

# Len A Pennacchio

## List of Publications by Year in descending order

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154  
papers

34,259  
citations

6486

82  
h-index

7427

157  
g-index

177  
all docs

177  
docs citations

177  
times ranked

46177  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation in PNPLA3 confers susceptibility to nonalcoholic fatty liver disease. <i>Nature Genetics</i> , 2008, 40, 1461-1465.	9.4	2,764
2	A Common Allele on Chromosome 9 Associated with Coronary Heart Disease. <i>Science</i> , 2007, 316, 1488-1491.	6.0	1,591
3	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	13.7	1,526
4	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	13.7	1,496
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
6	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	6.0	1,135
7	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	13.7	1,072
8	VISTA Enhancer Browser--a database of tissue-specific human enhancers. <i>Nucleic Acids Research</i> , 2007, 35, D88-D92.	6.5	950
9	Dicer, Drosha, and Outcomes in Patients with Ovarian Cancer. <i>New England Journal of Medicine</i> , 2008, 359, 2641-2650.	13.9	633
10	Gain-of-function RAF1 mutations cause Noonan and LEOPARD syndromes with hypertrophic cardiomyopathy. <i>Nature Genetics</i> , 2007, 39, 1007-1012.	9.4	624
11	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17921-17926.	3.3	606
12	Genomic views of distant-acting enhancers. <i>Nature</i> , 2009, 461, 199-205.	13.7	549
13	Most Rare Missense Alleles Are Deleterious in Humans: Implications for Complex Disease and Association Studies. <i>American Journal of Human Genetics</i> , 2007, 80, 727-739.	2.6	547
14	Gain-of-function SOS1 mutations cause a distinctive form of Noonan syndrome. <i>Nature Genetics</i> , 2007, 39, 75-79.	9.4	523
15	Enhancer redundancy provides phenotypic robustness in mammalian development. <i>Nature</i> , 2018, 554, 239-243.	13.7	514
16	Population-based resequencing of ANGPTL4 uncovers variations that reduce triglycerides and increase HDL. <i>Nature Genetics</i> , 2007, 39, 513-516.	9.4	473
17	Massively parallel functional dissection of mammalian enhancers in vivo. <i>Nature Biotechnology</i> , 2012, 30, 265-270.	9.4	468
18	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456

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19	Enhancers: five essential questions. <i>Nature Reviews Genetics</i> , 2013, 14, 288-295.	7.7	455
20	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. <i>Nature</i> , 2010, 464, 409-412.	13.7	425
21	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	9.4	395
22	Disruption of an AP-2 binding site in an IRF6 enhancer is associated with cleft lip. <i>Nature Genetics</i> , 2008, 40, 1341-1347.	9.4	382
23	Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. <i>Nature Genetics</i> , 2009, 41, 1022-1026.	9.4	358
24	Two independent apolipoprotein A5 haplotypes influence human plasma triglyceride levels. <i>Human Molecular Genetics</i> , 2002, 11, 3031-3038.	1.4	352
25	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348
26	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. <i>Cell</i> , 2013, 155, 1521-1531.	13.5	342
27	Genomic strategies to identify mammalian regulatory sequences. <i>Nature Reviews Genetics</i> , 2001, 2, 100-109.	7.7	341
28	Relative contribution of variation within the APOC3/A4/A5 gene cluster in determining plasma triglycerides. <i>Human Molecular Genetics</i> , 2002, 11, 3039-3046.	1.4	335
29	Progressive ataxia, myoclonic epilepsy and cerebellar apoptosis in cystatin B-deficient mice. <i>Nature Genetics</i> , 1998, 20, 251-258.	9.4	332
30	Human-Specific Gain of Function in a Developmental Enhancer. <i>Science</i> , 2008, 321, 1346-1350.	6.0	330
31	Rare loss-of-function mutations in ANGPTL family members contribute to plasma triglyceride levels in humans. <i>Journal of Clinical Investigation</i> , 2009, 119, 70-9.	3.9	322
32	Genetic dissection of the $\beta$ -globin super-enhancer in vivo. <i>Nature Genetics</i> , 2016, 48, 895-903.	9.4	308
33	Genomic Patterns of De Novo Mutation in Simplex Autism. <i>Cell</i> , 2017, 171, 710-722.e12.	13.5	308
34	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. <i>Cell</i> , 2008, 135, 1053-1064.	13.5	306
35	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. <i>Nature Genetics</i> , 2008, 40, 158-160.	9.4	299
36	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	13.7	298

