

# 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

270111

25  
h-index

511568

30  
g-index

40  
all docs

40  
docs citations

40  
times ranked

50982  
citing authors

#	ARTICLE	IF	CITATIONS
1	Correlation of preterm infant illness severity with placental histology. <i>Placenta</i> , 2016, 39, 61-69.	0.7	27
2	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015, 11, e1004220.	1.5	158
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
4	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
5	Causal signals between codon bias, $\langle scp \rangle mRNA \langle /scp \rangle$ structure, and the efficiency of translation and elongation. <i>Molecular Systems Biology</i> , 2014, 10, 770.	3.2	231
6	Variation and Genetic Control of Gene Expression in Primary Immunocytes across Inbred Mouse Strains. <i>Journal of Immunology</i> , 2014, 193, 4485-4496.	0.4	44
7	Programming Pluralism: Using Learning Analytics to Detect Patterns in the Learning of Computer Programming. <i>Journal of the Learning Sciences</i> , 2014, 23, 561-599.	2.0	201
8	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. <i>Genome Research</i> , 2014, 24, 14-24.	2.4	547
9	Human Responses to Influenza Vaccination Show Seroconversion Signatures and Convergent Antibody Rearrangements. <i>Cell Host and Microbe</i> , 2014, 16, 105-114.	5.1	246
10	Apoptosis and other immune biomarkers predict influenza vaccine responsiveness. <i>Molecular Systems Biology</i> , 2013, 9, 659.	3.2	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2946-2951.	3.3	296
13	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	9.4	6,815
14	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. <i>PLoS ONE</i> , 2013, 8, e68141.	1.1	68
15	Imputing gene expression from selectively reduced probe sets. <i>Nature Methods</i> , 2012, 9, 1120-1125.	9.0	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.	0.2	0
23	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	1.5	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.	0.6	52
26	Multi-Class Segmentation with Relative Location Prior. International Journal of Computer Vision, 2008, 80, 300-316.	10.9	379
27	The Immunological Genome Project: networks of gene expression in immune cells. Nature Immunology, 2008, 9, 1091-1094.	7.0	1,576
28	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	9.4	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.	3.3	126
30	From signatures to models: understanding cancer using microarrays. Nature Genetics, 2005, 37, S38-S45.	9.4	331
31	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	9.4	622
32	Title is missing!. Machine Learning, 2003, 50, 95-125.	3.4	516
33	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	9.4	1,543
34	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. Science, 2003, 302, 249-255.	6.0	2,034
35	Selectivity estimation using probabilistic models. SIGMOD Record, 2001, 30, 461-472.	0.7	71
36	Adaptive Probabilistic Networks with Hidden Variables. Machine Learning, 1997, 29, 213-244.	3.4	233

#	ARTICLE	IF	CITATIONS
37	Asymptotic conditional probabilities: The non-unary case. Journal of Symbolic Logic, 1996, 61, 250-276.	0.4	15
38	Structured representations and intractability. ACM Computing Surveys, 1996, 28, 8.	16.1	1
39	A RESPONSE TO "BELIEVING ON THE BASIS OF THE EVIDENCE": Computational Intelligence, 1994, 10, 21-25. 2.1		3