

Kevin P White

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

80
papers

5,717
citations

41
h-index

75
g-index

85
ext. papers

8,464
ext. citations

16.3
avg, IF

4.93
L-index

#	Paper	IF	Citations
80	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. <i>Genome Medicine</i> , 2021 , 13, 158	14.4	2
79	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021 , 12, 3968	17.4	2
78	To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. <i>Nucleic Acids Research</i> , 2021 , 49, e17	20.1	2
77	A pan-cancer organoid platform for precision medicine. <i>Cell Reports</i> , 2021 , 36, 109429	10.6	10
76	Validation of a liquid biopsy assay with molecular and clinical profiling of circulating tumor DNA. <i>Npj Precision Oncology</i> , 2021 , 5, 63	9.8	3
75	STARRPeaker: uniform processing and accurate identification of STARR-seq active regions. <i>Genome Biology</i> , 2020 , 21, 298	18.3	12
74	Tumor Mutational Burden From Tumor-Only Sequencing Compared With Germline Subtraction From Paired Tumor and Normal Specimens. <i>JAMA Network Open</i> , 2020 , 3, e200202	10.4	12
73	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020 , 11,	7.8	79
72	The Drosophila MLR COMPASS complex is essential for programming cis-regulatory information and maintaining epigenetic memory during development. <i>Nucleic Acids Research</i> , 2020 , 48, 3476-3495	20.1	2
71	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. <i>PLoS Computational Biology</i> , 2020 , 16, e1007522	5	3
70	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. <i>Journal of Clinical Investigation</i> , 2020 , 130, 3005-3020	15.9	4
69	Automated microfluidic platform for dynamic and combinatorial drug screening of tumor organoids. <i>Nature Communications</i> , 2020 , 11, 5271	17.4	64
68	Integrating Next-Generation Sequencing with Morphology Improves Prognostic and Biologic Classification of Spitz Neoplasms. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 1599-1608	4.3	20
67	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020 , 11, 3696	17.4	28
66	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	10.4	360
65	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent and enhancer hijacking in primary gastric adenocarcinoma. <i>Gut</i> , 2020 , 69, 1039-1052	19.2	21
64	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data 2020 , 16, e1007522		

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62	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data 2020 , 16, e1007522		
61	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data 2020 , 16, e1007522		
60	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data 2020 , 16, e1007522		
59	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data 2020 , 16, e1007522		
58	Clinical validation of the tempus xT next-generation targeted oncology sequencing assay. <i>Oncotarget</i> , 2019 , 10, 2384-2396	3.3	51
57	Activating Structural Alterations in MAPK Genes Are Distinct Genetic Drivers in a Unique Subgroup Of Spitzoid Neoplasms. <i>American Journal of Surgical Pathology</i> , 2019 , 43, 538-548	6.7	23
56	Integrated genomic profiling expands clinical options for patients with cancer. <i>Nature Biotechnology</i> , 2019 , 37, 1351-1360	44.5	47
55	Human Organoids Share Structural and Genetic Features with Primary Pancreatic Adenocarcinoma Tumors. <i>Molecular Cancer Research</i> , 2019 , 17, 70-83	6.6	45
54	Giant tortoise genomes provide insights into longevity and age-related disease. <i>Nature Ecology and Evolution</i> , 2019 , 3, 87-95	12.3	43
53	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018 , 359, 693-697	33.3	547
52	Nuclear receptors in cancer - uncovering new and evolving roles through genomic analysis. <i>Nature Reviews Genetics</i> , 2018 , 19, 160-174	30.1	46
51	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of and Transcription Factors. <i>Genetics</i> , 2018 , 208, 937-949	4	71
50	Integrated molecular subtyping defines a curable oligometastatic state in colorectal liver metastasis. <i>Nature Communications</i> , 2018 , 9, 1793	17.4	114
49	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018 , 9, 3121	17.4	74
48	Clinical validation of the Tempus xO assay. <i>Oncotarget</i> , 2018 , 9, 25826-25832	3.3	20
47	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018 , 362,	33.3	142
46	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277

