

Carol A Rohl

List of Publications by Year in Descending Order

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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	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012 , 22, 1173-83	9.7	415
34	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <i>BMC Genomics</i> , 2010 , 11, 244	4.5	42
33	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. <i>BMC Genomics</i> , 2010 , 11, 473	4.5	27
32	Digital genome-wide ncRNA expression, including SnoRNAs, across 11 human tissues using polyA-neutral amplification. <i>PLoS ONE</i> , 2010 , 5, e11779	3.7	96
31	Pokefind: a novel topological filter for use with protein structure prediction. <i>Bioinformatics</i> , 2009 , 25, i281-8	7.2	8
30	Definition, conservation and epigenetics of housekeeping and tissue-enriched genes. <i>BMC Genomics</i> , 2009 , 10, 269	4.5	103
29	Knowledge based identification of essential signaling from genome-scale siRNA experiments. <i>BMC Systems Biology</i> , 2009 , 3, 80	3.5	11
28	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009 , 6, 647-9	21.6	139
27	Mapping the genetic architecture of gene expression in human liver. <i>PLoS Biology</i> , 2008 , 6, e107	9.7	768
26	Rapid knot detection and application to protein structure prediction. <i>Bioinformatics</i> , 2006 , 22, e252-9	7.2	32
25	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, 5361-6	11.5	138
24	Cataloging the relationships between proteins: a review of interaction databases. <i>Molecular Biotechnology</i> , 2006 , 34, 69-93	3	5
23	Prediction of CASP6 structures using automated Robetta protocols. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 157-66	4.2	114
22	Protein structure estimation from minimal restraints using Rosetta. <i>Methods in Enzymology</i> , 2005 , 394, 244-60	1.7	27
21	Modeling structurally variable regions in homologous proteins with rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 656-77	4.2	264
20	Protein structure prediction using Rosetta. <i>Methods in Enzymology</i> , 2004 , 383, 66-93	1.7	1142
19	An improved protein decoy set for testing energy functions for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 76-87	4.2	140

18	Automated prediction of CASP-5 structures using the Robetta server. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 524-33	4.2	241
17	Rosetta predictions in CASP5: successes, failures, and prospects for complete automation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 457-68	4.2	142
16	Protein-protein docking with simultaneous optimization of rigid-body displacement and side-chain conformations. <i>Journal of Molecular Biology</i> , 2003 , 331, 281-99	6.5	858
15	Exact solutions for chemical bond orientations from residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2002 , 22, 137-51	3	28
14	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, 15416-21	11.5	114
13	De novo determination of protein backbone structure from residual dipolar couplings using Rosetta. <i>Journal of the American Chemical Society</i> , 2002 , 124, 2723-9	16.4	153
12	De novo prediction of three-dimensional structures for major protein families. <i>Journal of Molecular Biology</i> , 2002 , 322, 65-78	6.5	206
11	Rosetta in CASP4: progress in ab initio protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 119-26	4.2	204
10	Solution structure of the sodium channel inactivation gate. <i>Biochemistry</i> , 1999 , 38, 855-61	3.2	116
9	Deciphering rules of helix stability in peptides. <i>Methods in Enzymology</i> , 1998 , 295, 1-26	1.7	103
8	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, 8435-42	3.2	149
7	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> , 1996 , 5, 1687-96	6.3	67
6	Helix propagation and N-cap propensities of the amino acids measured in alanine-based peptides in 40 volume percent trifluoroethanol. <i>Protein Science</i> , 1996 , 5, 2623-37	6.3	239
5	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, 2383-91	6.3	86
4	Exchange kinetics of individual amide protons in ¹⁵ N-labeled helical peptides measured by isotope-edited NMR. <i>Biochemistry</i> , 1994 , 33, 7760-7	3.2	90
3	Kinetics of amide proton exchange in helical peptides of varying chain lengths. Interpretation by the Lifson-Roig equation. <i>Biochemistry</i> , 1992 , 31, 1263-9	3.2	119
2	BEDT-TTF Salts with Square-Planar Gold(III) Complex Anions: [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		2
1	Crystal structure and electrical properties of (BEDT-TTF) ₂ Cp(CN) ₅ [(solvent) _x . <i>Synthetic Metals</i> , 1989 , 33, 1-9	3.6	13

