Robert O Fox

List of Publications by Year in descending order

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49 papers 3,395 citations

26 h-index 205818 48 g-index

49 all docs 49 docs citations

49 times ranked 2308 citing authors

#	Article	IF	CITATIONS
1	A voltage-gated ion channel model inferred from the crystal structure of alamethicin at 1.5-Ã resolution. Nature, 1982, 300, 325-330.	13.7	751
2	Structural determinants of peptide-binding orientation and of sequence specificity in SH3 domains. Nature, 1994, 372, 375-379.	13.7	518
3	Recombinant antibodies possessing novel effector functions. Nature, 1984, 312, 604-608.	13.7	304
4	The crystal structure of staphylococcal nuclease refined at $1.7~\tilde{A}$ resolution. Proteins: Structure, Function and Bioinformatics, 1991 , 10 , $92-105$.	1.5	256
5	Proline isomerism in staphylococcal nuclease characterized by NMR and site-directed mutagenesis. Nature, 1987, 329, 266-268.	13.7	180
6	A magnetization-transfer nuclear magnetic resonance study of the folding of staphylococcal nuclease. Biochemistry, 1989, 28, 362-370.	1.2	143
7	Multiple conformations of a protein demonstrated by magnetization transfer NMR spectroscopy. Nature, 1986, 320, 192-194.	13.7	114
8	Transfer of a Î ² -turn structure to a new protein context. Nature, 1989, 339, 73-76.	13.7	97
9	Oxidative polypeptide cleavage mediated by EDTA-iron covalently linked to cysteine residues. Biochemistry, 1993, 32, 12761-12767.	1.2	81
10	Stability and peptide binding affinity of an SH3 domain from the <i>Caenorhabditis elegans</i> signaling protein Semâ€5. Protein Science, 1994, 3, 1261-1266.	3.1	63
11	Conformational substrates and uncertainty in macromolecular free energy calculations. The Journal of Physical Chemistry, 1993, 97, 3409-3417.	2.9	52
12	Capillary electrophoresis of S. nuclease mutants. Journal of Chromatography A, 1995, 705, 135-154.	1.8	52
13	Mapping RNA-protein interactions in ribonuclease P from Escherichia coli using disulfide-linked EDTA-fe 1 1Edited by K. Nagai. Journal of Molecular Biology, 2000, 296, 19-31.	2.0	50
14	Fluorescence and conformational stability studies of Staphylococcus nuclease and its mutants, including the less stable nuclease-concanavalin A hybrids. Biochemistry, 1991, 30, 1193-1199.	1.2	47
15	Mapping the structure of a non-native state of staphylococcal nuclease. Nature Structural Biology, 1996, 3, 59-66.	9.7	47
16	Structural and Functional Linkages Between Subunit Interfaces in Mammalian Pyruvate Kinase. Journal of Molecular Biology, 2001, 312, 525-540.	2.0	47
17	Mapping Staphylococcal Nuclease Conformation Using an EDTA-Fe Derivative Attached to Genetically Engineered Cysteine Residues. Biochemistry, 1994, 33, 13625-13641.	1.2	46
18	Mapping interactions between the catalytic domain of resolvase and its DNA substrate using cysteine-coupled EDTA-iron. Biochemistry, 1993, 32, 2979-2986.	1.2	45

