

George D Rose

List of Publications by Year in descending order

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67
papers

8,471
citations

76326

40
h-index

118850

62
g-index

72
all docs

72
docs citations

72
times ranked

6173
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein folding â€œseeing is deceiving. Protein Science, 2021, 30, 1606-1616.	7.6	26
2	Building blocks of protein structures: Physics meets biology. Physical Review E, 2021, 104, 014402.	2.1	10
3	Reframing the Protein Folding Problem: Entropy as Organizer. Biochemistry, 2021, 60, 3753-3761.	2.5	18
4	Cover Image, Volume 87, Issue 5. Proteins: Structure, Function and Bioinformatics, 2019, 87, C1.	2.6	0
5	What is life? Part II. Proteins: Structure, Function and Bioinformatics, 2019, 87, 174-175.	2.6	4
6	Ramachandran maps for side chains in globular proteins. Proteins: Structure, Function and Bioinformatics, 2019, 87, 357-364.	2.6	18
7	How the hydrophobic factor drives protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12462-12466.	7.1	67
8	On interpretation of protein Xâ€ray structures: Planarity of the peptide unit. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1687-1692.	2.6	7
9	Molten globules, entropy-driven conformational change and protein folding. Current Opinion in Structural Biology, 2013, 23, 4-10.	5.7	112
10	THE OPEN-ENDED INTELLECTUAL LEGACY OF GNR. , 2013, , 38-45.		1
11	Reducing the dimensionality of the proteinâ€folding search problem. Protein Science, 2012, 21, 1231-1240.	7.6	7
12	A thermodynamic definition of protein domains. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9420-9425.	7.1	45
13	Counting peptideâ€water hydrogen bonds in unfolded proteins. Protein Science, 2011, 20, 417-427.	7.6	19
14	Comment on â€œRevisiting the Ramachandran plot from a new angleâ€ Protein Science, 2011, 20, 1771-1773.	7.6	4
15	Redrawing the Ramachandran plot after inclusion of hydrogen-bonding constraints. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 109-113.	7.1	71
16	Physicalâ€chemical determinants of coil conformations in globular proteins. Protein Science, 2010, 19, 1127-1136.	7.6	13
17	Dry molten globule intermediates and the mechanism of protein unfolding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2725-2737.	2.6	100
18	In memoriam. Proteins: Structure, Function and Bioinformatics, 2009, 75, 535-539.	2.6	0

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19	A simple model for polyproline II structure in unfolded states of alanine-based peptides. <i>Protein Science</i> , 2009, 11, 2437-2455.	7.6	124
20	A novel method reveals that solvent water favors polyproline II over $\hat{\nu}^2$ -strand conformation in peptides and unfolded proteins: conditional hydrophobic accessible surface area (CHASA). <i>Protein Science</i> , 2009, 14, 111-118.	7.6	76
21	Structures, basins, and energies: A deconstruction of the Protein Coil Library. <i>Protein Science</i> , 2008, 17, 1151-1161.	7.6	42
22	Structure and Energetics of the Hydrogen-Bonded Backbone in Protein Folding. <i>Annual Review of Biochemistry</i> , 2008, 77, 339-362.	11.1	355
23	Assessing the solvent-dependent surface area of unfolded proteins using an ensemble model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3321-3326.	7.1	38
24	Physical-chemical determinants of turn conformations in globular proteins. <i>Protein Science</i> , 2007, 16, 1720-1727.	7.6	24
25	Building native protein conformation from NMR backbone chemical shifts using Monte Carlo fragment assembly. <i>Protein Science</i> , 2007, 16, 1515-1521.	7.6	33
26	A molecular mechanism for osmolyte-induced protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13997-14002.	7.1	594
27	Secondary structure determines protein topology. <i>Protein Science</i> , 2006, 15, 1829-1834.	7.6	35
28	A backbone-based theory of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16623-16633.	7.1	433
29	Do all backbone polar groups in proteins form hydrogen bonds?. <i>Protein Science</i> , 2005, 14, 1911-1917.	7.6	151
30	Hydrogen-bonded turns in proteins: The case for a recount. <i>Protein Science</i> , 2005, 14, 2910-2914.	7.6	41
31	Are proteins made from a limited parts list?. <i>Trends in Biochemical Sciences</i> , 2005, 30, 73-80.	7.5	59
32	The Protein Coil Library: A structural database of nonhelix, nonstrand fragments derived from the PDB. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 58, 852-854.	2.6	92
33	Does secondary structure determine tertiary structure in proteins?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 338-343.	2.6	17
34	From The Cover: Building native protein conformation from highly approximate backbone torsion angles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16227-16232.	7.1	56
35	Sterics and Solvation Winnow Accessible Conformational Space for Unfolded Proteins. <i>Journal of Molecular Biology</i> , 2005, 353, 873-887.	4.2	42
36	Reassessing random-coil statistics in unfolded proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12497-12502.	7.1	306

