Lucy J Colwell

List of Publications by Year
in descending order

| 28 papers | 3,265 citations | 304743
22 h-index | 526287
27 g-index |
| 32 all docs | 32 docs citations | 32 times ranked | 3996 citing authors |

#	Article	IF	Citations
1	Protein 3D Structure Computed from Evolutionary Sequence Variation. PLoS ONE, 2011, 6, e28766.	2.5	975
2	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. Cell, 2012, 149, 1607-1621.	28.9	478
3	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
4	Deep diversification of an AAV capsid protein by machine learning. Nature Biotechnology, 2021, 39, 691-696.	17.5	165
5	Comparative analysis of nanobody sequence and structure data. Proteins: Structure, Function and Bioinformatics, 2018, 86, 697-706.	2.6	151
6	Using deep learning to annotate the protein universe. Nature Biotechnology, 2022, 40, 932-937.	17.5	133
7	Inferring interaction partners from protein sequences. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12180-12185.	7.1	126
8	Computational approaches to therapeutic antibody design: established methods and emerging trends. Briefings in Bioinformatics, 2020, 21, 1549-1567.	6.5	126
9	A core subunit of Polycomb repressive complex 1 is broadly conserved in function but not primary sequence. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1063-71.	7.1	104
10	Analysis of nanobody paratopes reveals greater diversity than classical antibodies. Protein Engineering, Design and Selection, 2018, 31, 267-275.	2.1	81
11	Charge as a Selection Criterion for Translocation through the Nuclear Pore Complex. PLoS Computational Biology, 2010, 6, e1000747.	3.2	78
12	The emergence of protein complexes: quaternary structure, dynamics and allostery. Biochemical Society Transactions, 2012, 40, 475-491.	3.4	75
13	Protein Sectors: Statistical Coupling Analysis versus Conservation. PLoS Computational Biology, 2015, 11, e1004091.	3.2	70
14	Rapid discovery and evolution of orthogonal aminoacyl-tRNA synthetase–tRNA pairs. Nature Biotechnology, 2020, 38, 989-999.	17.5	67
15	Power law tails in phylogenetic systems. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 690-695.	7.1	59
16	Glycation changes molecular organization and charge distribution in type I collagen fibrils. Scientific Reports, 2020, 10, 3397.	3.3	56
17	Using attribution to decode binding mechanism in neural network models for chemistry. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11624-11629.	7.1	53
18	Statistical and machine learning approaches to predicting protein–ligand interactions. Current Opinion in Structural Biology, 2018, 49, 123-128.	5.7	52

#	Article	IF	Citations
19	Proline provides site-specific flexibility for in vivo collagen. Scientific Reports, 2018, 8, 13809.	3.3	40
20	The Role of Protein-Ligand Contacts in Allosteric Regulation of the Escherichia coli Catabolite Activator Protein. Journal of Biological Chemistry, 2015, 290, 22225-22235.	3.4	37
21	Action Potential Initiation in the Hodgkin-Huxley Model. PLoS Computational Biology, 2009, 5, e1000265.	3.2	25
22	Predicting protein–ligand affinity with a random matrix framework. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13564-13569.	7.1	24
23	A Polymer Physics Framework for the Entropy of Arbitrary Pseudoknots. Biophysical Journal, 2019, 117, 520-532.	0.5	12
24	The Effect of Debiasing Protein–Ligand Binding Data on Generalization. Journal of Chemical Information and Modeling, 2020, 60, 56-62.	5.4	12
25	Optimal Design of Experiments by Combining Coarse and Fine Measurements. Physical Review Letters, 2017, 119, 208101.	7.8	5
26	Improving Protein Function Annotation via Unsupervised Pre-training: Robustness, Efficiency, and Insights. , 2021, , .		5
27	Collagen-Inspired Self-Assembly of Twisted Filaments. Physical Review Letters, 2019, 123, 238102.	7.8	3
28	Minding the gaps: The importance of navigating holes in protein fitness landscapes. Cell Systems, 2021, 12, 1019-1020.	6.2	2