

Vincent J Magrini

List of Publications by Year in descending order

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Version: 2024-02-01

119
papers

53,359
citations

38742

50
h-index

25787

108
g-index

132
all docs

132
docs citations

132
times ranked

73169
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-read whole genome sequencing reveals HOXD13 alterations in synpolydactyly. <i>Human Mutation</i> , 2022, 43, 189-199.	2.5	7
2	A deletion in the N gene of SARS-CoV-2 may reduce test sensitivity for detection of SARS-CoV-2. <i>Diagnostic Microbiology and Infectious Disease</i> , 2022, 102, 115631.	1.8	12
3	Expanding the Clinical Phenotype of FGFR1 Internal Tandem Duplication. <i>Journal of Physical Education and Sports Management</i> , 2022, , mcs.a006174.	1.2	4
4	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. <i>Cancer Genetics</i> , 2022, 264-265, 90-99.	0.4	3
5	Detection of brain somatic variation in epilepsy-associated developmental lesions. <i>Epilepsia</i> , 2022, 63, 1981-1997.	5.1	29
6	Novel morphologic findings in <i>PLAG1</i> rearranged soft tissue tumors. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 577-585.	2.8	9
7	Expanding the phenotypic spectrum of internal tandem duplications in somatic disease. <i>Molecular Genetics and Metabolism</i> , 2021, 132, S44.	1.1	0
8	Molecular classification of a complex structural rearrangement of the RB1 locus in an infant with sporadic, isolated, intracranial, sellar region retinoblastoma. <i>Acta Neuropathologica Communications</i> , 2021, 9, 61.	5.2	5
9	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	7.6	23
10	Somatic PIK3R1 variation as a cause of vascular malformations and overgrowth. <i>Genetics in Medicine</i> , 2021, 23, 1882-1888.	2.4	26
11	Gastroblastoma with a novel <i>EWSR1</i> - <i>CTBP1</i> fusion presenting in adolescence. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 640-646.	2.8	12
12	A novel sialic acid-binding adhesin present in multiple species contributes to the pathogenesis of Infective endocarditis. <i>PLoS Pathogens</i> , 2021, 17, e1009222.	4.7	11
13	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. <i>American Journal of Surgical Pathology</i> , 2021, 45, 329-340.	3.7	14
14	Somatic variation as an incidental finding in the pediatric next-generation sequencing era. <i>Journal of Physical Education and Sports Management</i> , 2021, 7, a006135.	1.2	3
15	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021, 22, 872.	2.8	13
16	Clinically aggressive pediatric spinal ependymoma with novel MYC amplification demonstrates molecular and histopathologic similarity to newly described MYCN-amplified spinal ependymomas. <i>Acta Neuropathologica Communications</i> , 2021, 9, 192.	5.2	5
17	Infantile fibrosarcoma-like tumor driven by novel <i>RBPMS-MET</i> fusion consolidated with cabozantinib. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005645.	1.2	17
18	Disease-associated mosaic variation in clinical exome sequencing: a two-year pediatric tertiary care experience. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005231.	1.2	15

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19	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. <i>Neurology: Genetics</i> , 2020, 6, e460.	1.9	26
20	<i>De novo</i> primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) <i>NFIA/CBFA2T3</i> translocation. <i>Haematologica</i> , 2020, 105, e194-e197.	3.5	9
21	<i>Streptococcus oralis</i> subsp. <i>dentisani</i> Produces Monolateral Serine-Rich Repeat Protein Fibrils, One of Which Contributes to Saliva Binding via Sialic Acid. <i>Infection and Immunity</i> , 2019, 87, .	2.2	14
22	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. <i>IScience</i> , 2019, 18, 1-10.	4.1	6
23	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. <i>European Journal of Medical Genetics</i> , 2019, 62, 103701.	1.3	12
24	Comprehensive gene expression meta-analysis identifies signature genes that distinguish microglia from peripheral monocytes/macrophages in health and glioma. <i>Acta Neuropathologica Communications</i> , 2019, 7, 20.	5.2	124
25	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23662-23670.	7.1	40
26	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	28.9	364
27	Abstract 1651: Utilization of an ensemble approach for identification of driver fusions in pediatric cancer. , 2019, , .		0
28	Abstract 484: Molecular profiling identifies a second malignancy in a patient with medulloblastoma. , 2019, , .		0
29	Abstract 4551: Expression profiling-based characterization of immune cell populations in pediatric brain cancers. , 2019, , .		0
30	Abstract 4949: Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigen. , 2019, , .		0
31	Genome sequencing identifies somatic BRAF duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002618.	1.2	7
32	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , 2018, 19, 172.	2.8	17
33	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	12.8	89
34	Compartmentalization of functions and predicted miRNA regulation among contiguous regions of the nematode intestine. <i>RNA Biology</i> , 2017, 14, 1335-1352.	3.1	11
35	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017, 27, 849-864.	5.5	728
36	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.4	9

