

# Alberto Riva

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | Pyrosequencing enumerates and contrasts soil microbial diversity. <i>ISME Journal</i> , 2007, 1, 283-290.                                                                 | 4.4 | 1,615     |
| 2  | Kaposi's Sarcoma-Associated Herpesvirus Encodes an Ortholog of miR-155. <i>Journal of Virology</i> , 2007, 81, 12836-12845.                                               | 1.5 | 421       |
| 3  | JAGGED1 Expression Is Associated with Prostate Cancer Metastasis and Recurrence. <i>Cancer Research</i> , 2004, 64, 6854-6857.                                            | 0.4 | 310       |
| 4  | Identification of Cellular Genes Targeted by KSHV-Encoded MicroRNAs. <i>PLoS Pathogens</i> , 2007, 3, e65.                                                                | 2.1 | 277       |
| 5  | Single nucleotide polymorphisms in innate immunity genes: abundant variation and potential role in complex human disease. <i>Immunological Reviews</i> , 2002, 190, 9-25. | 2.8 | 185       |
| 6  | MAPPER: a search engine for the computational identification of putative transcription factor binding sites in multiple genomes. <i>BMC Bioinformatics</i> , 2005, 6, 79. | 1.2 | 178       |
| 7  | Distantly sampled soils carry few species in common. <i>ISME Journal</i> , 2008, 2, 901-910.                                                                              | 4.4 | 137       |
| 8  | The MAPPER database: a multi-genome catalog of putative transcription factor binding sites. <i>Nucleic Acids Research</i> , 2004, 33, D91-D97.                            | 6.5 | 111       |
| 9  | A telemedicine support for diabetes management: the T-IDDM project. <i>Computer Methods and Programs in Biomedicine</i> , 2002, 69, 147-161.                              | 2.6 | 109       |
| 10 | GR and HMGB1 Interact Only within Chromatin and Influence Each Other's Residence Time. <i>Molecular Cell</i> , 2005, 18, 109-121.                                         | 4.5 | 108       |
| 11 | UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. <i>Cell Reports</i> , 2017, 21, 628-640.                     | 2.9 | 106       |
| 12 | PANGEA: pipeline for analysis of next generation amplicons. <i>ISME Journal</i> , 2010, 4, 852-861.                                                                       | 4.4 | 103       |
| 13 | Web-based telemedicine systems for home-care: technical issues and experiences. <i>Computer Methods and Programs in Biomedicine</i> , 2001, 64, 175-187.                  | 2.6 | 93        |
| 14 | Defining Aggressive Prostate Cancer Using a 12-Gene Model. <i>Neoplasia</i> , 2006, 8, 59-68.                                                                             | 2.3 | 90        |
| 15 | Genetic modifiers of the severity of sickle cell anemia identified through a genome-wide association study. <i>American Journal of Hematology</i> , 2010, 85, 29-35.      | 2.0 | 83        |
| 16 | RNA Editing Genes Associated with Extreme Old Age in Humans and with Lifespan in <i>C. elegans</i> . <i>PLoS ONE</i> , 2009, 4, e8210.                                    | 1.1 | 81        |
| 17 | A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. <i>Cancer Discovery</i> , 2019, 9, 1438-1451.                                                       | 7.7 | 65        |
| 18 | A SNP-centric database for the investigation of the human genome. <i>BMC Bioinformatics</i> , 2004, 5, 33.                                                                | 1.2 | 64        |

| #  | ARTICLE                                                                                                                                                                                                                  | IF  | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Whole Genome Sequences of a Male and Female Supercentenarian, Ages Greater than 114 Years. <i>Frontiers in Genetics</i> , 2011, 2, 90.                                                                                   | 1.1 | 51        |
| 20 | Multiplex mapping of chromatin accessibility and DNA methylation within targeted single molecules identifies epigenetic heterogeneity in neural stem cells and glioblastoma. <i>Genome Research</i> , 2014, 24, 329-339. | 2.4 | 51        |
| 21 | DNA Methylation of Synaptic Genes in the Prefrontal Cortex Is Associated with Aging and Age-Related Cognitive Impairment. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 249.                                         | 1.7 | 51        |
| 22 | The MAPPER2 Database: a multi-genome catalog of putative transcription factor binding sites. <i>Nucleic Acids Research</i> , 2012, 40, D155-D161.                                                                        | 6.5 | 50        |
| 23 | Large-scale computational identification of regulatory SNPs with rSNP-MAPPER. <i>BMC Genomics</i> , 2012, 13, S7.                                                                                                        | 1.2 | 40        |
| 24 | Bayesian approach to discovering pathogenic SNPs in conserved protein domains. <i>Human Mutation</i> , 2004, 24, 178-184.                                                                                                | 1.1 | 38        |