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37	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018, 21, 432-439.	7.1	290
38	Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16224-16229.	3.3	285
39	Cathepsin L is required for endothelial progenitor cell-induced neovascularization. <i>Nature Medicine</i> , 2005, 11, 206-213.	15.2	278
40	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. <i>Cell</i> , 2016, 167, 633-642.e11.	13.5	275
41	A restricted spectrum of NRAS mutations causes Noonan syndrome. <i>Nature Genetics</i> , 2010, 42, 27-29.	9.4	271
42	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259
43	Large-scale discovery of enhancers from human heart tissue. <i>Nature Genetics</i> , 2012, 44, 89-93.	9.4	257
44	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
45	Deletion of Ultraconserved Elements Yields Viable Mice. <i>PLoS Biology</i> , 2007, 5, e234.	2.6	255
46	Apolipoprotein AV Accelerates Plasma Hydrolysis of Triglyceride-rich Lipoproteins by Interaction with Proteoglycan-bound Lipoprotein Lipase. <i>Journal of Biological Chemistry</i> , 2005, 280, 21553-21560.	1.6	253
47	A High-Resolution Enhancer Atlas of the Developing Telencephalon. <i>Cell</i> , 2013, 152, 895-908.	13.5	241
48	Germline Chd8 haploinsufficiency alters brain development in mouse. <i>Nature Neuroscience</i> , 2017, 20, 1062-1073.	7.1	210
49	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. <i>Science</i> , 2013, 342, 1241006.	6.0	209
50	Unstable minisatellite expansion causing recessively inherited myoclonus epilepsy, EPM1. <i>Nature Genetics</i> , 1997, 15, 393-396.	9.4	207
51	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. <i>Genome Research</i> , 2010, 20, 565-577.	2.4	203
52	Medical Sequencing at the Extremes of Human Body Mass. <i>American Journal of Human Genetics</i> , 2007, 80, 779-791.	2.6	199
53	Apolipoprotein A5, a Crucial Determinant of Plasma Triglyceride Levels, Is Highly Responsive to Peroxisome Proliferator-activated Receptor $\delta$ Activators. <i>Journal of Biological Chemistry</i> , 2003, 278, 17982-17985.	1.6	186
54	Mechanism of triglyceride lowering in mice expressing human apolipoprotein A5. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 397-404.	1.0	183

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55	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	3.5	173
56	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	13.5	169
57	Close sequence comparisons are sufficient to identify human cis-regulatory elements. <i>Genome Research</i> , 2006, 16, 855-863.	2.4	164
58	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	13.7	156
59	Apolipoprotein A5, a Newly Identified Gene That Affects Plasma Triglyceride Levels in Humans and Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2003, 23, 529-534.	1.1	150
60	Apoa5 Q139X truncation predisposes to late-onset hyperchylomicronemia due to lipoprotein lipase impairment. <i>Journal of Clinical Investigation</i> , 2005, 115, 2862-2869.	3.9	147
61	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. <i>Nature Communications</i> , 2014, 5, 4907.	5.8	142
62	Dlx1&2-Dependent Expression of Zfhx1b (Sip1, Zeb2) Regulates the Fate Switch between Cortical and Striatal Interneurons. <i>Neuron</i> , 2013, 77, 83-98.	3.8	140
63	Directed Evolution of Ionizing Radiation Resistance in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5240-5252.	1.0	131
64	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	131
65	Apolipoprotein A-V Deficiency Results in Marked Hypertriglyceridemia Attributable to Decreased Lipolysis of Triglyceride-Rich Lipoproteins and Removal of Their Remnants. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2005, 25, 2573-2579.	1.1	125
66	Functional importance of cardiac enhancer-associated noncoding RNAs in heart development and disease. <i>Journal of Molecular and Cellular Cardiology</i> , 2014, 76, 55-70.	0.9	124
67	Predicting tissue-specific enhancers in the human genome. <i>Genome Research</i> , 2007, 17, 201-211.	2.4	117
68	A large genomic deletion leads to enhancer adoption by the lamin B1 gene: a second path to autosomal dominant adult-onset demyelinating leukodystrophy (ADLD). <i>Human Molecular Genetics</i> , 2015, 24, 3143-3154.	1.4	117
69	A Cryptochrome 2 mutation yields advanced sleep phase in humans. <i>ELife</i> , 2016, 5, .	2.8	114
70	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
71	Association of functionally significant Melanocortin-4 but not Melanocortin-3 receptor mutations with severe adult obesity in a large North American case-control study. <i>Human Molecular Genetics</i> , 2009, 18, 1140-1147.	1.4	112
72	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. <i>Cell</i> , 2016, 167, 355-368.e10.	13.5	112

