

Doug Barrick

List of Publications by Year in descending order

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72
papers

3,563
citations

109137

35
h-index

143772

57
g-index

77
all docs

77
docs citations

77
times ranked

2900
citing authors

#	ARTICLE	IF	CITATIONS
1	A collection of programs for one-dimensional Ising analysis of linear repeat proteins with point substitutions. <i>Protein Science</i> , 2021, 30, 168-186.	3.1	4
2	Analysis of Tandem Repeat Protein Folding Using Nearest-Neighbor Models. <i>Annual Review of Biophysics</i> , 2021, 50, 245-265.	4.5	12
3	Surface residues and nonadditive interactions stabilize a consensus homeodomain protein. <i>Biophysical Journal</i> , 2021, 120, 5267-5278.	0.2	2
4	The use of consensus sequence information to engineer stability and activity in proteins. <i>Methods in Enzymology</i> , 2020, 643, 149-179.	0.4	23
5	A Second Backbone: The Contribution of a Buried Asparagine Ladder to the Global and Local Stability of a Leucine-Rich Repeat Protein. <i>Biochemistry</i> , 2019, 58, 3480-3493.	1.2	11
6	Consensus sequence design as a general strategy to create hyperstable, biologically active proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11275-11284.	3.3	105
7	Functional instability allows access to DNA in longer transcription Activator-Like effector (TALE) arrays. <i>ELife</i> , 2019, 8, .	2.8	8
8	High-Pressure NMR and SAXS Reveals How Capping Modulates Folding Cooperativity of the pp32 Leucine-rich Repeat Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 1336-1349.	2.0	7
9	Extreme stability in de novo-designed repeat arrays is determined by unusually stable short-range interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7539-7544.	3.3	25
10	The consequences of cavity creation on the folding landscape of a repeat protein depend upon context. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8153-E8161.	3.3	17
11	Creating a Homeodomain with High Stability and DNA Binding Affinity by Sequence Averaging. <i>Journal of the American Chemical Society</i> , 2017, 139, 5051-5060.	6.6	24
12	Control of transcriptional activity by design of charge patterning in the intrinsically disordered RAM region of the Notch receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9243-E9252.	3.3	95
13	Synergistic enhancement of cellulase pairs linked by consensus ankyrin repeats: Determination of the roles of spacing, orientation, and enzyme identity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1043-1054.	1.5	4
14	High-Resolution Mapping of a Repeat Protein Folding Free Energy Landscape. <i>Biophysical Journal</i> , 2016, 111, 2368-2376.	0.2	32
15	Broken TALEs: Transcription Activator-like Effectors Populate Partly Folded States. <i>Biophysical Journal</i> , 2016, 111, 2395-2403.	0.2	10
16	Direct NMR Detection of Bifurcated Hydrogen Bonding in the \pm -Helix N-Caps of Ankyrin Repeat Proteins. <i>Journal of the American Chemical Society</i> , 2015, 137, 1008-1011.	6.6	22
17	Highly polarized C-terminal transition state of the leucine-rich repeat domain of PP32 is governed by local stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2298-306.	3.3	19
18	A Naturally Occurring Repeat Protein with High Internal Sequence Identity Defines a New Class of TPR-like Proteins. <i>Structure</i> , 2015, 23, 2055-2065.	1.6	28

