

Axel Visel

List of Publications by Year in descending order

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127
papers

43,817
citations

14655

66
h-index

13379

130
g-index

166
all docs

166
docs citations

166
times ranked

63562
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	27.8	15,516
2	Genome-wide atlas of gene expression in the adult mouse brain. <i>Nature</i> , 2007, 445, 168-176.	27.8	4,863
3	Disruptions of Topological Chromatin Domains Cause Pathogenic Rewiring of Gene-Enhancer Interactions. <i>Cell</i> , 2015, 161, 1012-1025.	28.9	1,725
4	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	27.8	1,526
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
6	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	12.6	1,135
7	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	27.8	1,072
8	VISTA Enhancer Browser--a database of tissue-specific human enhancers. <i>Nucleic Acids Research</i> , 2007, 35, D88-D92.	14.5	950
9	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	7.3	663
10	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.	7.1	606
11	Genomic views of distant-acting enhancers. <i>Nature</i> , 2009, 461, 199-205.	27.8	549
12	Enhancer redundancy provides phenotypic robustness in mammalian development. <i>Nature</i> , 2018, 554, 239-243.	27.8	514
13	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
14	GenePaint.org: an atlas of gene expression patterns in the mouse embryo. <i>Nucleic Acids Research</i> , 2004, 32, 552D-556.	14.5	455
15	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	27.8	433
16	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. <i>Nature</i> , 2010, 464, 409-412.	27.8	425
17	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	21.4	395
18	Disruption of an AP-2 binding site in an IRF6 enhancer is associated with cleft lip. <i>Nature Genetics</i> , 2008, 40, 1341-1347.	21.4	382

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19	The Epigenomic Landscape of Prokaryotes. PLoS Genetics, 2016, 12, e1005854.	3.5	348
20	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531.	28.9	342
21	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. Genome Research, 2014, 24, 1517-1525.	5.5	332
22	Human-Specific Gain of Function in a Developmental Enhancer. Science, 2008, 321, 1346-1350.	12.6	330
23	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. Cell, 2008, 135, 1053-1064.	28.9	306
24	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. Nature Genetics, 2008, 40, 158-160.	21.4	299
25	Widespread adenine N6-methylation of active genes in fungi. Nature Genetics, 2017, 49, 964-968.	21.4	292
26	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
27	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. Cell, 2016, 167, 633-642.e11.	28.9	275
28	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	27.8	259
29	Large-scale discovery of enhancers from human heart tissue. Nature Genetics, 2012, 44, 89-93.	21.4	257
30	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	27.8	257
31	Deletion of Ultraconserved Elements Yields Viable Mice. PLoS Biology, 2007, 5, e234.	5.6	255
32	A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908.	28.9	241
33	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. Nature Biotechnology, 2017, 35, 676-683.	17.5	222
34	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. Frontiers in Microbiology, 2016, 7, 150.	3.5	219
35	Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073.	14.8	210
36	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	12.6	209

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37	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
38	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. <i>Genome Research</i> , 2010, 20, 565-577.	5.5	203
39	Genome-wide identification of bacterial plant colonization genes. <i>PLoS Biology</i> , 2017, 15, e2002860.	5.6	173
40	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	28.9	169
41	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. <i>Nature Genetics</i> , 2018, 50, 1463-1473.	21.4	147
42	Comprehensive expression atlas of fibroblast growth factors and their receptors generated by a novel robotic in situ hybridization platform. <i>Developmental Dynamics</i> , 2005, 234, 371-386.	1.8	142
43	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. <i>Nature Communications</i> , 2014, 5, 4907.	12.8	142
44	Dlx1&2-Dependent Expression of Zfhx1b (Sip1, Zeb2) Regulates the Fate Switch between Cortical and Striatal Interneurons. <i>Neuron</i> , 2013, 77, 83-98.	8.1	140
45	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. <i>Neuron</i> , 2015, 85, 27-47.	8.1	136
46	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	27.8	131
47	Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 27124-27132.	7.1	129
48	Scaffolding by ERK3 regulates MK5 in development. <i>EMBO Journal</i> , 2004, 23, 4770-4779.	7.8	124
49	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	12.6	124
50	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
51	Transcriptional Networks Controlled by NKX2-1 in the Development of Forebrain GABAergic Neurons. <i>Neuron</i> , 2016, 91, 1260-1275.	8.1	120
52	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . <i>BMC Genomics</i> , 2013, 14, 563.	2.8	115
53	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.8	113
54	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. <i>Cell</i> , 2019, 177, 32-37.	28.9	113

