

# Sorana A Morrissy

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1689747/publications.pdf>

Version: 2024-02-01

54  
papers

8,156  
citations

136740

32  
h-index

168136

53  
g-index

62  
all docs

62  
docs citations

62  
times ranked

12211  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations in the RAS/MAPK Pathway Drive Replication Repairâ€“Deficient Hypermuted Tumors and Confer Sensitivity to MEK Inhibition. <i>Cancer Discovery</i> , 2021, 11, 1454-1467.	7.7	19
2	Profiling Chromatin Accessibility at Single-cell Resolution. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 172-190.	3.0	18
3	Reconstruction of Microbial Haplotypes by Integration of Statistical and Physical Linkage in Scaffolding. <i>Molecular Biology and Evolution</i> , 2021, 38, 2660-2672.	3.5	8
4	Histologyâ€“based molecular profiling improves mutation detection for advanced thyroid cancer. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 531-545.	1.5	5
5	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
6	Single allele loss-of-function mutations select and sculpt conditional cooperative networks in breast cancer. <i>Nature Communications</i> , 2021, 12, 5238.	5.8	8
7	DNA Polymerase and Mismatch Repair Exert Distinct Microsatellite Instability Signatures in Normal and Malignant Human Cells. <i>Cancer Discovery</i> , 2021, 11, 1176-1191.	7.7	46
8	Copy-scAT: Deconvoluting single-cell chromatin accessibility of genetic subclones in cancer. <i>Science Advances</i> , 2021, 7, eabg6045.	4.7	19
9	Locoregional delivery of CAR T cells to the cerebrospinal fluid for treatment of metastatic medulloblastoma and ependymoma. <i>Nature Medicine</i> , 2020, 26, 720-731.	15.2	141
10	ID1 Is Critical for Tumorigenesis and Regulates Chemoresistance in Glioblastoma. <i>Cancer Research</i> , 2019, 79, 4057-4071.	0.4	39
11	Single-Cell Transcriptomics in Medulloblastoma Reveals Tumor-Initiating Progenitors and Oncogenic Cascades during Tumorigenesis and Relapse. <i>Cancer Cell</i> , 2019, 36, 302-318.e7.	7.7	96
12	Engineering Genetic Predisposition in Human Neuroepithelial Stem Cells Recapitulates Medulloblastoma Tumorigenesis. <i>Cell Stem Cell</i> , 2019, 25, 433-446.e7.	5.2	56
13	IMMU-03. TUMOR NECROSIS FACTOR OVERCOMES IMMUNE EVASION IN P53-MUTANT MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2019, 21, ii93-ii93.	0.6	1
14	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019, 572, 67-73.	13.7	293
15	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. <i>Cancer Research</i> , 2019, 79, 2111-2123.	0.4	28
16	Recurrent noncoding U1â€“snRNA mutations drive cryptic splicing in SHH medulloblastoma. <i>Nature</i> , 2019, 574, 707-711.	13.7	129
17	MEDU-28. ELIMINATING THE ROOT OF MEDULLOBLASTOMA BY TARGETING A VOLTAGE-GATED POTASSIUM CHANNEL. <i>Neuro-Oncology</i> , 2019, 21, ii109-ii109.	0.6	1
18	p53 Function Is Compromised by Inhibitor 2 of Phosphatase 2A in Sonic Hedgehog Medulloblastoma. <i>Molecular Cancer Research</i> , 2019, 17, 186-198.	1.5	10

