

Pouya Kheradpour

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.

26
papers

18,832
citations

24
h-index

28
g-index

28
ext. papers

23,094
ext. citations

28
avg, IF

5.21
L-index

#	Paper	IF	Citations
26	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
25	Evidence of reduced recombination rate in human regulatory domains. <i>Genome Biology</i> , 2017 , 18, 193	18.3	23
24	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , 2015 , 348, 648-60	33.3	3242
23	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015 , 348, 666-9	33.3	170
22	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
21	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014 , 512, 453-6	50.4	135
20	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014 , 24, 1224-35	9.7	27
19	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. <i>Nucleic Acids Research</i> , 2014 , 42, 2976-87	20.1	302
18	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013 , 23, 800-11	9.7	191
17	Analysis of variation at transcription factor binding sites in <i>Drosophila</i> and humans. <i>Genome Biology</i> , 2012 , 13, R49	18.3	71
16	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
15	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011 , 473, 43-9	50.4	2153
14	A cis-regulatory map of the <i>Drosophila</i> genome. <i>Nature</i> , 2011 , 471, 527-31	50.4	390
13	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011 , 478, 476-82	50.4	802
12	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. <i>Genome Research</i> , 2011 , 21, 1916-28	9.7	71
11	A comprehensive map of insulator elements for the <i>Drosophila</i> genome. <i>PLoS Genetics</i> , 2010 , 6, e1000814	14	255
10	Identification of functional elements and regulatory circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010 , 330, 1787-97	33.3	892

9	Histone modifications at human enhancers reflect global cell-type-specific gene expression. <i>Nature</i> , 2009 , 459, 108-12	50.4	1832
8	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
7	A single Hox locus in <i>Drosophila</i> produces functional microRNAs from opposite DNA strands. <i>Genes and Development</i> , 2008 , 22, 8-13	12.6	188
6	Conservation of small RNA pathways in platypus. <i>Genome Research</i> , 2008 , 18, 995-1004	9.7	34
5	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007 , 450, 219-32	50.4	506
4	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
3	Systematic discovery and characterization of fly microRNAs using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007 , 17, 1865-79	9.7	158
2	Reliable prediction of regulator targets using 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2007 , 17, 1919-31	9.7	123
1	Dissection of multiple sclerosis genetics identifies B and CD4+ T cells as driver cell subsets		1