Vincent J Magrini

List of Publications by Year
in descending order

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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	An obesity-associated gut microbiome with increased capacity for energy harvest. Nature, 2006, 444, 1027-1031.	27.8	10,136
2	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
3	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
4	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
5	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
6	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
7	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
8	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
9	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
10	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	8.1	1,311
11	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
12	A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells. Science, 2015, 348, 803-808.	12.6	1,139
13	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
14	Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting. Nature, 2012, 482, 400-404.	27.8	1,075
15	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	5.5	728
16	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
17	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
18	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541

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19	Identification of genes subject to positive selection in uropathogenic strains of Escherichia coli: A comparative genomics approach. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5977-5982.	7.1	509
20	Viral Discovery and Sequence Recovery Using DNA Microarrays. PLoS Biology, 2003, 1, e2.	5.6	386
21	Whole-genome sequencing and variant discovery in C. elegans. Nature Methods, 2008, 5, 183-188.	19.0	380
22	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. Nature Genetics, 2004, 36, 1268-1274.	21.4	367
23	Characterizing the Major Structural Variant Alleles of the Human Genome. Cell, 2019, 176, 663-675.e19.	28.9	364
24	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
25	Comparative analysis of the small RNA transcriptomes of Pinus contorta and Oryza sativa. Genome Research, 2008, 18, 571-584.	5.5	305
26	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
27	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing InÂVivo. Cancer Cell, 2015, 27, 631-643.	16.8	259
28	Extending assembly of short DNA sequences to handle error. Bioinformatics, 2007, 23, 2942-2944.	4.1	223
29	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	5.6	198
30	Optimizing Cancer Genome Sequencing and Analysis. Cell Systems, 2015, 1, 210-223.	6.2	174
31	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. BMC Genomics, 2006, 7, 246.	2.8	173
32	Next-generation sequencing identifies the natural killer cell microRNA transcriptome. Genome Research, 2010, 20, 1590-1604.	5.5	144
33	Genomic impact of transient low-dose decitabine treatment on primary AML cells. Blood, 2013, 121, 1633-1643.	1.4	137
34	The repetitive landscape of the chicken genome. Genome Research, 2005, 15, 126-136.	5.5	136
35	A precise reconstruction of the emergence and constrained radiations of Escherichia coli 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
36	Comprehensive gene expression meta-analysis identifies signature genes that distinguish microglia from peripheral monocytes/macrophages in health and glioma. Acta Neuropathologica Communications, 2019, 7, 20.	5.2	124

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37	Clonal Architecture of Secondary Acute Myeloid Leukemia Defined by Single-Cell Sequencing. PLoS Genetics, 2014, 10, e1004462.	3.5	115
38	The repetitive landscape of the chicken genome. Genome Research, 2004, 15, 126-136.	5.5	108
39	Conifers have a unique small RNA silencing signature. Rna, 2008, 14, 1508-1515.	3.5	108
40	Silencing of Germline-Expressed Genes by DNA Elimination in Somatic Cells. Developmental Cell, 2012, 23, 1072-1080.	7.0	101
41	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research, 2013, 23, 431-439.	5.5	99
42	Hybrid Capture and Next-Generation Sequencing Identify Viral Integration Sites from Formalin-Fixed, Paraffin-Embedded Tissue. Journal of Molecular Diagnostics, 2011, 13, 325-333.	2.8	98
43	Epigenomic analysis of the HOX gene loci reveals mechanisms that may control canonical expression patterns in AML and normal hematopoietic cells. Leukemia, 2015, 29, 1279-1289.	7.2	96
44	The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications, 2018, 9, 3476.	12.8	89
45	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
46	The value of avian genomics to the conservation of wildlife. BMC Genomics, 2009, 10, S10.	2.8	75
47	RNA Sequencing of Tumor-Associated Microglia Reveals Ccl5 as a Stromal Chemokine Critical for Neurofibromatosis-1 Glioma Growth. Neoplasia, 2015, 17, 776-788.	5.3	75
48	Complete characterization of the microRNAome in a patient with acute myeloid leukemia. Blood, 2010, 116, 5316-5326.	1.4	63
49	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	3.5	57
50	The Oxytricha trifallax Mitochondrial Genome. Genome Biology and Evolution, 2012, 4, 136-154.	2.5	52
51	SLOPE: a quick and accurate method for locating non-SNP structural variation from targeted next-generation sequence data. Bioinformatics, 2010, 26, 2684-2688.	4.1	51
52	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
53	Transcriptome analysis for Caenorhabditis elegansbased on novel expressed sequence tags. BMC Biology, 2008, 6, 30.	3.8	46
54	RNAâ€sequencing reveals oligodendrocyte and neuronal transcripts in microglia relevant to central nervous system disease. Glia, 2015, 63, 531-548.	4.9	44

