuCl ₄ and (ET) ₂ Au(CN) ₂ Cl ₂ . <i>Molecular Crystals and Liquid Crystals Incorporating Nonlinear Optics</i> , 1990, 181, 105-116.	0.3	2