# Len A Pennacchio

List of Publications by Year
in descending order



| 154 | 34,259 | 5574 82 | 6471 157 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 177 | 177 | 177 | 41531 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Genetic variation in PNPLA3 confers susceptibility to nonalcoholic fatty liver disease. Nature Genetics, 2008, 40, 1461-1465. | 21.4 | 2,764 |
| 2 | A Common Allele on Chromosome 9 Associated with Coronary Heart Disease. Science, 2007, 316, 1488-1491. | 12.6 | 1,591 |
| 3 | ChIP-seq accurately predicts tissue-specific activity of enhancers. Nature, 2009, 457, 854-858. | 27.8 | 1,526 |
| 4 | The amphioxus genome and the evolution of the chordate karyotype. Nature, 2008, 453, 1064-1071. | 27.8 | 1,496 |
| 5 | Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710. | 27.8 | 1,252 |
| 6 | Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. Science, 2011, 331, 463-467. | 12.6 | 1,135 |
| 7 | In vivo enhancer analysis of human conserved non-coding sequences. Nature, 2006, 444, 499-502. | 27.8 | 1,072 |
| 8 | VISTA Enhancer Browser--a database of tissue-specific human enhancers. Nucleic Acids Research, 2007, 35, D88-D92. | 14.5 | 950 |
| 9 | Dicer, Drosha, and Outcomes in Patients with Ovarian Cancer. New England Journal of Medicine, 2008, 359, 2641-2650. | 27.0 | 633 |
| 10 | Gain-of-function RAF1 mutations cause Noonan and LEOPARD syndromes with hypertrophic cardiomyopathy. Nature Genetics, 2007, 39, 1007-1012. | 21.4 | 624 |
| 11 | 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. | 7.1 | 606 |
| 12 | Genomic views of distant-acting enhancers. Nature, 2009, 461, 199-205. | 27.8 | 549 |
| 13 | Most Rare Missense Alleles Are Deleterious in Humans: Implications for Complex Disease and Association Studies. American Journal of Human Genetics, 2007, 80, 727-739. | 6.2 | 547 |
| 14 | Gain-of-function SOS1 mutations cause a distinctive form of Noonan syndrome. Nature Genetics, 2007, 39, 75-79. | 21.4 | 523 |
| 15 | Enhancer redundancy provides phenotypic robustness in mammalian development. Nature, 2018, 554, 239-243. | 27.8 | 514 |
| 16 | Population-based resequencing of ANGPTL4 uncovers variations that reduce triglycerides and increase HDL. Nature Genetics, 2007, 39, 513-516. | 21.4 | 473 |
| 17 | Massively parallel functional dissection of mammalian enhancers in vivo. Nature Biotechnology, 2012, 30, 265-270. | 17.5 | 468 |
| 18 | The amphioxus genome illuminates vertebrate origins and cephalochordate biology. Genome Research, 2008, 18, 1100-1111. | 5.5 | 456 |

