Sebastian M Waszak

List of Publications by Year in Descending Order

62 papers	6,046 citations	34 h-index	73 g-index
73 ext. papers	8,712 ext. citations	17.8 avg, IF	7.1 L-index

#	Paper	IF	Citations
62	Imipridones affect tumor bioenergetics and promote cell lineage differentiation in diffuse midline gliomas.. *Neuro-Oncology*, **2022**,	1	2
61	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation.. *Nature Communications*, **2022**, 13, 2042	17.4	1
60	MEDB-14. Clinical outcome of pediatric medulloblastoma patients with Li-Fraumeni syndrome. *Neuro-Oncology*, **2022**, 24, i107-i107	1	
59	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	1	
58	Pharmaco-proteogenomic profiling of pediatric diffuse midline glioma to inform future treatment strategies. *Oncogene*, **2021**,	9.2	5
57	Versatile workflow for cell type-resolved transcriptional and epigenetic profiles from cryopreserved human lung. *JCI Insight*, **2021**, 6,	9.9	2
56	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. *Leukemia*, **2021**, 35, 2002-2016	10.7	3
55	HGG-32. ONC201 AND ONC206 TARGET TUMOR CELL METABOLISM IN PEDIATRIC DIFFUSE MIDLINE GLIOMA PRECLINICAL MODELS. *Neuro-Oncology*, **2021**, 23, i23-i24	1	
54	Mechanisms of imipridones in targeting mitochondrial metabolism in cancer cells. *Neuro-Oncology*, **2021**, 23, 542-556	1	11
53	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. *Nature*, **2020**, 580, 396-401	50.4	47
52	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
51	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
50	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
49	Genomic basis for RNA alterations in cancer. *Nature*, **2020**, 578, 129-136	50.4	148
48	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
47	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	10.6	11
46	DIPG-64. INTERNATIONAL PRECLINICAL DRUG DISCOVERY AND BIOMARKER PROGRAM INFORMING AN ADOPTIVE COMBINATORIAL TRIAL FOR DIFFUSE MIDLINE GLIOMAS. *Neuro-Oncology*, **2020**, 22, iii300-iii300	1	78

45	MBCL-21. GERMLINE ELONGATOR MUTATIONS IN SONIC HEDGEHOG MEDULLOBLASTOMA. *Neuro-Oncology*, **2020**, 22, iii392-iii393	1	78
44	Butler enables rapid cloud-based analysis of thousands of human genomes. *Nature Biotechnology*, **2020**, 38, 288-292	44.5	9
43	Chromatin accessibility landscape of pediatric T-lymphoblastic leukemia and human T-cell precursors. *EMBO Molecular Medicine*, **2020**, 12, e12104	12	3
42	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
41	Germline Mutations Predispose to Pediatric Medulloblastoma. *Journal of Clinical Oncology*, **2020**, 38, 43-50	2.2	28
40	NCoR1: Putting the Brakes on the Dendritic Cell Immune Tolerance. *IScience*, **2019**, 19, 996-1011	6.1	10
39	Antibiotics-induced monodominance of a novel gut bacterial order. *Gut*, **2019**, 68, 1781-1790	19.2	33
38	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. *Nature Communications*, **2019**, 10, 1459	17.4	49
37	MEDU-11. MOLECULAR CHARACTERIZATION OF ETMRs REVEALS A ROLE FOR R-LOOP MEDIATED CHROMOSOMAL INSTABILITY. *Neuro-Oncology*, **2019**, 21, ii105-ii105	1	78
36	The molecular landscape of ETMR at diagnosis and relapse. *Nature*, **2019**, 576, 274-280	50.4	46
35	The landscape of genomic alterations across childhood cancers. *Nature*, **2018**, 555, 321-327	50.4	603
34	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	21.7	159
33	EMBR-10. GENOMIC COMPLEXITY AND EVOLUTION OF EMBRYONAL TUMORS WITH MULTILAYERED ROSETTES (ETMR). *Neuro-Oncology*, **2018**, 20, i70-i70	1	78
32	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	2.2	
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	1	78
30	PDX models recapitulate the genetic and epigenetic landscape of pediatric T-cell leukemia. *EMBO Molecular Medicine*, **2018**, 10,	12	20
29	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. *Cancer Cell*, **2018**, 34, 996-1011.e8	24.3	89
28	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	21.7	95

27	Chromosomal contacts connect loci associated with autism, BMI and head circumference phenotypes. *Molecular Psychiatry*, **2017**, 22, 836-849	15.1	43
26	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
25	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. *Nature Genetics*, **2017**, 49, 65-74	36.3	220
24	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. *Nature*, **2016**, 530, 57-62	50.4	234
23	No correlation between NF1 mutation position and risk of optic pathway glioma in 77 unrelated NF1 patients. *Human Genetics*, **2016**, 135, 469-475	6.3	21
22	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. *Cell*, **2015**, 162, 1039-50	56.2	156
21	EPIG-04THE CHROMATIN LANDSCAPE OF MEDULLOBLASTOMA. *Neuro-Oncology*, **2015**, 17, v86.4-v87	1	78
20	A cell-based model system links chromothripsis with hyperploidy. *Molecular Systems Biology*, **2015**, 11, 828	12.2	88
19	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. *Bioinformatics*, **2014**, 30, 165-71	7.2	17
18	A dual program for translation regulation in cellular proliferation and differentiation. *Cell*, **2014**, 158, 1281-1292	56.2	278
17	A common microdeletion affecting a hippocampus- and amygdala-specific isoform of tryptophan hydroxylase 2 is not associated with affective disorders. *Bipolar Disorders*, **2014**, 16, 764-8	3.8	2
16	Identification of the transcription factor ZEB1 as a central component of the adipogenic gene regulatory network. *ELife*, **2014**, 3, e03346	8.9	60
15	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. *Science*, **2013**, 342, 744-7	33.3	278
14	Rounding up natural gene expression variation during development. *Developmental Cell*, **2013**, 27, 601-3	10.2	0
13	A yeast one-hybrid and microfluidics-based pipeline to map mammalian gene regulatory networks. *Molecular Systems Biology*, **2013**, 9, 682	12.2	31
12	Personal receptor repertoires: olfaction as a model. *BMC Genomics*, **2012**, 13, 414	4.5	74
11	Integrative genomics identifies the corepressor SMRT as a gatekeeper of adipogenesis through the transcription factors C/EBP and KAISO. *Molecular Cell*, **2012**, 46, 335-50	17.6	62
10	Genomic variation and its impact on gene expression in Drosophila melanogaster. *PLoS Genetics*, **2012**, 8, e1003055	6	85

List of Publications

9	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, 2004-13	9.7	80
8	Systematic inference of copy-number genotypes from personal genome sequencing data reveals extensive olfactory receptor gene content diversity. *PLoS Computational Biology*, **2010**, 6, e1000988	5	54
7	Variation in transcription factor binding among humans. *Science*, **2010**, 328, 232-5	33.3	447
6	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
5	Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types		10
4	Enabling rapid cloud-based analysis of thousands of human genomes via Butler		2
3	The whole-genome panorama of cancer drivers		38
2	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
1	Assessing the Gene Regulatory Landscape in 1,188 Human Tumors		3