

Jesper TegnÃ©r

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

5,682
citations

304743

22
h-index

395702

33
g-index

36
all docs

36
docs citations

36
times ranked

10668
citing authors

#	ARTICLE	IF	CITATIONS
1	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. <i>Bioinformatics</i> , 2013, 29, 189-196.	4.1	1,295
2	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667
3	Reverse engineering gene networks using singular value decomposition and robust regression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6163-6168.	7.1	582
4	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
5	Reverse engineering gene networks: Integrating genetic perturbations with dynamical modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5944-5949.	7.1	380
6	Mechanism for top-down control of working memory capacity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6802-6807.	7.1	305
7	Data integration in the era of omics: current and future challenges. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	300
8	Temporally Irregular Mnemonic Persistent Activity in Prefrontal Neurons of Monkeys During a Delayed Response Task. <i>Journal of Neurophysiology</i> , 2003, 90, 3441-3454.	1.8	235
9	Intrinsic function of a neuronal network – a vertebrate central pattern generator. <i>Brain Research Reviews</i> , 1998, 26, 184-197.	9.0	217
10	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346.	2.7	192
11	An integrative analysis reveals coordinated reprogramming of the epigenome and the transcriptome in human skeletal muscle after training. <i>Epigenetics</i> , 2014, 9, 1557-1569.	2.7	184
12	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397.	12.8	147
13	The dynamical stability of reverberatory neural circuits. <i>Biological Cybernetics</i> , 2002, 87, 471-481.	1.3	130
14	Stronger Synaptic Connectivity as a Mechanism behind Development of Working Memory-related Brain Activity during Childhood. <i>Journal of Cognitive Neuroscience</i> , 2007, 19, 750-760.	2.3	103
15	Monozygotic twins discordant for common variable immunodeficiency reveal impaired DNA demethylation during naïve-to-memory B-cell transition. <i>Nature Communications</i> , 2015, 6, 7335.	12.8	81
16	Transcriptional Profiling Uncovers a Network of Cholesterol-Responsive Atherosclerosis Target Genes. <i>PLoS Genetics</i> , 2008, 4, e1000036.	3.5	67
17	Low-Voltage-Activated Calcium Channels in the Lamprey Locomotor Network: Simulation and Experiment. <i>Journal of Neurophysiology</i> , 1997, 77, 1795-1812.	1.8	53
18	Perturbations to uncover gene networks. <i>Trends in Genetics</i> , 2007, 23, 34-41.	6.7	51

#	ARTICLE	IF	CITATIONS
19	Combining evidence from four immune cell types identifies DNA methylation patterns that implicate functionally distinct pathways during Multiple Sclerosis progression. <i>EBioMedicine</i> , 2019, 43, 411-423.	6.1	45
20	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. <i>Genomics</i> , 2008, 91, 219-231.	2.9	38
21	Systems Biology Is Taking Off. <i>Genome Research</i> , 2003, 13, 2377-2380.	5.5	36
22	Modulation of burst frequency by calcium-dependent potassium channels in the lamprey locomotor system: dependence of the activity level. <i>Journal of Computational Neuroscience</i> , 1998, 5, 121-140.	1.0	30
23	Neuronal methylome reveals CREB-associated neuro-axonal impairment in multiple sclerosis. <i>Clinical Epigenetics</i> , 2019, 11, 86.	4.1	24
24	Thematic review series: Systems Biology Approaches to Metabolic and Cardiovascular Disorders. Multi-organ whole-genome measurements and reverse engineering to uncover gene networks underlying complex traits. <i>Journal of Lipid Research</i> , 2007, 48, 267-277.	4.2	19
25	Interactive Effects of the GABAergic Modulation of Calcium Channels and Calcium-Dependent Potassium Channels in Lamprey. <i>Journal of Neurophysiology</i> , 1999, 81, 1318-1329.	1.8	17
26	Neuronal firing rates account for distractor effects on mnemonic accuracy in a visuo-spatial working memory task. <i>Biological Cybernetics</i> , 2007, 96, 407-419.	1.3	17
27	Detection of compound mode of action by computational integration of whole-genome measurements and genetic perturbations. <i>BMC Bioinformatics</i> , 2006, 7, 51.	2.6	16
28	A perspective on bridging scales and design of models using low-dimensional manifolds and data-driven model inference. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20160144.	3.4	14
29	HiDi: an efficient reverse engineering schema for large-scale dynamic regulatory network reconstruction using adaptive differentiation. <i>Bioinformatics</i> , 2017, 33, 3964-3972.	4.1	11
30	GABAB-ergic modulation of burst rate and intersegmental coordination in lamprey: experiments and simulations. <i>Brain Research</i> , 2000, 864, 81-86.	2.2	8
31	The Information-Theoretic and Algorithmic Approach to Human, Animal, and Artificial Cognition. <i>Studies in Applied Philosophy, Epistemology and Rational Ethics</i> , 2017, , 117-139.	0.3	4
32	Activity Dependent Modulation of the Burst Rate by Calcium-Dependent Potassium Channels in Lamprey. , 1998, , 549-554.		3
33	Introduction to Data Types in Epigenomics. <i>Translational Bioinformatics</i> , 2015, , 3-34.	0.0	2
34	Evidence of Highly Regulated Genes (in-Hubs) in Gene Networks of <i>Saccharomyces Cerevisiae</i> . <i>Bioinformatics and Biology Insights</i> , 2008, 2, BBI.S853.	2.0	1
35	Adaptive input data transformation for improved network reconstruction with information theoretic algorithms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2016, 15, 507-520.	0.6	0
36	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0