

# Robert O Fox

## 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.

48  
papers

3,067  
citations

23  
h-index

49  
g-index

49  
ext. papers

3,195  
ext. citations

11  
avg, IF

4.5  
L-index

#	Paper	IF	Citations
48	Characterizing the role of ensemble modulation in mutation-induced changes in binding affinity. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 6785-93	16.4	12
47	Exploring the impact of polyproline II (PII) conformational bias on the binding of peptides to the SEM-5 SH3 domain. <i>Protein Science</i> , <b>2008</b> , 17, 1200-11	6.3	19
46	Overexpression and functional characterization of the extracellular domain of the human alpha1 glycine receptor. <i>Biochemistry</i> , <b>2008</b> , 47, 9803-10	3.2	8
45	NMR solution structure and backbone dynamics of domain III of the E protein of tick-borne Langat flavivirus suggests a potential site for molecular recognition. <i>Protein Science</i> , <b>2006</b> , 15, 1342-55	6.3	20
44	The crystal structure of the E. coli stress protein YciF. <i>Protein Science</i> , <b>2006</b> , 15, 2605-11	6.3	20
43	The crystal structure of the cis-proline to glycine variant (P114G) of ribonuclease A. <i>Protein Science</i> , <b>2005</b> , 14, 2862-70	6.3	12
42	Directed discovery of bivalent peptide ligands to an SH3 domain. <i>Protein Science</i> , <b>2004</b> , 13, 626-32	6.3	16
41	Backbone and side chain resonance assignments of domain III of the tick-borne Langat flavivirus envelope protein. <i>Journal of Biomolecular NMR</i> , <b>2004</b> , 29, 535-6	3	2
40	Escherichia coli stress protein YciF: expression, crystallization and preliminary crystallographic analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2004</b> , 60, 2389-90		2
39	Functional reconstitution and characterization of recombinant human alpha 1-glycine receptors. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 20981-8	5.4	27
38	Structural and functional linkages between subunit interfaces in mammalian pyruvate kinase. <i>Journal of Molecular Biology</i> , <b>2001</b> , 312, 525-40	6.5	44
37	The development of the GPCPC protein crystallography beamline at CAMD. <i>AIP Conference Proceedings</i> , <b>2001</b> ,	0	1
36	Mapping RNA-protein interactions in ribonuclease P from Escherichia coli using disulfide-linked EDTA-Fe. <i>Journal of Molecular Biology</i> , <b>2000</b> , 296, 19-31	6.5	48
35	Calibration of spiral-readout image-plate detectors. <i>Journal of Applied Crystallography</i> , <b>1999</b> , 32, 65-70	3.8	1
34	Directed cleavage of RNA with protein-tethered EDTA-Fe. <i>Methods</i> , <b>1999</b> , 18, 78-84	4.6	19
33	Stability studies of amino acid substitutions at tyrosine 27 of the staphylococcal nuclease beta-barrel. <i>Biochemistry</i> , <b>1997</b> , 36, 12167-74	3.2	7
32	Comparison of straight chain and cyclic unnatural amino acids embedded in the core of staphylococcal nuclease. <i>Protein Science</i> , <b>1997</b> , 6, 1621-6	6.3	15

