Lenore J Cowen

List of Publications by Year
in descending order

49 papers	2,008 citations	516710 16 h-index	315739 38 g-index
57 all docs	57 docs citations	57 times ranked	2304 citing authors

#	Article	IF	Citations
1	MUNDO: protein function prediction embedded in a multispecies world. Bioinformatics Advances, 2022, 2, .	2.4	2
2	Bioengineered models of Parkinson's disease using patient-derived dopaminergic neurons exhibit distinct biological profiles in a 3D microenvironment. Cellular and Molecular Life Sciences, 2022, 79, 78.	5.4	12
3	Cognitive cascades: How to model (and potentially counter) the spread of fake news. PLoS ONE, 2022, 17, e0261811.	2.5	10
4	Topsy-Turvy: integrating a global view into sequence-based PPI prediction. Bioinformatics, 2022, 38, i264-i272.	4.1	28
5	GLIDER: function prediction from GLIDE-based neighborhoods. Bioinformatics, 2022, 38, 3395-3406.	4.1	3
6	Embodied Notes: A Cognitive Support Tool For Remote Scientific Collaboration in VR. , 2022, , .		2
7	Bioinformatics of Corals: Investigating Heterogeneous Omics Data from Coral Holobionts for Insight into Reef Health and Resilience. Annual Review of Biomedical Data Science, 2022, 5, 205-231.	6.5	4
8	Identifying Cognitive and Creative Support Needs for Remote Scientific Collaboration using VR: Practices, Affordances, and Design Implications. , 2022, , .		2
9	D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions. Cell Systems, 2021, 12, 969-982.e6.	6.2	78
10	Bioinformatics of corals: Investigating heterogeneous omics data from coral holobionts for insight into reef health and resilience. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 336-340.	0.7	0
11	GLIDE: combining local methods and diffusion state embeddings to predict missing interactions in biological networks. Bioinformatics, 2020, 36, i464-i473.	4.1	11
12	Bioinformatics of corals: Investigating heterogeneous omics data from coral holobionts for insight into reef health and resilience. , 2020, , .		0
13	Cell shape, and not 2D migration, predicts extracellular matrix-driven 3D cell invasion in breast cancer. APL Bioengineering, 2020, 4, 026105.	6.2	50
14	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	19.0	213
15	Computing the diffusion state distance on graphs via algebraic multigrid and random projections. Numerical Linear Algebra With Applications, 2018, 25, e2156.	1.6	7
16	Network propagation: a universal amplifier of genetic associations. Nature Reviews Genetics, 2017, 18, 551-562.	16.3	514
17	New directions for diffusion-based network prediction of protein function: incorporating pathways with confidence. Bioinformatics, 2014, 30, i219-i227.	4.1	108
18	MRFy. , 2013, , .		1

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19	Going the Distance for Protein Function Prediction: A New Distance Metric for Protein Interaction Networks. PLoS ONE, 2013, 8, e76339.	2.5	94
20	SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins into the twilight zone. Bioinformatics, 2012, 28, 1216-1222.	4.1	25
21	Touring Protein Space with Matt. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 286-293.	3.0	12
22	Molli: Interactive Visualization for Exploratory Protein Analysis. IEEE Computer Graphics and Applications, 2012, 32, 62-69.	1.2	0
23	Formatt: Correcting protein multiple structural alignments by incorporating sequence alignment. BMC Bioinformatics, 2012, 13, 259.	2.6	15
24	STITCHER: Dynamic assembly of likely amyloid and prion β-structures from secondary structure predictions. Proteins: Structure, Function and Bioinformatics, 2012, 80, 410-420.	2.6	19
25	Markov random fields reveal an N-terminal double beta-propeller motif as part of a bacterial hybrid two-component sensor system. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4069-4074.	7.1	27
26	Recognition of beta-structural motifs using hidden Markov models trained with simulated evolution. Bioinformatics, 2010, 26, i287-i293.	4.1	14
27	Touring Protein Space with Matt. Lecture Notes in Computer Science, 2010, , 18-28.	1.3	5
28	Compact roundtrip routing with topology-independent node names. Journal of Computer and System Sciences, 2008, 74, 775-795.	1.2	0
29	Matt: Local Flexibility Aids Protein Multiple Structure Alignment. PLoS Computational Biology, 2008, 4, e10.	3.2	185
30	Packet Routing. , 2008, , 616-618.		0
31	Compact Routing with Name Independence. SIAM Journal on Discrete Mathematics, 2006, 20, 705-726.	0.8	6
32	Exact Distance Labelings Yield Additive-Stretch Compact Routing Schemes. Lecture Notes in Computer Science, 2006, , 339-354.	1.3	1
33	Microarray Data Analysis of Survival Times of Patients with Lung Adenocarcinomas Using ADC and K-Medians Clustering. , 2005, , 175-190.		0
34	Approximation Algorithms for the Class Cover Problem. Annals of Mathematics and Artificial Intelligence, 2004, 40, 215-223.	1.3	26
35	Compact roundtrip routing in directed networks. Journal of Algorithms, 2004, 50, 79-95.	0.9	57
36	The distinguishing number of the hypercube. Discrete Mathematics, 2004, 283, 29-35.	0.7	56

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37	Compact routing with name independence. , 2003, , .		20
38	Compact Routing with Minimum Stretch. Journal of Algorithms, 2001, 38, 170-183.	0.9	158
39	A formal framework for evaluating heuristic programs. Annals of Mathematics and Artificial Intelligence, 1998, 22, 193-206.	1.3	1
40	Near-Linear Time Construction of Sparse Neighborhood Covers. SIAM Journal on Computing, 1998, 28, 263-277.	1.0	79
41	Mine detection via generalized Wilcoxon-Mann-Whitney classification. , 1998, 3392, 906.		1
42	The Offset Problem. Combinatorics Probability and Computing, 1997, 6, 159-164.	1.3	0
43	Defective coloring revisited. Journal of Graph Theory, 1997, 24, 205-219.	0.9	88
44	Randomized Nonlinear Projections Uncover High-Dimensional Structure. Advances in Applied Mathematics, 1997, 19, 319-331.	0.7	10
45	Hypercube sandwich approach to conferencing. Journal of Supercomputing, 1996, 10, 271-283.	3.6	8
46	A formal framework for evaluating heuristic programs. Lecture Notes in Computer Science, 1996, , 634-645.	1.3	1
47	Concurrence probabilities for a locally slotted packet radio network by combinatorial methods. Performance Evaluation, 1993, 17, 43-51.	1.2	3
48	Fast network decomposition. , 1992, , .		21
49	Low-diameter graph decomposition is in NC. Lecture Notes in Computer Science, 1992, , 83-93.	1.3	8