Alberto Riva

List of Publications by Year
in descending order

90 papers	5,036 citations	201385 27 h-index	91712 69 g-index
100 all docs	100 docs citations	100 times ranked	8321 citing authors

#	Article	IF	Citations
1	PRC2 Inhibitors Overcome Glucocorticoid Resistance Driven by *NSD2* Mutation in Pediatric Acute Lymphoblastic Leukemia. Cancer Discovery, 2022, 12, 186-203.	7.7	17
2	Rapid Emergence and Spread of Severe Acute Respiratory Syndrome Coronavirus 2 Gamma (P.1) Variant in Haiti. Clinical Infectious Diseases, 2022, 74, 2057-2060.	2.9	12
3	Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDiS) for phylogenetics. Bioinformatics, 2022, 38, 856-860.	1.8	10
4	DNMT3A Harboring Leukemia-Associated Mutations Directs Sensitivity to DNA Damage at Replication Forks. Clinical Cancer Research, 2022, 28, 756-769.	3.2	9
5	Acquired Resistance to EZH2 Inhibitor GSK343 Promotes the Differentiation of Human DLBCL Cell Lines toward an ABC-Like Phenotype. Molecular Cancer Therapeutics, 2022, 21, 511-521.	1.9	3
6	Severe Acute Respiratory Syndrome Coronavirus 2 Delta Vaccine Breakthrough Transmissibility in Alachua County, Florida. Clinical Infectious Diseases, 2022, 75, 1618-1627.	2.9	4
7	Low‐frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled‐edged sword. Journal of Medical Virology, 2022, , .	2.5	8
8	Discordance between HIV-1 Population in Plasma at Rebound after Structured Treatment Interruption and Archived Provirus Population in Peripheral Blood Mononuclear Cells. Microbiology Spectrum, 2022, 10, .	1.2	1
9	Exertional heat stroke leads to concurrent long‐term epigenetic memory, immunosuppression and altered heat shock response in female mice. Journal of Physiology, 2021, 599, 119-141.	1.3	24
10	Analysis of canine myeloid-derived suppressor cells (MDSCs) utilizing fluorescence-activated cell sorting, RNA protection mediums to yield quality RNA for single-cell RNA sequencing. Veterinary Immunology and Immunopathology, 2021, 231, 110144.	0.5	10
11	Decreases in different Dnmt3b activities drive distinct development of hematologic malignancies in mice. Journal of Biological Chemistry, 2021, 296, 100285.	1.6	6
12	Dnmt3b catalytic activity is critical for its tumour suppressor function in lymphomagenesis and is associated with c-Met oncogenic signalling. EBioMedicine, 2021, 63, 103191.	2.7	9
13	Novel application of single-cell next-generation sequencing for determination of intratumoral heterogeneity of canine osteosarcoma cell lines. Journal of Veterinary Diagnostic Investigation, 2021, 33, 261-278.	0.5	15
14	Brain tissue transcriptomic analysis of SIV-infected macaques identifies several altered metabolic pathways linked to neuropathogenesis and poly (ADP-ribose) polymerases (PARPs) as potential therapeutic targets. Journal of NeuroVirology, 2021, 27, 101-115.	1.0	6
15	Islet sympathetic innervation and islet neuropathology in patients with type 1 diabetes. Scientific Reports, 2021, 11, 6562.	1.6	18
16	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. Communications Biology, 2021, 4, 489.	2.0	23
17	Methylscaper: an R/Shiny app for joint visualization of DNA methylation and nucleosome occupancy in single-molecule and single-cell data. Bioinformatics, 2021, 37, 4857-4859.	1.8	4
18	Examination of CA1 Hippocampal DNA Methylation as a Mechanism for Closing of Estrogen's Critical Window. Frontiers in Aging Neuroscience, 2021, 13, 717032.	1.7	4