45	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018 , 362,	33.3	434
44	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018 , 362,	33.3	319
43	The long noncoding RNA may regulate expression of several schizophrenia-related genes. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	42
42	The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	46
41	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. <i>Nature Communications</i> , 2018 , 9, 4181	17.4	45
40	Genomic Fusions in Pigmented Spindle Cell Nevus of Reed. <i>American Journal of Surgical Pathology</i> , 2018 , 42, 1042-1051	6.7	39
39	Integration of temporal and spatial patterning generates neural diversity. <i>Nature</i> , 2017 , 541, 365-370	50.4	72
38	Evolution of transcript modification by -methyladenosine in primates. <i>Genome Research</i> , 2017 , 27, 385-397	37	34
37	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017 , 8, 1221	17.4	40
36	Systematic identification of regulatory variants associated with cancer risk. <i>Genome Biology</i> , 2017 , 18, 194	18.3	44
35	Identification of Novel Protein Expression Changes Following Cisplatin Treatment and Application to Combination Therapy. <i>Journal of Proteome Research</i> , 2017 , 16, 4227-4236	5.6	3
34	Clinical Validation of a Next-Generation Sequencing Genomic Oncology Panel via Cross-Platform Benchmarking against Established Amplicon Sequencing Assays. <i>Journal of Molecular Diagnostics</i> , 2017 , 19, 43-56	5.1	69
33	Functional assessment of human enhancer activities using whole-genome STARR-sequencing. <i>Genome Biology</i> , 2017 , 18, 219	18.3	47
32	Robust stratification of breast cancer subtypes using differential patterns of transcript isoform expression. <i>PLoS Genetics</i> , 2017 , 13, e1006589	6	36
31	GSK-3 inhibition overcomes chemoresistance in human breast cancer. <i>Cancer Letters</i> , 2016 , 380, 384-392	9.9	42
30	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. <i>Oncotarget</i> , 2016 , 7, 76816-76826	3.3	26
29	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. <i>Genome Biology</i> , 2016 , 17, 250	18.3	48
28	Shared Genetic Signals of Hypoxia Adaptation in <i>Drosophila</i> and in High-Altitude Human Populations. <i>Molecular Biology and Evolution</i> , 2016 , 33, 501-17	8.3	30

27	Metabolic Regulation of Gene Expression by Histone Lysine ϵ -Hydroxybutyrylation. <i>Molecular Cell</i> , 2016 , 62, 194-206	17.6	240
26	Zodiac: A Comprehensive Depiction of Genetic Interactions in Cancer by Integrating TCGA Data. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	23
25	A Conserved Bicycle Model for Circadian Clock Control of Membrane Excitability. <i>Cell</i> , 2015 , 162, 836-48	56.2	133
24	Centrosomin represses dendrite branching by orienting microtubule nucleation. <i>Nature Neuroscience</i> , 2015 , 18, 1437-45	25.5	80
23	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
22	Integrative analysis of head and neck cancer identifies two biologically distinct HPV and three non-HPV subtypes. <i>Clinical Cancer Research</i> , 2015 , 21, 870-81	12.9	242
21	Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. <i>Clinical Cancer Research</i> , 2015 , 21, 632-41	12.9	398
20	Whole-Genome Resequencing of Experimental Populations Reveals Polygenic Basis of Egg-Size Variation in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2015 , 32, 2616-32	8.3	46
19	Regulation of Gene Expression Patterns in Mosquito Reproduction. <i>PLoS Genetics</i> , 2015 , 11, e1005450	6	39
18	Widespread genetic epistasis among cancer genes. <i>Nature Communications</i> , 2014 , 5, 4828	17.4	45
17	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014 , 512, 453-6	50.4	135
16	Yorkie promotes transcription by recruiting a histone methyltransferase complex. <i>Cell Reports</i> , 2014 , 8, 449-59	10.6	52
15	Identification and validation of genetic variants that influence transcription factor and cell signaling protein levels. <i>American Journal of Human Genetics</i> , 2014 , 95, 194-208	11	42
14	Su(H)-mediated repression positions gene boundaries along the dorsal-ventral axis of <i>Drosophila</i> embryos. <i>Developmental Cell</i> , 2014 , 31, 100-13	10.2	25
13	SPOP promotes tumorigenesis by acting as a key regulatory hub in kidney cancer. <i>Cancer Cell</i> , 2014 , 25, 455-68	24.3	110
12	Transcription factor networks in <i>Drosophila melanogaster</i> . <i>Cell Reports</i> , 2014 , 8, 2031-2043	10.6	56
11	Pri peptides are mediators of ecdysone for the temporal control of development. <i>Nature Cell Biology</i> , 2014 , 16, 1035-44	23.4	57
10	Protein quantitative trait loci identify novel candidates modulating cellular response to chemotherapy. <i>PLoS Genetics</i> , 2014 , 10, e1004192	6	20

9	Bionimbus: a cloud for managing, analyzing and sharing large genomics datasets. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014 , 21, 969-75	8.6	56
8	Evolution of H3K27me3-marked chromatin is linked to gene expression evolution and to patterns of gene duplication and diversification. <i>Genome Research</i> , 2014 , 24, 1115-24	9.7	16
7	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014 , 24, 1224-35	9.7	27
6	miR-9a minimizes the phenotypic impact of genomic diversity by buffering a transcription factor. <i>Cell</i> , 2013 , 155, 1556-67	56.2	70
5	Next-generation sequencing of disseminated tumor cells. <i>Frontiers in Oncology</i> , 2013 , 3, 320	5.3	29
4	Groucho-mediated long-range transcriptional repression: roles for discontinuous spreading and an HDAC-dependent increase in nucleosome density. <i>FASEB Journal</i> , 2010 , 24, 713.1	0.9	
3	Next-Generation Sequencing Analysis of 23 Therapy-Related Acute Myeloid Leukemia Transcriptomes. <i>Blood</i> , 2010 , 116, 850-850	2.2	
2	STARRPeaker: Uniform processing and accurate identification of STARR-seq active regions		3
1	Integrative Epigenomic and High-Throughput Functional Enhancer Profiling Reveals Determinants of Enhancer Heterogeneity in Gastric Cancer		1