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55	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.4	44
56	Site-Specific Recombination of Temperate Myxococcus xanthus Phage Mx8: Genetic Elements Required for Integration. Journal of Bacteriology, 1999, 181, 4050-4061.	2.2	41
57	F11R Is a Novel Monocyte Prognostic Biomarker for Malignant Glioma. PLoS ONE, 2013, 8, e77571.	2.5	40
58	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. Journal of Molecular Diagnostics, 2014, 16, 440-451.	2.8	40
59	Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23662-23670.	7.1	40
60	PML-RARA requires DNA methyltransferase 3A to initiate acute promyelocytic leukemia. Journal of Clinical Investigation, 2015, 126, 85-98.	8.2	36
61	Genome Sequence of Enterovirus D68 from St. Louis, Missouri, USA. Emerging Infectious Diseases, 2015, 21, 184-186.	4.3	35
62	Temperate Myxococcus xanthus phage Mx8 encodes a DNA adenine methylase, Mox. Journal of Bacteriology, 1997, 179, 4254-4263.	2.2	29
63	Detection of brain somatic variation in epilepsyâ€associated developmental lesions. Epilepsia, 2022, 63, 1981-1997.	5.1	29
64	Genetic Determinants of Immunity and Integration of Temperate Myxococcus xanthus Phage Mx8. Journal of Bacteriology, 1998, 180, 614-621.	2.2	28
65	Molecular mycology: a genetic toolbox for Histoplasma capsulatum. Trends in Microbiology, 2001, 9, 541-546.	7.7	26
66	Somatic SLC35A2 mosaicism correlates with clinical findings in epilepsy brain tissue. Neurology: Genetics, 2020, 6, e460.	1.9	26
67	Somatic PIK3R1 variation as a cause of vascular malformations and overgrowth. Genetics in Medicine, 2021, 23, 1882-1888.	2.4	26
68	Fosmid-Based Physical Mapping of the Histoplasma capsulatum Genome. Genome Research, 2004, 14, 1603-1609.	5.5	23
69	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. Brain, 2021, 144, 2971-2978.	7.6	23
70	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. Molecular and Cellular Endocrinology, 2016, 420, 159-168.	3.2	18
71	A genomic case study of mixed fibrolamellar hepatocellular carcinoma. Annals of Oncology, 2016, 27, 1148-1154.	1.2	18
72	A genomic analysis of Philadelphia chromosome-negative AML arising in patients with CML. Blood Cancer Journal, 2016, 6, e413-e413.	6.2	18

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73	Biome representational in silico karyotyping. Genome Research, 2011, 21, 626-633.	5.5	17
74	Improving eukaryotic genome annotation using single molecule mRNA sequencing. BMC Genomics, 2018, 19, 172.	2.8	17
75	Infantile fibrosarcomaâ€“like tumor driven by novel RBPMS-MET fusion consolidated with cabozantinib. Journal of Physical Education and Sports Management, 2020, 6, a005645.	1.2	17
76	Site-Specific Recombination of Temperate Myxococcus xanthus Phage Mx8: Regulation of Integrase Activity by Reversible, Covalent Modification. Journal of Bacteriology, 1999, 181, 4062-4070.	2.2	17
77	A common founding clone with TP53 and PTEN mutations gives rise to a concurrent germ cell tumor and acute megakaryoblastic leukemia. Journal of Physical Education and Sports Management, 2016, 2, a000687.	1.2	15
78	Disease-associated mosaic variation in clinical exome sequencing: a two-year pediatric tertiary care experience. Journal of Physical Education and Sports Management, 2020, 6, a005231.	1.2	15
79	Streptococcus oralis subsp. dentisani Produces Monolateral Serine-Rich Repeat Protein Fibrils, One of Which Contributes to Saliva Binding via Sialic Acid. Infection and Immunity, 2019, 87, .	2.2	14
80	YAP1-FAM118B Fusion Defines a Rare Subset of Childhood and Young Adulthood Meningiomas. American Journal of Surgical Pathology, 2021, 45, 329-340.	3.7	14
81	The aadA Gene of Plasmid R100 Confers Resistance to Spectinomycin and Streptomycin in Myxococcus xanthus. Journal of Bacteriology, 1998, 180, 6757-6760.	2.2	14
82	Discovery of clinically relevant fusions in pediatric cancer. BMC Genomics, 2021, 22, 872.	2.8	13
83	A method for isolating and analyzing human mRNA from newborn stool. Journal of Immunological Methods, 2009, 349, 56-60.	1.4	12
84	Expanding the clinical history associated with syndromic Klippel-Feil: A unique case of comorbidity with medulloblastoma. European Journal of Medical Genetics, 2019, 62, 103701.	1.3	12
85	Gastroblastoma with a novel <scp>EWSR1â€CTBP1</scp> fusion presenting in adolescence. Genes Chromosomes and Cancer, 2021, 60, 640-646.	2.8	12
86	A deletion in the N gene of SARS-CoV-2 may reduce test sensitivity for detection of SARS-CoV-2. Diagnostic Microbiology and Infectious Disease, 2022, 102, 115631.	1.8	12
87	Exploiting Oxytricha trifallax nanochromosomes to screen for non-coding RNA genes. Nucleic Acids Research, 2011, 39, 7529-7547.	14.5	11
88	Compartmentalization of functions and predicted miRNA regulation among contiguous regions of the nematode intestine. RNA Biology, 2017, 14, 1335-1352.	3.1	11
89	A novel sialic acid-binding adhesin present in multiple species contributes to the pathogenesis of Infective endocarditis. PLoS Pathogens, 2021, 17, e1009222.	4.7	11
90	Gallus GBrowse: a unified genomic database for the chicken. Nucleic Acids Research, 2007, 36, D719-D723.	14.5	9

