Len A Pennacchio

List of Publications by Year
in descending order

154	34,259	6486 82	7427 157
papers	citations	h-index	g-index

177	177	177	46177
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Perfect and imperfect views of ultraconserved sequences. Nature Reviews Genetics, 2022, 23, 182-194.	7.7	16
2	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in Molecular Biology, 2022, 2403, 147-186.	0.4	20
3	Differential Etv2 threshold requirement for endothelial and erythropoietic development. Cell Reports, 2022, 39, 110881.	2.9	9
4	Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528.	9.4	39
5	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. Genome Medicine, 2021, 13, 69.	3.6	15
6	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	5.8	19
7	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
8	HAND transcription factors cooperatively specify the aorta and pulmonary trunk. Developmental Biology, 2021, 476, 1-10.	0.9	7
9	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. Communications Biology, 2021, 4, 1302.	2.0	21
10	Transcriptional network orchestrating regional patterning of cortical progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
11	ATAC-Seq Reveals an Isl1 Enhancer That Regulates Sinoatrial Node Development and Function. Circulation Research, 2020, 127, 1502-1518.	2.0	35
12	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
13	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
14	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
15	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767.	13.7	131
16	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	9.0	71
17	Presynaptic Homeostasis Opposes Disease Progression in Mouse Models of ALS-Like Degeneration: Evidence for Homeostatic Neuroprotection. Neuron, 2020, 107, 95-111.e6.	3.8	43
18	Comprehensive InÂVivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. Cell, 2020, 180, 1262-1271.e15.	13.5	100

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19	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68
20	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. Genome Biology, 2019, 20, 140.	3.8	11
21	Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111.	13.7	24
22	TIMELESS mutation alters phase responsiveness and causes advanced sleep phase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12045-12053.	3.3	50
23	Dynamic BAF chromatin remodeling complex subunit inclusion promotes temporally distinct gene expression programs in cardiogenesis. Development (Cambridge), 2019, 146, .	1.2	39
24	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	7.1	290
25	Enhancer redundancy provides phenotypic robustness in mammalian development. Nature, 2018, 554, 239-243.	13.7	514
26	Ultraconserved Enhancers Are Required for Normal Development. Cell, 2018, 172, 491-499.e15.	13.5	169
27	Relationship between genetic variation at PPP1R3B and levels of liver glycogen and triglyceride. Hepatology, 2018, 67, 2182-2195.	3.6	51
28	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	2.6	30
29	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1633-E1640.	3.3	78
30	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	13.5	308
31	Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073.	7.1	210
32	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720.	1.5	17
33	Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903.	9.4	308
34	Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. Cell, 2016, 167, 355-368.e10.	13.5	112
35	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
36	Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923.	5.8	83

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37	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. Cell, 2016, 167, 633-642.e11.	13.5	275
38	The Epigenomic Landscape of Prokaryotes. PLoS Genetics, 2016, 12, e1005854.	1.5	348
39	A Cryptochrome 2 mutation yields advanced sleep phase in humans. ELife, 2016, 5, .	2.8	114
40	Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. Human Mutation, 2015, 36, 1080-1087.	1.1	67
41	Occupancy by key transcription factors is a more accurate predictor of enhancer activity than histone modifications or chromatin accessibility. Epigenetics and Chromatin, 2015, 8, 16.	1.8	100
42	Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. Development (Cambridge), 2015, 142, 4092-4106.	1.2	30
43	A large genomic deletion leads to enhancer adoption by the lamin B1 gene: a second path to autosomal dominant adult-onset demyelinating leukodystrophy (ADLD). Human Molecular Genetics, 2015, 24, 3143-3154.	1.4	117
44	Brg1 modulates enhancer activation in mesoderm lineage commitment. Development (Cambridge), 2015, 142, 1418-30.	1.2	81
45	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. PLoS Genetics, 2014, 10, e1004610.	1.5	105
46	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. Neuron, 2014, 82, 989-1003.	3.8	99
47	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	9.0	71
48	An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. Human Molecular Genetics, 2014, 23, 2711-2720.	1.4	55
49	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	2.4	63
50	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	13.7	259
51	Functional importance of cardiac enhancer-associated noncoding RNAs in heart development and disease. Journal of Molecular and Cellular Cardiology, 2014, 76, 55-70.	0.9	124
52	Identification of Novel Craniofacial Regulatory Domains Located far Upstream ofSOX9and Disrupted in Pierre Robin Sequence. Human Mutation, 2014, 35, 1011-1020.	1.1	69
53	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. Nature Communications, 2014, 5, 4907.	5.8	142
54	Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. ELife, 2014, 3, e01322.	2.8	80

