

# Sean D Mcgrath

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

15,482  
citations

218677

26  
h-index

197818

49  
g-index

56  
all docs

56  
docs citations

56  
times ranked

24271  
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	Detection of brain somatic variation in epilepsy-associated developmental lesions. <i>Epilepsia</i> , 2022, 63, 1981-1997.	5.1	29
5	Novel morphologic findings in <sc>PLAG1</sc>-rearranged soft tissue tumors. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 577-585.	2.8	9
6	Expanding the phenotypic spectrum of internal tandem duplications in somatic disease. <i>Molecular Genetics and Metabolism</i> , 2021, 132, S44.	1.1	0
7	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
8	PTEN somatic mutations contribute to spectrum of cerebral overgrowth. <i>Brain</i> , 2021, 144, 2971-2978.	7.6	23
9	Gastroblastoma with a novel <sc><i>EWSR1</i>-CTBP1</sc> fusion presenting in adolescence. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 640-646.	2.8	12
10	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
11	Discovery of clinically relevant fusions in pediatric cancer. <i>BMC Genomics</i> , 2021, 22, 872.	2.8	13
12	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
13	<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
14	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	28.9	364
15	Abstract 1651: Utilization of an ensemble approach for identification of driver fusions in pediatric cancer. , 2019, , .		0
16	Improving eukaryotic genome annotation using single molecule mRNA sequencing. <i>BMC Genomics</i> , 2018, 19, 172.	2.8	17
17	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
18	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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19	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
20	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
21	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	6.2	174
22	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. <i>Cancer Cell</i> , 2015, 27, 631-643.	16.8	259
23	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	2.8	40
24	The <i>Oxytricha trifallax</i> Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. <i>PLoS Biology</i> , 2013, 11, e1001473.	5.6	198
25	Dysregulation and Recurrent Mutation Of miRNA-142 In De Novo AML. <i>Blood</i> , 2013, 122, 472-472.	1.4	3
26	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. <i>Nature</i> , 2012, 481, 506-510.	27.8	1,795
27	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. <i>Cell</i> , 2012, 150, 264-278.	28.9	1,365
28	Dysregulation of the Imprinted DLK1-DIO3 Locus in Promyelocytic Leukemia. <i>Blood</i> , 2012, 120, 3500-3500.	1.4	0
29	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. <i>Journal of Clinical Investigation</i> , 2011, 121, 1445-1455.	8.2	91
30	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
31	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. <i>Nature</i> , 2010, 463, 536-539.	27.8	381
32	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	27.8	1,077
33	DNMT3A Mutations in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2010, 363, 2424-2433.	27.0	1,777
34	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
35	The value of avian genomics to the conservation of wildlife. <i>BMC Genomics</i> , 2009, 10, S10.	2.8	75
36	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. <i>Nature Methods</i> , 2009, 6, 677-681.	19.0	1,322

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37	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. <i>New England Journal of Medicine</i> , 2009, 361, 1058-1066.	27.0	2,009
38	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. <i>Nature</i> , 2008, 456, 66-72.	27.8	1,275
39	A Sequence Motif within Chromatin Entry Sites Directs MSL Establishment on the <i>Drosophila</i> X Chromosome. <i>Cell</i> , 2008, 134, 599-609.	28.9	256
40	Transcriptome-Wide Identification of Novel Imprinted Genes in Neonatal Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3839.	2.5	170
41	Gallus GBrowse: a unified genomic database for the chicken. <i>Nucleic Acids Research</i> , 2007, 36, D719-D723.	14.5	9
42	Hotspots for copy number variation in chimpanzees and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8006-8011.	7.1	231
43	Linkage Disequilibrium and Heritability of Copy-Number Polymorphisms within Duplicated Regions of the Human Genome. <i>American Journal of Human Genetics</i> , 2006, 79, 275-290.	6.2	283
44	Lineage-Specific Expansions of Retroviral Insertions within the Genomes of African Great Apes but Not Humans and Orangutans. <i>PLoS Biology</i> , 2005, 3, e110.	5.6	84
45	A genome-wide survey of structural variation between human and chimpanzee. <i>Genome Research</i> , 2005, 15, 1344-1356.	5.5	153
46	Segmental Duplications and Copy-Number Variation in the Human Genome. <i>American Journal of Human Genetics</i> , 2005, 77, 78-88.	6.2	872
47	Template-Directed Dye-Terminator Incorporation with Fluorescence Polarization Detection for Analysis of Single Nucleotide Polymorphisms Implicated in Sepsis. <i>Journal of Molecular Diagnostics</i> , 2002, 4, 209-215.	2.8	13
48	The Frequency and Effects of Cytochrome P450 (CYP) 2C9 Polymorphisms in Patients Receiving Warfarin. <i>Journal of the American College of Surgeons</i> , 2002, 194, 267-273.	0.5	86
49	Extreme warfarin sensitivity in siblings associated with multiple cytochrome P450 polymorphisms. <i>American Journal of Hematology</i> , 2001, 67, 144-146.	4.1	12
50	Factor V Leiden mutation in a patient with warfarin-associated skin necrosis. <i>Surgery</i> , 2000, 127, 595-596.	1.9	8
51	Cytochrome P450 polymorphisms are associated with reduced warfarin dose. <i>Surgery</i> , 2000, 128, 281-285.	1.9	75
52	Partial T-Cell Receptor Gene Rearrangement: A Source of Pseudo-clonal Populations in Thymomas and Other Thymic Tissues. <i>American Journal of Clinical Pathology</i> , 1996, 105, 262-267.	0.7	6