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73	Comparative genomic analysis as a tool for biological discovery. <i>Journal of Physiology</i> , 2004, 554, 31-39.	1.3	105
74	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. <i>PLoS Genetics</i> , 2014, 10, e1004610.	1.5	105
75	Cathepsin B but not cathepsins L or S contributes to the pathogenesis of Unverricht-Lundborg progressive myoclonus epilepsy (EPM1). <i>Journal of Neurobiology</i> , 2003, 56, 315-327.	3.7	102
76	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004, 431, 268-274.	13.7	102
77	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. <i>Epigenetics and Chromatin</i> , 2015, 8, 16.	1.8	100
78	Comprehensive In Vivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. <i>Cell</i> , 2020, 180, 1262-1271.e15.	13.5	100
79	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. <i>Neuron</i> , 2014, 82, 989-1003.	3.8	99
80	Lack of MEF2A mutations in coronary artery disease. <i>Journal of Clinical Investigation</i> , 2005, 115, 1016-1020.	3.9	99
81	Linkage and Association Between Distinct Variants of the APOA1/C3/A4/A5 Gene Cluster and Familial Combined Hyperlipidemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 167-174.	1.1	97
82	Enhancer identification through comparative genomics. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 140-152.	2.3	97
83	Haplotype analysis of the apolipoprotein gene cluster on human chromosome 11. <i>Genomics</i> , 2004, 83, 912-923.	1.3	95
84	Array comparative genomic hybridization in patients with congenital diaphragmatic hernia: mapping of four CDH-critical regions and sequencing of candidate genes at 15q26.1-15q26.2. <i>European Journal of Human Genetics</i> , 2006, 14, 999-1008.	1.4	91
85	Insulin-Mediated Down-Regulation of Apolipoprotein A5 Gene Expression through the Phosphatidylinositol 3-Kinase Pathway: Role of Upstream Stimulatory Factor. <i>Molecular and Cellular Biology</i> , 2005, 25, 1537-1548.	1.1	88
86	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
87	Genome-wide compendium and functional assessment of in vivo heart enhancers. <i>Nature Communications</i> , 2016, 7, 12923.	5.8	83
88	Brg1 modulates enhancer activation in mesoderm lineage commitment. <i>Development (Cambridge)</i> , 2015, 142, 1418-30.	1.2	81
89	Gain-of-Function R225W Mutation in Human AMPK $\beta$ 3 Causing Increased Glycogen and Decreased Triglyceride in Skeletal Muscle. <i>PLoS ONE</i> , 2007, 2, e903.	1.1	80
90	Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. <i>ELife</i> , 2014, 3, e01322.	2.8	80