| # | Article | IF | Citations |
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| 19 | Enhancers: five essential questions. Nature Reviews Genetics, 2013, 14, 288-295. | 16.3 | 455 |
| 20 | Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. Nature, 2010, 464, 409-412. | 27.8 | 425 |
| 21 | ChIP-Seq identification of weakly conserved heart enhancers. Nature Genetics, 2010, 42, 806-810. | 21.4 | 395 |
| 22 | Disruption of an AP-2Î± binding site in an IRF6 enhancer is associated with cleft lip. Nature Genetics, 2008, 40, 1341-1347. | 21.4 | 382 |
| 23 | Mutation of SHOC2 promotes aberrant protein N-myristoylation and causes Noonan-like syndrome with loose anagen hair. Nature Genetics, 2009, 41, 1022-1026. | 21.4 | 358 |
| 24 | Two independent apolipoprotein A5 haplotypes influence human plasma triglyceride levels. Human Molecular Genetics, 2002, 11, 3031-3038. | 2.9 | 352 |
| 25 | The Epigenomic Landscape of Prokaryotes. PLoS Genetics, 2016, 12, e1005854. | 3.5 | 348 |
| 26 | Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531. | 28.9 | 342 |
| 27 | Genomic strategies to identify mammalian regulatory sequences. Nature Reviews Genetics, 2001, 2, 100-109. | 16.3 | 341 |
| 28 | Relative contribution of variation within the APOC3/A4/A5 gene cluster in determining plasma triglycerides. Human Molecular Genetics, 2002, 11, 3039-3046. | 2.9 | 335 |
| 29 | Progressive ataxia, myoclonic epilepsy and cerebellar apoptosis in cystatin B-deficient mice. Nature Genetics, 1998, 20, 251-258. | 21.4 | 332 |
| 30 | Human-Specific Gain of Function in a Developmental Enhancer. Science, 2008, 321, 1346-1350. | 12.6 | 330 |
| 31 | Rare loss-of-function mutations in ANGPTL family members contribute to plasma triglyceride levels in humans. Journal of Clinical Investigation, 2009, 119, 70-9. | 8.2 | 322 |
| 32 | Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903. | 21.4 | 308 |
| 33 | Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12. | 28.9 | 308 |
| 34 | Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. Cell, 2008, 135, 1053-1064. | 28.9 | 306 |
| 35 | Ultraconservation identifies a small subset of extremely constrained developmental enhancers. Nature Genetics, 2008, 40, 158-160. | 21.4 | 299 |
| 36 | The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535. | 27.8 | 298 |

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| 37 | Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439. | 14.8 | 290 |
| 38 | 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. | 7.1 | 285 |
| 39 | Cathepsin L is required for endothelial progenitor cellâ€“induced neovascularization. Nature Medicine, 2005, 11, 206-213. | 30.7 | 278 |
| 40 | Progressive Loss of Function in a Limb Enhancer during Snake Evolution. Cell, 2016, 167, 633-642.e11. | 28.9 | 275 |
| 41 | A restricted spectrum of NRAS mutations causes Noonan syndrome. Nature Genetics, 2010, 42, 27-29. | 21.4 | 271 |
| 42 | Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375. | 27.8 | 259 |
| 43 | Large-scale discovery of enhancers from human heart tissue. Nature Genetics, 2012, 44, 89-93. | 21.4 | 257 |
| 44 | An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751. | 27.8 | 257 |
| 45 | Deletion of Ultraconserved Elements Yields Viable Mice. PLoS Biology, 2007, 5, e234. | 5.6 | 255 |
| 46 | Apolipoprotein AV Accelerates Plasma Hydrolysis of Triglyceriderich Lipoproteins by Interaction with Proteoglycan-bound Lipoprotein Lipase. Journal of Biological Chemistry, 2005, 280, 21553-21560. | 3.4 | 253 |
| 47 | A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908. | 28.9 | 241 |
| 48 | Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073. | 14.8 | 210 |
| 49 | Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006. | 12.6 | 209 |
| 50 | Unstable minisatellite expansion causing recessively inherited myoclonus epilepsy, EPM1. Nature Genetics, 1997, 15, 393-396. | 21.4 | 207 |
| 51 | Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. Genome Research, 2010, 20, 565-577. | 5.5 | 203 |
| 52 | Medical Sequencing at the Extremes of Human Body Mass. American Journal of Human Genetics, 2007, 80, 779-791. | 6.2 | 199 |
| 53 | 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. | 3.4 | 186 |
| 54 | Mechanism of triglyceride lowering in mice expressing human apolipoprotein A5. Biochemical and Biophysical Research Communications, 2004, 319, 397-404. | 2.1 | 183 |