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55	Single site-specific integration targeting coupled with embryonic stem cell differentiation provides a high-throughput alternative to in vivo enhancer analyses. Biology Open, 2013, 2, 1229-1238.	0.6	11
56	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531.	13.5	342
57	Dlx1&2-Dependent Expression of Zfhx1b (Sip1, Zeb2) Regulates the Fate Switch between Cortical and Striatal Interneurons. Neuron, 2013, 77, 83-98.	3.8	140
58	Enhancers: five essential questions. Nature Reviews Genetics, 2013, 14, 288-295.	7.7	455
59	A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908.	13.5	241
60	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	6.0	209
61	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17921-17926.	3.3	606
62	Congenital Heart Defects in Patients with Deletions Upstream ofSOX9. Human Mutation, 2013, 34, 1628-1631.	1.1	33
63	Use of â€œMGE Enhancersâ€•for Labeling and Selection of Embryonic Stem Cell-Derived Medial Ganglionic Eminence (MGE) Progenitors and Neurons. PLoS ONE, 2013, 8, e61956.	1.1	28
64	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree Populus trichocarpa. New Phytologist, 2012, 196, 713-725.	3.5	173
65	Large-scale discovery of enhancers from human heart tissue. Nature Genetics, 2012, 44, 89-93.	9.4	257
66	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. BMC Genomics, 2012, 13, 713.	1.2	16
67	Massively parallel functional dissection of mammalian enhancers in vivo. Nature Biotechnology, 2012, 30, 265-270.	9.4	468
68	Generation of Long Insert Pairs Using a Cre-LoxP Inverse PCR Approach. PLoS ONE, 2012, 7, e29437.	1.1	26
69	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. Science, 2011, 331, 463-467.	6.0	1,135
70	A Genetic Signature of Spina Bifida Risk from Pathway-Informed Comprehensive Gene-Variant Analysis. PLoS ONE, 2011, 6, e28408.	1.1	29
71	Genetic and functional analyses identify DISC1 as a novel callosal agenesis candidate gene. American Journal of Medical Genetics, Part A, 2011, 155, 1865-1876.	0.7	38
72	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. Nature, 2010, 464, 409-412.	13.7	425

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73	A restricted spectrum of NRAS mutations causes Noonan syndrome. Nature Genetics, 2010, 42, 27-29.	9.4	271
74	ChIP-Seq identification of weakly conserved heart enhancers. Nature Genetics, 2010, 42, 806-810.	9.4	395
75	Limits of sequence and functional conservation. Nature Genetics, 2010, 42, 557-558.	9.4	15
76	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. Genome Research, 2010, 20, 565-577.	2.4	203
77	Massively parallel sequencing identifies the gene Megf8 with ENU-induced mutation causing heterotaxy. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3219-3224.	3.3	57
78	Association of functionally significant Melanocortin-4 but not Melanocortin-3 receptor mutations with severe adult obesity in a large North American case-control study. Human Molecular Genetics, 2009, 18, 1140-1147.	1.4	112
79	Directed Evolution of Ionizing Radiation Resistance in Escherichia coli. Journal of Bacteriology, 2009, 191, 5240-5252.	1.0	131
80	Contrasting Patterns of Sequence Evolution at the Functionally Redundant bric Ã brac Paralogs in Drosophila melanogaster. Journal of Molecular Evolution, 2009, 69, 194-202.	0.8	5
81	The INSIG2 rs7566605 genetic variant does not play a major role in obesity in a sample of 24,722 individuals from four cohorts. BMC Medical Genetics, 2009, 10, 56.	2.1	17
82	ChIP-seq accurately predicts tissue-specific activity of enhancers. Nature, 2009, 457, 854-858.	13.7	1,526
83	Genomic views of distant-acting enhancers. Nature, 2009, 461, 199-205.	13.7	549
84	Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. Nature Genetics, 2009, 41, 1022-1026.	9.4	358
85	Functional autonomy of distant-acting human enhancers. Genomics, 2009, 93, 509-513.	1.3	56
86	Rare loss-of-function mutations in ANGPTL family members contribute to plasma triglyceride levels in humans. Journal of Clinical Investigation, 2009, 119, 70-9.	3.9	322
87	The amphioxus genome and the evolution of the chordate karyotype. Nature, 2008, 453, 1064-1071.	13.7	1,496
88	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. Nature Genetics, 2008, 40, 158-160.	9.4	299
89	Disruption of an AP-2Î± binding site in an IRF6 enhancer is associated with cleft lip. Nature Genetics, 2008, 40, 1341-1347.	9.4	382
90	Genetic variation in PNPLA3 confers susceptibility to nonalcoholic fatty liver disease. Nature Genetics, 2008, 40, 1461-1465.	9.4	2,764

