

Lucy J Colwell

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Using deep learning to annotate the protein universe. <i>Nature Biotechnology</i> , 2022, 40, 932-937. | 17.5 | 133 |
| 2 | Deep diversification of an AAV capsid protein by machine learning. <i>Nature Biotechnology</i> , 2021, 39, 691-696. | 17.5 | 165 |
| 3 | Improving Protein Function Annotation via Unsupervised Pre-training: Robustness, Efficiency, and Insights. , 2021, , . | | 5 |
| 4 | Minding the gaps: The importance of navigating holes in protein fitness landscapes. <i>Cell Systems</i> , 2021, 12, 1019-1020. | 6.2 | 2 |
| 5 | Computational approaches to therapeutic antibody design: established methods and emerging trends. <i>Briefings in Bioinformatics</i> , 2020, 21, 1549-1567. | 6.5 | 126 |
| 6 | The Effect of Debiasing Protein-Ligand Binding Data on Generalization. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 56-62. | 5.4 | 12 |
| 7 | Glycation changes molecular organization and charge distribution in type I collagen fibrils. <i>Scientific Reports</i> , 2020, 10, 3397. | 3.3 | 56 |
| 8 | Rapid discovery and evolution of orthogonal aminoacyl-tRNA synthetase-tRNA pairs. <i>Nature Biotechnology</i> , 2020, 38, 989-999. | 17.5 | 67 |
| 9 | A Polymer Physics Framework for the Entropy of Arbitrary Pseudoknots. <i>Biophysical Journal</i> , 2019, 117, 520-532. | 0.5 | 12 |
| 10 | Using attribution to decode binding mechanism in neural network models for chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11624-11629. | 7.1 | 53 |
| 11 | Collagen-Inspired Self-Assembly of Twisted Filaments. <i>Physical Review Letters</i> , 2019, 123, 238102. | 7.8 | 3 |
| 12 | Statistical and machine learning approaches to predicting protein-ligand interactions. <i>Current Opinion in Structural Biology</i> , 2018, 49, 123-128. | 5.7 | 52 |
| 13 | Comparative analysis of nanobody sequence and structure data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 697-706. | 2.6 | 151 |
| 14 | Power law tails in phylogenetic systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 690-695. | 7.1 | 59 |
| 15 | Proline provides site-specific flexibility for in vivo collagen. <i>Scientific Reports</i> , 2018, 8, 13809. | 3.3 | 40 |
| 16 | Analysis of nanobody paratopes reveals greater diversity than classical antibodies. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 267-275. | 2.1 | 81 |
| 17 | Optimal Design of Experiments by Combining Coarse and Fine Measurements. <i>Physical Review Letters</i> , 2017, 119, 208101. | 7.8 | 5 |
| 18 | Inferring interaction partners from protein sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12180-12185. | 7.1 | 126 |

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|----|--|------|-----------|
| 19 | Predicting protein–ligand affinity with a random matrix framework. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13564-13569. | 7.1 | 24 |
| 20 | Protein Sectors: Statistical Coupling Analysis versus Conservation. <i>PLoS Computational Biology</i> , 2015, 11, e1004091. | 3.2 | 70 |
| 21 | The Role of Protein-Ligand Contacts in Allosteric Regulation of the <i>Escherichia coli</i> Catabolite Activator Protein. <i>Journal of Biological Chemistry</i> , 2015, 290, 22225-22235. | 3.4 | 37 |
| 22 | A core subunit of Polycomb repressive complex 1 is broadly conserved in function but not primary sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1063-71. | 7.1 | 104 |
| 23 | Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. <i>Cell</i> , 2012, 149, 1607-1621. | 28.9 | 478 |
| 24 | The emergence of protein complexes: quaternary structure, dynamics and allostery. <i>Biochemical Society Transactions</i> , 2012, 40, 475-491. | 3.4 | 75 |
| 25 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785. | 7.6 | 188 |
| 26 | Protein 3D Structure Computed from Evolutionary Sequence Variation. <i>PLoS ONE</i> , 2011, 6, e28766. | 2.5 | 975 |
| 27 | Charge as a Selection Criterion for Translocation through the Nuclear Pore Complex. <i>PLoS Computational Biology</i> , 2010, 6, e1000747. | 3.2 | 78 |
| 28 | Action Potential Initiation in the Hodgkin-Huxley Model. <i>PLoS Computational Biology</i> , 2009, 5, e1000265. | 3.2 | 25 |