

John A Stamatoyannopoulos

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

28,768
citations

81900

39
h-index

197818

49
g-index

56
all docs

56
docs citations

56
times ranked

40709
citing authors

#	ARTICLE	IF	CITATIONS
1	Myasthenia gravis genome-wide association study implicates AGRN as a risk locus. <i>Journal of Medical Genetics</i> , 2022, 59, 801-809.	3.2	5
2	Differences in nanoscale organization of regulatory active and inactive human chromatin. <i>Biophysical Journal</i> , 2022, 121, 977-990.	0.5	6
3	Inaccessible LCG Promoters Act as Safeguards to Restrict T Cell Development to Appropriate Notch Signaling Environments. <i>Stem Cell Reports</i> , 2021, 16, 717-726.	4.8	0
4	Tissue context determines the penetrance of regulatory DNA variation. <i>Nature Communications</i> , 2021, 12, 2850.	12.8	13
5	Discrete regulatory modules instruct hematopoietic lineage commitment and differentiation. <i>Nature Communications</i> , 2021, 12, 6790.	12.8	6
6	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
7	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
8	Global reference mapping of human transcription factor footprints. <i>Nature</i> , 2020, 583, 729-736.	27.8	228
9	Index and biological spectrum of human DNase I hypersensitive sites. <i>Nature</i> , 2020, 584, 244-251.	27.8	207
10	De novo design of protein logic gates. <i>Science</i> , 2020, 368, 78-84.	12.6	151
11	Single-molecule regulatory architectures captured by chromatin fiber sequencing. <i>Science</i> , 2020, 368, 1449-1454.	12.6	106
12	Genetic history of the population of Crete. <i>Annals of Human Genetics</i> , 2019, 83, 373-388.	0.8	2
13	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	27.8	203
14	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 1465-1474.	5.6	20
15	Cross-Platform DNA Encoding for Single-Cell Imaging of Gene Expression. <i>Angewandte Chemie</i> , 2016, 128, 9121-9124.	2.0	0
16	Genomic footprinting. <i>Nature Methods</i> , 2016, 13, 213-221.	19.0	97
17	APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. <i>Cell Reports</i> , 2015, 13, 1103-1109.	6.4	80
18	Taking Stock of Regulatory Variation. <i>Cell Systems</i> , 2015, 1, 18-21.	6.2	4

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19	Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. <i>PLoS Genetics</i> , 2015, 11, e1005573.	3.5	16
20	Role of DNA Methylation in Modulating Transcription Factor Occupancy. <i>Cell Reports</i> , 2015, 12, 1184-1195.	6.4	249
21	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
22	Cell-of-origin chromatin organization shapes the mutational landscape of cancer. <i>Nature</i> , 2015, 518, 360-364.	27.8	491
23	Genomic discovery of potent chromatin insulators for human gene therapy. <i>Nature Biotechnology</i> , 2015, 33, 198-203.	17.5	98
24	2p15-p16.1 microdeletions encompassing and proximal to BCL11A are associated with elevated HbF in addition to neurologic impairment. <i>Blood</i> , 2015, 126, 89-93.	1.4	62
25	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. <i>Cell</i> , 2015, 161, 541-554.	28.9	342
26	Methylated Cytosines Mutate to Transcription Factor Binding Sites that Drive Tetrapod Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 3155-3169.	2.5	20
27	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. <i>Nature Genetics</i> , 2015, 47, 1393-1401.	21.4	202
28	Functional footprinting of regulatory DNA. <i>Nature Methods</i> , 2015, 12, 927-930.	19.0	123
29	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	7.1	635
30	Coupling transcription factor occupancy to nucleosome architecture with DNase-FLASH. <i>Nature Methods</i> , 2014, 11, 66-72.	19.0	58
31	Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. <i>Nature Biotechnology</i> , 2014, 32, 71-75.	17.5	120
32	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	27.8	211
33	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	12.6	244
34	Maritime route of colonization of Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9211-9216.	7.1	71
35	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	28.9	329
36	Genome-scale Mapping of DNase I Hypersensitivity. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 21.27.	2.9	82

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37	Probing DNA shape and methylation state on a genomic scale with DNase I. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6376-6381.	7.1	151
38	Widespread Site-Dependent Buffering of Human Regulatory Polymorphism. PLoS Genetics, 2012, 8, e1002599.	3.5	65
39	Personal and population genomics of human regulatory variation. Genome Research, 2012, 22, 1689-1697.	5.5	98
40	BEDOPS: high-performance genomic feature operations. Bioinformatics, 2012, 28, 1919-1920.	4.1	840
41	An expansive human regulatory lexicon encoded in transcription factor footprints. Nature, 2012, 489, 83-90.	27.8	715
42	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. Science, 2012, 337, 1190-1195.	12.6	3,129
43	Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. Cell, 2012, 150, 1274-1286.	28.9	451
44	The accessible chromatin landscape of the human genome. Nature, 2012, 489, 75-82.	27.8	2,434
45	Dynamic Exchange at Regulatory Elements during Chromatin Remodeling Underlies Assisted Loading Mechanism. Cell, 2011, 146, 544-554.	28.9	282
46	Chromatin accessibility pre-determines glucocorticoid receptor binding patterns. Nature Genetics, 2011, 43, 264-268.	21.4	854
47	Human mutation rate associated with DNA replication timing. Nature Genetics, 2009, 41, 393-395.	21.4	371
48	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. Nature Methods, 2009, 6, 283-289.	19.0	533
49	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	12.6	7,170
50	Discovery of functional noncoding elements by digital analysis of chromatin structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16837-16842.	7.1	135