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91	Dicer, Drosha, and Outcomes in Patients with Ovarian Cancer. New England Journal of Medicine, 2008, 359, 2641-2650.	13.9	633
92	Human-Specific Gain of Function in a Developmental Enhancer. Science, 2008, 321, 1346-1350.	6.0	330
93	Glucose Regulates the Expression of the Apolipoprotein A5 Gene. Journal of Molecular Biology, 2008, 380, 789-798.	2.0	16
94	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. Cell, 2008, 135, 1053-1064.	13.5	306
95	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. Genome Research, 2008, 18, 1100-1111.	2.4	456
96	Association of common variants in the Joubert syndrome gene (AHI1) with autism. Human Molecular Genetics, 2008, 17, 3887-3896.	1.4	79
97	Integrated analysis of homozygous deletions, focal amplifications, and sequence alterations in breast and colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16224-16229.	3.3	285
98	VISTA Enhancer Browser--a database of tissue-specific human enhancers. Nucleic Acids Research, 2007, 35, D88-D92.	6.5	950
99	Deletion of Ultraconserved Elements Yields Viable Mice. PLoS Biology, 2007, 5, e234.	2.6	255
100	Predicting tissue-specific enhancers in the human genome. Genome Research, 2007, 17, 201-211.	2.4	117
101	Enhancer identification through comparative genomics. Seminars in Cell and Developmental Biology, 2007, 18, 140-152.	2.3	97
102	In vivo characterization of human APOA5 haplotypes. Genomics, 2007, 90, 674-679.	1.3	25
103	Medical Sequencing at the Extremes of Human Body Mass. American Journal of Human Genetics, 2007, 80, 779-791.	2.6	199
104	Most Rare Missense Alleles Are Deleterious in Humans: Implications for Complex Disease and Association Studies. American Journal of Human Genetics, 2007, 80, 727-739.	2.6	547
105	A Common Allele on Chromosome 9 Associated with Coronary Heart Disease. Science, 2007, 316, 1488-1491.	6.0	1,591
106	Gain-of-function SOS1 mutations cause a distinctive form of Noonan syndrome. Nature Genetics, 2007, 39, 75-79.	9.4	523
107	Population-based resequencing of ANGPTL4 uncovers variations that reduce triglycerides and increase HDL. Nature Genetics, 2007, 39, 513-516.	9.4	473
108	Gain-of-function RAF1 mutations cause Noonan and LEOPARD syndromes with hypertrophic cardiomyopathy. Nature Genetics, 2007, 39, 1007-1012.	9.4	624

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109	Comparative Genomics. Methods in Molecular Biology, 2007, 366, 229-251.	0.4	4
110	Gain-of-Function R225W Mutation in Human AMPKÎ³3 Causing Increased Glycogen and Decreased Triglyceride in Skeletal Muscle. PLoS ONE, 2007, 2, e903.	1.1	80
111	Human cathepsin L rescues the neurodegeneration and lethality in cathepsin B/L double-deficient mice. Biological Chemistry, 2006, 387, 885-891.	1.2	49
112	In vivo enhancer analysis of human conserved non-coding sequences. Nature, 2006, 444, 499-502.	13.7	1,072
113	Array comparative genomic hybridization in patients with congenital diaphragmatic hernia: mapping of four CDH-critical regions and sequencing of candidate genes at 15q26.1â€“15q26.2. European Journal of Human Genetics, 2006, 14, 999-1008.	1.4	91
114	A PYY Q62P variant linked to human obesity. Human Molecular Genetics, 2006, 15, 387-391.	1.4	28
115	Close sequence comparisons are sufficient to identify human cis-regulatory elements. Genome Research, 2006, 16, 855-863.	2.4	164
116	Cathepsin L is required for endothelial progenitor cellâ€“induced neovascularization. Nature Medicine, 2005, 11, 206-213.	15.2	278
117	Comparative genomic analysis reveals a distant liver enhancer upstream of the COUP-TFII gene. Mammalian Genome, 2005, 16, 91-95.	1.0	16
118	Lack of Support for the Association between GAD2 Polymorphisms and Severe Human Obesity. PLoS Biology, 2005, 3, e315.	2.6	44
119	Insulin-Mediated Down-Regulation of Apolipoprotein A5 Gene Expression through the Phosphatidylinositol 3-Kinase Pathway: Role of Upstream Stimulatory Factor. Molecular and Cellular Biology, 2005, 25, 1537-1548.	1.1	88
120	Apolipoprotein AV Accelerates Plasma Hydrolysis of Triglyceriderich Lipoproteins by Interaction with Proteoglycan-bound Lipoprotein Lipase. Journal of Biological Chemistry, 2005, 280, 21553-21560.	1.6	253
121	Apolipoprotein A-V Deficiency Results in Marked Hypertriglyceridemia Attributable to Decreased Lipolysis of Triglyceride-Rich Lipoproteins and Removal of Their Remnants. Arteriosclerosis, Thrombosis, and Vascular Biology, 2005, 25, 2573-2579.	1.1	125
122	Transcriptional Regulation of Apolipoprotein A5 Gene Expression by the Nuclear Receptor RORÎ±. Arteriosclerosis, Thrombosis, and Vascular Biology, 2005, 25, 1186-1192.	1.1	50
123	In vivo characterization of a vertebrate ultraconserved enhancer. Genomics, 2005, 85, 774-781.	1.3	77
124	Lack of MEF2A mutations in coronary artery disease. Journal of Clinical Investigation, 2005, 115, 1016-1020.	3.9	99
125	Apoa5 Q139X truncation predisposes to late-onset hyperchylomicronemia due to lipoprotein lipase impairment. Journal of Clinical Investigation, 2005, 115, 2862-2869.	3.9	147
126	The Liver X Receptor Ligand T0901317 Down-regulates APOA5 Gene Expression through Activation of SREBP-1c. Journal of Biological Chemistry, 2004, 279, 45462-45469.	1.6	76