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37	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. <i>Molecular and Cellular Endocrinology</i> , 2016, 420, 159-168.	3.2	18
38	A common founding clone with <i>TP53</i> and <i>PTEN</i> mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000687.	1.2	15
39	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. <i>Annals of Oncology</i> , 2016, 27, 1148-1154.	1.2	18
40	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. <i>Blood Cancer Journal</i> , 2016, 6, e413-e413.	6.2	18
41	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.4	44
42	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	6.2	174
43	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	3.2	83
44	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen <i>Blastomyces</i> and Close Relative <i>Emmonsia</i> . <i>PLoS Genetics</i> , 2015, 11, e1005493.	3.5	57
45	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. <i>Leukemia</i> , 2015, 29, 1279-1289.	7.2	96
46	RNA-seq reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. <i>Glia</i> , 2015, 63, 531-548.	4.9	44
47	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. <i>Cancer Cell</i> , 2015, 27, 631-643.	16.8	259
48	A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. <i>Science</i> , 2015, 348, 803-808.	12.6	1,139
49	Genome Sequence of Enterovirus D68 from St. Louis, Missouri, USA. <i>Emerging Infectious Diseases</i> , 2015, 21, 184-186.	4.3	35
50	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 811.	7.4	302
51	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. <i>Neoplasia</i> , 2015, 17, 776-788.	5.3	75
52	PML-RARA requires DNA methyltransferase 3A to initiate acute promyelocytic leukemia. <i>Journal of Clinical Investigation</i> , 2015, 126, 85-98.	8.2	36
53	Abstract LB-237: Vaccination increases the breadth and diversity of melanoma neoantigen-specific T cells in humans. , 2015, , .		1
54	Abstract PR03: Genomic approaches for risk assessment in acute myeloid leukemia. , 2015, , .		0

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55	Abstract PR11: Genomic approaches for risk assessment in acute myeloid leukemia. , 2015, , .		0
56	Abstract A1-13: Ultra-deep whole-genome sequencing reveals clinically relevant low-frequency subclones in an acute myeloid leukemia. , 2015, , .		0
57	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	3.5	115
58	Draft Genome Sequence of Acetobacter aceti Strain 1023, a Vinegar Factory Isolate. Genome Announcements, 2014, 2, .	0.8	4
59	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
60	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
61	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	2.8	40
62	Abstract 1074: Tumor-associated microglia secrete paracrine factors that promote Nf1-deficient optic glial cell growth. , 2014, , .		0
63	Whole Genome Bisulfite Sequencing of Purified Mouse Promyelocytes Reveals Differentially Methylated Regions in Cells Expressing PML-Rara. Blood, 2014, 124, 3531-3531.	1.4	0
64	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	5.6	198
65	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research, 2013, 23, 431-439.	5.5	99
66	Genomic impact of transient low-dose decitabine treatment on primary AML cells. Blood, 2013, 121, 1633-1643.	1.4	137
67	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. PLoS ONE, 2013, 8, e77571.	2.5	40
68	Dysregulation and Recurrent Mutation Of miRNA-142 In De Novo AML. Blood, 2013, 122, 472-472.	1.4	3
69	The Oxytricha trifallax Mitochondrial Genome. Genome Biology and Evolution, 2012, 4, 136-154.	2.5	52
70	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. Developmental Cell, 2012, 23, 1072-1080.	7.0	101
71	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
72	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249

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73	De Novo Gene Disruptions in Children on the Autistic Spectrum. <i>Neuron</i> , 2012, 74, 285-299.	8.1	1,311
74	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	27.0	688
75	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. <i>Nature</i> , 2012, 481, 506-510.	27.8	1,795
76	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. <i>Cell</i> , 2012, 150, 264-278.	28.9	1,365
77	Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting. <i>Nature</i> , 2012, 482, 400-404.	27.8	1,075
78	Dysregulation of the Imprinted DLK1-DIO3 Locus in Promyelocytic Leukemia. <i>Blood</i> , 2012, 120, 3500-3500.	1.4	0
79	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	27.8	6,541
80	Hybrid Capture and Next-Generation Sequencing Identify Viral Integration Sites from Formalin-Fixed, Paraffin-Embedded Tissue. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 325-333.	2.8	98
81	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
82	Biome representational in silico karyotyping. <i>Genome Research</i> , 2011, 21, 626-633.	5.5	17
83	Exploiting <i>Oxytricha trifallax</i> nanochromosomes to screen for non-coding RNA genes. <i>Nucleic Acids Research</i> , 2011, 39, 7529-7547.	14.5	11
84	Complete Sequencing and Comparison of 12 Normal Karyotype M1 AML Genomes with 12 t(15;17) Positive M3-APL Genomes. <i>Blood</i> , 2011, 118, 404-404.	1.4	1
85	Complete characterization of the microRNAome in a patient with acute myeloid leukemia. <i>Blood</i> , 2010, 116, 5316-5326.	1.4	63
86	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	27.8	1,077
87	SLOPE: a quick and accurate method for locating non-SNP structural variation from targeted next-generation sequence data. <i>Bioinformatics</i> , 2010, 26, 2684-2688.	4.1	51
88	Next-generation sequencing identifies the natural killer cell microRNA transcriptome. <i>Genome Research</i> , 2010, 20, 1590-1604.	5.5	144
89	<i>DNMT3A</i> Mutations in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2010, 363, 2424-2433.	27.0	1,777
90	Mutations In the DNA Methyltransferase Gene DNMT3A Are Highly Recurrent In Patients with Intermediate Risk Acute Myeloid Leukemia, and Predict Poor Outcomes. <i>Blood</i> , 2010, 116, 99-99.	1.4	9

