

Robert O Fox

List of Publications by Year in descending order

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49
papers

3,395
citations

218677

26
h-index

206112

48
g-index

49
all docs

49
docs citations

49
times ranked

2308
citing authors

#	ARTICLE	IF	CITATIONS
1	Frederic Richards (1925–2009). <i>Nature</i> , 2009, 457, 976-976.	27.8	0
2	Characterizing the Role of Ensemble Modulation in Mutation-Induced Changes in Binding Affinity. <i>Journal of the American Chemical Society</i> , 2009, 131, 6785-6793.	13.7	14
3	Exploring the impact of polyproline II (P _{II}) conformational bias on the binding of peptides to the SEM5 SH3 domain. <i>Protein Science</i> , 2008, 17, 1200-1211.	7.6	21
4	Overexpression and Functional Characterization of the Extracellular Domain of the Human $\alpha 1$ Glycine Receptor. <i>Biochemistry</i> , 2008, 47, 9803-9810.	2.5	10
5	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> , 2006, 15, 1342-1355.	7.6	26
6	The crystal structure of the E. coli stress protein YciF. <i>Protein Science</i> , 2006, 15, 2605-2611.	7.6	24
7	The crystal structure of the cis-proline to glycine variant (P114G) of ribonuclease A. <i>Protein Science</i> , 2005, 14, 2862-2870.	7.6	14
8	Directed discovery of bivalent peptide ligands to an SH3 domain. <i>Protein Science</i> , 2004, 13, 626-632.	7.6	17
9	Letter to the Editor: Backbone and side chain resonance assignments of domain III of the tick-borne Langat flavivirus envelope protein. <i>Journal of Biomolecular NMR</i> , 2004, 29, 535-536.	2.8	2
10	Escherichia coli stress protein YciF: expression, crystallization and preliminary crystallographic analysis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2389-2390.	2.5	2
11	Structural and Functional Linkages Between Subunit Interfaces in Mammalian Pyruvate Kinase. <i>Journal of Molecular Biology</i> , 2001, 312, 525-540.	4.2	47
12	The development of the GPCPC protein crystallography beamline at CAMD. <i>AIP Conference Proceedings</i> , 2001, , .	0.4	1
13	Functional Reconstitution and Characterization of Recombinant Human $\alpha 1$ -Glycine Receptors. <i>Journal of Biological Chemistry</i> , 2001, 276, 20981-20988.	3.4	34
14	Mapping RNA-protein interactions in ribonuclease P from Escherichia coli using disulfide-linked EDTA-Fe ¹ Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 2000, 296, 19-31.	4.2	50
15	Calibration of spiral-readout image-plate detectors. <i>Journal of Applied Crystallography</i> , 1999, 32, 65-70.	4.5	5
16	Directed Cleavage of RNA with Protein-Tethered EDTA-Fe. <i>Methods</i> , 1999, 18, 78-84.	3.8	19
17	Stability Studies of Amino Acid Substitutions at Tyrosine 27 of the Staphylococcal Nuclease $\beta 2$ -Barrel. <i>Biochemistry</i> , 1997, 36, 12167-12174.	2.5	7
18	Comparison of straight chain and cyclic unnatural amino acids embedded in the core of staphylococcal nuclease. <i>Protein Science</i> , 1997, 6, 1621-1626.	7.6	16