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127	Haplotypes in the APOA1-C3-A4-A5 gene cluster affect plasma lipids in both humans and baboons. Human Molecular Genetics, 2004, 13, 1049-1056.	1.4	25
128	Analysis of Apolipoprotein A5, C3, and Plasma Triglyceride Concentrations in Genetically Engineered Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 1297-1302.	1.1	76
129	Linkage and Association Between Distinct Variants of theAPOA1/C3/A4/A5Gene Cluster and Familial Combined Hyperlipidemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 167-174.	1.1	97
130	The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535.	13.7	298
131	The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274.	13.7	102
132	The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994.	13.7	156
133	Comparative genomic analysis as a tool for biological discovery. Journal of Physiology, 2004, 554, 31-39.	1.3	105
134	Identification of a novel enhancer of brain expression near the apoE gene cluster by comparative genomics. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1676, 41-50.	2.4	26
135	Mechanism of triglyceride lowering in mice expressing human apolipoprotein A5. Biochemical and Biophysical Research Communications, 2004, 319, 397-404.	1.0	183
136	Haplotype analysis of the apolipoprotein gene cluster on human chromosome 11. Genomics, 2004, 83, 912-923.	1.3	95
137	Insights from human/mouse genome comparisons. Mammalian Genome, 2003, 14, 429-436.	1.0	68
138	Cathepsin B but not cathepsins L or S contributes to the pathogenesis of Unverricht-Lundborg progressive myoclonus epilepsy (EPM1). Journal of Neurobiology, 2003, 56, 315-327.	3.7	102
139	Apolipoprotein A5, a Newly Identified Gene That Affects Plasma Triglyceride Levels in Humans and Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2003, 23, 529-534.	1.1	150
140	Apolipoprotein AIV Gene Variant S347 Is Associated With Increased Risk of Coronary Heart Disease and Lower Plasma Apolipoprotein AIV Levels. Circulation Research, 2003, 92, 969-975.	2.0	71
141	Apolipoprotein A5, a Crucial Determinant of Plasma Triglyceride Levels, Is Highly Responsive to Peroxisome Proliferator-activated Receptor Î± Activators. Journal of Biological Chemistry, 2003, 278, 17982-17985.	1.6	186
142	Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106.	3.9	60
143	Comparative and functional analysis of cardiovascular-related genes. Pharmacogenomics, 2003, 4, 571-582.	0.6	1
144	Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106.	3.9	20

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145	Relative contribution of variation within the APOC3/A4/A5 gene cluster in determining plasma triglycerides. Human Molecular Genetics, 2002, 11, 3039-3046.	1.4	335
146	Neuropathological Changes in a Mouse Model of Progressive Myoclonus Epilepsy: Cystatin B Deficiency and Unverricht-Lundborg Disease. Journal of Neuropathology and Experimental Neurology, 2002, 61, 1085-1091.	0.9	72
147	Two independent apolipoprotein A5 haplotypes influence human plasma triglyceride levels. Human Molecular Genetics, 2002, 11, 3031-3038.	1.4	352
148	Genomic strategies to identify mammalian regulatory sequences. Nature Reviews Genetics, 2001, 2, 100-109.	7.7	341
149	Progressive ataxia, myoclonic epilepsy and cerebellar apoptosis in cystatin B-deficient mice. Nature Genetics, 1998, 20, 251-258.	9.4	332
150	Characterization of the human neurocan gene, CSPG3. Gene, 1998, 221, 199-205.	1.0	18
151	Unstable minisatellite expansion causing recessively inherited myoclonus epilepsy, EPM1. Nature Genetics, 1997, 15, 393-396.	9.4	207
152	Structure, sequence and location of the UQCRFS1 gene for the human Rieske Fe-S protein. Gene, 1995, 155, 207-211.	1.0	10
153	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0
154	Comparative Genomics: A Tool to Functionally Annotate Human DNA. , 0, , 229-252.		0