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55	Composition and dosage of a multipartite enhancer cluster control developmental expression of <i>lhh</i> (Indian hedgehog). <i>Nature Genetics</i> , 2017, 49, 1539-1545.	21.4	107
56	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. <i>PLoS Genetics</i> , 2014, 10, e1004610.	3.5	105
57	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. <i>Cell Stem Cell</i> , 2020, 27, 765-783.e14.	11.1	101
58	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.	3.9	100
59	Comprehensive In Vivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. <i>Cell</i> , 2020, 180, 1262-1271.e15.	28.9	100
60	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. <i>Neuron</i> , 2014, 82, 989-1003.	8.1	99
61	HAND2 Targets Define a Network of Transcriptional Regulators that Compartmentalize the Early Limb Bud Mesenchyme. <i>Developmental Cell</i> , 2014, 31, 345-357.	7.0	98
62	Enhancer identification through comparative genomics. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 140-152.	5.0	97
63	Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae. <i>Nature Plants</i> , 2015, 1, 15107.	9.3	89
64	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. <i>Nature Microbiology</i> , 2019, 4, 2498-2510.	13.3	85
65	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	27.8	84
66	Genome-wide compendium and functional assessment of in vivo heart enhancers. <i>Nature Communications</i> , 2016, 7, 12923.	12.8	83
67	Transcriptional control of axonal guidance and sorting in dorsal interneurons by the Lim-HD proteins <i>Lhx9</i> and <i>Lhx1</i> . <i>Neural Development</i> , 2009, 4, 21.	2.4	79
68	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.	7.1	78
69	The FaceBase Consortium: A comprehensive program to facilitate craniofacial research. <i>Developmental Biology</i> , 2011, 355, 175-182.	2.0	72
70	Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by <i>HOX13</i> . <i>Cell Reports</i> , 2016, 17, 2913-2926.	6.4	72
71	<i>Dlx1</i> and <i>Dlx2</i> Promote Interneuron GABA Synthesis, Synaptogenesis, and Dendritogenesis. <i>Cerebral Cortex</i> , 2018, 28, 3797-3815.	2.9	72
72	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. <i>Cell Stem Cell</i> , 2019, 25, 69-86.e5.	11.1	72

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73	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	19.0	71
74	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	19.0	71
75	Identification of Novel Craniofacial Regulatory Domains Located far Upstream of <i>SOX9</i> and Disrupted in Pierre Robin Sequence. Human Mutation, 2014, 35, 1011-1020.	2.5	69
76	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	6.4	68
77	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics, 2018, 19, 588.	2.8	64
78	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	5.5	63
79	Subpallial Enhancer Transgenic Lines: a Data and Tool Resource to Study Transcriptional Regulation of GABAergic Cell Fate. Neuron, 2016, 92, 59-74.	8.1	62
80	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. Development (Cambridge), 2016, 143, 2677-88.	2.5	62
81	Pbx Regulates Patterning of the Cerebral Cortex in Progenitors and Postmitotic Neurons. Neuron, 2015, 88, 1192-1207.	8.1	58
82	Comprehensive analysis of the expression patterns of the adenylate cyclase gene family in the developing and adult mouse brain. Journal of Comparative Neurology, 2006, 496, 684-697.	1.6	56
83	Functional autonomy of distant-acting human enhancers. Genomics, 2009, 93, 509-513.	2.9	56
84	Regulatory Pathway Analysis by High-Throughput In Situ Hybridization. PLoS Genetics, 2007, 3, e178.	3.5	55
85	An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. Human Molecular Genetics, 2014, 23, 2711-2720.	2.9	55
86	Multilab EcoFAB study shows highly reproducible physiology and depletion of soil metabolites by a model grass. New Phytologist, 2019, 222, 1149-1160.	7.3	55
87	HAND2 Target Gene Regulatory Networks Control Atrioventricular Canal and Cardiac Valve Development. Cell Reports, 2017, 19, 1602-1613.	6.4	50
88	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. Science, 2020, 370, 208-214.	12.6	41
89	Functional anatomy of distant-acting mammalian enhancers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120359.	4.0	40
90	Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528.	21.4	39