#	ARTICLE	IF	CITATIONS
19	Dual Regulatory Functions of SUFU and Targetome of GLI2 in SHH Subgroup Medulloblastoma. <i>Developmental Cell</i> , 2019, 48, 167-183.e5.	3.1	39
20	BMI1 is a therapeutic target in recurrent medulloblastoma. <i>Oncogene</i> , 2019, 38, 1702-1716.	2.6	20
21	A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. <i>Cell</i> , 2018, 172, 1050-1062.e14.	13.5	85
22	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. <i>Developmental Cell</i> , 2018, 44, 709-724.e6.	3.1	35
23	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	5.1	268
24	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	9.4	112
25	ATOH1 Promotes Leptomeningeal Dissemination and Metastasis of Sonic Hedgehog Subgroup Medulloblastomas. <i>Cancer Research</i> , 2017, 77, 3766-3777.	0.4	29
26	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. <i>Cancer Research</i> , 2017, 77, 3217-3230.	0.4	45
27	Intertumoral Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2017, 31, 737-754.e6.	7.7	836
28	Identification of GPC2 as an Oncoprotein and Candidate Immunotherapeutic Target in High-Risk Neuroblastoma. <i>Cancer Cell</i> , 2017, 32, 295-309.e12.	7.7	148
29	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
30	TMOD-11. HUMAN STEM CELL BASED MODEL OF MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2017, 19, vi256-vi257.	0.6	0
31	Highlights of Children with Cancer UK's Workshop on Drug Delivery in Paediatric Brain Tumours. <i>Ecancermedalscience</i> , 2016, 10, 630.	0.6	2
32	MB-102HEMATOGENOUS DISSEMINATION OF MEDULLOBLASTOMA DRIVES LEPTOMENINGEAL DISEASE. <i>Neuro-Oncology</i> , 2016, 18, iii120.2-iii120.	0.6	0
33	TMOD-17. CONVERGENCE OF BMI1 AND CHD7 ON ERK SIGNALLING IN MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2016, 18, vi210-vi210.	0.6	0
34	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. <i>Cancer Cell</i> , 2016, 30, 891-908.	7.7	191
35	MB-100DIVERGENT CLONAL SELECTION DOMINATES MEDULLOBLASTOMA AT RECURRENCE. <i>Neuro-Oncology</i> , 2016, 18, iii119.4-iii119.	0.6	0
36	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266

#	ARTICLE	IF	CITATIONS
37	HDAC and PI3K Antagonists Cooperate to Inhibit Growth of MYC- Driven Medulloblastoma. <i>Cancer Cell</i> , 2016, 29, 311-323.	7.7	204
38	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	0.8	62
39	Sleeping Beauty Mouse Models Identify Candidate Genes Involved in Gliomagenesis. <i>PLoS ONE</i> , 2014, 9, e113489.	1.1	21
40	Integrative Genomic Analyses of Atypical Teratoid Rhabdoid Tumours (ATRTs). <i>Cancer Genetics</i> , 2014, 207, 447-448.	0.2	2
41	Hippo Signaling Influences HNF4A and FOXA2 Enhancer Switching during Hepatocyte Differentiation. <i>Cell Reports</i> , 2014, 9, 261-271.	2.9	89
42	Cytogenetic Prognostication Within Medulloblastoma Subgroups. <i>Journal of Clinical Oncology</i> , 2014, 32, 886-896.	0.8	263
43	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. <i>Cancer Cell</i> , 2014, 26, 33-47.	7.7	241
44	Aberrant patterns of H3K4 and H3K27 histone lysine methylation occur across subgroups in medulloblastoma. <i>Acta Neuropathologica</i> , 2013, 125, 373-384.	3.9	169
45	TERT promoter mutations are highly recurrent in SHH subgroup medulloblastoma. <i>Acta Neuropathologica</i> , 2013, 126, 917-929.	3.9	146
46	Tissue-specific alternative polyadenylation at the imprinted gene Mest regulates allelic usage at Copg2. <i>Nucleic Acids Research</i> , 2012, 40, 1523-1535.	6.5	22
47	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
48	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. <i>Cancer Cell</i> , 2012, 22, 425-437.	7.7	1,551
49	Subgroup-specific alternative splicing in medulloblastoma. <i>Acta Neuropathologica</i> , 2012, 123, 485-499.	3.9	28
50	Abstract 1430: Characterization of the medulloblastoma splice-ome reveals subgroup-specific changes in alternative splicing and isoform expression patterns. , 2012, , .		0
51	Extensive relationship between antisense transcription and alternative splicing in the human genome. <i>Genome Research</i> , 2011, 21, 1203-1212.	2.4	68
52	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	9.0	283
53	Digital Gene Expression by Tag Sequencing on the Illumina Genome Analyzer. <i>Current Protocols in Human Genetics</i> , 2010, 65, Unit 11.11.1-36.	3.5	15
54	Next-generation tag sequencing for cancer gene expression profiling. <i>Genome Research</i> , 2009, 19, 1825-1835.	2.4	306