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19	Dysregulation of Epigenetic Landscape Uncovered the Mechanisms Underlying the Relapse of Pediatric Acute Lymphoblastic Leukemia with NSD2 Mutation. Blood, 2021, 138, 3297-3297.	0.6	0
20	Adenylate Kinase 2 Is a Selective Multiple Myeloma Cell Dependency That Is Preferentially Essential in NSD2-Overexpressing Cells. Blood, 2021, 138, 1586-1586.	0.6	0
21	Clinical Utility of Pharmacogene Panelâ€Based Testing in Patients Undergoing Percutaneous Coronary Intervention. Clinical and Translational Science, 2020, 13, 473-481.	1.5	9
22	A Bayesian data fusion based approach for learning genome-wide transcriptional regulatory networks. BMC Bioinformatics, 2020, 21, 219.	1.2	3
23	Bioinformatics Core Survey Highlights the Challenges Facing Data Analysis Facilities. Journal of Biomolecular Techniques, 2020, 31, jbt.20-3102-005.	0.8	2
24	3141 â€" LEUKEMIA-ASSOCIATED MUTATIONS IN DNMT3A MEDIATE SENSITIVITY TO REPLICATION STRESS INDUCED BY NUCLEOSIDE ANALOGS. Experimental Hematology, 2020, 88, S82.	0.2	0
25	KDM6A Controls Genes Modulating Immune Surveillance in Multiple Myeloma. Blood, 2020, 136, 14-14.	0.6	1
26	NSD2-E1099K Mutation Leads to Glucocorticoid-Resistant B Cell Lymphocytic Leukemia in Mice. Blood, 2020, 136, 3-4.	0.6	0
27	Adenylate Kinase 2 Is a Selective Dependency in NSD2-High Multiple Myeloma. Blood, 2020, 136, 31-31.	0.6	0
28	A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. Cancer Discovery, 2019, 9, 1438-1451.	7.7	65
29	Catalytically inactive Dnmt3b rescues mouse embryonic development by accessory and repressive functions. Nature Communications, 2019, 10, 4374.	5.8	28
30	Probabilistic Reasoning under Ignorance. , 2019, , 733-738.		1
31	Identification of Genetic Vulnerabilities and Synthetic-Lethal Targets in NSD2-High Multiple Myeloma. Blood, 2019, 134, 3757-3757.	0.6	1
32	DNMT3A with Leukemia-Associated Mutations Directs Sensitivity to DNA Damage at Replication Forks. Blood, 2019, 134, 535-535.	0.6	1
33	A Gain of Function Mutation in the NSD2 Histone Methyltransferase Drives Glucocorticoid Resistance Via Blocking Receptor Auto-Induction and BIM/Bmf Expression in ALL. Blood, 2019, 134, 3758-3758.	0.6	1
34	Abstract 3042: Splicing repressor *HNRNPC* is an indispensable and 'druggable' target in acute myeloid leukemia. , 2019, , .		0
35	Abstract 2456: NetZen: A comprehensive network-based pathway and target discovery platform. , 2019, , .		0
36	*SIRT1/HERC4* Locus Associated With Bisphosphonate-Induced Osteonecrosis of the Jaw: An Exome-Wide Association Analysis. Journal of Bone and Mineral Research, 2018, 33, 91-98.	3.1	31

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37	Mechanism Sharing Between Genetic and Gestational Hypoxia-Induced Cardiac Anomalies. Frontiers in Cardiovascular Medicine, 2018, 5, 100.	1.1	5
38	A Gain of Function Mutation in the NSD2 Histone Methyltransferase Drives Glucocorticoid Resistance of Acute Lymphoblastic Leukemia. Blood, 2018, 132, 653-653.	0.6	7
39	Genome-Wide Prioritization and Transcriptomics Reveal Novel Signatures Associated With Thiazide Diuretics Blood Pressure Response. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	11
40	UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. Cell Reports, 2017, 21, 628-640.	2.9	106
41	Patterns of Arabidopsis gene expression in the face of hypobaric stress. AoB PLANTS, 2017, 9, .	1.2	10
42	Dissecting Low Atmospheric Pressure Stress: Transcriptome Responses to the Components of Hypobaria in Arabidopsis. Frontiers in Plant Science, 2017, 8, 528.	1.7	16
43	DNA Methylation of Synaptic Genes in the Prefrontal Cortex Is Associated with Aging and Age-Related Cognitive Impairment. Frontiers in Aging Neuroscience, 2017, 9, 249.	1.7	51
44	Data Fusion Approach for Learning Transcriptional Bayesian Networks. Lecture Notes in Computer Science, 2017, , 76-80.	1.0	1
45	BigQ: a NoSQL based framework to handle genomic variants in i2b2. BMC Bioinformatics, 2015, 16, 415.	1.2	20
46	The Murine Pbx1-d Lupus Susceptibility Allele Accelerates Mesenchymal Stem Cell Differentiation and Impairs Their Immunosuppressive Function. Journal of Immunology, 2015, 194, 43-55.	0.4	14
47	Multiplex mapping of chromatin accessibility and DNA methylation within targeted single molecules identifies epigenetic heterogeneity in neural stem cells and glioblastoma. Genome Research, 2014, 24, 329-339.	2.4	51
48	PASTA: splice junction identification from RNA-Sequencing data. BMC Bioinformatics, 2013, 14, 116.	1.2	19
49	The MAPPER2 Database: a multi-genome catalog of putative transcription factor binding sites. Nucleic Acids Research, 2012, 40, D155-D161.	6.5	50
50	DNA Methyltransferase Accessibility Protocol for Individual Templates by Deep Sequencing. Methods in Enzymology, 2012, 513, 185-204.	0.4	13
51	A Knowledge-Based Method for Association Studies on Complex Diseases. PLoS ONE, 2012, 7, e44162.	1.1	1
52	Large-scale computational identification of regulatory SNPs with rSNP-MAPPER. BMC Genomics, 2012, 13, S7.	1.2	40
53	An innovative Positional Pattern Detection tool applied to GAL4 Binding Sites in yeast. , 2011, , .		0
54	Whole Genome Sequences of a Male and Female Supercentenarian, Ages Greater than 114â€‰Years. Frontiers in Genetics, 2011, 2, 90.	1.1	51