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| 55 | Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree Populus trichocarpa. New Phytologist, 2012, 196, 713-725. | 7.3 | 173 |
| 56 | Ultraconserved Enhancers Are Required for Normal Development. Cell, 2018, 172, 491-499.e15. | 28.9 | 169 |
| 57 | Close sequence comparisons are sufficient to identify human cis-regulatory elements. Genome Research, 2006, 16, 855-863. | 5.5 | 164 |
| 58 | The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994. | 27.8 | 156 |
| 59 | Apolipoprotein A5 , a Newly Identified Gene That Affects Plasma Triglyceride Levels in Humans and Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2003, 23, 529-534. | 2.4 | 150 |
| 60 | Apoa5 Q139X truncation predisposes to late-onset hyperchylomicronemia due to lipoprotein lipase impairment. Journal of Clinical Investigation, 2005, 115, 2862-2869. | 8.2 | 147 |
| 61 | Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. Nature Communications, 2014, 5, 4907. | 12.8 | 142 |
| 62 | Dlx1&2-Dependent Expression of Zfhx1b (Sip1, Zeb2) Regulates the Fate Switch between Cortical and Striatal Interneurons. Neuron, 2013, 77, 83-98. | 8.1 | 140 |
| 63 | Directed Evolution of Ionizing Radiation Resistance in Escherichia coli. Journal of Bacteriology, 2009, 191, 5240-5252. | 2.2 | 131 |
| 64 | The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767. | 27.8 | 131 |
| 65 | 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. | 2.4 | 125 |
| 66 | Functional importance of cardiac enhancer-associated noncoding RNAs in heart development and disease. Journal of Molecular and Cellular Cardiology, 2014, 76, 55-70. | 1.9 | 124 |
| 67 | Predicting tissue-specific enhancers in the human genome. Genome Research, 2007, 17, 201-211. | 5.5 | 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). Human Molecular Genetics, 2015, 24, 3143-3154. | 2.9 | 117 |
| 69 | A Cryptochrome 2 mutation yields advanced sleep phase in humans. ELife, 2016, 5, . | 6.0 | 114 |
| 70 | 52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448. | 2.8 | 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. Human Molecular Genetics, 2009, 18, 1140-1147. | 2.9 | 112 |
| 72 | Enhancer Variants Synergistically Drive Dysfunction of a Gene Regulatory Network In Hirschsprung Disease. Cell, 2016, 167, 355-368.e10. | 28.9 | 112 |

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|---|---|---|---|
| 73 | Comparative genomic analysis as a tool for biological discovery. Journal of Physiology, 2004, 554, 31-39. | 2.9 | 105 |
| 74 | Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. PLoS Genetics, 2014, 10, e1004610. | 3.5 | 105 |
| 75 | 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. | 3.6 | 102 |
| 76 | The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274. | 27.8 | 102 |
| 77 | 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. | 3.9 | 100 |
| 78 | Comprehensive InÂVivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. Cell, 2020, 180, 1262-1271.e15. | 28.9 | 100 |
| 79 | Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. Neuron, 2014, 82, 989-1003. | 8.1 | 99 |
| 80 | Lack of MEF2A mutations in coronary artery disease. Journal of Clinical Investigation, 2005, 115, 1016-1020. | 8.2 | 99 |
| 81 | 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. | 2.4 | 97 |
| 82 | Enhancer identification through comparative genomics. Seminars in Cell and Developmental Biology, 2007, 18, 140-152. | 5.0 | 97 |
| 83 | Haplotype analysis of the apolipoprotein gene cluster on human chromosome 11. Genomics, 2004, 83, 912-923. | 2.9 | 95 |
| 84 | Array comparative genomic hybridization in patients with congenital diaphragmatic hernia: mapping of four CDH-critical regions and sequencing of candidate genes at 15q26.1â€“15q26.2. European Journal of Human Genetics, 2006, 14, 999-1008. | 2.8 | 91 |
| 85 | 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. | 2.3 | 88 |
| 86 | Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759. | 27.8 | 84 |
| 87 | Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923. | 12.8 | 83 |
| 88 | Brg1 modulates enhancer activation in mesoderm lineage commitment. Development (Cambridge), 2015, 142, 1418-30. | 2.5 | 81 |
| 89 | Gain-of-Function R225W Mutation in Human AMPKÎ³3 Causing Increased Glycogen and Decreased Triglyceride in Skeletal Muscle. PLoS ONE, 2007, 2, e903. | 2.5 | 80 |
| 90 | Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. ELife, 2014, 3, e01322. | 6.0 | 80 |