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37	Steric restrictions in protein folding: An α -helix cannot be followed by a contiguous α -strand. <i>Protein Science</i> , 2004, 13, 633-639.	7.6	58
38	Polyproline II helix is the preferred conformation for unfolded polyalanine in water. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 502-507.	2.6	158
39	Ab Initio Protein Folding Using LINUS. <i>Methods in Enzymology</i> , 2004, 383, 48-66.	1.0	31
40	Local Secondary Structure Content Predicts Folding Rates for Simple, Two-state Proteins. <i>Journal of Molecular Biology</i> , 2003, 327, 1149-1154.	4.2	105
41	RNABase: an annotated database of RNA structures. <i>Nucleic Acids Research</i> , 2003, 31, 502-504.	14.5	37
42	Protein structure prediction "An Ab initio approach. , 2003, , .		0
43	Polyproline II structure in a sequence of seven alanine residues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9190-9195.	7.1	478
44	Methinks it is like a folding curve. <i>Biophysical Chemistry</i> , 2002, 101-102, 167-171.	2.8	11
45	Ab initio prediction of protein structure using LINUS. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 489-495.	2.6	66
46	Perspective. <i>Protein Science</i> , 2001, 10, 1691-1693.	7.6	3
47	A protein taxonomy based on secondary structure. <i>Nature Structural Biology</i> , 1999, 6, 672-682.	9.7	105
48	Identifying two ancient enzymes in Archaea using predicted secondary structure alignment. <i>Nature Structural Biology</i> , 1999, 6, 750-754.	9.7	42
49	Is protein folding hierarchic? II. Folding intermediates and transition states. <i>Trends in Biochemical Sciences</i> , 1999, 24, 77-83.	7.5	379
50	Is protein folding hierarchic? I. Local structure and peptide folding. <i>Trends in Biochemical Sciences</i> , 1999, 24, 26-33.	7.5	488
51	A Complete Conformational Map for RNA. <i>Journal of Molecular Biology</i> , 1999, 291, 313-327.	4.2	56
52	Local Interactions in Protein Folding: Lessons from the α -Helix. <i>Journal of Biological Chemistry</i> , 1997, 272, 1413-1416.	3.4	136
53	Modeling Unfolded States of Proteins and Peptides. II. Backbone Solvent Accessibility. <i>Biochemistry</i> , 1997, 36, 2832-2835.	2.5	129
54	Protein folding and the Paracelsus challenge. <i>Nature Structural Biology</i> , 1997, 4, 512-514.	9.7	27

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55	LINUS: A hierarchic procedure to predict the fold of a protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 81-99.	2.6	257
56	Rigid domains in proteins: An algorithmic approach to their identification. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 38-48.	2.6	71
57	Interactions between hydrophobic side chains within α -helices. <i>Protein Science</i> , 1995, 4, 1305-1314.	7.6	79
58	<i>Response</i> : Possible Exceptions to Rules for α -Helix Termination by Glycine. <i>Science</i> , 1995, 269, 1451-1452.	12.6	0
59	Sequence determinants of the capping box, a stabilizing motif at the N-termini of α -helices. <i>Protein Science</i> , 1994, 3, 1741-1745.	7.6	120
60	Protein folding: Predicting predicting. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 1-3.	2.6	68
61	α -Helix-forming propensities in peptides and proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 85-97.	2.6	167
62	Molten globular characteristics of the native state of apomyoglobin. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 447-452.	8.2	67
63	Effects of alanine substitutions in α -helices of sperm whale myoglobin on protein stability. <i>Protein Science</i> , 1993, 2, 1099-1105.	7.6	51
64	Hydrogen bonding in globular proteins. <i>Journal of Molecular Biology</i> , 1992, 226, 1143-1159.	4.2	408
65	Turns in Peptides and Proteins. <i>Advances in Protein Chemistry</i> , 1985, 37, 1-109.	4.4	1,532
66	Hierarchic organization of domains in globular proteins. <i>Journal of Molecular Biology</i> , 1979, 134, 447-470.	4.2	228
67	A new algorithm for finding the peptide chain turns in a globular protein. <i>Journal of Molecular Biology</i> , 1977, 113, 153-164.	4.2	60