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91	Association of common variants in the Joubert syndrome gene (AHI1) with autism. <i>Human Molecular Genetics</i> , 2008, 17, 3887-3896.	1.4	79
92	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1633-E1640.	3.3	78
93	In vivo characterization of a vertebrate ultraconserved enhancer. <i>Genomics</i> , 2005, 85, 774-781.	1.3	77
94	The Liver X Receptor Ligand T0901317 Down-regulates APOA5 Gene Expression through Activation of SREBP-1c. <i>Journal of Biological Chemistry</i> , 2004, 279, 45462-45469.	1.6	76
95	Analysis of Apolipoprotein A5, C3, and Plasma Triglyceride Concentrations in Genetically Engineered Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 1297-1302.	1.1	76
96	Neuropathological Changes in a Mouse Model of Progressive Myoclonus Epilepsy: Cystatin B Deficiency and Unverricht-Lundborg Disease. <i>Journal of Neuropathology and Experimental Neurology</i> , 2002, 61, 1085-1091.	0.9	72
97	Apolipoprotein AIV Gene Variant S347 Is Associated With Increased Risk of Coronary Heart Disease and Lower Plasma Apolipoprotein AIV Levels. <i>Circulation Research</i> , 2003, 92, 969-975.	2.0	71
98	Function-based identification of mammalian enhancers using site-specific integration. <i>Nature Methods</i> , 2014, 11, 566-571.	9.0	71
99	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020, 17, 807-814.	9.0	71
100	Identification of Novel Craniofacial Regulatory Domains Located far Upstream of <i>SOX9</i> and Disrupted in Pierre Robin Sequence. <i>Human Mutation</i> , 2014, 35, 1011-1020.	1.1	69
101	Insights from human/mouse genome comparisons. <i>Mammalian Genome</i> , 2003, 14, 429-436.	1.0	68
102	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>Cell Reports</i> , 2019, 28, 2048-2063.e8.	2.9	68
103	Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. <i>Human Mutation</i> , 2015, 36, 1080-1087.	1.1	67
104	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014, 24, 920-929.	2.4	63
105	Comparative genomic tools and databases: providing insights into the human genome. <i>Journal of Clinical Investigation</i> , 2003, 111, 1099-1106.	3.9	60
106	Massively parallel sequencing identifies the gene <i>Megf8</i> with ENU-induced mutation causing heterotaxy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3219-3224.	3.3	57
107	Functional autonomy of distant-acting human enhancers. <i>Genomics</i> , 2009, 93, 509-513.	1.3	56
108	An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. <i>Human Molecular Genetics</i> , 2014, 23, 2711-2720.	1.4	55

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109	Relationship between genetic variation at PPP1R3B and levels of liver glycogen and triglyceride. <i>Hepatology</i> , 2018, 67, 2182-2195.	3.6	51
110	Transcriptional Regulation of Apolipoprotein A5 Gene Expression by the Nuclear Receptor ROR $\alpha$ . <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2005, 25, 1186-1192.	1.1	50
111	TIMELESS mutation alters phase responsiveness and causes advanced sleep phase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12045-12053.	3.3	50
112	Human cathepsin L rescues the neurodegeneration and lethality in cathepsin B/L double-deficient mice. <i>Biological Chemistry</i> , 2006, 387, 885-891.	1.2	49
113	Lack of Support for the Association between GAD2 Polymorphisms and Severe Human Obesity. <i>PLoS Biology</i> , 2005, 3, e315.	2.6	44
114	Presynaptic Homeostasis Opposes Disease Progression in Mouse Models of ALS-Like Degeneration: Evidence for Homeostatic Neuroprotection. <i>Neuron</i> , 2020, 107, 95-111.e6.	3.8	43
115	Dynamic BAF chromatin remodeling complex subunit inclusion promotes temporally distinct gene expression programs in cardiogenesis. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	39
116	Ultraconserved enhancer function does not require perfect sequence conservation. <i>Nature Genetics</i> , 2021, 53, 521-528.	9.4	39
117	Genetic and functional analyses identify <i>DISC1</i> as a novel callosal agenesis candidate gene. <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 1865-1876.	0.7	38
118	ATAC-Seq Reveals an <i>Isl1</i> Enhancer That Regulates Sinoatrial Node Development and Function. <i>Circulation Research</i> , 2020, 127, 1502-1518.	2.0	35
119	Congenital Heart Defects in Patients with Deletions Upstream of <i>SOX9</i> . <i>Human Mutation</i> , 2013, 34, 1628-1631.	1.1	33
120	Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. <i>Development (Cambridge)</i> , 2015, 142, 4092-4106.	1.2	30
121	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. <i>American Journal of Human Genetics</i> , 2018, 103, 874-892.	2.6	30
122	A Genetic Signature of Spina Bifida Risk from Pathway-Informed Comprehensive Gene-Variant Analysis. <i>PLoS ONE</i> , 2011, 6, e28408.	1.1	29
123	A PYY Q62P variant linked to human obesity. <i>Human Molecular Genetics</i> , 2006, 15, 387-391.	1.4	28
124	Use of "MGE Enhancers" for Labeling and Selection of Embryonic Stem Cell-Derived Medial Ganglionic Eminence (MGE) Progenitors and Neurons. <i>PLoS ONE</i> , 2013, 8, e61956.	1.1	28
125	Identification of a novel enhancer of brain expression near the apoE gene cluster by comparative genomics. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1676, 41-50.	2.4	26
126	Generation of Long Insert Pairs Using a Cre-LoxP Inverse PCR Approach. <i>PLoS ONE</i> , 2012, 7, e29437.	1.1	26