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19	Water cluster calibration reduces mass error in electrospray ionization mass spectrometry of proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 1997, 8, 1158-1164.	2.8	24
20	Mobile unnatural amino acid side chains in the core of staphylococcal nuclease. <i>Protein Science</i> , 1996, 5, 1026-1031.	7.6	30
21	Mapping the structure of a non-native state of staphylococcal nuclease. <i>Nature Structural Biology</i> , 1996, 3, 59-66.	9.7	47
22	Charge and size effects in the capillary zone electrophoresis of nuclease A and its variants. <i>Electrophoresis</i> , 1995, 16, 595-603.	2.4	13
23	Crystallization and preliminary X-ray investigation of the recombinant <i>Trypanosoma brucei</i> rhodesiense calmodulin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 354-357.	2.6	1
24	Interactions in nonnative and truncated forms of staphylococcal nuclease as indicated by mutational free energy changes. <i>Protein Science</i> , 1995, 4, 1815-1823.	7.6	10
25	Capillary electrophoresis of <i>S. nuclease</i> mutants. <i>Journal of Chromatography A</i> , 1995, 705, 135-154.	3.7	52
26	Stabilization of a strained protein loop conformation through protein engineering. <i>Protein Science</i> , 1995, 4, 484-495.	7.6	11
27	Proline <i>cis</i> → <i>trans</i> isomerization in staphylococcal nuclease: Multi-state free energy perturbation calculations. <i>Protein Science</i> , 1995, 4, 636-654.	7.6	21
28	The importance of anchorage in determining a strained protein loop conformation. <i>Protein Science</i> , 1994, 3, 549-556.	7.6	13
29	Stability and peptide binding affinity of an SH3 domain from the <i>Caenorhabditis elegans</i> signaling protein Sem-5. <i>Protein Science</i> , 1994, 3, 1261-1266.	7.6	63
30	Structural determinants of peptide-binding orientation and of sequence specificity in SH3 domains. <i>Nature</i> , 1994, 372, 375-379.	27.8	518
31	Engineering Alternative β -Turn Types in Staphylococcal Nuclease. <i>Biochemistry</i> , 1994, 33, 5021-5030.	2.5	27
32	Mapping Staphylococcal Nuclease Conformation Using an EDTA-Fe Derivative Attached to Genetically Engineered Cysteine Residues. <i>Biochemistry</i> , 1994, 33, 13625-13641.	2.5	46
33	Protein Folding Intermediates Characterized by Pulsed Hydrogen Exchange. <i>Techniques in Protein Chemistry</i> , 1994, 5, 447-454.	0.3	1
34	Stress and strain in staphylococcal nuclease. <i>Protein Science</i> , 1993, 2, 838-850.	7.6	32
35	NMR analysis of staphylococcal nuclease thermal quench refolding kinetics. <i>Protein Science</i> , 1993, 2, 851-858.	7.6	28
36	Effect of proline mutations on the stability and kinetics of folding of staphylococcal nuclease. <i>Biochemistry</i> , 1993, 32, 2534-2541.	2.5	42

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37	Oxidative polypeptide cleavage mediated by EDTA-iron covalently linked to cysteine residues. <i>Biochemistry</i> , 1993, 32, 12761-12767.	2.5	81
38	Mapping interactions between the catalytic domain of resolvase and its DNA substrate using cysteine-coupled EDTA-iron. <i>Biochemistry</i> , 1993, 32, 2979-2986.	2.5	45
39	Conformational substrates and uncertainty in macromolecular free energy calculations. <i>The Journal of Physical Chemistry</i> , 1993, 97, 3409-3417.	2.9	52
40	2.9 Å resolution structure of an anti-dinitrophenyl-spin-label monoclonal antibody Fab fragment with bound hapten. <i>Journal of Molecular Biology</i> , 1991, 221, 239-256.	4.2	28
41	Fluorescence and conformational stability studies of <i>Staphylococcus</i> nuclease and its mutants, including the less stable nuclease-concanavalin A hybrids. <i>Biochemistry</i> , 1991, 30, 1193-1199.	2.5	47
42	The crystal structure of staphylococcal nuclease refined at 1.7 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 92-105.	2.6	256
43	Transfer of a β -turn structure to a new protein context. <i>Nature</i> , 1989, 339, 73-76.	27.8	97
44	A magnetization-transfer nuclear magnetic resonance study of the folding of staphylococcal nuclease. <i>Biochemistry</i> , 1989, 28, 362-370.	2.5	143
45	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> , 1988, 203, 829-830.	4.2	9
46	Proline isomerism in staphylococcal nuclease characterized by NMR and site-directed mutagenesis. <i>Nature</i> , 1987, 329, 266-268.	27.8	180
47	Multiple conformations of a protein demonstrated by magnetization transfer NMR spectroscopy. <i>Nature</i> , 1986, 320, 192-194.	27.8	114
48	Recombinant antibodies possessing novel effector functions. <i>Nature</i> , 1984, 312, 604-608.	27.8	304
49	A voltage-gated ion channel model inferred from the crystal structure of alamethicin at 1.5 Å resolution. <i>Nature</i> , 1982, 300, 325-330.	27.8	751