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91	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. Experimental Hematology, 2017, 55, 19-33.	0.4	9
92	De novo primary central nervous system pure erythroid leukemia/sarcoma with t(1;16)(p31;q24) NFIA/CBFA2T3 translocation. Haematologica, 2020, 105, e194-e197.	3.5	9
93	Novel morphologic findings in <scp>PLAG1â€rearranged</scp> soft tissue tumors. Genes Chromosomes and Cancer, 2021, 60, 577-585.	2.8	9
94	Mutations In the DNA Methyltransferase Gene DNMT3A Are Highly Recurrent In Patients with Intermediate Risk Acute Myeloid Leukemia, and Predict Poor Outcomes. Blood, 2010, 116, 99-99.	1.4	9
95	Genome sequencing identifies somatic BRAF duplication c.1794_1796dupTAC;p.Thr599dup in pediatric patient with low-grade ganglioglioma. Journal of Physical Education and Sports Management, 2018, 4, a002618.	1.2	7
96	Longâ€read whole genome sequencing reveals HOXD13 alterations in synpolydactyly. Human Mutation, 2022, 43, 189-199.	2.5	7
97	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. IScience, 2019, 18, 1-10.	4.1	6
98	Molecular classification of a complex structural rearrangement of the RB1 locus in an infant with sporadic, isolated, intracranial, sellar region retinoblastoma. Acta Neuropathologica Communications, 2021, 9, 61.	5.2	5
99	Clinically aggressive pediatric spinal ependymoma with novel MYC amplification demonstrates molecular and histopathologic similarity to newly described MYCN-amplified spinal ependymomas. Acta Neuropathologica Communications, 2021, 9, 192.	5.2	5
100	Draft Genome Sequence of Acetobacter aceti Strain 1023, a Vinegar Factory Isolate. Genome Announcements, 2014, 2, .	0.8	4
101	Expanding the Clinical Phenotype of FGFR1 Internal Tandem Duplication. Journal of Physical Education and Sports Management, 2022, , mcs.a006174.	1.2	4
102	Dysregulation and Recurrent Mutation Of miRNA-142 In De Novo AML. Blood, 2013, 122, 472-472.	1.4	3
103	Somatic variation as an incidental finding in the pediatric next-generation sequencing era. Journal of Physical Education and Sports Management, 2021, 7, a006135.	1.2	3
104	Genomic and transcriptomic somatic alterations of hepatocellular carcinoma in non-cirrhotic livers. Cancer Genetics, 2022, 264-265, 90-99.	0.4	3
105	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
106	Complete Sequencing and Comparison of 12 Normal Karyotype M1 AML Genomes with 12 t(15;17) Positive M3-APL Genomes. Blood, 2011, 118, 404-404.	1.4	1
107	Abstract LB-237: Vaccination increases the breadth and diversity of melanoma neoantigen-specific T cells in humans. , 2015, , .		1
108	Expanding the phenotypic spectrum of internal tandem duplications in somatic disease. Molecular Genetics and Metabolism, 2021, 132, S44.	1.1	0

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109	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
110	Dysregulation of the Imprinted DLK1-DIO3 Locus in Promyelocytic Leukemia. Blood, 2012, 120, 3500-3500.	1.4	0
111	Abstract 1074: Tumor-associated microglia secrete paracrine factors that promote Nf1-deficient optic glial cell growth. , 2014, , .		0
112	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
113	Abstract PR03: Genomic approaches for risk assessment in acute myeloid leukemia. , 2015, , .		0
114	Abstract PR11: Genomic approaches for risk assessment in acute myeloid leukemia. , 2015, , .		0
115	Abstract A1-13: Ultra-deep whole-genome sequencing reveals clinically relevant low-frequency subclones in an acute myeloid leukemia. , 2015, , .		0
116	Abstract 1651: Utilization of an ensemble approach for identification of driver fusions in pediatric cancer. , 2019, , .		0
117	Abstract 484: Molecular profiling identifies a second malignancy in a patient with medulloblastoma. , 2019, , .		0
118	Abstract 4551: Expression profiling-based characterization of immune cell populations in pediatric brain cancers. , 2019, , .		0
119	Abstract 4949: Immunological ignorance is an enabling feature of the oligo-clonal T cell response to melanoma neoantigen. , 2019, , .		0