Sharon J Diskin

List of Publications by Year
in descending order

72 papers	8,284 citations	71102 41 h-index	102487 66 g-index
79 all docs	79 docs citations	79 times ranked	13318 citing authors

#	Article	IF	Citations
1	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. Journal of the National Cancer Institute, 2022, 114, 910-913.	6.3	4
2	Genetic analysis in African American children supports ancestry specific neuroblastoma susceptibility. Cancer Epidemiology Biomarkers and Prevention, 2022, , cebp.EPI-21-0782-A.2021.	2.5	1
3	svpluscnv: analysis and visualization of complex structural variation data. Bioinformatics, 2021, 37, 1912-1914.	4.1	13
4	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. Cancers, 2021, 13, 1807.	3.7	4
5	OMIC-12. PREVALENCE AND SPECTRUM OF GERMLINE PATHOGENIC VARIANTS IN CANCER PREDISPOSITION GENES ACROSS THE CHILDRENâ€™S BRAIN TUMOR NETWORK (CBTN). Neuro-Oncology, 2021, 23, i39-i40.	1.2	0
6	Abstract 3028: Integrative genomics reveals lncRNAs associated with pediatric cancer. , 2021, , .		1
7	Neural crest-derived tumor neuroblastoma and melanoma share 1p13.2 as susceptibility locus that shows a long-range interaction with the SLC16A1 gene. Carcinogenesis, 2020, 41, 284-295.	2.8	18
8	Pediatric high-grade glioma resources from the Childrenâ€™s Brain Tumor Tissue Consortium. Neuro-Oncology, 2020, 22, 163-165.	1.2	29
9	European genetic ancestry associated with risk of childhood ependymoma. Neuro-Oncology, 2020, 22, 1637-1646.	1.2	16
10	Genetic predisposition to longer telomere length and risk of childhood, adolescent and adult-onset ependymoma. Acta Neuropathologica Communications, 2020, 8, 173.	5.2	15
11	Somatic structural variation targets neurodevelopmental genes and identifies SHANK2 as a tumor suppressor in neuroblastoma. Genome Research, 2020, 30, 1228-1242.	5.5	20
12	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2020, 112, 1259-1266.	6.3	10
13	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
14	Epigenomic profiling of neuroblastoma cell lines. Scientific Data, 2020, 7, 116.	5.3	32
15	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. Cancer Research, 2020, 80, 2663-2675.	0.9	55
16	BIOM-50. GENETIC PREDISPOSITION TO LONGER TELOMERE LENGTH AND RISK OF CHILDHOOD, ADOLESCENT AND ADULT-ONSET EPENDYMOMA. Neuro-Oncology, 2020, 22, ii12-ii12.	1.2	0
17	Neuroblastoma in relation to joint effects of vitamin A and maternal and offspring variants in vitamin A-related genes: A report of the Childrenâ€™s Oncology Group. Cancer Epidemiology, 2019, 61, 165-171.	1.9	6
18	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9.	6.4	103

