

# Eric Haugen

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

16,113  
citations

136740

32  
h-index

288905

40  
g-index

46  
all docs

46  
docs citations

46  
times ranked

28249  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	3.8	19
2	Differences in nanoscale organization of regulatory active and inactive human chromatin. <i>Biophysical Journal</i> , 2022, 121, 977-990.	0.2	6
3	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
4	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736.	13.7	228
5	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	13.7	207
6	Single-molecule regulatory architectures captured by chromatin fiber sequencing. <i>Science</i> , 2020, 368, 1449-1454.	6.0	106
7	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. <i>EBioMedicine</i> , 2019, 41, 427-442.	2.7	26
8	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
9	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.	1.0	10
10	Epigenetic Regulation by Chromatin Activation Mark H3K4me3 in Primate Progenitor Cells within Adult Neurogenic Niche. <i>Scientific Reports</i> , 2015, 4, 5371.	1.6	45
11	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. <i>Nature Genetics</i> , 2015, 47, 1393-1401.	9.4	202
12	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A. thaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	2.9	249
13	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. <i>Nature Biotechnology</i> , 2014, 32, 71-75.	9.4	120
14	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	13.7	211
15	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
16	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	6.0	244
17	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	13.5	329
18	Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution. <i>Science</i> , 2013, 342, 1367-1372.	6.0	267

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19	Polymyxin Resistance of <i>Pseudomonas aeruginosa</i> phoQ Mutants Is Dependent on Additional Two-Component Regulatory Systems. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 2204-2215.	1.4	114
20	Genome Sequence of <i>Francisella tularensis</i> subspecies <i>holarctica</i> Strain FSC200, Isolated from a Child with Tularemia. <i>Journal of Bacteriology</i> , 2012, 194, 6965-6966.	1.0	34
21	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920.	1.8	840
22	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	13.7	715
23	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. <i>Science</i> , 2012, 337, 1190-1195.	6.0	3,129
24	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	13.7	2,434
25	Evolution of <i>Burkholderia pseudomallei</i> in Recurrent Melioidosis. <i>PLoS ONE</i> , 2012, 7, e36507.	1.1	96
26	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	13.5	716
27	ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: <i>AUREOCOCCUS ANOPHAGEFFERENS</i> CCMP1984 AND <i>AUREOUMBRA LAGUNENSIS</i> CCMP1507 <sup>1</sup> . <i>Journal of Phycology</i> , 2010, 46, 602-615.	1.0	32
28	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.	1.1	204
29	Analysis of the Genome of the <i>Escherichia coli</i> O157:H7 2006 Spinach-Associated Outbreak Isolate Indicates Candidate Genes That May Enhance Virulence. <i>Infection and Immunity</i> , 2009, 77, 3713-3721.	1.0	163
30	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	13.7	983
31	Closing gaps in the human genome with fosmid resources generated from multiple individuals. <i>Nature Genetics</i> , 2008, 40, 96-101.	9.4	50
32	Large-insert genome analysis technology detects structural variation in <i>Pseudomonas aeruginosa</i> clinical strains from cystic fibrosis patients. <i>Genomics</i> , 2008, 91, 530-537.	1.3	22
33	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.	13.9	245
34	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	13.7	53
35	Potential Source of <i>Francisella tularensis</i> Live Vaccine Strain Attenuation Determined by Genome Comparison. <i>Infection and Immunity</i> , 2006, 74, 6895-6906.	1.0	83
36	Fine-scale structural variation of the human genome. <i>Nature Genetics</i> , 2005, 37, 727-732.	9.4	897

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37	Ancient haplotypes of the HLA Class II region. <i>Genome Research</i> , 2005, 15, 1250-1257.	2.4	54
38	Targeted, haplotype-resolved resequencing of long segments of the human genome. <i>Genomics</i> , 2005, 86, 759-766.	1.3	23
39	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	13.7	236
40	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, 14339-14344.	3.3	1,017