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127	Haplotypes in the APOA1-C3-A4-A5 gene cluster affect plasma lipids in both humans and baboons. <i>Human Molecular Genetics</i> , 2004, 13, 1049-1056.	1.4	25
128	In vivo characterization of human APOA5 haplotypes. <i>Genomics</i> , 2007, 90, 674-679.	1.3	25
129	Transcriptional network orchestrating regional patterning of cortical progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
130	Noncoding deletions reveal a gene that is critical for intestinal function. <i>Nature</i> , 2019, 571, 107-111.	13.7	24
131	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. <i>Communications Biology</i> , 2021, 4, 1302.	2.0	21
132	Comparative genomic tools and databases: providing insights into the human genome. <i>Journal of Clinical Investigation</i> , 2003, 111, 1099-1106.	3.9	20
133	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. <i>Methods in Molecular Biology</i> , 2022, 2403, 147-186.	0.4	20
134	Reactivation of a developmentally silenced embryonic globin gene. <i>Nature Communications</i> , 2021, 12, 4439.	5.8	19
135	Characterization of the human neurocan gene, CSPG3. <i>Gene</i> , 1998, 221, 199-205.	1.0	18
136	The INSIG2 rs7566605 genetic variant does not play a major role in obesity in a sample of 24,722 individuals from four cohorts. <i>BMC Medical Genetics</i> , 2009, 10, 56.	2.1	17
137	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. <i>PLoS Computational Biology</i> , 2017, 13, e1005720.	1.5	17
138	Comparative genomic analysis reveals a distant liver enhancer upstream of the COUP-TFII gene. <i>Mammalian Genome</i> , 2005, 16, 91-95.	1.0	16
139	Glucose Regulates the Expression of the Apolipoprotein A5 Gene. <i>Journal of Molecular Biology</i> , 2008, 380, 789-798.	2.0	16
140	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. <i>BMC Genomics</i> , 2012, 13, 713.	1.2	16
141	Coding and noncoding variants in EBF3 are involved in HADDs and simplex autism. <i>Human Genomics</i> , 2021, 15, 44.	1.4	16
142	Perfect and imperfect views of ultraconserved sequences. <i>Nature Reviews Genetics</i> , 2022, 23, 182-194.	7.7	16
143	Limits of sequence and functional conservation. <i>Nature Genetics</i> , 2010, 42, 557-558.	9.4	15
144	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. <i>Genome Medicine</i> , 2021, 13, 69.	3.6	15

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145	Single site-specific integration targeting coupled with embryonic stem cell differentiation provides a high-throughput alternative to in vivo enhancer analyses. <i>Biology Open</i> , 2013, 2, 1229-1238.	0.6	11
146	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. <i>Genome Biology</i> , 2019, 20, 140.	3.8	11
147	Structure, sequence and location of the UQCRFS1 gene for the human Rieske Fe-S protein. <i>Gene</i> , 1995, 155, 207-211.	1.0	10
148	Differential Etv2 threshold requirement for endothelial and erythropoietic development. <i>Cell Reports</i> , 2022, 39, 110881.	2.9	9
149	HAND transcription factors cooperatively specify the aorta and pulmonary trunk. <i>Developmental Biology</i> , 2021, 476, 1-10.	0.9	7
150	Contrasting Patterns of Sequence Evolution at the Functionally Redundant bric À brac Paralogs in <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 2009, 69, 194-202.	0.8	5
151	Comparative Genomics. <i>Methods in Molecular Biology</i> , 2007, 366, 229-251.	0.4	4
152	Comparative and functional analysis of cardiovascular-related genes. <i>Pharmacogenomics</i> , 2003, 4, 571-582.	0.6	1
153	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
154	Comparative Genomics: A Tool to Functionally Annotate Human DNA. , 0, , 229-252.		0