

Hamid Bolouri

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

8,101
citations

147801

31
h-index

128289

60
g-index

73
all docs

73
docs citations

73
times ranked

12328
citing authors

#	ARTICLE	IF	CITATIONS
1	A Genomic Regulatory Network for Development. <i>Science</i> , 2002, 295, 1669-1678.	12.6	1,399
2	Systems biology approaches identify ATF3 as a negative regulator of Toll-like receptor 4. <i>Nature</i> , 2006, 441, 173-178.	27.8	755
3	Genomic Cis-Regulatory Logic: Experimental and Computational Analysis of a Sea Urchin Gene. <i>Science</i> , 1998, 279, 1896-1902.	12.6	637
4	Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer. <i>Nature Medicine</i> , 2016, 22, 369-378.	30.7	572
5	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018, 24, 103-112.	30.7	525
6	A Provisional Regulatory Gene Network for Specification of Endomesoderm in the Sea Urchin Embryo. <i>Developmental Biology</i> , 2002, 246, 162-190.	2.0	319
7	Mutant IDH1 regulates the tumor-associated immune system in gliomas. <i>Genes and Development</i> , 2017, 31, 774-786.	5.9	313
8	A data integration methodology for systems biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17296-17301.	7.1	293
9	Modeling transcriptional regulatory networks. <i>BioEssays</i> , 2002, 24, 1118-1129.	2.5	268
10	Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 355-372.	2.0	254
11	Robustness as a Measure of Plausibility in Models of Biochemical Networks. <i>Journal of Theoretical Biology</i> , 2002, 216, 19-30.	1.7	226
12	Computational representation of developmental genetic regulatory networks. <i>Developmental Biology</i> , 2005, 283, 1-16.	2.0	207
13	DIZZY: STOCHASTIC SIMULATION OF LARGE-SCALE GENETIC REGULATORY NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 415-436.	0.8	195
14	Transcriptional regulatory cascades in development: Initial rates, not steady state, determine network kinetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9371-9376.	7.1	193
15	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
16	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. <i>Cell Reports</i> , 2015, 13, 2425-2439.	6.4	146
17	<i>Crebbp</i> Loss Drives Small Cell Lung Cancer and Increases Sensitivity to HDAC Inhibition. <i>Cancer Discovery</i> , 2018, 8, 1422-1437.	9.4	126
18	Multidimensional scaling of diffuse gliomas: application to the 2016 World Health Organization classification system with prognostically relevant molecular subtype discovery. <i>Acta Neuropathologica Communications</i> , 2017, 5, 39.	5.2	110

