Sebastianâ€M Waszak

List of Publications by Year
in descending order

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62	9,761	147726	197736
papers	citations	31 h-index	49 g-index

73	73	73	17930
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pharmaco-proteogenomic profiling of pediatric diffuse midline glioma to inform future treatment strategies. Oncogene, 2022, 41, 461-475.	2.6	39
2	Imipridones affect tumor bioenergetics and promote cell lineage differentiation in diffuse midline gliomas. Neuro-Oncology, 2022, 24, 1438-1451.	0.6	36
3	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. Nature Communications, 2022, 13, 2042.	5.8	6
4	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. European Urology, 2022, 82, 201-211.	0.9	2
5	MEDB-14. Clinical outcome of pediatric medulloblastoma patients with Li-Fraumeni syndrome. Neuro-Oncology, 2022, 24, i107-i107.	0.6	1
6	DIPG-07. Preclinical and case study results underpinning the phase II clinical trial testing the combination of ONC201 and paxalisib for the treatment of patients with diffuse midline glioma (NCT05009992). Neuro-Oncology, 2022, 24, i18-i19.	0.6	0
7	Cancer risk and tumour spectrum in 172 patients with a germlineSUFUpathogenic variation: a collaborative study of the SIOPE Host Genome Working Group. Journal of Medical Genetics, 2022, 59, 1123-1132.	1.5	4
8	Mechanisms of imipridones in targeting mitochondrial metabolism in cancer cells. Neuro-Oncology, 2021, 23, 542-556.	0.6	30
9	Versatile workflow for cell typeâ€“resolved transcriptional and epigenetic profiles from cryopreserved human lung. JCI Insight, 2021, 6, .	2.3	8
10	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
11	HGG-32. ONC201 AND ONC206 TARGET TUMOR CELL METABOLISM IN PEDIATRIC DIFFUSE MIDLINE GLIOMA PRECLINICAL MODELS. Neuro-Oncology, 2021, 23, i23-i24.	0.6	2
12	Germline GPR161 Mutations Predispose to Pediatric Medulloblastoma. Journal of Clinical Oncology, 2020, 38, 43-50.	0.8	50
13	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	3.3	13
14	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
15	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	13.7	94
16	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
17	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
18	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966

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19	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
20	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
21	Genome-wide Screens Implicate Loss of Cullin Ring Ligase 3 in Persistent Proliferation and Genome Instability in TP53-Deficient Cells. Cell Reports, 2020, 31, 107465.	2.9	24
22	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
23	DIPG-64. INTERNATIONAL PRECLINICAL DRUG DISCOVERY AND BIOMARKER PROGRAM INFORMING AN ADOPTIVE COMBINATORIAL TRIAL FOR DIFFUSE MIDLINE GLIOMAS. Neuro-Oncology, 2020, 22, iii300-iii300.	0.6	0
24	MBCL-21. GERMLINE ELONGATOR MUTATIONS IN SONIC HEDGEHOG MEDULLOBLASTOMA. Neuro-Oncology, 2020, 22, iii392-iii393.	0.6	0
25	MEDU-11. MOLECULAR CHARACTERIZATION OF ETMRs REVEALS A ROLE FOR R-LOOP MEDIATED CHROMOSOMAL INSTABILITY. Neuro-Oncology, 2019, 21, ii105-ii105.	0.6	0
26	NCoR1: Putting the Brakes on the Dendritic Cell Immune Tolerance. IScience, 2019, 19, 996-1011.	1.9	20
27	Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790.	6.1	73
28	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
29	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	13.7	94
30	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
31	MBCL-44. THE MOLECULAR AND CLINICAL LANDSCAPE OF INFANT MEDULLOBLASTOMA (iMB): RESULTS AND MOLECULAR ANALYSIS FROM A PROSPECTIVE, MULTICENTER PHASE II TRIAL (SJYC07). Neuro-Oncology, 2018, 20, i126-i127.	0.6	0
32	<scp>PDX</scp> models recapitulate the genetic and epigenetic landscape of pediatric Tâ€cell leukemia. EMBO Molecular Medicine, 2018, 10, .	3.3	38
33	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
34	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. Lancet Oncology, The, 2018, 19, 768-784.	5.1	151
35	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	5.1	268
36	EMBR-10. GENOMIC COMPLEXITY AND EVOLUTION OF EMBRYONAL TUMORS WITH MULTILAYERED ROSETTES (ETMR). Neuro-Oncology, 2018, 20, i70-i70.	0.6	0