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19	Effect of proline mutations on the stability and kinetics of folding of staphylococcal nuclease. Biochemistry, 1993, 32, 2534-2541.	1.2	42
20	Functional Reconstitution and Characterization of Recombinant Human $\hat{l}\pm 1$ -Glycine Receptors. Journal of Biological Chemistry, 2001, 276, 20981-20988.	1.6	34
21	Stress and strain in staphylococcal nuclease. Protein Science, 1993, 2, 838-850.	3.1	32
22	Mobile unnatural amino acid side chains in the core of staphylococcal nuclease. Protein Science, 1996, 5, 1026-1031.	3.1	30
23	2·9Åresolution structure of an anti-dinitrophenyl-spin-label monoclonal antibody Fab fragment with bound hapten. Journal of Molecular Biology, 1991, 221, 239-256.	2.0	28
24	NMR analysis of staphylococcal nuclease thermal quench refolding kinetics. Protein Science, 1993, 2, 851-858.	3.1	28
25	Engineering Alternative .betaTurn Types in Staphylococcal Nuclease. Biochemistry, 1994, 33, 5021-5030.	1.2	27
26	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. Protein Science, 2006, 15, 1342-1355.	3.1	26
27	Water cluster calibration reduces mass error in electrospray ionization mass spectrometry of proteins. Journal of the American Society for Mass Spectrometry, 1997, 8, 1158-1164.	1.2	24
28	The crystal structure of the E. colistress protein YciF. Protein Science, 2006, 15, 2605-2611.	3.1	24
29	Proline <i>cisâ€trans</i> isomerization in staphylococcal nuclease: Multiâ€substate free energy perturbation calculations. Protein Science, 1995, 4, 636-654.	3.1	21
30	Exploring the impact of polyproline II (P _{II}) conformational bias on the binding of peptides to the SEMâ€5 SH3 domain. Protein Science, 2008, 17, 1200-1211.	3.1	21
31	Directed Cleavage of RNA with Protein-Tethered EDTA–Fe. Methods, 1999, 18, 78-84.	1.9	19
32	Directed discovery of bivalent peptide ligands to an SH3 domain. Protein Science, 2004, 13, 626-632.	3.1	17
33	Comparison of straight chain and cyclic unnatural amino acids embedded in the core of staphylococcal nuclease. Protein Science, 1997, 6, 1621-1626.	3.1	16
34	The crystal structure of thecis-proline to glycine variant (P114G) of ribonuclease A. Protein Science, 2005, 14, 2862-2870.	3.1	14
35	Characterizing the Role of Ensemble Modulation in Mutation-Induced Changes in Binding Affinity. Journal of the American Chemical Society, 2009, 131, 6785-6793.	6.6	14
36	The importance of anchorage in determining a strained protein loop conformation. Protein Science, 1994, 3, 549-556.	3.1	13

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37	Charge and size effects in the capillary zone electrophoresis of nuclease A and its variants. Electrophoresis, 1995, 16, 595-603.	1.3	13
38	Stabilization of a strained protein loop conformation through protein engineering. Protein Science, 1995, 4, 484-495.	3.1	11
39	Interactions in nonnative and truncated forms of staphylococcal nuclease as indicated by mutational free energy changes. Protein Science, 1995, 4, 1815-1823.	3.1	10
40	Overexpression and Functional Characterization of the Extracellular Domain of the Human $\hat{l}\pm 1$ Glycine Receptor. Biochemistry, 2008, 47, 9803-9810.	1.2	10
41	Crystallization of an anti-2,2,6,6-tetramethyl-1-piperidinyloxy-dinitrophenyl monoclonal antibody Fab fragment with and without bound hapten. Journal of Molecular Biology, 1988, 203, 829-830.	2.0	9
42	Stability Studies of Amino Acid Substitutions at Tyrosine 27 of the Staphylococcal Nuclease β-Barrelâ€. Biochemistry, 1997, 36, 12167-12174.	1.2	7
43	Calibration of spiral-readout image-plate detectors. Journal of Applied Crystallography, 1999, 32, 65-70.	1.9	5
44	Letter to the Editor: Backbone and side chain resonance assignments of domain III of the tick-borne Langat flavivirus envelope protein. Journal of Biomolecular NMR, 2004, 29, 535-536.	1.6	2
45	Escherichia colistress protein YciF: expression, crystallization and preliminary crystallographic analysis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2389-2390.	2.5	2
46	Crystallization and preliminary X-ray investigation of the recombinantTrypanosoma brucei rhodesiense calmodulin. Proteins: Structure, Function and Bioinformatics, 1995, 21, 354-357.	1.5	1
47	The development of the GCPCC protein crystallography beamline at CAMD. AIP Conference Proceedings, 2001, , .	0.3	1
48	Protein Folding Intermediates Characterized by Pulsed Hydrogen Exchange. Techniques in Protein Chemistry, 1994, 5, 447-454.	0.3	1
49	Frederic Richards (1925–2009). Nature, 2009, 457, 976-976.	13.7	O