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	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
2	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
3	Relapsed neuroblastomas show frequent RAS-MAPK pathway mutations. Nature Genetics, 2015, 47, 864-871.	21.4	451
4	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
5	Copy number variation at 1q21.1 associated with neuroblastoma. Nature, 2009, 459, 987-991.	27.8	329
6	Dual CDK4/CDK6 Inhibition Induces Cell-Cycle Arrest and Senescence in Neuroblastoma. Clinical Cancer Research, 2013, 19, 6173-6182.	7.0	323
7	A Functional Screen Identifies miR-34a as a Candidate Neuroblastoma Tumor Suppressor Gene. Molecular Cancer Research, 2008, 6, 735-742.	3.4	298
8	Adjustment of genomic waves in signal intensities from whole-genome SNP genotyping platforms. Nucleic Acids Research, 2008, 36, e126-e126.	14.5	297
9	Integrative genomics identifies LMO1 as a neuroblastoma oncogene. Nature, 2011, 469, 216-220.	27.8	276
10	Chromosome 6p22 Locus Associated with Clinically Aggressive Neuroblastoma. New England Journal of Medicine, 2008, 358, 2585-2593.	27.0	271
11	Common variations in BARD1 influence susceptibility to high-risk neuroblastoma. Nature Genetics, 2009, 41, 718-723.	21.4	266
12	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. Nature, 2015, 528, 418-421.	27.8	263
13	Common variation at 6q16 within HACE1 and LIN28B influences susceptibility to neuroblastoma. Nature Genetics, 2012, 44, 1126-1130.	21.4	231
14	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
15	MYC Disrupts the Circadian Clock and Metabolism in Cancer Cells. Cell Metabolism, 2015, 22, 1009-1019.	16.2	217
16	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
17	The Plasmodium genome database. Nature, 2002, 419, 490-492.	27.8	156
18	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

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19	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
20	CASC15-S Is a Tumor Suppressor lncRNA at the 6p22 Neuroblastoma Susceptibility Locus. Cancer Research, 2015, 75, 3155-3166.	0.9	132
21	CODEX: a normalization and copy number variation detection method for whole exome sequencing. Nucleic Acids Research, 2015, 43, e39-e39.	14.5	126
22	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
23	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
24	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
25	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
26	Rare Variants in TP53 and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2014, 106, dju047.	6.3	100
27	A LIN28B-RAN-AURKA Signaling Network Promotes Neuroblastoma Tumorigenesis. Cancer Cell, 2015, 28, 599-609.	16.8	99
28	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
29	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
30	Imaging genomics in cancer research: limitations and promises. British Journal of Radiology, 2016, 89, 20151030.	2.2	90
31	Predicting Gene Ontology Functions from ProDom and CDD Protein Domains. Genome Research, 2002, 12, 648-655.	5.5	81
32	Common Genetic Variants in NEFL Influence Gene Expression and Neuroblastoma Risk. Cancer Research, 2014, 74, 6913-6924.	0.9	74
33	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
34	Common variants upstream of MLF1 at 3q25 and within CPZ at 4p16 associated with neuroblastoma. PLoS Genetics, 2017, 13, e1006787.	3.5	62
35	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
36	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57

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37	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. Cancer Research, 2020, 80, 2663-2675.	0.9	55
38	Replication of Neuroblastoma SNP Association at the BARD1 Locus in African-Americans. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 658-663.	2.5	54
39	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
40	Genetic susceptibility to neuroblastoma: current knowledge and future directions. Cell and Tissue Research, 2018, 372, 287-307.	2.9	49
41	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
42	Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. PLoS Genetics, 2007, 3, e143.	3.5	41
43	Epigenomic profiling of neuroblastoma cell lines. Scientific Data, 2020, 7, 116.	5.3	32
44	Germline 16p11.2 Microdeletion Predisposes to Neuroblastoma. American Journal of Human Genetics, 2019, 105, 658-668.	6.2	31
45	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
46	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
47	Pediatric high-grade glioma resources from the Childrenâ€™s Brain Tumor Tissue Consortium. Neuro-Oncology, 2020, 22, 163-165.	1.2	29
48	Common variants in MMP20 at 11q22.2 predispose to 11q deletion and neuroblastoma risk. Nature Communications, 2017, 8, 569.	12.8	22
49	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. Journal of the National Cancer Institute, 2017, 109, .	6.3	20
50	Somatic structural variation targets neurodevelopmental genes and identifies SHANK2 as a tumor suppressor in neuroblastoma. Genome Research, 2020, 30, 1228-1242.	5.5	20
51	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
52	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
53	European genetic ancestry associated with risk of childhood ependymoma. Neuro-Oncology, 2020, 22, 1637-1646.	1.2	16
54	Genetic predisposition to longer telomere length and risk of childhood, adolescent and adult-onset ependymoma. Acta Neuropathologica Communications, 2020, 8, 173.	5.2	15

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55	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
56	Exploring Shared Susceptibility between Two Neural Crest Cells Originating Conditions: Neuroblastoma and Congenital Heart Disease. Genes, 2019, 10, 663.	2.4	14
57	svpluscnv: analysis and visualization of complex structural variation data. Bioinformatics, 2021, 37, 1912-1914.	4.1	13
58	LIN28B: an orchestrator of oncogenic signaling in neuroblastoma. Cell Cycle, 2016, 15, 772-774.	2.6	12
59	Mitochondrial DNA Haplogroups and Susceptibility to Neuroblastoma. Journal of the National Cancer Institute, 2020, 112, 1259-1266.	6.3	10
60	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
61	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
62	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. Cancers, 2021, 13, 1807.	3.7	4
63	Identification of Mitochondrial DNA Variants Associated With Risk of Neuroblastoma. Journal of the National Cancer Institute, 2022, 114, 910-913.	6.3	4
64	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
65	Abstract 3028: Integrative genomics reveals lncRNAs associated with pediatric cancer. , 2021, , .		1
66	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
67	PDTM-33. EUROPEAN GENETIC ANCESTRY ASSOCIATED WITH RISK OF CHILDHOOD EPENDYMOMA. Neuro-Oncology, 2019, 21, vi194-vi194.	1.2	0
68	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
69	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
70	Second malignancies in neuroblastoma patients: A report from the International Neuroblastoma Risk Group.. Journal of Clinical Oncology, 2015, 33, 10019-10019.	1.6	0
71	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
72	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