

Charles DeLisi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5194545/publications.pdf>

Version: 2024-02-01

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	Constructive principles for gene editing oversight. <i>Nature Biotechnology</i> , 2022, 40, 17-18.	17.5	1
2	The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. <i>BioDesign Research</i> , 2020, 2020, .	1.9	24
3	The role of synthetic biology in climate change mitigation. <i>Biology Direct</i> , 2019, 14, 14.	4.6	10
4	Visualization of Metabolic Interaction Networks in Microbial Communities Using VisANT 5.0. <i>PLoS Computational Biology</i> , 2016, 12, e1004875.	3.2	26
5	A network based approach to drug repositioning identifies plausible candidates for breast cancer and prostate cancer. <i>BMC Medical Genomics</i> , 2016, 9, 51.	1.5	42
6	Mutated Pathways as a Guide to Adjuvant Therapy Treatments for Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 184-189.	4.1	2
7	Igf1 and Pacap rescue cerebellar granule neurons from apoptosis via a common transcriptional program. <i>Cell Death Discovery</i> , 2015, 1, .	4.7	9
8	Evaluation and integration of cancer gene classifiers: identification and ranking of plausible drivers. <i>Scientific Reports</i> , 2015, 5, 10204.	3.3	18
9	VisANT 4.0: Integrative network platform to connect genes, drugs, diseases and therapies. <i>Nucleic Acids Research</i> , 2013, 41, W225-W231.	14.5	123
10	Using Functional Signatures to Identify Repositioned Drugs for Breast, Myelogenous Leukemia and Prostate Cancer. <i>PLoS Computational Biology</i> , 2012, 8, e1002347.	3.2	56
11	ROBUST GENE NETWORK ANALYSIS REVEALS ALTERATION OF THE STAT5a NETWORK AS A HALLMARK OF PROSTATE CANCER. , 2010, , .		3
12	Identification of functional modules that correlate with phenotypic difference: the influence of network topology. <i>Genome Biology</i> , 2010, 11, R23.	9.6	67
13	Smoothing Gene Expression Using Biological Networks. , 2010, , .		1
14	Robust gene network analysis reveals alteration of the STAT5a network as a hallmark of prostate cancer. <i>Genome Informatics</i> , 2010, 24, 139-53.	0.4	5
15	VisANT 3.5: multi-scale network visualization, analysis and inference based on the gene ontology. <i>Nucleic Acids Research</i> , 2009, 37, W115-W121.	14.5	170
16	Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network. <i>Genome Biology</i> , 2009, 10, R91.	9.6	196
17	Santa Fe 1986: Human genome baby-steps. <i>Nature</i> , 2008, 455, 876-877.	27.8	27
18	Classifying transcription factor targets and discovering relevant biological features. <i>Biology Direct</i> , 2008, 3, 22.	4.6	9

#	ARTICLE	IF	CITATIONS
19	In silico regulatory analysis for exploring human disease progression. <i>Biology Direct</i> , 2008, 3, 24.	4.6	6
20	Ensemble Machine Methods for DNA Binding. , 2008, , .		2
21	VisANT: an integrative framework for networks in systems biology. <i>Briefings in Bioinformatics</i> , 2008, 9, 317-325.	6.5	121
22	Learning Methods for DNA Binding in Computational Biology. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	0
23	VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. <i>Nucleic Acids Research</i> , 2007, 35, W625-W632.	14.5	66
24	SVMotif: A Machine Learning Motif Algorithm. , 2007, , .		5
25	Towards zoomable multidimensional maps of the cell. <i>Nature Biotechnology</i> , 2007, 25, 547-554.	17.5	84
26	Machine learning for regulatory analysis and transcription factor target prediction in yeast. <i>Systems and Synthetic Biology</i> , 2007, 1, 25-46.	1.0	21
27	The interaction map of yeast: terra incognita?. <i>Journal of Biology</i> , 2006, 5, 10.	2.7	2
28	VisANT: data-integrating visual framework for biological networks and modules. <i>Nucleic Acids Research</i> , 2005, 33, W352-W357.	14.5	172
29	Binding Site Graphs: A New Graph Theoretical Framework for Prediction of Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2005, preprint, e90.	3.2	0
30	VisANT: an online visualization and analysis tool for biological interaction data. <i>BMC Bioinformatics</i> , 2004, 5, 17.	2.6	220
31	Analyzing Networks with VisANT. <i>Current Protocols in Bioinformatics</i> , 2004, 8, Unit 8.8.	25.8	13
32	Constructing networks with correlation maximization methods. <i>Genome Informatics</i> , 2004, 15, 149-59.	0.4	1
33	Predictome: a database of putative functional links between proteins. <i>Nucleic Acids Research</i> , 2002, 30, 306-309.	14.5	129
34	Toward a predictive understanding of molecular recognition. <i>Immunological Reviews</i> , 1998, 163, 251-266.	6.0	14
35	Hedgehogs, foxes, and a new science. <i>Nature Biotechnology</i> , 1997, 15, 819-819.	17.5	1
36	Consistency in structural energetics of protein folding and peptide recognition. <i>Protein Science</i> , 1997, 6, 1057-1064.	7.6	47

#	ARTICLE	IF	CITATIONS
37	Empirical free energy calculation: Comparison to calorimetric data. Protein Science, 1997, 6, 1976-1984.	7.6	29
38	Peptide docking using dynamic programming. , 1996, 17, 418-428.		21
39	Prediction of protein complexes using empirical free energy functions. Protein Science, 1996, 5, 614-626.	7.6	91
40	Multiple copy sampling in protein loop modeling: Computational efficiency and sensitivity to dihedral angle perturbations. Protein Science, 1994, 3, 493-506.	7.6	46
41	Monte Carlo study of the effect of \hat{I}^2 microglobulin on the binding cleft of the HLA A2 complex. Protein Science, 1994, 3, 911-919.	7.6	2
42	Determining protein loop conformation using scaling relaxation techniques. Protein Science, 1993, 2, 1242-1248.	7.6	69