| 25 | Learning temporal probabilistic causal models from longitudinal data. <i>Artificial Intelligence in Medicine</i> , 1996, 8, 217-234.                                                                                     | 3.8 | 37        |
| 26 | <i>SIRT1/HERC4</i> Locus Associated With Bisphosphonate-Induced Osteonecrosis of the Jaw: An Exome-Wide Association Analysis. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 91-98.                             | 3.1 | 31        |
| 27 | The Personal Interneted Notary and Guardian. <i>International Journal of Medical Informatics</i> , 2001, 62, 27-40.                                                                                                      | 1.6 | 28        |
| 28 | Catalytically inactive Dnmt3b rescues mouse embryonic development by accessory and repressive functions. <i>Nature Communications</i> , 2019, 10, 4374.                                                                  | 5.8 | 28        |
| 29 | A hierarchical and modular approach to the discovery of robust associations in genome-wide association studies from pooled DNA samples. <i>BMC Genetics</i> , 2008, 9, 6.                                                | 2.7 | 26        |
| 30 | Exertional heat stroke leads to concurrent long-term epigenetic memory, immunosuppression and altered heat shock response in female mice. <i>Journal of Physiology</i> , 2021, 599, 119-141.                             | 1.3 | 24        |
| 31 | SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021, 4, 489.                                        | 2.0 | 23        |
| 32 | Temporal Abstractions for diabetic patients management. <i>Lecture Notes in Computer Science</i> , 1997, , 319-330.                                                                                                      | 1.0 | 22        |
| 33 | BigQ: a NoSQL based framework to handle genomic variants in i2b2. <i>BMC Bioinformatics</i> , 2015, 16, 415.                                                                                                             | 1.2 | 20        |
| 34 | PASTA: splice junction identification from RNA-Sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 116.                                                                                                               | 1.2 | 19        |
| 35 | Islet sympathetic innervation and islet neuropathology in patients with type 1 diabetes. <i>Scientific Reports</i> , 2021, 11, 6562.                                                                                     | 1.6 | 18        |
| 36 | PRC2 Inhibitors Overcome Glucocorticoid Resistance Driven by <i>NSD2</i> Mutation in Pediatric Acute Lymphoblastic Leukemia. <i>Cancer Discovery</i> , 2022, 12, 186-203.                                                | 7.7 | 17        |

| #  | ARTICLE                                                                                                                                                                                                                                                      | IF  | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Dissecting Low Atmospheric Pressure Stress: Transcriptome Responses to the Components of Hypobaria in Arabidopsis. <i>Frontiers in Plant Science</i> , 2017, 8, 528.                                                                                         | 1.7 | 16        |
| 38 | Novel application of single-cell next-generation sequencing for determination of intratumoral heterogeneity of canine osteosarcoma cell lines. <i>Journal of Veterinary Diagnostic Investigation</i> , 2021, 33, 261-278.                                    | 0.5 | 15        |
| 39 | The Murine Pbx1-d Lupus Susceptibility Allele Accelerates Mesenchymal Stem Cell Differentiation and Impairs Their Immunosuppressive Function. <i>Journal of Immunology</i> , 2015, 194, 43-55.                                                               | 0.4 | 14        |
| 40 | An ignorant belief network to forecast glucose concentration from clinical databases. <i>Artificial Intelligence in Medicine</i> , 1995, 7, 541-559.                                                                                                         | 3.8 | 13        |
| 41 | DNA Methyltransferase Accessibility Protocol for Individual Templates by Deep Sequencing. <i>Methods in Enzymology</i> , 2012, 513, 185-204.                                                                                                                 | 0.4 | 13        |
| 42 | Rapid Emergence and Spread of Severe Acute Respiratory Syndrome Coronavirus 2 Gamma (P.1) Variant in Haiti. <i>Clinical Infectious Diseases</i> , 2022, 74, 2057-2060.                                                                                       | 2.9 | 12        |
| 43 | Genome-Wide Prioritization and Transcriptomics Reveal Novel Signatures Associated With Thiazide Diuretics Blood Pressure Response. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .                                                                 | 5.1 | 11        |
| 44 | Internet-based Profiler system as integrative framework to support translational research. <i>BMC Bioinformatics</i> , 2005, 6, 304.                                                                                                                         | 1.2 | 10        |