31	Water cluster calibration reduces mass error in electrospray ionization mass spectrometry of proteins. <i>Journal of the American Society for Mass Spectrometry</i> , <b>1997</b> , 8, 1158-1164	3.5	23
30	Mobile unnatural amino acid side chains in the core of staphylococcal nuclease. <i>Protein Science</i> , <b>1996</b> , 5, 1026-31	6.3	30
29	Mapping the structure of a non-native state of staphylococcal nuclease. <i>Nature Structural Biology</i> , <b>1996</b> , 3, 59-66		46
28	Stabilization of a strained protein loop conformation through protein engineering. <i>Protein Science</i> , <b>1995</b> , 4, 484-95	6.3	9
27	Proline cis-trans isomerization in staphylococcal nuclease: multi-substrate free energy perturbation calculations. <i>Protein Science</i> , <b>1995</b> , 4, 636-54	6.3	18
26	Crystallization and preliminary X-ray investigation of the recombinant <i>Trypanosoma brucei</i> rhodesiense calmodulin. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1995</b> , 21, 354-7	4.2	1
25	Interactions in nonnative and truncated forms of staphylococcal nuclease as indicated by mutational free energy changes. <i>Protein Science</i> , <b>1995</b> , 4, 1815-23	6.3	10
24	Capillary electrophoresis of <i>S. nuclease</i> mutants. <i>Journal of Chromatography A</i> , <b>1995</b> , 705, 135-54	4.5	49
23	Charge and size effects in the capillary zone electrophoresis of nuclease A and its variants. <i>Electrophoresis</i> , <b>1995</b> , 16, 595-603	3.6	10
22	The importance of anchorage in determining a strained protein loop conformation. <i>Protein Science</i> , <b>1994</b> , 3, 549-56	6.3	12
21	Stability and peptide binding affinity of an SH3 domain from the <i>Caenorhabditis elegans</i> signaling protein Sem-5. <i>Protein Science</i> , <b>1994</b> , 3, 1261-6	6.3	59
20	Structural determinants of peptide-binding orientation and of sequence specificity in SH3 domains. <i>Nature</i> , <b>1994</b> , 372, 375-9	50.4	472
19	Engineering alternative beta-turn types in staphylococcal nuclease. <i>Biochemistry</i> , <b>1994</b> , 33, 5021-30	3.2	22
18	Mapping staphylococcal nuclease conformation using an EDTA-Fe derivative attached to genetically engineered cysteine residues. <i>Biochemistry</i> , <b>1994</b> , 33, 13625-41	3.2	42
17	Protein Folding Intermediates Characterized by Pulsed Hydrogen Exchange. <i>Techniques in Protein Chemistry</i> , <b>1994</b> , 5, 447-454		1
16	Effect of proline mutations on the stability and kinetics of folding of staphylococcal nuclease. <i>Biochemistry</i> , <b>1993</b> , 32, 2534-41	3.2	39
15	Oxidative polypeptide cleavage mediated by EDTA-Fe covalently linked to cysteine residues. <i>Biochemistry</i> , <b>1993</b> , 32, 12761-7	3.2	76
14	Mapping interactions between the catalytic domain of resolvase and its DNA substrate using cysteine-coupled EDTA-iron. <i>Biochemistry</i> , <b>1993</b> , 32, 2979-86	3.2	39

13	Conformational substrates and uncertainty in macromolecular free energy calculations. <i>The Journal of Physical Chemistry</i> , <b>1993</b> , 97, 3409-3417		49
12	Stress and strain in staphylococcal nuclease. <i>Protein Science</i> , <b>1993</b> , 2, 838-50	6.3	30
11	NMR analysis of staphylococcal nuclease thermal quench refolding kinetics. <i>Protein Science</i> , <b>1993</b> , 2, 851-8	6.3	25
10	The crystal structure of staphylococcal nuclease refined at 1.7 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1991</b> , 10, 92-105	4.2	232
9	2.9 Å resolution structure of an anti-dinitrophenyl-spin-label monoclonal antibody Fab fragment with bound hapten. <i>Journal of Molecular Biology</i> , <b>1991</b> , 221, 239-56	6.5	16
8	Fluorescence and conformational stability studies of Staphylococcus nuclease and its mutants, including the less stable nuclease-concanavalin A hybrids. <i>Biochemistry</i> , <b>1991</b> , 30, 1193-9	3.2	41
7	Transfer of a beta-turn structure to a new protein context. <i>Nature</i> , <b>1989</b> , 339, 73-6	50.4	91
6	A magnetization-transfer nuclear magnetic resonance study of the folding of staphylococcal nuclease. <i>Biochemistry</i> , <b>1989</b> , 28, 362-70	3.2	131
5	Crystallization of an anti-2,2,6,6-tetramethyl-1-piperidinyloxy-dinitrophenyl monoclonal antibody Fab fragment with and without bound hapten. <i>Journal of Molecular Biology</i> , <b>1988</b> , 203, 829-30	6.5	8
4	Proline isomerism in staphylococcal nuclease characterized by NMR and site-directed mutagenesis. <i>Nature</i> , <b>1987</b> , 329, 266-8	50.4	165
3	Multiple conformations of a protein demonstrated by magnetization transfer NMR spectroscopy. <i>Nature</i> , <b>1986</b> , 320, 192-4	50.4	97
2	Recombinant antibodies possessing novel effector functions. <i>Nature</i> , <b>1984</b> , 312, 604-8	50.4	266
1	A voltage-gated ion channel model inferred from the crystal structure of alamethicin at 1.5-Å resolution. <i>Nature</i> , <b>1982</b> , 300, 325-30	50.4	685