

Eric Haugen

List of Publications by Citations

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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.

42
papers

12,130
citations

30
h-index

46
g-index

46
ext. papers

14,754
ext. citations

24.8
avg, IF

4.91
L-index

#	Paper	IF	Citations
42	Systematic localization of common disease-associated variation in regulatory DNA. <i>Science</i> , 2012 , 337, 1190-5	33.3	2262
41	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012 , 489, 75-82	50.4	1900
40	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
39	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008 , 453, 56-64	50.4	878
38	Comprehensive transposon mutant library of <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 14339-44	11.5	864
37	Fine-scale structural variation of the human genome. <i>Nature Genetics</i> , 2005 , 37, 727-32	36.3	811
36	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012 , 489, 83-90	50.4	589
35	The human mitochondrial transcriptome. <i>Cell</i> , 2011 , 146, 645-58	56.2	561
34	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012 , 28, 1919-20	7.2	472
33	Developmental fate and cellular maturity encoded in human regulatory DNA landscapes. <i>Cell</i> , 2013 , 154, 888-903	56.2	255
32	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003 , 424, 157-64	50.4	202
31	Exonic transcription factor binding directs codon choice and affects protein evolution. <i>Science</i> , 2013 , 342, 1367-72	33.3	201
30	Comparison of <i>Francisella tularensis</i> genomes reveals evolutionary events associated with the emergence of human pathogenic strains. <i>Genome Biology</i> , 2007 , 8, R102	18.3	192
29	Mapping and dynamics of regulatory DNA and transcription factor networks in <i>A. thaliana</i> . <i>Cell Reports</i> , 2014 , 8, 2015-2030	10.6	191
28	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014 , 346, 1007-12	33.3	184
27	Methylobacterium genome sequences: a reference blueprint to investigate microbial metabolism of C1 compounds from natural and industrial sources. <i>PLoS ONE</i> , 2009 , 4, e5584	3.7	172
26	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014 , 515, 365-70	50.4	164

25	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. <i>Nature Genetics</i> , 2015 , 47, 1393-401	36.3	160
24	Analysis of the genome of the Escherichia coli O157:H7 2006 spinach-associated outbreak isolate indicates candidate genes that may enhance virulence. <i>Infection and Immunity</i> , 2009 , 77, 3713-21	3.7	122
23	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. <i>Nature Biotechnology</i> , 2014 , 32, 71-5	44.5	92
22	Polymyxin resistance of Pseudomonas aeruginosa phoQ mutants is dependent on additional two-component regulatory systems. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 2204-15	5.9	83
21	Evolution of Burkholderia pseudomallei in recurrent melioidosis. <i>PLoS ONE</i> , 2012 , 7, e36507	3.7	83
20	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
19	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020 , 583, 729-736	50.4	76
18	Potential source of Francisella tularensis live vaccine strain attenuation determined by genome comparison. <i>Infection and Immunity</i> , 2006 , 74, 6895-906	3.7	71
17	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020 , 584, 244-251	50.4	64
16	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
15	Ancient haplotypes of the HLA Class II region. <i>Genome Research</i> , 2005 , 15, 1250-7	9.7	48
14	Closing gaps in the human genome with fosmid resources generated from multiple individuals. <i>Nature Genetics</i> , 2008 , 40, 96-101	36.3	47
13	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006 , 440, 1194-8	50.4	43
12	Single-molecule regulatory architectures captured by chromatin fiber sequencing. <i>Science</i> , 2020 , 368, 1449-1454	33.3	28
11	Genome sequence of Francisella tularensis subspecies holarctica strain FSC200, isolated from a child with tularemia. <i>Journal of Bacteriology</i> , 2012 , 194, 6965-6	3.5	24
10	ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: AUREOCOCCUS ANOPHAGEFFERENS CCMP1984 AND AUREOUMBRA LAGUNENSIS CCMP15071. <i>Journal of Phycology</i> , 2010 , 46, 602-615	3	23
9	Targeted, haplotype-resolved resequencing of long segments of the human genome. <i>Genomics</i> , 2005 , 86, 759-66	4.3	23
8	Large-insert genome analysis technology detects structural variation in Pseudomonas aeruginosa clinical strains from cystic fibrosis patients. <i>Genomics</i> , 2008 , 91, 530-7	4.3	22

7	Epigenetic regulation by chromatin activation mark H3K4me3 in primate progenitor cells within adult neurogenic niche. <i>Scientific Reports</i> , 2014 , 4, 5371	4.9	21
6	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. <i>EBioMedicine</i> , 2019 , 41, 427-442	8.8	16
5	Rare Variants of the Serotonin Transporter Are Associated With Psychiatric Comorbidity in Irritable Bowel Syndrome. <i>Biological Research for Nursing</i> , 2016 , 18, 394-400	2.6	9
4	Atlas and developmental dynamics of mouse DNase I hypersensitive sites		5
3	Index and biological spectrum of accessible DNA elements in the human genome		5
2	Global reference mapping and dynamics of human transcription factor footprints		3
1	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations.. <i>Genome Biology</i> , 2022 , 23, 13	18.3	1