| 45 | Patterns of Arabidopsis gene expression in the face of hypobaric stress. <i>AoB PLANTS</i> , 2017, 9, .                                                                                                                                                      | 1.2 | 10        |
| 46 | 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. <i>Veterinary Immunology and Immunopathology</i> , 2021, 231, 110144. | 0.5 | 10        |
| 47 | Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDiS) for phylogenetics. <i>Bioinformatics</i> , 2022, 38, 856-860.                                                                                                    | 1.8 | 10        |
| 48 | Clinical Utility of Pharmacogene Panel-Based Testing in Patients Undergoing Percutaneous Coronary Intervention. <i>Clinical and Translational Science</i> , 2020, 13, 473-481.                                                                               | 1.5 | 9         |
| 49 | Dnmt3b catalytic activity is critical for its tumour suppressor function in lymphomagenesis and is associated with c-Met oncogenic signalling. <i>EBioMedicine</i> , 2021, 63, 103191.                                                                       | 2.7 | 9         |
| 50 | DNMT3A Harboring Leukemia-Associated Mutations Directs Sensitivity to DNA Damage at Replication Forks. <i>Clinical Cancer Research</i> , 2022, 28, 756-769.                                                                                                  | 3.2 | 9         |
| 51 | A Unique, Consistent Identifier for Alternatively Spliced Transcript Variants. <i>PLoS ONE</i> , 2009, 4, e7631.                                                                                                                                             | 1.1 | 8         |
| 52 | Genephony: a knowledge management tool for genome-wide research. <i>BMC Bioinformatics</i> , 2009, 10, 278.                                                                                                                                                  | 1.2 | 8         |
| 53 | Low-frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled-edged sword. <i>Journal of Medical Virology</i> , 2022, , .                                                                                                  | 2.5 | 8         |
| 54 | High level control strategies for diabetes therapy. <i>Lecture Notes in Computer Science</i> , 1995, , 185-196.                                                                                                                                              | 1.0 | 7         |

| #  | ARTICLE                                                                                                                                                                                                                                                          | IF  | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Phenotypic and genotypic data integration and exploration through a web-service architecture. BMC Bioinformatics, 2009, 10, S5.                                                                                                                                  | 1.2 | 7         |
| 56 | An automated reasoning framework for translational research. Journal of Biomedical Informatics, 2010, 43, 419-427.                                                                                                                                               | 2.5 | 7         |
| 57 | Belief Maintenance in Bayesian Networks. , 1994, , 498-505.                                                                                                                                                                                                      |     | 7         |
| 58 | 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         |
| 59 | Decreases in different Dnmt3b activities drive distinct development of hematologic malignancies in mice. Journal of Biological Chemistry, 2021, 296, 100285.                                                                                                     | 1.6 | 6         |
| 60 | 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         |
| 61 | START: an automated tool for serial analysis of chromatin occupancy data. Bioinformatics, 2006, 22, 999-1001.                                                                                                                                                    | 1.8 | 5         |
| 62 | Mechanism Sharing Between Genetic and Gestational Hypoxia-Induced Cardiac Anomalies. Frontiers in Cardiovascular Medicine, 2018, 5, 100.                                                                                                                         | 1.1 | 5         |
| 63 | 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         |
| 64 | 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         |
| 65 | Cooperative Intelligent Data Analysis: An Application to Diabetic Patients Management. , 1997, , 81-98.                                                                                                                                                          |     | 4         |
| 66 | Severe Acute Respiratory Syndrome Coronavirus 2 Delta Vaccine Breakthrough Transmissibility in Alachua County, Florida. Clinical Infectious Diseases, 2022, 75, 1618-1627.                                                                                       | 2.9 | 4         |