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| 91 | Association of common variants in the Joubert syndrome gene (AHI1) with autism. Human Molecular Genetics, 2008, 17, 3887-3896. | 2.9 | 79 |
| 92 | 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. | 7.1 | 78 |
| 93 | In vivo characterization of a vertebrate ultraconserved enhancer. Genomics, 2005, 85, 774-781. | 2.9 | 77 |
| 94 | The Liver X Receptor Ligand T0901317 Down-regulates APOA5 Gene Expression through Activation of SREBP-1c. Journal of Biological Chemistry, 2004, 279, 45462-45469. | 3.4 | 76 |
| 95 | Analysis of Apolipoprotein A5, C3, and Plasma Triglyceride Concentrations in Genetically Engineered Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 1297-1302. | 2.4 | 76 |
| 96 | 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. | 1.7 | 72 |
| 97 | 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. | 4.5 | 71 |
| 98 | Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571. | 19.0 | 71 |
| 99 | Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814. | 19.0 | 71 |
| 100 | Identification of Novel Craniofacial Regulatory Domains Located far Upstream ofSOX9and Disrupted in Pierre Robin Sequence. Human Mutation, 2014, 35, 1011-1020. | 2.5 | 69 |
| 101 | Insights from human/mouse genome comparisons. Mammalian Genome, 2003, 14, 429-436. | 2.2 | 68 |
| 102 | Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8. | 6.4 | 68 |
| 103 | Activating Mutations Affecting the Dbl Homology Domain of SOS2 Cause Noonan Syndrome. Human Mutation, 2015, 36, 1080-1087. | 2.5 | 67 |
| 104 | Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929. | 5.5 | 63 |
| 105 | Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106. | 8.2 | 60 |
| 106 | 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. | 7.1 | 57 |
| 107 | Functional autonomy of distant-acting human enhancers. Genomics, 2009, 93, 509-513. | 2.9 | 56 |
| 108 | An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. Human Molecular Genetics, 2014, 23, 2711-2720. | 2.9 | 55 |

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| 109 | Relationship between genetic variation at PPP1R3B and levels of liver glycogen and triglyceride. Hepatology, 2018, 67, 2182-2195. | 7.3 | 51 |
| 110 | Transcriptional Regulation of Apolipoprotein A5 Gene Expression by the Nuclear Receptor RORÎ±. Arteriosclerosis, Thrombosis, and Vascular Biology, 2005, 25, 1186-1192. | 2.4 | 50 |
| 111 | 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. | 7.1 | 50 |
| 112 | Human cathepsin L rescues the neurodegeneration and lethality in cathepsin B/L double-deficient mice. Biological Chemistry, 2006, 387, 885-891. | 2.5 | 49 |
| 113 | Lack of Support for the Association between GAD2 Polymorphisms and Severe Human Obesity. PLoS Biology, 2005, 3, e315. | 5.6 | 44 |
| 114 | Presynaptic Homeostasis Opposes Disease Progression in Mouse Models of ALS-Like Degeneration: Evidence for Homeostatic Neuroprotection. Neuron, 2020, 107, 95-111.e6. | 8.1 | 43 |
| 115 | Dynamic BAF chromatin remodeling complex subunit inclusion promotes temporally distinct gene expression programs in cardiogenesis. Development (Cambridge), 2019, 146, . | 2.5 | 39 |
| 116 | Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528. | 21.4 | 39 |
| 117 | Genetic and functional analyses identify DISC1 as a novel callosal agenesis candidate gene. American Journal of Medical Genetics, Part A, 2011, 155, 1865-1876. | 1.2 | 38 |
| 118 | ATAC-Seq Reveals an Isl1 Enhancer That Regulates Sinoatrial Node Development and Function. Circulation Research, 2020, 127, 1502-1518. | 4.5 | 35 |
| 119 | Congenital Heart Defects in Patients with Deletions Upstream ofSOX9. Human Mutation, 2013, 34, 1628-1631. | 2.5 | 33 |
| 120 | Brg1 coordinates multiple processes during retinogenesis and is a tumor suppressor in retinoblastoma. Development (Cambridge), 2015, 142, 4092-4106. | 2.5 | 30 |
| 121 | Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892. | 6.2 | 30 |
| 122 | A Genetic Signature of Spina Bifida Risk from Pathway-Informed Comprehensive Gene-Variant Analysis. PLoS ONE, 2011, 6, e28408. | 2.5 | 29 |
| 123 | A PYY Q62P variant linked to human obesity. Human Molecular Genetics, 2006, 15, 387-391. | 2.9 | 28 |
| 124 | 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. | 2.5 | 28 |
| 125 | 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 |
| 126 | Generation of Long Insert Pairs Using a Cre-LoxP Inverse PCR Approach. PLoS ONE, 2012, 7, e29437. | 2.5 | 26 |