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19	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. Genes, 2019, 10, 663.	2.4	14
20	Germline 16p11.2 Microdeletion Predisposes to Neuroblastoma. American Journal of Human Genetics, 2019, 105, 658-668.	6.2	31
21	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
22	PDTM-16. PEDIATRIC HIGH GRADE GLIOMA RESOURCES FROM THE CHILDRENâ€™S BRAIN TUMOR TISSUE CONSORTIUM (CBTTC) AND PEDIATRIC BRAIN TUMOR ATLAS (PBTA). Neuro-Oncology, 2019, 21, vi190-vi190.	1.2	1
23	PDTM-33. EUROPEAN GENETIC ANCESTRY ASSOCIATED WITH RISK OF CHILDHOOD EPENDYMOMA. Neuro-Oncology, 2019, 21, vi194-vi194.	1.2	0
24	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
25	Genetic susceptibility to neuroblastoma: current knowledge and future directions. Cell and Tissue Research, 2018, 372, 287-307.	2.9	49
26	Graphical Interpretation and Analysis of Proteins and their Ontologies (GiaPronto): A One-Click Graph Visualization Software for Proteomics Data Sets. Molecular and Cellular Proteomics, 2018, 17, 1426-1431.	3.8	14
27	Fine mapping of 2q35 highâ€risk neuroblastoma locus reveals independent functional risk variants and suggests fullâ€length BARD1 as tumorâ€suppressor. International Journal of Cancer, 2018, 143, 2828-2837.	5.1	54
28	MIBG avidity correlates with clinical features, tumor biology, and outcomes in neuroblastoma: A report from the Children's Oncology Group. Pediatric Blood and Cancer, 2017, 64, e26545.	1.5	30
29	Neuroblastoma survivors are at increased risk for second malignancies: A report from the International Neuroblastoma Risk Group Project. European Journal of Cancer, 2017, 72, 177-185.	2.8	59
30	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. Nature Communications, 2017, 8, 569.	12.8	22
31	The functional variant rs34330 of CDKN1B is associated with risk of neuroblastoma. Journal of Cellular and Molecular Medicine, 2017, 21, 3224-3230.	3.6	47
32	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. Journal of the National Cancer Institute, 2017, 109, .	6.3	20
33	Common variants upstream of MLF1 at 3q25 and within CPZ at 4p16 associated with neuroblastoma. PLoS Genetics, 2017, 13, e1006787.	3.5	62
34	A family-based study of gene variants and maternal folate and choline in neuroblastoma: a report from the Childrenâ€™s Oncology Group. Cancer Causes and Control, 2016, 27, 1209-1218.	1.8	8
35	LIN28B: an orchestrator of oncogenic signaling in neuroblastoma. Cell Cycle, 2016, 15, 772-774.	2.6	12
36	Imaging genomics in cancer research: limitations and promises. British Journal of Radiology, 2016, 89, 20151030.	2.2	90

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37	Second malignancies in patients with neuroblastoma: A report from the International Neuroblastoma Risk Group Project.. Journal of Clinical Oncology, 2016, 34, 10547-10547.	1.6	0
38	CODEX: a normalization and copy number variation detection method for whole exome sequencing. Nucleic Acids Research, 2015, 43, e39-e39.	14.5	126
39	Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations. Nature Genetics, 2015, 47, 864-871.	21.4	451
40	CASC15-S Is a Tumor Suppressor lncRNA at the 6p22 Neuroblastoma Susceptibility Locus. Cancer Research, 2015, 75, 3155-3166.	0.9	132
41	A LIN28B-RAN-AURKA Signaling Network Promotes Neuroblastoma Tumorigenesis. Cancer Cell, 2015, 28, 599-609.	16.8	99
42	MYC Disrupts the Circadian Clock and Metabolism in Cancer Cells. Cell Metabolism, 2015, 22, 1009-1019.	16.2	217
43	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. Nature, 2015, 528, 418-421.	27.8	263
44	Second malignancies in neuroblastoma patients: A report from the International Neuroblastoma Risk Group.. Journal of Clinical Oncology, 2015, 33, 10019-10019.	1.6	0
45	Common Genetic Variants in NEFL Influence Gene Expression and Neuroblastoma Risk. Cancer Research, 2014, 74, 6913-6924.	0.9	74
46	Rare Variants in TP53 and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2014, 106, dju047.	6.3	100
47	Mitogenâ€activated protein kinase (MEK/ERK) inhibition sensitizes cancer cells to centromereâ€associated protein E inhibition. International Journal of Cancer, 2013, 132, E149-57.	5.1	16
48	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
49	Dual CDK4/CDK6 Inhibition Induces Cell-Cycle Arrest and Senescence in Neuroblastoma. Clinical Cancer Research, 2013, 19, 6173-6182.	7.0	323
50	Replication of GWAS-identified neuroblastoma risk loci strengthens the role of BARD1 and affirms the cumulative effect of genetic variations on disease susceptibility. Carcinogenesis, 2013, 34, 605-611.	2.8	95
51	Replication of Neuroblastoma SNP Association at the BARD1 Locus in African-Americans. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 658-663.	2.5	54
52	Trans-population Analysis of Genetic Mechanisms of Ethnic Disparities in Neuroblastoma Survival. Journal of the National Cancer Institute, 2012, 105, 302-309.	6.3	30
53	Common Variation at BARD1 Results in the Expression of an Oncogenic Isoform That Influences Neuroblastoma Susceptibility and Oncogenicity. Cancer Research, 2012, 72, 2068-2078.	0.9	97
54	Common variation at 6q16 within HACE1 and LIN28B influences susceptibility to neuroblastoma. Nature Genetics, 2012, 44, 1126-1130.	21.4	231

