

Daphne Koller

List of Publications by Year in descending order

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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	Correlation of preterm infant illness severity with placental histology. Placenta, 2016, 39, 61-69.	1.5	27
2	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	3.2	158
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
4	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
5	Causal signals between codon bias, $\langle \text{scp} \rangle \text{mRNA} \langle / \text{scp} \rangle$ structure, and the efficiency of translation and elongation. Molecular Systems Biology, 2014, 10, 770.	7.2	231
6	Variation and Genetic Control of Gene Expression in Primary Immunocytes across Inbred Mouse Strains. Journal of Immunology, 2014, 193, 4485-4496.	0.8	44
7	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
8	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. Genome Research, 2014, 24, 14-24.	5.5	547
9	Human Responses to Influenza Vaccination Show Seroconversion Signatures and Convergent Antibody Rearrangements. Cell Host and Microbe, 2014, 16, 105-114.	11.0	246
10	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. Molecular Systems Biology, 2013, 9, 659.	7.2	173
11	Combining the Right Features for Complex Event Recognition. , 2013, , .		58
12	Conservation and divergence in the transcriptional programs of the human and mouse immune systems. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2946-2951.	7.1	296
13	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
14	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141.	2.5	68
15	Imputing gene expression from selectively reduced probe sets. Nature Methods, 2012, 9, 1120-1125.	19.0	26
16	Learning latent temporal structure for complex event detection. , 2012, , .		239
17	Discriminative learning of relaxed hierarchy for large-scale visual recognition. , 2011, , .		29
18	Multi-level inference by relaxed dual decomposition for human pose segmentation. , 2011, , .		25

#	ARTICLE	IF	CITATIONS
19	A segmentation-aware object detection model with occlusion handling. , 2011, , .		82
20	Real time motion capture using a single time-of-flight camera. , 2010, , .		254
21	Single image depth estimation from predicted semantic labels. , 2010, , .		328
22	Understanding Gene Regulatory Networks and Their Variations. FASEB Journal, 2010, 24, 81.2.	0.5	0
23	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	3.5	177
24	Decomposing a scene into geometric and semantically consistent regions. , 2009, , .		437
25	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. Blood, 2009, 114, 3158-3166.	1.4	52
26	Multi-Class Segmentation with Relative Location Prior. International Journal of Computer Vision, 2008, 80, 300-316.	15.6	379
27	The Immunological Genome Project: networks of gene expression in immune cells. Nature Immunology, 2008, 9, 1091-1094.	14.5	1,576
28	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	21.4	1,072
29	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
30	From signatures to models: understanding cancer using microarrays. Nature Genetics, 2005, 37, S38-S45.	21.4	331
31	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	21.4	622
32	Title is missing!. Machine Learning, 2003, 50, 95-125.	5.4	516
33	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543
34	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. Science, 2003, 302, 249-255.	12.6	2,034
35	Selectivity estimation using probabilistic models. SIGMOD Record, 2001, 30, 461-472.	1.2	71
36	Adaptive Probabilistic Networks with Hidden Variables. Machine Learning, 1997, 29, 213-244.	5.4	233

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37	Asymptotic conditional probabilities: The non-unary case. Journal of Symbolic Logic, 1996, 61, 250-276.	0.5	15
38	Structured representations and intractability. ACM Computing Surveys, 1996, 28, 8.	23.0	1
39	A RESPONSE TO "BELIEVING ON THE BASIS OF THE EVIDENCE". Computational Intelligence, 1994, 10, 21-25. 3.2		3