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19	New Computational Approaches for Analysis of cis-Regulatory Networks. <i>Developmental Biology</i> , 2002, 246, 86-102.	2.0	103
20	ERG Activates the YAP1 Transcriptional Program and Induces the Development of Age-Related Prostate Tumors. <i>Cancer Cell</i> , 2015, 27, 797-808.	16.8	100
21	Visualization, documentation, analysis, and communication of large-scale gene regulatory networks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 363-374.	1.9	98
22	A gene regulatory network armature for T lymphocyte specification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20100-20105.	7.1	87
23	Dual feedback loops in the GAL regulon suppress cellular heterogeneity in yeast. <i>Nature Genetics</i> , 2006, 38, 1082-1087.	21.4	86
24	Modeling DNA Sequence-Based cis-Regulatory Gene Networks. <i>Developmental Biology</i> , 2002, 246, 2-13.	2.0	76
25	Control of internal and external noise in genetic regulatory networks. <i>Journal of Theoretical Biology</i> , 2004, 230, 301-312.	1.7	59
26	The gene regulatory network basis of the "community effect," and analysis of a sea urchin embryo example. <i>Developmental Biology</i> , 2010, 340, 170-178.	2.0	54
27	Modeling genomic regulatory networks with big data. <i>Trends in Genetics</i> , 2014, 30, 182-191.	6.7	53
28	A De Novo Mouse Model of C11orf95-RELA Fusion-Driven Ependymoma Identifies Driver Functions in Addition to NF- κ B. <i>Cell Reports</i> , 2018, 23, 3787-3797.	6.4	53
29	Big data visualization identifies the multidimensional molecular landscape of human gliomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5394-5399.	7.1	45
30	Variability in estimated gene expression among commonly used RNA-seq pipelines. <i>Scientific Reports</i> , 2020, 10, 2734.	3.3	43
31	Oncogenic Signaling Is Dominant to Cell of Origin and Dictates Astrocytic or Oligodendroglial Tumor Development from Oligodendrocyte Precursor Cells. <i>Journal of Neuroscience</i> , 2014, 34, 14644-14651.	3.6	42
32	Comprehensive Transcriptome Profiling of Cryptic <i>CBFA2T3-GLIS2</i> Fusion Positive AML Defines Novel Therapeutic Options: A COG and TARGET Pediatric AML Study. <i>Clinical Cancer Research</i> , 2020, 26, 726-737.	7.0	42
33	Network dynamics in the tumor microenvironment. <i>Seminars in Cancer Biology</i> , 2015, 30, 52-59.	9.6	36
34	The COVID-19 immune landscape is dynamically and reversibly correlated with disease severity. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	32
35	Genomic distinctions between metastatic lower and upper tract urothelial carcinoma revealed through rapid autopsy. <i>JCI Insight</i> , 2019, 4, .	5.0	30
36	Copy number profiling across glioblastoma populations has implications for clinical trial design. <i>Neuro-Oncology</i> , 2018, 20, 1368-1373.	1.2	28

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37	A kinase-deficient NTRK2 splice variant predominates in glioma and amplifies several oncogenic signaling pathways. <i>Nature Communications</i> , 2020, 11, 2977.	12.8	26
38	DIZZY: STOCHASTIC SIMULATION OF LARGE-SCALE GENETIC REGULATORY NETWORKS (SUPPLEMENTARY) Tj ETQq0,0 0 rgBT, /Overlock	0.8	24
39	Neural G0: a quiescent-like state found in neuroepithelial-derived cells and glioma. <i>Molecular Systems Biology</i> , 2021, 17, e9522.	7.2	24
40	Multimodal analysis for human ex vivo studies shows extensive molecular changes from delays in blood processing. <i>IScience</i> , 2021, 24, 102404.	4.1	22
41	miR-155 expression and correlation with clinical outcome in pediatric AML: A report from Children's Oncology Group. <i>Pediatric Blood and Cancer</i> , 2016, 63, 2096-2103.	1.5	21
42	Dissecting innate immune responses with the tools of systems biology. <i>Current Opinion in Immunology</i> , 2005, 17, 49-54.	5.5	18
43	Object-oriented regression for building predictive models with high dimensional omics data from translational studies. <i>Journal of Biomedical Informatics</i> , 2016, 60, 431-445.	4.3	15
44	Integrative network modeling reveals mechanisms underlying T cell exhaustion. <i>Scientific Reports</i> , 2020, 10, 1915.	3.3	14
45	Understanding the Dynamic Behavior of Genetic Regulatory Networks by Functional Decomposition. <i>Current Genomics</i> , 2006, 7, 333-341.	1.6	13
46	Embryonic pattern formation without morphogens. <i>BioEssays</i> , 2008, 30, 412-417.	2.5	10
47	An Object-Oriented Regression for Building Disease Predictive Models with Multiallelic HLA Genes. <i>Genetic Epidemiology</i> , 2016, 40, 315-332.	1.3	10
48	Analysis and visualization of linked molecular and clinical cancer data by using Oncoscape. <i>Nature Genetics</i> , 2018, 50, 1203-1204.	21.4	10
49	Feedback control of stochastic noise in the yeast galactose utilization pathway. <i>Physica D: Nonlinear Phenomena</i> , 2006, 217, 64-76.	2.8	9
50	Alteration of Chromatin Modifiers and Misregulation of Transcription Factors Define the Genomic Profile of Infant AML. <i>Blood</i> , 2016, 128, 774-774.	1.4	8
51	Integration of 198 ChIP-seq Datasets Reveals Humancis-Regulatory Regions. <i>Journal of Computational Biology</i> , 2012, 19, 989-997.	1.6	6
52	Computational Challenges of Personal Genomics. <i>Current Genomics</i> , 2008, 9, 80-87.	1.6	5
53	Integrative Network Analysis of Pediatric AML Whole Genomes, cDNA Expression and Clinical Data Elements Reveals Shared As Well As t(8;21), Inv16 and MLL Specific Pathways; A Report From COG/NCI Target AML Initiative. <i>Blood</i> , 2012, 120, 3519-3519.	1.4	5
54	A B-cell developmental gene regulatory network is activated in infant AML. <i>PLoS ONE</i> , 2021, 16, e0259197.	2.5	5

