Carl Herrmann

List of Publications by Citations

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65	4,561	27	67
papers	citations	h-index	g-index
72	6,485	13.7	7.09
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
65	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
64	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. *Nature*, **2015**, 526, 700-4	50.4	347
63	Identification of regulatory networks in HSCs and their immediate progeny via integrated proteome, transcriptome, and DNA methylome analysis. *Cell Stem Cell*, **2014**, 15, 507-522	18	320
62	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. *Cancer Cell*, **2016**, 29, 379-393	24.3	319
61	Myelodysplastic cells in patients reprogram mesenchymal stromal cells to establish a transplantable stem cell niche disease unit. *Cell Stem Cell*, **2014**, 14, 824-37	18	267
60	Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cell state. *Nature Communications*, **2015**, 6, 6683	17.4	235
59	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
58	RSAT 2015: Regulatory Sequence Analysis Tools. *Nucleic Acids Research*, **2015**, 43, W50-6	20.1	193
57	RSAT 2011: regulatory sequence analysis tools. *Nucleic Acids Research*, **2011**, 39, W86-91	20.1	192
56	RSAT peak-motifs: motif analysis in full-size ChIP-seq datasets. *Nucleic Acids Research*, **2012**, 40, e31	20.1	159
55	BCAT1 restricts □KG levels in AML stem cells leading to IDHmut-like DNA hypermethylation. *Nature* , **2017**, 551, 384-388	50.4	154
54	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. *Nature Immunology*, **2017**, 18, 1160-1172	19.1	125
53	i-cisTarget: an integrative genomics method for the prediction of regulatory features and cis-regulatory modules. *Nucleic Acids Research*, **2012**, 40, e114	20.1	98
52	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. *Nature Communications*, **2019**, 10, 470	17.4	84
51	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. *Molecular Systems Biology*, **2016**, 12, 861	12.2	71
50	A complete workflow for the analysis of full-size ChIP-seq (and similar) data sets using peak-motifs. *Nature Protocols*, **2012**, 7, 1551-68	18.8	64
49	A comprehensive comparison of tools for differential ChIP-seq analysis. *Briefings in Bioinformatics*, **2016**, 17, 953-966	13.4	62

48	Connectivity distribution of spatial networks. *Physical Review E*, **2003**, 68, 026128	2.4	60
47	Compactification of type IIB string theory on Calabi–Yau threefolds. *Nuclear Physics B*, **2000**, 569, 229-246	2.8	54
46	Integrative Genome-Scale Analysis Identifies Epigenetic Mechanisms of Transcriptional Deregulation in Unfavorable Neuroblastomas. *Cancer Research*, **2016**, 76, 5523-37	10.1	52
45	Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation. *Scientific Reports*, **2016**, 6, 28616	4.9	44
44	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. *Nature Communications*, **2018**, 9, 4866	17.4	42
43	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. *Cell*, **2020**, 180, 915-927.e16	56.2	38
42	Domain walls in five dimensional supergravity with non-trivial hypermultiplets. *Journal of High Energy Physics*, **2001**, 2001, 011-011	5.4	35
41	Increased vitamin D levels at birth and in early infancy increase offspring allergy risk-evidence for involvement of epigenetic mechanisms. *Journal of Allergy and Clinical Immunology*, **2016**, 137, 610-3	11.5	32
40	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. *Cancer Letters*, **2015**, 366, 123-32	9.9	31
39	Identification of DNA methylation changes at cis-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. *Cell Cycle*, **2014**, 13, 3476-87	4.7	31
38	Single-cell transcriptomic analyses provide insights into the developmental origins of neuroblastoma. *Nature Genetics*, **2021**, 53, 683-693	36.3	26
37	Ab initio identification of putative human transcription factor binding sites by comparative genomics. *BMC Bioinformatics*, **2005**, 6, 110	3.6	24
36	Identification of Embryonic Neural Plate Border Stem Cells and Their Generation by Direct Reprogramming from Adult Human Blood Cells. *Cell Stem Cell*, **2019**, 24, 166-182.e13	18	24
35	Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut. *Molecular Systems Biology*, **2021**, 17, e10232	12.2	23
34	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. *Blood*, **2020**, 136, 1507-1519	2.2	22
33	From single genes to co-expression networks: extracting knowledge from barley functional genomics. *Plant Molecular Biology*, **2005**, 58, 739-50	4.6	22
32	THE N=2 VECTOR–TENSOR MULTIPLET, CENTRAL CHARGE SUPERSPACE, AND CHERN–SIMONS COUPLINGS. *International Journal of Modern Physics A*, **1998**, 13, 1805-1816	1.2	19
31	Metagenome annotation using a distributed grid of undergraduate students. *PLoS Biology*, **2008**, 6, e296	9.7	19