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55	Genetic modifiers of the severity of sickle cell anemia identified through a genome‑wide association study. American Journal of Hematology, 2010, 85, 29-35.	2.0	83
56	An automated reasoning framework for translational research. Journal of Biomedical Informatics, 2010, 43, 419-427.	2.5	7
57	PANGEA: pipeline for analysis of next generation amplicons. ISME Journal, 2010, 4, 852-861.	4.4	103
58	Evolving Spiking Neural Networks for predicting transcription factor binding sites. , 2010, , .		1
59	A Unique, Consistent Identifier for Alternatively Spliced Transcript Variants. PLoS ONE, 2009, 4, e7631.	1.1	8
60	RNA Editing Genes Associated with Extreme Old Age in Humans and with Lifespan in C. elegans. PLoS ONE, 2009, 4, e8210.	1.1	81
61	Genephony: a knowledge management tool for genome-wide research. BMC Bioinformatics, 2009, 10, 278.	1.2	8
62	Phenotypic and genotypic data integration and exploration through a web-service architecture. BMC Bioinformatics, 2009, 10, S5.	1.2	7
63	An Architecture for Automated Reasoning Systems for Genome-Wide Studies. Lecture Notes in Computer Science, 2009, , 426-430.	1.0	1
64	A hierarchical and modular approach to the discovery of robust associations in genome-wide association studies from pooled DNA samples. BMC Genetics, 2008, 9, 6.	2.7	26
65	Distantly sampled soils carry few species in common. ISME Journal, 2008, 2, 901-910.	4.4	137
66	Identification of Cellular Genes Targeted by KSHV-Encoded MicroRNAs. PLoS Pathogens, 2007, 3, e65.	2.1	277
67	Kaposi's Sarcoma-Associated Herpesvirus Encodes an Ortholog of miR-155. Journal of Virology, 2007, 81, 12836-12845.	1.5	421
68	Pyrosequencing enumerates and contrasts soil microbial diversity. ISME Journal, 2007, 1, 283-290.	4.4	1,615
69	Defining Aggressive Prostate Cancer Using a 12-Gene Model. Neoplasia, 2006, 8, 59-68.	2.3	90
70	START: an automated tool for serial analysis of chromatin occupancy data. Bioinformatics, 2006, 22, 999-1001.	1.8	5
71	Internet-based Profiler system as integrative framework to support translational research. BMC Bioinformatics, 2005, 6, 304.	1.2	10
72	MAPPER: a search engine for the computational identification of putative transcription factor binding sites in multiple genomes. BMC Bioinformatics, 2005, 6, 79.	1.2	178

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73	GR and HMGB1 Interact Only within Chromatin and Influence Each Other's Residence Time. Molecular Cell, 2005, 18, 109-121.	4.5	108
74	The MAPPER database: a multi-genome catalog of putative transcription factor binding sites. Nucleic Acids Research, 2004, 33, D91-D97.	6.5	111
75	JAGGED1 Expression Is Associated with Prostate Cancer Metastasis and Recurrence. Cancer Research, 2004, 64, 6854-6857.	0.4	310
76	A SNP-centric database for the investigation of the human genome. BMC Bioinformatics, 2004, 5, 33.	1.2	64
77	Bayesian approach to discovering pathogenic SNPs in conserved protein domains. Human Mutation, 2004, 24, 178-184.	1.1	38
78	A telemedicine support for diabetes management: the T-IDDM project. Computer Methods and Programs in Biomedicine, 2002, 69, 147-161.	2.6	109
79	Single nucleotide polymorphisms in innate immunity genes: abundant variation and potential role in complex human disease. Immunological Reviews, 2002, 190, 9-25.	2.8	185
80	Accessing genomic data through XML-based remote procedure calls. Proceedings, 2002, , 662-6.	0.6	1
81	Web-based telemedicine systems for home-care: technical issues and experiences. Computer Methods and Programs in Biomedicine, 2001, 64, 175-187.	2.6	93
82	The Personal Internetworked Notary and Guardian. International Journal of Medical Informatics, 2001, 62, 27-40.	1.6	28
83	Temporal Abstractions for diabetic patients management. Lecture Notes in Computer Science, 1997, , 319-330.	1.0	22
84	Interpreting longitudinal data through temporal abstractions: An application to diabetic patients monitoring. Lecture Notes in Computer Science, 1997, , 287-298.	1.0	2
85	Cooperative Intelligent Data Analysis: An Application to Diabetic Patients Management. , 1997, , 81-98.		4
86	Learning temporal probabilistic causal models from longitudinal data. Artificial Intelligence in Medicine, 1996, 8, 217-234.	3.8	37
87	An ignorant belief network to forecast glucose concentration from clinical databases. Artificial Intelligence in Medicine, 1995, 7, 541-559.	3.8	13
88	High level control strategies for diabetes therapy. Lecture Notes in Computer Science, 1995, , 185-196.	1.0	7
89	Medical decision making using Ignorant Influence Diagrams. Lecture Notes in Computer Science, 1995, , 139-150.	1.0	1
90	Belief Maintenance in Bayesian Networks. , 1994, , 498-505.		7