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55	Comprehensive Transcriptome Profiling of Cryptic CBFA2T3-GLIS2 Fusion-Positive AML Defines Novel Therapeutic Options in a COG and Target Pediatric AML Study. <i>Blood</i> , 2018, 132, 881-881.	1.4	3
56	Improving reinforcement learning in stochastic RAM-based neural networks. <i>Neural Processing Letters</i> , 1996, 3, 11-15.	3.2	2
57	Building and validating a prediction model for paediatric type 1 diabetes risk using next generation targeted sequencing of class II HLA genes. <i>Diabetes/Metabolism Research and Reviews</i> , 2017, 33, e2921.	4.0	2
58	Marked Differences in the Genomic Landscape of Pediatric Compared to Adult Acute Myeloid Leukemia: A Report from the Children's Oncology Group and NCI/COG Therapeutically Applicable Research to Generate Effective Treatments (TARGET) Initiative. <i>Blood</i> , 2016, 128, 595-595.	1.4	1
59	Menu-driven cloud computing and resource sharing for R and Bioconductor. <i>Bioinformatics</i> , 2011, 27, 2309-2310.	4.1	0
60	PATH-51. DNA COPY NUMBER PROFILING ACROSS GLIOBLASTOMA POPULATIONS HAS IMPLICATIONS FOR CLINICAL TRIAL DESIGN. <i>Neuro-Oncology</i> , 2018, 20, vi169-vi170.	1.2	0
61	CSIG-17. CHARACTERIZATION OF AN ALTERNATIVELY SPLICED NTRK2 VARIANT IN GLIOMA: EMPLOYING NOVEL REAGENTS TO UNCOVER NOVEL FUNCTIONS. <i>Neuro-Oncology</i> , 2018, 20, vi46-vi46.	1.2	0
62	Inherent Gene Expression Variabilities and the Need for Personalized Drug Dosage. <i>Letters in Drug Design and Discovery</i> , 2008, 5, 193-208.	0.7	0
63	Correlation of Mir-155 Expression with Clinical Outcome in Childhood AML: A Report from Children's Oncology Group. <i>Blood</i> , 2014, 124, 3545-3545.	1.4	0
64	Divergent Epigenomes in Pediatric and Adult Acute Myeloid Leukemia Implicate Cell of Origin and Transcriptional Silencing of Immune Responses As Sources of Clinically Relevant Heterogeneity: A Report from the Children's Oncology Group and NCI/COG Therapeutically Applicable Research to Generate Effective Treatments (TARGET) Initiative. <i>Blood</i> , 2016, 128, 1046-1046.	1.4	0
65	Selective Pressure from Chemotherapy Drives Convergent Evolution in Relapsing and Refractory AML across Age Groups. <i>Blood</i> , 2018, 132, 2609-2609.	1.4	0
66	A Distinct Oncofetal B-Cell Transcriptional Program Is Activated in Infant Acute Myeloid Leukemia and Reveals Novel Therapeutic Strategies. <i>Blood</i> , 2019, 134, 3768-3768.	1.4	0