30	Cis-regulatory characterization of sequence conservation surrounding the Hox4 genes. *Developmental Biology*, **2010**, 340, 269-82	3.1	16
29	Super enhancers define regulatory subtypes and cell identity in neuroblastoma.. *Nature Cancer*, **2021**, 2, 114-128	15.4	15
28	Automated 3D light-sheet screening with high spatiotemporal resolution reveals mitotic phenotypes. *Journal of Cell Science*, **2020**, 133,	5.3	14
27	Identifying Personal DNA Methylation Profiles by Genotype Inference **2017**,		14
26	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
25	Alternative lengthening of telomeres in childhood neuroblastoma from genome to proteome. *Nature Communications*, **2021**, 12, 1269	17.4	12
24	Evolutionary conserved gene co-expression drives generation of self-antigen diversity in medullary thymic epithelial cells. *Journal of Autoimmunity*, **2016**, 67, 65-75	15.5	11
23	Using cisTargetX to predict transcriptional targets and networks in Drosophila. *Methods in Molecular Biology*, **2012**, 786, 291-314	1.4	11
22	SimCT: a generic tool to visualize ontology-based relationships for biological objects. *Bioinformatics* , **2009**, 25, 3197-8	7.2	11
21	Impact of cancer mutational signatures on transcription factor motifs in the human genome. *BMC Medical Genomics*, **2019**, 12, 64	3.7	9
20	Transcriptional and epigenetic signatures of zygotic genome activation during early Drosophila embryogenesis. *BMC Genomics*, **2013**, 14, 226	4.5	9
19	Identification of cis-regulatory modules encoding temporal dynamics during development. *BMC Genomics*, **2014**, 15, 534	4.5	8
18	N = 2 central charge superspace and a minimal supergravity multiplet. *Classical and Quantum Gravity*, **1999**, 16, 1617-1623	3.3	8
17	PrOnto database : GO term functional dissimilarity inferred from biological data. *Frontiers in Genetics*, **2015**, 6, 200	4.5	7
16	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. *Nature Communications*, **2020**, 11, 6434	17.4	7
15	Deciphering programs of transcriptional regulation by combined deconvolution of multiple omics layers		6
14	Single-cell analyses reveal SARS-CoV-2 interference with intrinsic immune response in the human gut		6
13	MapMyFlu: visualizing spatio-temporal relationships between related influenza sequences. *Nucleic Acids Research*, **2015**, 43, W547-51	20.1	5

12	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity		5
11	Single-nucleus chromatin accessibility reveals intratumoral epigenetic heterogeneity in IDH1 mutant gliomas. *Acta Neuropathologica Communications*, **2019**, 7, 201	7.3	5
10	Passenger mutations in 2500 cancer genomes: Overall molecular functional impact and consequences		4
9	Identification of therapeutic targets of the hijacked super-enhancer complex in EVI1-rearranged leukemia. *Leukemia*, **2021**, 35, 3127-3138	10.7	4
8	LedPred: an R/bioconductor package to predict regulatory sequences using support vector machines. *Bioinformatics*, **2016**, 32, 1091-3	7.2	3
7	N = 4 supergravity with antisymmetric tensor in central charge superspace. *Classical and Quantum Gravity*, **2001**, 18, 1027-1037	3.3	3
6	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. *Biology Methods and Protocols*, **2020**, 5, bpaa022	2.4	2
5	Integrative Ranking Of Enhancer Networks Facilitates The Discovery Of Epigenetic Markers In Cancer		1
4	The endogenous cellular protease inhibitor SPINT2 controls SARS-CoV-2 viral infection and is associated to disease severity. *PLoS Pathogens*, **2021**, 17, e1009687	7.6	1
3	MYCN mediates cysteine addiction and sensitizes neuroblastoma to ferroptosis.. *Nature Cancer*, **2022**, 3, 471-485	15.4	0
2	Extended Gauged Supergravities and Holography. *Fortschritte Der Physik*, **2001**, 49, 535	5.7	
1	Integrative Ranking of Enhancer Networks Facilitates the Discovery of Epigenetic Markers in Cancer. *Frontiers in Genetics*, **2021**, 12, 664654	4.5	