Kevin P White

List of Publications by Citations

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	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. *Science*, **2018**, 359, 693-697	33.3	547
79	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
78	Integrative and comparative genomic analysis of HPV-positive and HPV-negative head and neck squamous cell carcinomas. *Clinical Cancer Research*, **2015**, 21, 632-41	12.9	398
77	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
76	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
75	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
74	Integrative analysis of head and neck cancer identifies two biologically distinct HPV and three non-HPV subtypes. *Clinical Cancer Research*, **2015**, 21, 870-81	12.9	242
73	Metabolic Regulation of Gene Expression by Histone Lysine βHydroxybutyrylation. *Molecular Cell*, **2016**, 62, 194-206	17.6	240
72	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
71	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
70	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135
69	A Conserved Bicycle Model for Circadian Clock Control of Membrane Excitability. *Cell*, **2015**, 162, 836-48	56.2	133
68	Integrated molecular subtyping defines a curable oligometastatic state in colorectal liver metastasis. *Nature Communications*, **2018**, 9, 1793	17.4	114
67	SPOP promotes tumorigenesis by acting as a key regulatory hub in kidney cancer. *Cancer Cell*, **2014**, 25, 455-68	24.3	110
66	Centrosomin represses dendrite branching by orienting microtubule nucleation. *Nature Neuroscience*, **2015**, 18, 1437-45	25.5	80
65	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. *MBio*, **2020**, 11,	7.8	79
64	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. *Nature Communications*, **2018**, 9, 3121	17.4	74

63	Integration of temporal and spatial patterning generates neural diversity. *Nature*, **2017**, 541, 365-370	50.4	72
62	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of and Transcription Factors. *Genetics*, **2018**, 208, 937-949	4	71
61	miR-9a minimizes the phenotypic impact of genomic diversity by buffering a transcription factor. *Cell*, **2013**, 155, 1556-67	56.2	70
60	Clinical Validation of a Next-Generation Sequencing Genomic Oncology Panel via Cross-Platform Benchmarking against Established Amplicon Sequencing Assays. *Journal of Molecular Diagnostics*, **2017**, 19, 43-56	5.1	69
59	Automated microfluidic platform for dynamic and combinatorial drug screening of tumor organoids. *Nature Communications*, **2020**, 11, 5271	17.4	64
58	Pri peptides are mediators of ecdysone for the temporal control of development. *Nature Cell Biology*, **2014**, 16, 1035-44	23.4	57
57	Transcription factor networks in Drosophila melanogaster. *Cell Reports*, **2014**, 8, 2031-2043	10.6	56
56	Bionimbus: a cloud for managing, analyzing and sharing large genomics datasets. *Journal of the American Medical Informatics Association: JAMIA*, **2014**, 21, 969-75	8.6	56
55	Yorkie promotes transcription by recruiting a histone methyltransferase complex. *Cell Reports*, **2014**, 8, 449-59	10.6	52
54	Clinical validation of the tempus xT next-generation targeted oncology sequencing assay. *Oncotarget*, **2019**, 10, 2384-2396	3.3	51
53	Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. *Genome Biology*, **2016**, 17, 250	18.3	48
52	Functional assessment of human enhancer activities using whole-genome STARR-sequencing. *Genome Biology*, **2017**, 18, 219	18.3	47
51	Integrated genomic profiling expands clinical options for patients with cancer. *Nature Biotechnology*, **2019**, 37, 1351-1360	44.5	47
50	Nuclear receptors in cancer - uncovering new and evolving roles through genomic analysis. *Nature Reviews Genetics*, **2018**, 19, 160-174	30.1	46
49	Whole-Genome Resequencing of Experimental Populations Reveals Polygenic Basis of Egg-Size Variation in Drosophila melanogaster. *Molecular Biology and Evolution*, **2015**, 32, 2616-32	8.3	46
48	The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. *Science Translational Medicine*, **2018**, 10,	17.5	46
47	Widespread genetic epistasis among cancer genes. *Nature Communications*, **2014**, 5, 4828	17.4	45
46	Human Organoids Share Structural and Genetic Features with Primary Pancreatic Adenocarcinoma Tumors. *Molecular Cancer Research*, **2019**, 17, 70-83	6.6	45