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37	Abstract 3172: Targeting genomic instability in embryonal tumors with multilayered rosettes (ETMR). , 2018, , .		0
38	Pediatric T-ALLs Developing into a Type 2 Relapse Originate from Cells That Carry the Potential of Variable Maturation into Subclones with Distinct Chromatin Landscapes. Blood, 2018, 132, 1545-1545.	0.6	0
39	Chromosomal contacts connect loci associated with autism, BMI and head circumference phenotypes. Molecular Psychiatry, 2017, 22, 836-849.	4.1	68
40	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
41	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	9.4	326
42	NCoR1 is a master repressor of the tolerogenic program in dendritic cells. Canadian Journal of Biotechnology, 2017, 1, 161-161.	0.3	0
43	No correlation between NF1 mutation position and risk of optic pathway glioma in 77 unrelated NF1 patients. Human Genetics, 2016, 135, 469-475.	1.8	29
44	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	13.7	318
45	EPIG-04THE CHROMATIN LANDSCAPE OF MEDULLOBLASTOMA. Neuro-Oncology, 2015, 17, v86.4-v87.	0.6	0
46	A cellâ€based model system links chromothripsis with hyperploidy. Molecular Systems Biology, 2015, 11, 828.	3.2	118
47	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. Cell, 2015, 162, 1039-1050.	13.5	210
48	Abstract LB-B23: Medulloblastoma regulatory circuitries reveal subgroup-specific cellular origins. , 2015, , .		0
49	A common microdeletion affecting a hippocampusâ€and amygdalaâ€specific isoform of tryptophan hydroxylase 2 is not associated with affective disorders. Bipolar Disorders, 2014, 16, 764-768.	1.1	2
50	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. Bioinformatics, 2014, 30, 165-171.	1.8	21
51	A Dual Program for Translation Regulation in Cellular Proliferation and Differentiation. Cell, 2014, 158, 1281-1292.	13.5	414
52	Identification of the transcription factor ZEB1 as a central component of the adipogenic gene regulatory network. ELife, 2014, 3, e03346.	2.8	101
53	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. Science, 2013, 342, 744-747.	6.0	364
54	Rounding Up Natural Gene Expression Variation during Development. Developmental Cell, 2013, 27, 601-603.	3.1	1

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55	A yeast oneâ€hybrid and microfluidicsâ€based pipeline to map mammalian gene regulatory networks. Molecular Systems Biology, 2013, 9, 682.	3.2	35
56	Genomic Variation and Its Impact on Gene Expression in Drosophila melanogaster. PLoS Genetics, 2012, 8, e1003055.	1.5	102
57	Personal receptor repertoires: olfaction as a model. BMC Genomics, 2012, 13, 414.	1.2	92
58	Integrative Genomics Identifies the Corepressor SMRT as a Gatekeeper of Adipogenesis through the Transcription Factors C/EBPÎ² and KAISO. Molecular Cell, 2012, 46, 335-350.	4.5	96
59	Relating CNVs to transcriptome data at fine resolution: Assessment of the effect of variant size, type, and overlap with functional regions. Genome Research, 2011, 21, 2004-2013.	2.4	109
60	Variation in transcription factor binding among humans. New Biotechnology, 2010, 27, S81.	2.4	3
61	Systematic Inference of Copy-Number Genotypes from Personal Genome Sequencing Data Reveals Extensive Olfactory Receptor Gene Content Diversity. PLoS Computational Biology, 2010, 6, e1000988.	1.5	56
62	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	6.0	521