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19	Effects of Linker Length and Transient Secondary Structure Elements in the Intrinsically Disordered Notch RAM Region on Notch Signaling. <i>Journal of Molecular Biology</i> , 2015, 427, 3587-3597.	2.0	18
20	Capping motifs stabilize the leucine-rich repeat protein PP32 and rigidify adjacent repeats. <i>Protein Science</i> , 2014, 23, 801-811.	3.1	19
21	Direct Observation of Parallel Folding Pathways Revealed Using a Symmetric Repeat Protein System. <i>Biophysical Journal</i> , 2014, 107, 220-232.	0.2	49
22	Insertion of Endocellulase Catalytic Domains into Thermostable Consensus Ankyrin Scaffolds: Effects on Stability and Cellulolytic Activity. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6684-6696.	1.4	16
23	Mapping the Deltex-Binding Surface on the Notch Ankyrin Domain Using Analytical Ultracentrifugation. <i>Journal of Molecular Biology</i> , 2011, 414, 243-259.	2.0	9
24	Size and Sequence and the Volume Change of Protein Folding. <i>Journal of the American Chemical Society</i> , 2011, 133, 6020-6027.	6.6	101
25	The Contribution of Entropy, Enthalpy, and Hydrophobic Desolvation to Cooperativity in Repeat-Protein Folding. <i>Structure</i> , 2011, 19, 349-360.	1.6	67
26	The folding of single domain proteinsâ€”have we reached a consensus?. <i>Current Opinion in Structural Biology</i> , 2011, 21, 12-24.	2.6	132
27	Deletion of internal structured repeats increases the stability of a leucine-rich repeat protein, YopM. <i>Biophysical Chemistry</i> , 2011, 159, 152-161.	1.5	14
28	Thermodynamic Analysis of the CSL-Notch Interaction. <i>Journal of Biological Chemistry</i> , 2010, 285, 6681-6692.	1.6	40
29	Unique Features of the Folding Landscape of a Repeat Protein Revealed by Pressure Perturbation. <i>Biophysical Journal</i> , 2010, 98, 2712-2721.	0.2	38
30	Predicting repeat protein folding kinetics from an experimentally determined folding energy landscape. <i>Protein Science</i> , 2009, 18, 58-68.	3.1	14
31	What have we learned from the studies of two-state folders, and what are the unanswered questions about two-state protein folding?. <i>Physical Biology</i> , 2009, 6, 015001.	0.8	44
32	Chapter 4 Analysis of Repeat-Protein Folding Using Nearest-Neighbor Statistical Mechanical Models. <i>Methods in Enzymology</i> , 2009, 455, 95-125.	0.4	41
33	C-terminal deletion of leucine-rich repeats from YopM reveals a heterogeneous distribution of stability in a cooperatively folded protein. <i>Protein Science</i> , 2009, 18, 1948-1960.	3.1	27
34	Structure and stability of the ankyrin domain of the <i>Drosophila</i> Notch receptor. <i>Protein Science</i> , 2009, 12, 2622-2632.	3.1	89
35	Biological Regulation via Ankyrin Repeat Folding. <i>ACS Chemical Biology</i> , 2009, 4, 19-22.	1.6	15
36	Folding thermodynamics and kinetics of the leucine-rich repeat domain of the virulence factor Internalin B. <i>Protein Science</i> , 2008, 17, 43-53.	3.1	24

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37	Folding landscapes of ankyrin repeat proteins: experiments meet theory. <i>Current Opinion in Structural Biology</i> , 2008, 18, 27-34.	2.6	92
38	The Leucine-Rich Repeat Domain of Internalin B Folds along a Polarized N-Terminal Pathway. <i>Structure</i> , 2008, 16, 705-714.	1.6	42
39	Protein Folding and Stability Using Denaturants. <i>Methods in Cell Biology</i> , 2008, 84, 295-325.	0.5	59
40	Thermodynamics, Kinetics, and Salt dependence of Folding of YopM, a Large Leucine-rich Repeat Protein. <i>Journal of Molecular Biology</i> , 2008, 383, 1195-1209.	2.0	22
41	Repeat-protein folding: New insights into origins of cooperativity, stability, and topology. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 83-99.	1.4	83
42	Rerouting the Folding Pathway of the Notch Ankyrin Domain by Reshaping the Energy Landscape. <i>Journal of the American Chemical Society</i> , 2008, 130, 5681-5688.	6.6	52
43	The effects of conformational heterogeneity on the binding of the Notch intracellular domain to effector proteins: a case of biologically tuned disorder. <i>Biochemical Society Transactions</i> , 2008, 36, 157-166.	1.6	46
44	Predicting coupling limits from an experimentally determined energy landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4907-4912.	3.3	34
45	Quantitative Dissection of the Notch:CSL Interaction: Insights into the Notch-mediated Transcriptional Switch. <i>Journal of Molecular Biology</i> , 2007, 365, 577-589.	2.0	89
46	Enhancing the Stability and Folding Rate of a Repeat Protein through the Addition of Consensus Repeats. <i>Journal of Molecular Biology</i> , 2007, 365, 1187-1200.	2.0	53
47	The Notch Transcription Activation Complex Makes Its Move. <i>Cell</i> , 2006, 124, 883-885.	13.5	43
48	The Role of Introns in Repeat Protein Gene Formation. <i>Journal of Molecular Biology</i> , 2006, 360, 258-266.	2.0	21
49	The Notch Ankyrin Domain Folds via a Discrete, Centralized Pathway. <i>Structure</i> , 2006, 14, 1303-1312.	1.6	49
50	An improved experimental system for determining small folding entropy changes resulting from proline to alanine substitutions. <i>Protein Science</i> , 2005, 14, 2429-2435.	3.1	12
51	Structure and Notch Receptor Binding of the Tandem WWE Domain of Deltex. <i>Structure</i> , 2005, 13, 1599-1611.	1.6	51
52	Effect of Multiple Prolyl Isomerization Reactions on the Stability and Folding Kinetics of the Notch Ankyrin Domain: Experiment and Theory. <i>Journal of Molecular Biology</i> , 2005, 352, 253-265.	2.0	21
53	Experimental Characterization of the Folding Kinetics of the Notch Ankyrin Domain. <i>Journal of Molecular Biology</i> , 2005, 352, 266-281.	2.0	40
54	Nonspecific hydrophobic interactions stabilize an equilibrium intermediate of apomyoglobin at a key position within the AGH region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12514-12519.	3.3	26

