

Charles DeLisi

List of Publications by Year in descending order

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42
papers

1,961
citations

394421

19
h-index

377865

34
g-index

44
all docs

44
docs citations

44
times ranked

2778
citing authors

#	ARTICLE	IF	CITATIONS
1	VisANT: an online visualization and analysis tool for biological interaction data. BMC Bioinformatics, 2004, 5, 17.	2.6	220
2	Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network. Genome Biology, 2009, 10, R91.	9.6	196
3	VisANT: data-integrating visual framework for biological networks and modules. Nucleic Acids Research, 2005, 33, W352-W357.	14.5	172
4	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. Nucleic Acids Research, 2009, 37, W115-W121.	14.5	170
5	Predictome: a database of putative functional links between proteins. Nucleic Acids Research, 2002, 30, 306-309.	14.5	129
6	VisANT 4.0: Integrative network platform to connect genes, drugs, diseases and therapies. Nucleic Acids Research, 2013, 41, W225-W231.	14.5	123
7	VisANT: an integrative framework for networks in systems biology. Briefings in Bioinformatics, 2008, 9, 317-325.	6.5	121
8	Prediction of protein complexes using empirical free energy functions. Protein Science, 1996, 5, 614-626.	7.6	91
9	Towards zoomable multidimensional maps of the cell. Nature Biotechnology, 2007, 25, 547-554.	17.5	84
10	Determining protein loop conformation using scaling&relaxation techniques. Protein Science, 1993, 2, 1242-1248.	7.6	69
11	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. Genome Biology, 2010, 11, R23.	9.6	67
12	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. Nucleic Acids Research, 2007, 35, W625-W632.	14.5	66
13	Using Functional Signatures to Identify Repositioned Drugs for Breast, Myelogenous Leukemia and Prostate Cancer. PLoS Computational Biology, 2012, 8, e1002347.	3.2	56
14	Consistency in structural energetics of protein folding and peptide recognition. Protein Science, 1997, 6, 1057-1064.	7.6	47
15	Multiple copy sampling in protein loop modeling: Computational efficiency and sensitivity to dihedral angle perturbations. Protein Science, 1994, 3, 493-506.	7.6	46
16	A network based approach to drug repositioning identifies plausible candidates for breast cancer and prostate cancer. BMC Medical Genomics, 2016, 9, 51.	1.5	42
17	Empirical free energy calculation: Comparison to calorimetric data. Protein Science, 1997, 6, 1976-1984.	7.6	29
18	Santa Fe 1986: Human genome baby-steps. Nature, 2008, 455, 876-877.	27.8	27

#	ARTICLE	IF	CITATIONS
19	Visualization of Metabolic Interaction Networks in Microbial Communities Using VisANT 5.0. PLoS Computational Biology, 2016, 12, e1004875.	3.2	26
20	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. Biodesign Research, 2020, 2020, .	1.9	24
21	Peptide docking using dynamic programming. , 1996, 17, 418-428.		21
22	Machine learning for regulatory analysis and transcription factor target prediction in yeast. Systems and Synthetic Biology, 2007, 1, 25-46.	1.0	21
23	Evaluation and integration of cancer gene classifiers: identification and ranking of plausible drivers. Scientific Reports, 2015, 5, 10204.	3.3	18
24	Toward a predictive understanding of molecular recognition. Immunological Reviews, 1998, 163, 251-266.	6.0	14
25	Analyzing Networks with VisANT. Current Protocols in Bioinformatics, 2004, 8, Unit 8.8.	25.8	13
26	The role of synthetic biology in climate change mitigation. Biology Direct, 2019, 14, 14.	4.6	10
27	Classifying transcription factor targets and discovering relevant biological features. Biology Direct, 2008, 3, 22.	4.6	9
28	Igf1 and Pacap rescue cerebellar granule neurons from apoptosis via a common transcriptional program. Cell Death Discovery, 2015, 1, .	4.7	9
29	In silico regulatory analysis for exploring human disease progression. Biology Direct, 2008, 3, 24.	4.6	6
30	SVMotif: A Machine Learning Motif Algorithm. , 2007, , .		5
31	Robust gene network analysis reveals alteration of the STAT5a network as a hallmark of prostate cancer. Genome Informatics, 2010, 24, 139-53.	0.4	5
32	ROBUST GENE NETWORK ANALYSIS REVEALS ALTERATION OF THE STAT5a NETWORK AS A HALLMARK OF PROSTATE CANCER. , 2010, , .		3
33	Monte Carlo study of the effect of $\hat{I}^2_{₂}$ microglobulin on the binding cleft of the HLA $\hat{A}2$ complex. Protein Science, 1994, 3, 911-919.	7.6	2
34	The interaction map of yeast: terra incognita?. Journal of Biology, 2006, 5, 10.	2.7	2
35	Ensemble Machine Methods for DNA Binding. , 2008, , .		2
36	Mutated Pathways as a Guide to Adjuvant Therapy Treatments for Breast Cancer. Molecular Cancer Therapeutics, 2016, 15, 184-189.	4.1	2

#	ARTICLE	IF	CITATIONS
37	Hedgehogs, foxes, and a new science. Nature Biotechnology, 1997, 15, 819-819.	17.5	1
38	Smoothing Gene Expression Using Biological Networks. , 2010, , .		1
39	Constructive principles for gene editing oversight. Nature Biotechnology, 2022, 40, 17-18.	17.5	1
40	Constructing networks with correlation maximization methods. Genome Informatics, 2004, 15, 149-59.	0.4	1
41	Learning Methods for DNA Binding in Computational Biology. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	0
42	Binding Site Graphs: A New Graph Theoretical Framework for Prediction of Transcription Factor Binding Sites. PLoS Computational Biology, 2005, preprint, e90.	3.2	0