

Eric Haugen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1170374/publications.pdf>

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	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. <i>Science</i> , 2012, 337, 1190-1195.	6.0	3,129
2	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	13.7	2,434
3	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
4	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
5	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	13.7	983
6	Fine-scale structural variation of the human genome. <i>Nature Genetics</i> , 2005, 37, 727-732.	9.4	897
7	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920.	1.8	840
8	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	13.5	716
9	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	13.7	715
10	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	13.5	329
11	Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution. <i>Science</i> , 2013, 342, 1367-1372.	6.0	267
12	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in <i>A.Âthaliana</i> . <i>Cell Reports</i> , 2014, 8, 2015-2030.	2.9	249
13	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
14	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	6.0	244
15	The DNA sequence of human chromosome 7. <i>Nature</i> , 2003, 424, 157-164.	13.7	236
16	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736.	13.7	228
17	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	13.7	211
18	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	13.7	207

#	ARTICLE	IF	CITATIONS
19	Methylobacterium Genome Sequences: A Reference Blueprint to Investigate Microbial Metabolism of C1 Compounds from Natural and Industrial Sources. PLoS ONE, 2009, 4, e5584.	1.1	204
20	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. Nature Genetics, 2015, 47, 1393-1401.	9.4	202
21	Analysis of the Genome of the <i>Escherichia coli</i> O157:H7 2006 Spinach-Associated Outbreak Isolate Indicates Candidate Genes That May Enhance Virulence. Infection and Immunity, 2009, 77, 3713-3721.	1.0	163
22	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
23	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. Nature Biotechnology, 2014, 32, 71-75.	9.4	120
24	Polymyxin Resistance of <i>Pseudomonas aeruginosa</i> <i>phoQ</i> Mutants Is Dependent on Additional Two-Component Regulatory Systems. Antimicrobial Agents and Chemotherapy, 2013, 57, 2204-2215.	1.4	114
25	52 Genetic Loci Influencing Myocardial Mass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
26	Single-molecule regulatory architectures captured by chromatin fiber sequencing. Science, 2020, 368, 1449-1454.	6.0	106
27	Evolution of <i>Burkholderia pseudomallei</i> in Recurrent Melioidosis. PLoS ONE, 2012, 7, e36507.	1.1	96
28	Potential Source of <i>Francisella tularensis</i> Live Vaccine Strain Attenuation Determined by Genome Comparison. Infection and Immunity, 2006, 74, 6895-6906.	1.0	83
29	Ancient haplotypes of the HLA Class II region. Genome Research, 2005, 15, 1250-1257.	2.4	54
30	The DNA sequence, annotation and analysis of human chromosome 3. Nature, 2006, 440, 1194-1198.	13.7	53
31	Closing gaps in the human genome with fosmid resources generated from multiple individuals. Nature Genetics, 2008, 40, 96-101.	9.4	50
32	Epigenetic Regulation by Chromatin Activation Mark H3K4me3 in Primate Progenitor Cells within Adult Neurogenic Niche. Scientific Reports, 2015, 4, 5371.	1.6	45
33	Genome Sequence of <i>Francisella tularensis</i> subspecies <i>holarctica</i> Strain FSC200, Isolated from a Child with Tularemia. Journal of Bacteriology, 2012, 194, 6965-6966.	1.0	34
34	ANALYSES OF THE COMPLETE CHLOROPLAST GENOME SEQUENCES OF TWO MEMBERS OF THE PELAGOPHYCEAE: <i>Aureococcus anophagefferens</i> CCMP1984 AND <i>Aureocymbra lagunensis</i> CCMP1507. Journal of Phycology, 2010, 46, 602-615.	1.0	32
35	Integrated epigenomic profiling reveals endogenous retrovirus reactivation in renal cell carcinoma. EBioMedicine, 2019, 41, 427-442.	2.7	26
36	Targeted, haplotype-resolved resequencing of long segments of the human genome. Genomics, 2005, 86, 759-766.	1.3	23

#	ARTICLE	IF	CITATIONS
37	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
38	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	3.8	19
39	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
40	Differences in nanoscale organization of regulatory active and inactive human chromatin. <i>Biophysical Journal</i> , 2022, 121, 977-990.	0.2	6