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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. | 2.9 | 25 |
| 128 | In vivo characterization of human APOA5 haplotypes. Genomics, 2007, 90, 674-679. | 2.9 | 25 |
| 129 | Transcriptional network orchestrating regional patterning of cortical progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 25 |
| 130 | Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111. | 27.8 | 24 |
| 131 | Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. Communications Biology, 2021, 4, 1302. | 4.4 | 21 |
| 132 | Comparative genomic tools and databases: providing insights into the human genome. Journal of Clinical Investigation, 2003, 111, 1099-1106. | 8.2 | 20 |
| 133 | Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in Molecular Biology, 2022, 2403, 147-186. | 0.9 | 20 |
| 134 | Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439. | 12.8 | 19 |
| 135 | Characterization of the human neurocan gene, CSPG3. Gene, 1998, 221, 199-205. | 2.2 | 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. BMC Medical Genetics, 2009, 10, 56. | 2.1 | 17 |
| 137 | Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720. | 3.2 | 17 |
| 138 | Comparative genomic analysis reveals a distant liver enhancer upstream of the COUP-TFII gene. Mammalian Genome, 2005, 16, 91-95. | 2.2 | 16 |
| 139 | Glucose Regulates the Expression of the Apolipoprotein A5 Gene. Journal of Molecular Biology, 2008, 380, 789-798. | 4.2 | 16 |
| 140 | Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. BMC Genomics, 2012, 13, 713. | 2.8 | 16 |
| 141 | Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44. | 2.9 | 16 |
| 142 | Perfect and imperfect views of ultraconserved sequences. Nature Reviews Genetics, 2022, 23, 182-194. | 16.3 | 16 |
| 143 | Limits of sequence and functional conservation. Nature Genetics, 2010, 42, 557-558. | 21.4 | 15 |
| 144 | Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. Genome Medicine, 2021, 13, 69. | 8.2 | 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. Biology Open, 2013, 2, 1229-1238. | 1.2 | 11 |
| 146 | Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. Genome Biology, 2019, 20, 140. | 8.8 | 11 |
| 147 | Structure, sequence and location of the UQCRFS1 gene for the human Rieske Fe-S protein. Gene, 1995, 155, 207-211. | 2.2 | 10 |
| 148 | Differential Etv2 threshold requirement for endothelial and erythropoietic development. Cell Reports, 2022, 39, 110881. | 6.4 | 9 |
| 149 | HAND transcription factors cooperatively specify the aorta and pulmonary trunk. Developmental Biology, 2021, 476, 1-10. | 2.0 | 7 |
| 150 | Contrasting Patterns of Sequence Evolution at the Functionally Redundant bric Ã brac Paralogs in Drosophila melanogaster. Journal of Molecular Evolution, 2009, 69, 194-202. | 1.8 | 5 |
| 151 | Comparative Genomics. Methods in Molecular Biology, 2007, 366, 229-251. | 0.9 | 4 |
| 152 | Comparative and functional analysis of cardiovascular-related genes. Pharmacogenomics, 2003, 4, 571-582. | 1.3 | 1 |
| 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 |