

Patricia L Clark

List of Publications by Year in descending order

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47
papers

2,252
citations

304743

22
h-index

276875

41
g-index

55
all docs

55
docs citations

55
times ranked

2381
citing authors

#	ARTICLE	IF	CITATIONS
1	Roles for Synonymous Codon Usage in Protein Biogenesis. Annual Review of Biophysics, 2015, 44, 143-166.	10.0	257
2	Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water. Science, 2017, 358, 238-241.	12.6	194
3	Pertactin beta-helix folding mechanism suggests common themes for the secretion and folding of autotransporter proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4918-4923.	7.1	187
4	Rare Codons Cluster. PLoS ONE, 2008, 3, e3412.	2.5	166
5	Protein folding in the cell: reshaping the folding funnel. Trends in Biochemical Sciences, 2004, 29, 527-534.	7.5	152
6	Synonymous codon substitutions perturb cotranslational protein folding in vivo and impair cell fitness. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3528-3534.	7.1	134
7	Expanding Anfinsen's Principle: Contributions of Synonymous Codon Selection to Rational Protein Design. Journal of the American Chemical Society, 2014, 136, 858-861.	13.7	125
8	Vectorial transport and folding of an autotransporter virulence protein during outer membrane secretion. Molecular Microbiology, 2009, 71, 1323-1332.	2.5	115
9	Folding the proteome. Trends in Biochemical Sciences, 2013, 38, 337-344.	7.5	100
10	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	3.2	98
11	Quality over quantity: optimizing co-translational protein folding with non-optimal synonymous codons. Current Opinion in Structural Biology, 2016, 38, 102-110.	5.7	65
12	A conserved stable core structure in the passenger domain α -helix of autotransporter virulence proteins. Biopolymers, 2008, 89, 420-427.	2.4	53
13	Dynamics and Energy Contributions for Transport of Unfolded Pertactin through a Protein Nanopore. ACS Nano, 2015, 9, 9050-9061.	14.6	52
14	Increased incidence of rare codon clusters at 5' and 3' gene termini: implications for function. BMC Genomics, 2010, 11, 118.	2.8	48
15	%MinMax: A versatile tool for calculating and comparing synonymous codon usage and its impact on protein folding. Protein Science, 2018, 27, 356-362.	7.6	47
16	Commonly used FRET fluorophores promote collapse of an otherwise disordered protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8889-8894.	7.1	43
17	ATP-Independent Control of Autotransporter Virulence Protein Transport via the Folding Properties of the Secreted Protein. Chemistry and Biology, 2012, 19, 287-296.	6.0	41
18	Properties of protein unfolded states suggest broad selection for expanded conformational ensembles. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23356-23364.	7.1	40

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19	Extracellular protease digestion to evaluate membrane protein cell surface localization. <i>Nature Protocols</i> , 2015, 10, 2074-2080.	12.0	38
20	Of linkers and autochaperones: an unambiguous nomenclature to identify common and uncommon themes for autotransporter secretion. <i>Molecular Microbiology</i> , 2015, 95, 1-16.	2.5	34
21	Response to Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018, 361, .	12.6	30
22	Water as a Good Solvent for Unfolded Proteins: Folding and Collapse are Fundamentally Different. <i>Journal of Molecular Biology</i> , 2020, 432, 2882-2889.	4.2	26
23	Multiple Driving Forces Required for Efficient Secretion of Autotransporter Virulence Proteins. <i>Journal of Biological Chemistry</i> , 2015, 290, 10104-10116.	3.4	22
24	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. <i>Scientific Reports</i> , 2017, 7, 14890.	3.3	21
25	Folding and unfolding of a non-fluorescent mutant of green fluorescent protein. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 285223.	1.8	20
26	Slow formation of aggregation-resistant β -sheet folding intermediates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 812-824.	2.6	20
27	Autotransporters: The Cellular Environment Reshapes a Folding Mechanism to Promote Protein Transport. <i>Journal of Physical Chemistry Letters</i> , 2012, 3, 1063-1071.	4.6	19
28	The comparison of aggregation and folding of enhanced green fluorescent protein (EGFP) by spectroscopic studies. <i>Spectroscopy</i> , 2010, 24, 343-348.	0.8	18
29	DegP Chaperone Suppresses Toxic Inner Membrane Translocation Intermediates. <i>PLoS ONE</i> , 2016, 11, e0162922.	2.5	14
30	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
31	Chapter 24 Measuring Cotranslational Folding of Nascent Polypeptide Chains on Ribosomes. <i>Methods in Enzymology</i> , 2009, 466, 567-590.	1.0	10
32	Molecular chaperones: providing a safe place to weather a midlife protein-folding crisis. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 621-623.	8.2	9
33	Analysis of computational codon usage models and their association with translationally slow codons. <i>PLoS ONE</i> , 2020, 15, e0232003.	2.5	9
34	Non-fluorescent mutant of green fluorescent protein sheds light on the mechanism of chromophore formation. <i>FEBS Letters</i> , 2018, 592, 1516-1523.	2.8	8
35	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. <i>Protein Science</i> , 2022, 31, 221-231.	7.6	8
36	Network analysis of synonymous codon usage. <i>Bioinformatics</i> , 2020, 36, 4876-4884.	4.1	6

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37	How to Build a Complex, Functional Propeller Protein, From Parts. Trends in Biochemical Sciences, 2016, 41, 290-292.	7.5	4
38	Proteins in the Cell. Protein Science, 2019, 28, 1175-1176.	7.6	2
39	Multi-layer sequential network analysis improves protein <scp>3D</scp> structural classification. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1721-1731.	2.6	2
40	Adding Protease Digestion to the Membrane Protein Toolbox. Journal of Molecular Biology, 2011, 406, 543-544.	4.2	1
41	Spectroscopic properties of two single-cysteine mutants of EGFP: C48S-EGFP and C70S-EGFP. Biomedical Spectroscopy and Imaging, 2014, 3, 231-236.	1.2	0
42	HarMinMax. , 2018, , .		0
43	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
44	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
45	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
46	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
47	A New Look at Codon Usage and Protein Expression. , 2019, 60, 104-112.		0