James P Noonan

List of Publications by Year
in descending order

40 papers	6,421 citations	196777 29 h-index	325983 40 g-index
49 all docs	49 docs citations	49 times ranked	12286 citing authors

#	Article	IF	Citations
1	Modeling uniquely human gene regulatory function via targeted humanization of the mouse genome. Nature Communications, 2022, 13, 304.	5.8	16
2	Massively parallel discovery of human-specific substitutions that alter enhancer activity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	67
3	Evidence against tetrapod-wide digit identities and for a limited frame shift in bird wings. Nature Communications, 2019, 10, 3244.	5.8	17
4	Genome‐wide analysis of the regulation of Cu metabolism in *Cryptococcus neoformans*. Molecular Microbiology, 2018, 108, 473-494.	1.2	34
5	High-Resolution Epigenomic Atlas of Human Embryonic Craniofacial Development. Cell Reports, 2018, 23, 1581-1597.	2.9	111
6	Disrupting the three-dimensional regulatory topology of the *Pitx1* locus results in overtly normal development. Development (Cambridge), 2018, 145, .	1.2	14
7	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
8	Marked Diversity of Unique Cortical Enhancers Enables Neuron-Specific Tools by Enhancer-Driven Gene Expression. Current Biology, 2018, 28, 2103-2114.e5.	1.8	66
9	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. American Journal of Human Genetics, 2018, 102, 1031-1047.	2.6	26
10	Molecular and cellular reorganization of neural circuits in the human lineage. Science, 2017, 358, 1027-1032.	6.0	192
11	Evolution of Gene Regulation in Humans. Annual Review of Genomics and Human Genetics, 2016, 17, 45-67.	2.5	52
12	Origin and evolution of developmental enhancers in the mammalian neocortex. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2617-26.	3.3	95
13	Evolutionary changes in promoter and enhancer activity during human corticogenesis. Science, 2015, 347, 1155-1159.	6.0	258
14	Chromatin Immunoprecipitation with Fixed Animal Tissues and Preparation for High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.prot084848.	0.2	25
15	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	5.8	316
16	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	2.6	111
17	Genomic Analysis of Non- *NF2* Meningiomas Reveals Mutations in *TRAF7* , *KLF4* , *AKT1* , and *SMO*. Science, 2013, 339, 1077-1080.	6.0	714
18	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825

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19	The Evolution of Lineage-Specific Regulatory Activities in the Human Embryonic Limb. Cell, 2013, 154, 185-196.	13.5	202
20	The genomic landscape of cohesin-associated chromatin interactions. Genome Research, 2013, 23, 1224-1234.	2.4	103
21	Genomic Correlates of Relationship QTL Involved in Fore- versus Hind Limb Divergence in Mice. Genome Biology and Evolution, 2013, 5, 1926-1936.	1.1	16
22	RNA-Seq Profiling of Spinal Cord Motor Neurons from a Presymptomatic SOD1 ALS Mouse. PLoS ONE, 2013, 8, e53575.	1.1	62
23	Time Course RNA-seq: A Potential Avenue with Somewhat Different Approach in Tandem of Differential Analysis. , 2012, , .		0
24	Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. Genome Research, 2012, 22, 1069-1080.	2.4	121
25	Transcriptional programs in transient embryonic zones of the cerebral cortex defined by high-resolution mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14950-14955.	3.3	144
26	Construction and maintenance of randomized retroviral expression libraries for transmembrane protein engineering. Protein Engineering, Design and Selection, 2011, 24, 311-320.	1.0	6
27	Gene regulation and the origins of human biological uniqueness. Trends in Genetics, 2010, 26, 110-118.	2.9	41
28	Neanderthal genomics and the evolution of modern humans: Figure 1.. Genome Research, 2010, 20, 547-553.	2.4	33
29	Genomics of Long-Range Regulatory Elements. Annual Review of Genomics and Human Genetics, 2010, 11, 1-23.	2.5	139
30	Regulatory DNAs and the evolution of human development. Current Opinion in Genetics and Development, 2009, 19, 557-564.	1.5	11
31	Human-Specific Gain of Function in a Developmental Enhancer. Science, 2008, 321, 1346-1350.	6.0	330
32	Sequencing and Analysis of Neanderthal Genomic DNA. Science, 2006, 314, 1113-1118.	6.0	547
33	Accelerated Evolution of Conserved Noncoding Sequences in Humans. Science, 2006, 314, 786-786.	6.0	395
34	Genomic Sequencing of Pleistocene Cave Bears. Science, 2005, 309, 597-599.	6.0	221
35	Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. Genome Research, 2004, 14, 2397-2405.	2.4	70
36	The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274.	13.7	102

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37	Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. Genome Research, 2004, 14, 354-366.	2.4	100
38	Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin α Cluster. American Journal of Human Genetics, 2003, 72, 621-635.	2.6	51
39	Comparative DNA Sequence Analysis of Mouse and Human Protocadherin Gene Clusters. Genome Research, 2001, 11, 389-404.	2.4	224
40	High Resolution Epigenomic Atlas of Human Embryonic Craniofacial Development. SSRN Electronic Journal, 0, , .	0.4	0