Philip N Bryan

List of Publications by Year
in descending order

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37 papers	2,574 citations	201385 27 h-index	329751 37 g-index
38 all docs	38 docs citations	38 times ranked	1912 citing authors

#	Article	IF	Citations
1	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. Biochemistry, 1992, 31, 3597-3603.	1.2	274
2	A minimal sequence code for switching protein structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21149-21154.	3.3	219
3	The prosegmentâ€“subtilisin BPNâ€² complex: crystal structure of a specific â€˜foldaseâ€™. Structure, 1995, 3, 907-914.	1.6	194
4	Kinetic analysis of folding and unfolding the 56 amino acid IgG-binding domain of streptococcal protein G. Biochemistry, 1992, 31, 7243-7248.	1.2	179
5	Proteins that switch folds. Current Opinion in Structural Biology, 2010, 20, 482-488.	2.6	170
6	The design and characterization of two proteins with 88% sequence identity but different structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11963-11968.	3.3	165
7	Catalysis of a protein folding reaction: Mechanistic implications of the 2.0 .ANG. structure of the subtilisin-prodomain complex. Biochemistry, 1995, 34, 10310-10318.	1.2	125
8	Energetics of folding subtilisin BPN'. Biochemistry, 1992, 31, 4937-4945.	1.2	108
9	Prodomains and Protein Folding Catalysisâ€. Chemical Reviews, 2002, 102, 4805-4816.	23.0	106
10	Mutational Tipping Points for Switching Protein Folds and Functions. Structure, 2012, 20, 283-291.	1.6	87
11	Directed Evolution of a Subtilisin with Calcium-Independent Stability. Nature Biotechnology, 1995, 13, 669-673.	9.4	76
12	Engineering Subtilisin into a Fluoride-Triggered Processing Protease Useful for One-Step Protein Purification. Biochemistry, 2004, 43, 14539-14546.	1.2	67
13	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€. Biochemistry, 1997, 36, 3580-3589.	1.2	62
14	De novo structure generation using chemical shifts for proteins with highâ€sequence identity but different folds. Protein Science, 2010, 19, 349-356.	3.1	59
15	Calcium-independent subtilisin by design. Proteins: Structure, Function and Bioinformatics, 1993, 16, 205-213.	1.5	57
16	Cation-Dependent Stability of Subtilisinâ€. Biochemistry, 2001, 40, 10634-10639.	1.2	50
17	Directed Evolution of Highly Homologous Proteins with Different Folds by Phage Display:Â Implications for the Protein Folding Codeâ€. Biochemistry, 2005, 44, 14045-14054.	1.2	46
18	Engineering the Independent Folding of the Subtilisin BPNâ€˜ Prodomain:â€‰ Analysis of Two-State Folding versus Protein Stability. Biochemistry, 1997, 36, 10414-10421.	1.2	44

#	Article	IF	Citations
19	Solution Structure of the Pro-hormone Convertase 1 Pro-domain from Mus musculus. Journal of Molecular Biology, 2002, 320, 801-812.	2.0	43
20	Stabilizing the subtilisin BPN' proâ€domain by phage display selection: How restrictive is the amino acid code for maximum protein stability?. Protein Science, 1998, 7, 2345-2353.	3.1	41
21	Directed Coevolution of Stability and Catalytic Activity in Calcium-free Subtilisinâ€. Biochemistry, 2005, 44, 3272-3279.	1.2	41
22	Engineering the Independent Folding of the Subtilisin BPNâ€˜ Pro-Domain:Â Correlation of Pro-Domain Stability with the Rate of Subtilisin Foldingâ€. Biochemistry, 1998, 37, 3165-3171.	1.2	39
23	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. Journal of Biological Chemistry, 2011, 286, 3863-3872.	1.6	37
24	Structure, Dynamics, and Stability Variation in Bacterial Albumin Binding Modules:Â Implications for Species Specificityâ€,â€¡. Biochemistry, 2006, 45, 10102-10109.	1.2	36
25	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. Protein Science, 2018, 27, 1557-1567.	3.1	34
26	Engineering Substrate Preference in Subtilisin: Structural and Kinetic Analysis of a Specificity Mutant. Biochemistry, 2008, 47, 6628-6636.	1.2	32
27	Rapid Folding of Calcium-Free Subtilisin by a Stabilized Pro-Domain Mutantâ€. Biochemistry, 1999, 38, 8562-8571.	1.2	31
28	Mechanism of the Kinetically-Controlled Folding Reaction of Subtilisinâ€. Biochemistry, 2007, 46, 640-651.	1.2	26
29	Subdomain Interactions Foster the Design of Two Protein Pairs withÂâˆ¼80%ÂSequence Identity but Different Folds. Biophysical Journal, 2015, 108, 154-162.	0.2	24
30	Using Offset Recombinant Polymerase Chain Reaction To Identify Functional Determinants in a Common Family of Bacterial Albumin Binding Domains. Biochemistry, 2006, 45, 3263-3271.	1.2	19
31	Implications of protein fold switching. Current Opinion in Structural Biology, 2013, 23, 314-316.	2.6	17
32	G148â€“GA3: A streptococcal virulence module with atypical thermodynamics of folding optimally binds human serum albumin at physiological temperatures. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 226-233.	1.1	15
33	An artificially evolved albumin binding module facilitates chemical shift epitope mapping of GA domain interactions with phylogenetically diverse albumins. Protein Science, 2007, 16, 1490-1494.	3.1	14
34	Hydrogenâˆ’Deuterium Exchange in Free and Prodomain-Complexed Subtilisinâ€. Biochemistry, 2007, 46, 652-658.	1.2	13
35	Engineering subtilisin proteases that specifically degrade active RAS. Communications Biology, 2021, 4, 299.	2.0	10
36	Solution NMR structure of a sheddase inhibitor prodomain from the malarial parasite Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2810-2817.	1.5	7

#	Article	IF	Citations
37	Structure of a Switchable Subtilisin Complexed with a Substrate and with the Activator Azide. Biochemistry, 2009, 48, 10389-10394.	1.2	4