

Jeff Vierstra

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/673039/publications.pdf>

Version: 2024-02-01

22
papers

7,950
citations

430442

18
h-index

676716

22
g-index

25
all docs

25
docs citations

25
times ranked

16067
citing authors

#	ARTICLE	IF	CITATIONS
1	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	13.7	2,434
2	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
3	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920.	1.8	840
4	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	13.7	715
5	An Erythroid Enhancer of <i>BCL11A</i> Subject to Genetic Variation Determines Fetal Hemoglobin Level. <i>Science</i> , 2013, 342, 253-257.	6.0	518
6	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554.	13.5	342
7	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	6.0	244
8	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736.	13.7	228
9	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	13.7	211
10	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	13.7	207
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	Functional footprinting of regulatory DNA. <i>Nature Methods</i> , 2015, 12, 927-930.	9.0	123
13	Personal and population genomics of human regulatory variation. <i>Genome Research</i> , 2012, 22, 1689-1697.	2.4	98
14	Genomic footprinting. <i>Nature Methods</i> , 2016, 13, 213-221.	9.0	97
15	Genome-scale Mapping of DNase I Hypersensitivity. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 21.27.	2.9	82
16	DNase I hypersensitivity analysis of the mouse brain and retina identifies region-specific regulatory elements. <i>Epigenetics and Chromatin</i> , 2015, 8, 8.	1.8	60
17	Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. <i>Nature Methods</i> , 2014, 11, 66-72.	9.0	58
18	Methylated Cytosines Mutate to Transcription Factor Binding Sites that Drive Tetrapod Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 3155-3169.	1.1	20

#	ARTICLE	IF	CITATIONS
19	Discrete regulatory modules instruct hematopoietic lineage commitment and differentiation. Nature Communications, 2021, 12, 6790.	5.8	6
20	53. From GWAS To the Clinic: Genome-Editing the Human BCL11A Erythroid Enhancer for Fetal Globin Elevation in the Hemoglobinopathies. Molecular Therapy, 2015, 23, S23-S24.	3.7	2
21	Unbiased phenotypic identification of functionally distinct hematopoietic progenitors. Journal of Biological Research, 2019, 26, 4.	2.2	2
22	Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. Blood, 2013, 122, 437-437.	0.6	1