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55	Relationship of divergent ancestral genetic variation on chromosome 6p22 and racial disparities in survival in neuroblastoma.. Journal of Clinical Oncology, 2012, 30, 9516-9516.	1.6	0
56	Phenotype Restricted Genome-Wide Association Study Using a Gene-Centric Approach Identifies Three Low-Risk Neuroblastoma Susceptibility Loci. PLoS Genetics, 2011, 7, e1002026.	3.5	141
57	Integrative genomics identifies LMO1 as a neuroblastoma oncogene. Nature, 2011, 469, 216-220.	27.8	276
58	RNAi screen of the protein kinome identifies checkpoint kinase 1 (CHK1) as a therapeutic target in neuroblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3336-3341.	7.1	227
59	Genomic copy number determination in cancer cells from single nucleotide polymorphism microarrays based on quantitative genotyping corrected for aneuploidy. Genome Research, 2009, 19, 276-283.	5.5	69
60	Copy number variation at 1q21.1 associated with neuroblastoma. Nature, 2009, 459, 987-991.	27.8	329
61	Common variations in BARD1 influence susceptibility to high-risk neuroblastoma. Nature Genetics, 2009, 41, 718-723.	21.4	266
62	A Functional Screen Identifies miR-34a as a Candidate Neuroblastoma Tumor Suppressor Gene. Molecular Cancer Research, 2008, 6, 735-742.	3.4	298
63	Adjustment of genomic waves in signal intensities from whole-genome SNP genotyping platforms. Nucleic Acids Research, 2008, 36, e126-e126.	14.5	297
64	Chromosome 6p22 Locus Associated with Clinically Aggressive Neuroblastoma. New England Journal of Medicine, 2008, 358, 2585-2593.	27.0	271
65	Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. PLoS Genetics, 2007, 3, e143.	3.5	41
66	Neuroblastomas have distinct genomic DNA profiles that predict clinical phenotype and regional gene expression. Genes Chromosomes and Cancer, 2007, 46, 936-949.	2.8	101
67	STAC: A method for testing the significance of DNA copy number aberrations across multiple array-CGH experiments. Genome Research, 2006, 16, 1149-1158.	5.5	152
68	Integrative Genomics Identifies Distinct Molecular Classes of Neuroblastoma and Shows That Multiple Genes Are Targeted by Regional Alterations in DNA Copy Number. Cancer Research, 2006, 66, 6050-6062.	0.9	178
69	1-Mb Resolution Array-Based Comparative Genomic Hybridization Using a BAC Clone Set Optimized for Cancer Gene Analysis. Genome Research, 2004, 14, 179-187.	5.5	100
70	Predicting Gene Ontology Functions from ProDom and CDD Protein Domains. Genome Research, 2002, 12, 648-655.	5.5	81
71	PlasmoDB: the Plasmodium genome resource. An integrated database providing tools for accessing, analyzing and mapping expression and sequence data (both finished and unfinished). Nucleic Acids Research, 2002, 30, 87-90.	14.5	110
72	The Plasmodium genome database. Nature, 2002, 419, 490-492.	27.8	156