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91	The NK Cell MicroRNA Transcriptome Defined by Next-Generation Sequencing Identifies IL-15-Signaled Alterations In Mature MiR-223 Expression, and MiR-223 as a Potential Regulator of Murine Granzyme B. Blood, 2010, 116, 104-104.	1.4	0
92	A precise reconstruction of the emergence and constrained radiations of <i>Escherichia coli</i> O157 portrayed by backbone concatenomic analysis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8713-8718.	7.1	126
93	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5859-5864.	7.1	612
94	A method for isolating and analyzing human mRNA from newborn stool. Journal of Immunological Methods, 2009, 349, 56-60.	1.4	12
95	The value of avian genomics to the conservation of wildlife. BMC Genomics, 2009, 10, S10.	2.8	75
96	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
97	Comprehensive Evaluation of MicroRNA Genes and Gene Expression Using Next Generation Sequencing in a Patient with Acute Myelogenous Leukemia.. Blood, 2009, 114, 271-271.	1.4	2
98	Transcriptome analysis for <i>Caenorhabditis elegans</i> based on novel expressed sequence tags. BMC Biology, 2008, 6, 30.	3.8	46
99	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
100	Whole-genome sequencing and variant discovery in <i>C. elegans</i> . Nature Methods, 2008, 5, 183-188.	19.0	380
101	Comparative analysis of the small RNA transcriptomes of <i>Pinus contorta</i> and <i>Oryza sativa</i> . Genome Research, 2008, 18, 571-584.	5.5	305
102	Conifers have a unique small RNA silencing signature. Rna, 2008, 14, 1508-1515.	3.5	108
103	Gallus GBrowse: a unified genomic database for the chicken. Nucleic Acids Research, 2007, 36, D719-D723.	14.5	9
104	Extending assembly of short DNA sequences to handle error. Bioinformatics, 2007, 23, 2942-2944.	4.1	223
105	An obesity-associated gut microbiome with increased capacity for energy harvest. Nature, 2006, 444, 1027-1031.	27.8	10,136
106	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246.	2.8	173
107	Identification of genes subject to positive selection in uropathogenic strains of <i>Escherichia coli</i> : A comparative genomics approach. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5977-5982.	7.1	509
108	The repetitive landscape of the chicken genome. Genome Research, 2005, 15, 126-136.	5.5	136

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109	Fosmid-Based Physical Mapping of the <i>Histoplasma capsulatum</i> Genome. <i>Genome Research</i> , 2004, 14, 1603-1609.	5.5	23
110	The repetitive landscape of the chicken genome. <i>Genome Research</i> , 2004, 15, 126-136.	5.5	108
111	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of <i>Salmonella enterica</i> that cause typhoid. <i>Nature Genetics</i> , 2004, 36, 1268-1274.	21.4	367
112	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	27.8	2,421
113	Viral Discovery and Sequence Recovery Using DNA Microarrays. <i>PLoS Biology</i> , 2003, 1, e2.	5.6	386
114	Molecular mycology: a genetic toolbox for <i>Histoplasma capsulatum</i> . <i>Trends in Microbiology</i> , 2001, 9, 541-546.	7.7	26
115	Site-Specific Recombination of Temperate <i>Myxococcus xanthus</i> Phage Mx8: Genetic Elements Required for Integration. <i>Journal of Bacteriology</i> , 1999, 181, 4050-4061.	2.2	41
116	Site-Specific Recombination of Temperate <i>Myxococcus xanthus</i> Phage Mx8: Regulation of Integrase Activity by Reversible, Covalent Modification. <i>Journal of Bacteriology</i> , 1999, 181, 4062-4070.	2.2	17
117	The <i>aadA</i> Gene of Plasmid R100 Confers Resistance to Spectinomycin and Streptomycin in <i>Myxococcus xanthus</i> . <i>Journal of Bacteriology</i> , 1998, 180, 6757-6760.	2.2	14
118	Genetic Determinants of Immunity and Integration of Temperate <i>Myxococcus xanthus</i> Phage Mx8. <i>Journal of Bacteriology</i> , 1998, 180, 614-621.	2.2	28
119	Temperate <i>Myxococcus xanthus</i> phage Mx8 encodes a DNA adenine methylase, Mox. <i>Journal of Bacteriology</i> , 1997, 179, 4254-4263.	2.2	29