45	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. *Nature Communications*, **2018**, 9, 4181	17.4	45
44	Systematic identification of regulatory variants associated with cancer risk. *Genome Biology*, **2017**, 18, 194	18.3	44
43	Giant tortoise genomes provide insights into longevity and age-related disease. *Nature Ecology and Evolution*, **2019**, 3, 87-95	12.3	43
42	GSK-3 inhibition overcomes chemoresistance in human breast cancer. *Cancer Letters*, **2016**, 380, 384-392	9.9	42
41	Identification and validation of genetic variants that influence transcription factor and cell signaling protein levels. *American Journal of Human Genetics*, **2014**, 95, 194-208	11	42
40	The long noncoding RNA may regulate expression of several schizophrenia-related genes. *Science Translational Medicine*, **2018**, 10,	17.5	42
39	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. *Nature Communications*, **2017**, 8, 1221	17.4	40
38	Regulation of Gene Expression Patterns in Mosquito Reproduction. *PLoS Genetics*, **2015**, 11, e1005450	6	39
37	Genomic Fusions in Pigmented Spindle Cell Nevus of Reed. *American Journal of Surgical Pathology*, **2018**, 42, 1042-1051	6.7	39
36	Robust stratification of breast cancer subtypes using differential patterns of transcript isoform expression. *PLoS Genetics*, **2017**, 13, e1006589	6	36
35	Evolution of transcript modification by -methyladenosine in primates. *Genome Research*, **2017**, 27, 385-392	9.7	34
34	Shared Genetic Signals of Hypoxia Adaptation in Drosophila and in High-Altitude Human Populations. *Molecular Biology and Evolution*, **2016**, 33, 501-17	8.3	30
33	Next-generation sequencing of disseminated tumor cells. *Frontiers in Oncology*, **2013**, 3, 320	5.3	29
32	An integrative ENCODE resource for cancer genomics. *Nature Communications*, **2020**, 11, 3696	17.4	28
31	Diverse patterns of genomic targeting by transcriptional regulators in Drosophila melanogaster. *Genome Research*, **2014**, 24, 1224-35	9.7	27
30	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. *Oncotarget*, **2016**, 7, 76816-76826	3.3	26
29	Su(H)-mediated repression positions gene boundaries along the dorsal-ventral axis of Drosophila embryos. *Developmental Cell*, **2014**, 31, 100-13	10.2	25
28	Zodiac: A Comprehensive Depiction of Genetic Interactions in Cancer by Integrating TCGA Data. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	23

27	Activating Structural Alterations in MAPK Genes Are Distinct Genetic Drivers in a Unique Subgroup Of Spitzoid Neoplasms. *American Journal of Surgical Pathology*, **2019**, 43, 538-548	6.7	23
26	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent and enhancer hijacking in primary gastric adenocarcinoma. *Gut*, **2020**, 69, 1039-1052	19.2	21
25	Protein quantitative trait loci identify novel candidates modulating cellular response to chemotherapy. *PLoS Genetics*, **2014**, 10, e1004192	6	20
24	Integrating Next-Generation Sequencing with Morphology Improves Prognostic and Biologic Classification of Spitz Neoplasms. *Journal of Investigative Dermatology*, **2020**, 140, 1599-1608	4.3	20
23	Clinical validation of the Tempus xO assay. *Oncotarget*, **2018**, 9, 25826-25832	3.3	20
22	Evolution of H3K27me3-marked chromatin is linked to gene expression evolution and to patterns of gene duplication and diversification. *Genome Research*, **2014**, 24, 1115-24	9.7	16
21	STARRPeaker: uniform processing and accurate identification of STARR-seq active regions. *Genome Biology*, **2020**, 21, 298	18.3	12
20	Tumor Mutational Burden From Tumor-Only Sequencing Compared With Germline Subtraction From Paired Tumor and Normal Specimens. *JAMA Network Open*, **2020**, 3, e200202	10.4	12
19	A pan-cancer organoid platform for precision medicine. *Cell Reports*, **2021**, 36, 109429	10.6	10
18	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. *Journal of Clinical Investigation*, **2020**, 130, 3005-3020	15.9	4
17	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. *PLoS Computational Biology*, **2020**, 16, e1007522	5	3
16	Identification of Novel Protein Expression Changes Following Cisplatin Treatment and Application to Combination Therapy. *Journal of Proteome Research*, **2017**, 16, 4227-4236	5.6	3
15	STARRPeaker: Uniform processing and accurate identification of STARR-seq active regions		3
14	Validation of a liquid biopsy assay with molecular and clinical profiling of circulating tumor DNA. *Npj Precision Oncology*, **2021**, 5, 63	9.8	3
13	The Drosophila MLR COMPASS complex is essential for programming cis-regulatory information and maintaining epigenetic memory during development. *Nucleic Acids Research*, **2020**, 48, 3476-3495	20.1	2
12	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. *Genome Medicine*, **2021**, 13, 158	14.4	2
11	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
10	To mock or not: a comprehensive comparison of mock IP and DNA input for ChIP-seq. *Nucleic Acids Research*, **2021**, 49, e17	20.1	2

9	Integrative Epigenomic and High-Throughput Functional Enhancer Profiling Reveals Determinants of Enhancer Heterogeneity in Gastric Cancer	1
8	Groucho-mediated long-range transcriptional repression: roles for discontinuous spreading and an HDAC-dependent increase in nucleosome density. *FASEB Journal*, **2010**, 24, 713.1	0.9
7	Next-Generation Sequencing Analysis of 23 Therapy-Related Acute Myeloid Leukemia Transcriptomes. *Blood*, **2010**, 116, 850-850	2.2
6	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	
5	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	
4	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	
3	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	
2	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	
1	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522	