

Philip N Bryan

List of Publications by Year in descending order

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201385

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times ranked

1912
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering subtilisin proteases that specifically degrade active RAS. <i>Communications Biology</i> , 2021, 4, 299.	2.0	10
2	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. <i>Protein Science</i> , 2018, 27, 1557-1567.	3.1	34
3	Subdomain Interactions Foster the Design of Two Protein Pairs with ~48% Sequence Identity but Different Folds. <i>Biophysical Journal</i> , 2015, 108, 154-162.	0.2	24
4	Implications of protein fold switching. <i>Current Opinion in Structural Biology</i> , 2013, 23, 314-316.	2.6	17
5	Solution NMR structure of a sheddase inhibitor prodomain from the malarial parasite <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2810-2817.	1.5	7
6	Mutational Tipping Points for Switching Protein Folds and Functions. <i>Structure</i> , 2012, 20, 283-291.	1.6	87
7	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 3863-3872.	1.6	37
8	Proteins that switch folds. <i>Current Opinion in Structural Biology</i> , 2010, 20, 482-488.	2.6	170
9	De novo structure generation using chemical shifts for proteins with high sequence identity but different folds. <i>Protein Science</i> , 2010, 19, 349-356.	3.1	59
10	A minimal sequence code for switching protein structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21149-21154.	3.3	219
11	Structure of a Switchable Subtilisin Complexed with a Substrate and with the Activator Azide. <i>Biochemistry</i> , 2009, 48, 10389-10394.	1.2	4
12	Engineering Substrate Preference in Subtilisin: Structural and Kinetic Analysis of a Specificity Mutant. <i>Biochemistry</i> , 2008, 47, 6628-6636.	1.2	32
13	The design and characterization of two proteins with 88% sequence identity but different structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11963-11968.	3.3	165
14	Hydrogen-Deuterium Exchange in Free and Prodomain-Complexed Subtilisin. <i>Biochemistry</i> , 2007, 46, 652-658.	1.2	13
15	Mechanism of the Kinetically-Controlled Folding Reaction of Subtilisin. <i>Biochemistry</i> , 2007, 46, 640-651.	1.2	26
16	An artificially evolved albumin binding module facilitates chemical shift epitope mapping of GA domain interactions with phylogenetically diverse albumins. <i>Protein Science</i> , 2007, 16, 1490-1494.	3.1	14
17	Structure, Dynamics, and Stability Variation in Bacterial Albumin Binding Modules: Implications for Species Specificity. <i>Biochemistry</i> , 2006, 45, 10102-10109.	1.2	36
18	Using Offset Recombinant Polymerase Chain Reaction To Identify Functional Determinants in a Common Family of Bacterial Albumin Binding Domains. <i>Biochemistry</i> , 2006, 45, 3263-3271.	1.2	19

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19	G148â€“GA3: A streptococcal virulence module with atypical thermodynamics of folding optimally binds human serum albumin at physiological temperatures. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1753, 226-233.	1.1	15
20	Directed Evolution of Highly Homologous Proteins with Different Folds by Phage Display:Â Implications for the Protein Folding Codeâ€. <i>Biochemistry</i> , 2005, 44, 14045-14054.	1.2	46
21	Directed Coevolution of Stability and Catalytic Activity in Calcium-free Subtilisinâ€. <i>Biochemistry</i> , 2005, 44, 3272-3279.	1.2	41
22	Engineering Subtilisin into a Fluoride-Triggered Processing Protease Useful for One-Step Protein Purification. <i>Biochemistry</i> , 2004, 43, 14539-14546.	1.2	67
23	Prodomains and Protein Folding Catalysisâ€. <i>Chemical Reviews</i> , 2002, 102, 4805-4816.	23.0	106
24	Solution Structure of the Pro-hormone Convertase 1 Pro-domain from <i>Mus musculus</i> . <i>Journal of Molecular Biology</i> , 2002, 320, 801-812.	2.0	43
25	Cation-Dependent Stability of Subtilisinâ€. <i>Biochemistry</i> , 2001, 40, 10634-10639.	1.2	50
26	Rapid Folding of Calcium-Free Subtilisin by a Stabilized Pro-Domain Mutantâ€. <i>Biochemistry</i> , 1999, 38, 8562-8571.	1.2	31
27	Stabilizing the subtilisin BPN' proâ€“domain by phage display selection: How restrictive is the amino acid code for maximum protein stability?. <i>Protein Science</i> , 1998, 7, 2345-2353.	3.1	41
28	Engineering the Independent Folding of the Subtilisin BPNâ€“ Pro-Domain:Â Correlation of Pro-Domain Stability with the Rate of Subtilisin Foldingâ€. <i>Biochemistry</i> , 1998, 37, 3165-3171.	1.2	39
29	Engineering the Independent Folding of the Subtilisin BPNâ€“ Prodomain:â€“ Analysis of Two-State Folding versus Protein Stability. <i>Biochemistry</i> , 1997, 36, 10414-10421.	1.2	44
30	pKaMeasurements from Nuclear Magnetic Resonance for the B1 and B2 Immunoglobulin G-Binding Domains of Protein G:Â Comparison with Calculated Values for Nuclear Magnetic Resonance and X-ray Structuresâ€. <i>Biochemistry</i> , 1997, 36, 3580-3589.	1.2	62
31	The prosegmentâ€“subtilisin BPNâ€“2 complex: crystal structure of a specific â€“foldaseâ€“™. <i>Structure</i> , 1995, 3, 907-914.	1.6	194
32	Directed Evolution of a Subtilisin with Calcium-Independent Stability. <i>Nature Biotechnology</i> , 1995, 13, 669-673.	9.4	76
33	Catalysis of a protein folding reaction: Mechanistic implications of the 2.0 .ANG. structure of the subtilisin-prodomain complex. <i>Biochemistry</i> , 1995, 34, 10310-10318.	1.2	125
34	Calcium-independent subtilisin by design. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 205-213.	1.5	57
35	Thermodynamic analysis of the folding of the streptococcal protein G IgG-binding domains B1 and B2: why small proteins tend to have high denaturation temperatures. <i>Biochemistry</i> , 1992, 31, 3597-3603.	1.2	274
36	Energetics of folding subtilisin BPN'. <i>Biochemistry</i> , 1992, 31, 4937-4945.	1.2	108

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37	Kinetic analysis of folding and unfolding the 56 amino acid IgG-binding domain of streptococcal protein G. <i>Biochemistry</i> , 1992, 31, 7243-7248.	1.2	179