

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	<scp>CHARMING</scp>: Harmonizing synonymous codon usage to replicate a desired codon usage pattern. Protein Science, 2022, 31, 221-231.	7.6	8
2	Multi-layer sequential network analysis improves protein <scp>3D</scp> structural classification. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1721-1731.	2.6	2
3	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	11
4	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
5	Analysis of computational codon usage models and their association with translationally slow codons. PLoS ONE, 2020, 15, e0232003.	2.5	9
6	Network analysis of synonymous codon usage. Bioinformatics, 2020, 36, 4876-4884.	4.1	6
7	Water as a Good Solvent for Unfolded Proteins: Folding and Collapse are Fundamentally Different. Journal of Molecular Biology, 2020, 432, 2882-2889.	4.2	26
8	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
9	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
10	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
11	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
12	Analysis of computational codon usage models and their association with translationally slow codons. , 2020, 15, e0232003.		0
13	Proteins in the Cell. Protein Science, 2019, 28, 1175-1176.	7.6	2
14	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
15	A New Look at Codon Usage and Protein Expression. , 2019, 60, 104-112.		0
16	Non-fluorescent mutant of green fluorescent protein sheds light on the mechanism of chromophore formation. FEBS Letters, 2018, 592, 1516-1523.	2.8	8
17	%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
18	Response to Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". Science, 2018, 361, .	12.6	30

#	ARTICLE	IF	CITATIONS
19	HarMinMax. , 2018, , .		0
20	Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water. Science, 2017, 358, 238-241.	12.6	194
21	GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison. Scientific Reports, 2017, 7, 14890.	3.3	21
22	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	3.2	98
23	DegP Chaperone Suppresses Toxic Inner Membrane Translocation Intermediates. PLoS ONE, 2016, 11, e0162922.	2.5	14
24	Molecular chaperones: providing a safe place to weather a midlife protein-folding crisis. Nature Structural and Molecular Biology, 2016, 23, 621-623.	8.2	9
25	Quality over quantity: optimizing co-translational protein folding with non-â€™optimalâ€™ synonymous codons. Current Opinion in Structural Biology, 2016, 38, 102-110.	5.7	65
26	How to Build a Complex, Functional Propeller Protein, From Parts. Trends in Biochemical Sciences, 2016, 41, 290-292.	7.5	4
27	Multiple Driving Forces Required for Efficient Secretion of Autotransporter Virulence Proteins. Journal of Biological Chemistry, 2015, 290, 10104-10116.	3.4	22
28	Of linkers and autochaperones: an unambiguous nomenclature to identify common and uncommon themes for autotransporter secretion. Molecular Microbiology, 2015, 95, 1-16.	2.5	34
29	Roles for Synonymous Codon Usage in Protein Biogenesis. Annual Review of Biophysics, 2015, 44, 143-166.	10.0	257
30	Dynamics and Energy Contributions for Transport of Unfolded Pertactin through a Protein Nanopore. ACS Nano, 2015, 9, 9050-9061.	14.6	52
31	Extracellular protease digestion to evaluate membrane protein cell surface localization. Nature Protocols, 2015, 10, 2074-2080.	12.0	38
32	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
33	Expanding Anfinsenâ€™s Principle: Contributions of Synonymous Codon Selection to Rational Protein Design. Journal of the American Chemical Society, 2014, 136, 858-861.	13.7	125
34	Folding the proteome. Trends in Biochemical Sciences, 2013, 38, 337-344.	7.5	100
35	Autotransporters: The Cellular Environment Reshapes a Folding Mechanism to Promote Protein Transport. Journal of Physical Chemistry Letters, 2012, 3, 1063-1071.	4.6	19
36	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

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37	Adding Protease Digestion to the Membrane Protein Toolbox. <i>Journal of Molecular Biology</i> , 2011, 406, 543-544.	4.2	1
38	Increased incidence of rare codon clusters at 5' and 3' gene termini: implications for function. <i>BMC Genomics</i> , 2010, 11, 118.	2.8	48
39	Slow formation of aggregation-resistant β -sheet folding intermediates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 812-824.	2.6	20
40	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
41	Chapter 24 Measuring Cotranslational Folding of Nascent Polypeptide Chains on Ribosomes. <i>Methods in Enzymology</i> , 2009, 466, 567-590.	1.0	10
42	Vectorial transport and folding of an autotransporter virulence protein during outer membrane secretion. <i>Molecular Microbiology</i> , 2009, 71, 1323-1332.	2.5	115
43	A conserved stable core structure in the passenger domain β -helix of autotransporter virulence proteins. <i>Biopolymers</i> , 2008, 89, 420-427.	2.4	53
44	Rare Codons Cluster. <i>PLoS ONE</i> , 2008, 3, e3412.	2.5	166
45	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
46	Pertactin beta-helix folding mechanism suggests common themes for the secretion and folding of autotransporter proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4918-4923.	7.1	187
47	Protein folding in the cell: reshaping the folding funnel. <i>Trends in Biochemical Sciences</i> , 2004, 29, 527-534.	7.5	152