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55	An experimentally determined protein folding energy landscape. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14102-14107.	3.3	153
56	Nuclear Magnetic Resonance Spectroscopy in the Study of Hemoglobin Cooperativity. Methods in Enzymology, 2004, 379, 28-54.	0.4	7
57	The Tolerance of a Modular Protein to Duplication and Deletion of Internal Repeats. Journal of Molecular Biology, 2004, 344, 169-178.	2.0	47
58	Folding by Consensus. Structure, 2003, 11, 486-487.	1.6	11
59	Measuring the stability of partly folded proteins using TMAO. Protein Science, 2003, 12, 1522-1529.	3.1	145
60	Limits of Cooperativity in a Structurally Modular Protein: Response of the Notch Ankyrin Domain to Analogous Alanine Substitutions in Each Repeat. Journal of Molecular Biology, 2002, 324, 373-386.	2.0	58
61	Relationships between the temperature dependence of solvent denaturation and the denaturant dependence of protein stability curves. Biophysical Chemistry, 2002, 101-102, 221-237.	1.5	39
62	Studies of the Ankyrin Repeats of the <i>Drosophila melanogaster</i> Notch Receptor. 2. Solution Stability and Cooperativity of Unfolding. Biochemistry, 2001, 40, 14357-14367.	1.2	89
63	Distal Ligand Reactivity and Quaternary Structure Studies of Proximally Detached Hemoglobins. Biochemistry, 2001, 40, 3780-3795.	1.2	30
64	Studies of the Ankyrin Repeats of the <i>Drosophila melanogaster</i> Notch Receptor. 1. Solution Conformational and Hydrodynamic Properties. Biochemistry, 2001, 40, 14344-14356.	1.2	58
65	Trans-substitution of the proximal hydrogen bond in myoglobin: I. Structural consequences of hydrogen bond deletion. , 2000, 39, 278-290.		16
66	Trans-substitution of the proximal hydrogen bond in myoglobin: II. Energetics, functional consequences, and implications for hemoglobin allostery. , 2000, 39, 291-308.		10
67	A test of the role of the proximal histidines in the Perutz model for cooperativity in haemoglobin. Nature Structural and Molecular Biology, 1997, 4, 78-83.	3.6	76
68	The Association Rate Constant for Heme Binding to Globin Is Independent of Protein Structure. Biochemistry, 1996, 35, 11293-11299.	1.2	221
69	Depletion and replacement of protein metal ligands. Current Opinion in Biotechnology, 1995, 6, 411-418.	3.3	35
70	Replacement of the Proximal Ligand of Sperm Whale Myoglobin with Free Imidazole in the Mutant His-93.fwdarw.Gly. Biochemistry, 1994, 33, 6546-6554.	1.2	183
71	Functional cavities in proteins: A general method for proximal ligand substitution in myoglobin. Journal of the American Chemical Society, 1994, 116, 6981-6982.	6.6	101
72	Three-state analysis of sperm whale apomyoglobin folding. Biochemistry, 1993, 32, 3790-3796.	1.2	241