

# Carol A Rohl

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35 papers	6,401 citations	28 h-index	35 g-index
35 ext. papers	7,033 ext. citations	5.7 avg, IF	5.19 L-index

#	Paper	IF	Citations
35	Protein structure prediction using Rosetta. <i>Methods in Enzymology</i> , <b>2004</b> , 383, 66-93	1.7	1142
34	Protein-protein docking with simultaneous optimization of rigid-body displacement and side-chain conformations. <i>Journal of Molecular Biology</i> , <b>2003</b> , 331, 281-99	6.5	858
33	Mapping the genetic architecture of gene expression in human liver. <i>PLoS Biology</i> , <b>2008</b> , 6, e107	9.7	768
32	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , <b>2012</b> , 22, 1173-83	9.7	415
31	Modeling structurally variable regions in homologous proteins with rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 55, 656-77	4.2	264
30	Automated prediction of CASP-5 structures using the Robetta server. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 524-33	4.2	241
29	Helix propagation and N-cap propensities of the amino acids measured in alanine-based peptides in 40 volume percent trifluoroethanol. <i>Protein Science</i> , <b>1996</b> , 5, 2623-37	6.3	239
28	De novo prediction of three-dimensional structures for major protein families. <i>Journal of Molecular Biology</i> , <b>2002</b> , 322, 65-78	6.5	206
27	Rosetta in CASP4: progress in ab initio protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2001</b> , Suppl 5, 119-26	4.2	204
26	De novo determination of protein backbone structure from residual dipolar couplings using Rosetta. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 2723-9	16.4	153
25	Comparison of NH exchange and circular dichroism as techniques for measuring the parameters of the helix-coil transition in peptides. <i>Biochemistry</i> , <b>1997</b> , 36, 8435-42	3.2	149
24	Rosetta predictions in CASP5: successes, failures, and prospects for complete automation. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53 Suppl 6, 457-68	4.2	142
23	An improved protein decoy set for testing energy functions for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2003</b> , 53, 76-87	4.2	140
22	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , <b>2009</b> , 6, 647-9	21.6	139
21	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> , <b>2006</b> , 103, 5361-6	11.5	138
20	Kinetics of amide proton exchange in helical peptides of varying chain lengths. Interpretation by the Lifson-Roig equation. <i>Biochemistry</i> , <b>1992</b> , 31, 1263-9	3.2	119
19	Solution structure of the sodium channel inactivation gate. <i>Biochemistry</i> , <b>1999</b> , 38, 855-61	3.2	116

18	Prediction of CASP6 structures using automated Robetta protocols. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 61 Suppl 7, 157-66	4.2	114
17	Circular dichroism spectra of short, fixed-nucleus alanine helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 15416-21	11.5	114
16	Definition, conservation and epigenetics of housekeeping and tissue-enriched genes. <i>BMC Genomics</i> , <b>2009</b> , 10, 269	4.5	103
15	Deciphering rules of helix stability in peptides. <i>Methods in Enzymology</i> , <b>1998</b> , 295, 1-26	1.7	103
14	Digital genome-wide ncRNA expression, including SnoRNAs, across 11 human tissues using polyA-neutral amplification. <i>PLoS ONE</i> , <b>2010</b> , 5, e11779	3.7	96
13	Exchange kinetics of individual amide protons in <sup>15</sup> N-labeled helical peptides measured by isotope-edited NMR. <i>Biochemistry</i> , <b>1994</b> , 33, 7760-7	3.2	90
12	Addition of side chain interactions to modified Lifson-Roig helix-coil theory: application to energetics of phenylalanine-methionine interactions. <i>Protein Science</i> , <b>1995</b> , 4, 2383-91	6.3	86
11	Models for the 3(10)-helix/coil, pi-helix/coil, and alpha-helix/3(10)-helix/coil transitions in isolated peptides. <i>Protein Science</i> , <b>1996</b> , 5, 1687-96	6.3	67
10	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <i>BMC Genomics</i> , <b>2010</b> , 11, 244	4.5	42
9	Rapid knot detection and application to protein structure prediction. <i>Bioinformatics</i> , <b>2006</b> , 22, e252-9	7.2	32
8	Exact solutions for chemical bond orientations from residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , <b>2002</b> , 22, 137-51	3	28
7	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. <i>BMC Genomics</i> , <b>2010</b> , 11, 473	4.5	27
6	Protein structure estimation from minimal restraints using Rosetta. <i>Methods in Enzymology</i> , <b>2005</b> , 394, 244-60	1.7	27
5	Crystal structure and electrical properties of (BEDT-TTF) <sub>2</sub> Cp(CN) <sub>5</sub> [solvent] <sub>x</sub> . <i>Synthetic Metals</i> , <b>1989</b> , 33, 1-9	3.6	13
4	Knowledge based identification of essential signaling from genome-scale siRNA experiments. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 80	3.5	11
3	Pokefind: a novel topological filter for use with protein structure prediction. <i>Bioinformatics</i> , <b>2009</b> , 25, i281-8	7.2	8
2	Cataloging the relationships between proteins: a review of interaction databases. <i>Molecular Biotechnology</i> , <b>2006</b> , 34, 69-93	3	5
1	BEDT-TTF Salts with Square-Planar Gold(III) Complex Anions: [ET] <sub>2</sub> AuCl <sub>4</sub> and (ET) <sub>2</sub> Au(CN) <sub>2</sub> Cl <sub>2</sub> . <i>Molecular Crystals and Liquid Crystals Incorporating Nonlinear Optics</i> , <b>1990</b> , 181, 105-116		2