| 67 | A Bayesian data fusion based approach for learning genome-wide transcriptional regulatory networks. BMC Bioinformatics, 2020, 21, 219.                                                                                                                           | 1.2 | 3         |
| 68 | 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         |
| 69 | Interpreting longitudinal data through temporal abstractions: An application to diabetic patients monitoring. Lecture Notes in Computer Science, 1997, , 287-298.                                                                                                | 1.0 | 2         |
| 70 | Bioinformatics Core Survey Highlights the Challenges Facing Data Analysis Facilities. Journal of Biomolecular Techniques, 2020, 31, jbt.20-3102-005.                                                                                                             | 0.8 | 2         |
| 71 | Evolving Spiking Neural Networks for predicting transcription factor binding sites. , 2010, ,                                                                                                                                                                    |     | 1         |
| 72 | A Knowledge-Based Method for Association Studies on Complex Diseases. PLoS ONE, 2012, 7, e44162.                                                                                                                                                                 | 1.1 | 1         |

| #  | ARTICLE                                                                                                                                                                                                      | IF  | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 73 | Medical decision making using Ignorant Influence Diagrams. Lecture Notes in Computer Science, 1995, , 139-150.                                                                                               | 1.0 | 1         |
| 74 | Data Fusion Approach for Learning Transcriptional Bayesian Networks. Lecture Notes in Computer Science, 2017, , 76-80.                                                                                       | 1.0 | 1         |
| 75 | An Architecture for Automated Reasoning Systems for Genome-Wide Studies. Lecture Notes in Computer Science, 2009, , 426-430.                                                                                 | 1.0 | 1         |
| 76 | Probabilistic Reasoning under Ignorance. , 2019, , 733-738.                                                                                                                                                  |     | 1         |
| 77 | Identification of Genetic Vulnerabilities and Synthetic-Lethal Targets in NSD2-High Multiple Myeloma. Blood, 2019, 134, 3757-3757.                                                                           | 0.6 | 1         |
| 78 | DNMT3A with Leukemia-Associated Mutations Directs Sensitivity to DNA Damage at Replication Forks. Blood, 2019, 134, 535-535.                                                                                 | 0.6 | 1         |
| 79 | 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         |
| 80 | Accessing genomic data through XML-based remote procedure calls. Proceedings, 2002, , 662-6.                                                                                                                 | 0.6 | 1         |
| 81 | KDM6A Controls Genes Modulating Immune Surveillance in Multiple Myeloma. Blood, 2020, 136, 14-14.                                                                                                            | 0.6 | 1         |
| 82 | 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         |
| 83 | An innovative Positional Pattern Detection tool applied to GAL4 Binding Sites in yeast. , 2011, , .                                                                                                          |     | 0         |
| 84 | 3141 " LEUKEMIA-ASSOCIATED MUTATIONS IN DNMT3A MEDIATE SENSITIVITY TO REPLICATION STRESS INDUCED BY NUCLEOSIDE ANALOGS. Experimental Hematology, 2020, 88, S82.                                              | 0.2 | 0         |
| 85 | 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         |
| 86 | 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         |
| 87 | NSD2-E1099K Mutation Leads to Glucocorticoid-Resistant B Cell Lymphocytic Leukemia in Mice. Blood, 2020, 136, 3-4.                                                                                           | 0.6 | 0         |
| 88 | Adenylate Kinase 2 Is a Selective Dependency in NSD2-High Multiple Myeloma. Blood, 2020, 136, 31-31.                                                                                                         | 0.6 | 0         |
| 89 | Abstract 3042: Splicing repressor <i>HNRNPC</i> is an indispensable and 'druggable' target in acute myeloid leukemia. , 2019, , .                                                                            |     | 0         |
| 90 | Abstract 2456: NetZen: A comprehensive network-based pathway and target discovery platform. , 2019, , .                                                                                                      |     | 0         |