Debra S Goldberg

List of Publications by Year
in descending order

20 papers	9,215 citations	687363 13 h-index	839539 18 g-index
22 all docs	22 docs citations	22 times ranked	10381 citing authors

#	Article	IF	Citations
1	Towards a proteome-scale map of the human protein–protein interaction network. Nature, 2005, 437, 1173-1178.	27.8	2,676
2	Global Mapping of the Yeast Genetic Interaction Network. Science, 2004, 303, 808-813.	12.6	1,908
3	Evidence for dynamically organized modularity in the yeast protein–protein interaction network. Nature, 2004, 430, 88-93.	27.8	1,683
4	A Map of the Interactome Network of the Metazoan <i>C. elegans</i>. Science, 2004, 303, 540-543.	12.6	1,587
5	Assessing experimentally derived interactions in a small world. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4372-4376.	7.1	387
6	Predictive models of molecular machines involved in Caenorhabditis elegans early embryogenesis. Nature, 2005, 436, 861-865.	27.8	260
7	Combining biological networks to predict genetic interactions. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15682-15687.	7.1	225
8	PREY PREFERENCE BY A TOP PREDATOR AND THE STABILITY OF LINKED FOOD CHAINS. Ecology, 2000, 81, 8-14.	3.2	187
9	Motifs, themes and thematic maps of an integrated Saccharomyces cerevisiae interaction network. Journal of Biology, 2005, 4, 6.	2.7	154
10	Questioning the Ubiquity of Neofunctionalization. PLoS Computational Biology, 2009, 5, e1000252.	3.2	37
11	Improving protein function prediction methods with integrated literature data. BMC Bioinformatics, 2008, 9, 198.	2.6	24
12	Improving evolutionary models of protein interaction networks. Bioinformatics, 2011, 27, 376-382.	4.1	24
13	Clustering Coefficients in Protein Interaction Hypernetworks. , 2013, , .		22
14	Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. PLoS ONE, 2017, 12, e0174052.	2.5	15
15	REVERSE ENGINEERING THE EVOLUTION OF PROTEIN INTERACTION NETWORKS. , 2008, , .		4
16	Characterization of known protein complexes using k-connectivity and other topological measures. F1000Research, 2013, 2, 172.	1.6	3
17	The Topological Profile of a Model of Protein Network Evolution Can Direct Model Improvement. Lecture Notes in Computer Science, 2015, , 40-52.	1.3	2
18	Characterization of known protein complexes using k-connectivity and other topological measures. F1000Research, 2013, 2, 172.	1.6	2

#	Article	IF	Citations
19	Evaluating theoretical models of protein interaction network evolution without seed graphs. , 2013, , .		0
20	Iâ€™m Like You, Just Not In That Way: Tag Networks to Improve Collaborative Filtering. F1000Research, 0, 2, 95.	1.6	0