

Daphne Koller

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10470622/publications.pdf>

Version: 2024-02-01

39
papers

23,947
citations

236925

25
h-index

454955

30
g-index

40
all docs

40
docs citations

40
times ranked

45838
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
3	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. <i>Science</i> , 2003, 302, 249-255.	12.6	2,034
4	The Immunological Genome Project: networks of gene expression in immune cells. <i>Nature Immunology</i> , 2008, 9, 1091-1094.	14.5	1,576
5	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	21.4	1,543
6	Population genomics of human gene expression. <i>Nature Genetics</i> , 2007, 39, 1217-1224.	21.4	1,072
7	A module map showing conditional activity of expression modules in cancer. <i>Nature Genetics</i> , 2004, 36, 1090-1098.	21.4	622
8	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. <i>Genome Research</i> , 2014, 24, 14-24.	5.5	547
9	Title is missing!. <i>Machine Learning</i> , 2003, 50, 95-125.	5.4	516
10	Decomposing a scene into geometric and semantically consistent regions. , 2009, , .		487
11	Multi-Class Segmentation with Relative Location Prior. <i>International Journal of Computer Vision</i> , 2008, 80, 300-316.	15.6	379
12	From signatures to models: understanding cancer using microarrays. <i>Nature Genetics</i> , 2005, 37, S38-S45.	21.4	331
13	Single image depth estimation from predicted semantic labels. , 2010, , .		328
14	Conservation and divergence in the transcriptional programs of the human and mouse immune systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2946-2951.	7.1	296
15	Real time motion capture using a single time-of-flight camera. , 2010, , .		254
16	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252
17	Human Responses to Influenza Vaccination Show Seroconversion Signatures and Convergent Antibody Rearrangements. <i>Cell Host and Microbe</i> , 2014, 16, 105-114.	11.0	246
18	Learning latent temporal structure for complex event detection. , 2012, , .		239

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19	Adaptive Probabilistic Networks with Hidden Variables. Machine Learning, 1997, 29, 213-244.	5.4	233
20	Causal signals between codon bias, <scp>mRNA</scp> structure, and the efficiency of translation and elongation. Molecular Systems Biology, 2014, 10, 770.	7.2	231
21	Programming Pluralism: Using Learning Analytics to Detect Patterns in the Learning of Computer Programming. Journal of the Learning Sciences, 2014, 23, 561-599.	2.9	201
22	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	3.5	177
23	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2013, 9, 659.	7.2	173
24	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	3.2	158
25	Identifying regulatory mechanisms using individual variation reveals key role for chromatin modification. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14062-14067.	7.1	126
26	A segmentation-aware object detection model with occlusion handling. , 2011, , .		82
27	Selectivity estimation using probabilistic models. SIGMOD Record, 2001, 30, 461-472.	1.2	71
28	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141.	2.5	68
29	Combining the Right Features for Complex Event Recognition. , 2013, , .		58
30	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. Blood, 2009, 114, 3158-3166.	1.4	52
31	Variation and Genetic Control of Gene Expression in Primary Immunocytes across Inbred Mouse Strains. Journal of Immunology, 2014, 193, 4485-4496.	0.8	44
32	Discriminative learning of relaxed hierarchy for large-scale visual recognition. , 2011, , .		29
33	Correlation of preterm infant illness severity with placental histology. Placenta, 2016, 39, 61-69.	1.5	27
34	Imputing gene expression from selectively reduced probe sets. Nature Methods, 2012, 9, 1120-1125.	19.0	26
35	Multi-level inference by relaxed dual decomposition for human pose segmentation. , 2011, , .		25
36	Asymptotic conditional probabilities: The non-unary case. Journal of Symbolic Logic, 1996, 61, 250-276.	0.5	15

#	ARTICLE	IF	CITATIONS
37	A RESPONSE TO "BELIEVING ON THE BASIS OF THE EVIDENCE", Computational Intelligence, 1994, 10, 21-25. 3.2		3
38	Structured representations and intractability. ACM Computing Surveys, 1996, 28, 8.	23.0	1
39	Understanding Gene Regulatory Networks and Their Variations. FASEB Journal, 2010, 24, 81.2.	0.5	0