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91	A single nucleotide polymorphism associated with isolated cleft lip and palate, thyroid cancer and hypothyroidism alters the activity of an oral epithelium and thyroid enhancer near FOXE1. Human Molecular Genetics, 2015, 24, 3895-3907.	2.9	36
92	Bi-fated tendon-to-bone attachment cells are regulated by shared enhancers and KLF transcription factors. ELife, 2021, 10, .	6.0	36
93	Congenital Heart Defects in Patients with Deletions Upstream of <i>SOX9</i> . Human Mutation, 2013, 34, 1628-1631.	2.5	33
94	Transmembrane protein 50b (C21orf4), a candidate for Down syndrome neurophenotypes, encodes an intracellular membrane protein expressed in the rodent brain. Neuroscience, 2008, 154, 1255-1266.	2.3	30
95	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
96	Use of "MGE Enhancers" for Labeling and Selection of Embryonic Stem Cell-Derived Medial Ganglionic Eminence (MGE) Progenitors and Neurons. PLoS ONE, 2013, 8, e61956.	2.5	28
97	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. Cell, 2016, 167, 1163-1166.	28.9	27
98	Fuzzy <sc>GIS</sc>-based multi-criteria evaluation for US <i>Agave</i> production as a bioenergy feedstock. GCB Bioenergy, 2015, 7, 84-99.	5.6	25
99	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. Development (Cambridge), 2020, 147, .	2.5	25
100	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
101	Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111.	27.8	24
102	Plant single-cell solutions for energy and the environment. Communications Biology, 2021, 4, 962.	4.4	23
103	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. ELife, 2020, 9, .	6.0	23
104	Multiple conserved regulatory domains promote Fezf2 expression in the developing cerebral cortex. Neural Development, 2014, 9, 6.	2.4	21
105	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. Communications Biology, 2021, 4, 1302.	4.4	21
106	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in Molecular Biology, 2022, 2403, 147-186.	0.9	20
107	Adenylate Cyclase 1 dependent refinement of retinotopic maps in the mouse. Vision Research, 2004, 44, 3357-3364.	1.4	19
108	Expression of the winged helix/forkhead gene, foxn4, during zebrafish development. Developmental Brain Research, 2004, 153, 115-119.	1.7	17

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109	A liver enhancer in the fibrinogen gene cluster. <i>Blood</i> , 2011, 117, 276-282.	1.4	17
110	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. <i>PLoS Computational Biology</i> , 2017, 13, e1005720.	3.2	17
111	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.	2.8	16
112	Perfect and imperfect views of ultraconserved sequences. <i>Nature Reviews Genetics</i> , 2022, 23, 182-194.	16.3	16
113	Limits of sequence and functional conservation. <i>Nature Genetics</i> , 2010, 42, 557-558.	21.4	15
114	A unique stylopod patterning mechanism by <i>Shox2</i> controlled osteogenesis. <i>Development (Cambridge)</i> , 2016, 143, 2548-60.	2.5	15
115	Deletion of a non-canonical regulatory sequence causes loss of <i>Scn1a</i> expression and epileptic phenotypes in mice. <i>Genome Medicine</i> , 2021, 13, 69.	8.2	15
116	A distal 594bp ECR specifies <i>Hmx1</i> expression in pinna and lateral facial morphogenesis and is regulated by Hox-Pbx-Meis. <i>Development (Cambridge)</i> , 2016, 143, 2582-92.	2.5	13
117	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. <i>Genome Biology</i> , 2019, 20, 140.	8.8	11
118	Interrogating the Grainyhead-like 2 (<i>Grlh2</i>) genomic locus identifies an enhancer element that regulates palatogenesis in mouse. <i>Developmental Biology</i> , 2020, 459, 194-203.	2.0	7
119	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	4
120	A Gene Expression Map of the Mouse Brain. , 2003, , 19-35.		3
121	MusMorph, a database of standardized mouse morphology data for morphometric meta-analyses. <i>Scientific Data</i> , 2022, 9, .	5.3	3
122	Power in isolation: insights from single cells. <i>Nature Reviews Microbiology</i> , 2020, 18, 364-364.	28.6	2
123	The Joint Genome Institute's synthetic biology internal review process. <i>Journal of Responsible Innovation</i> , 2015, 2, 133-136.	4.9	0
124	Fishing for Function in the Human Gene Pool. <i>Trends in Genetics</i> , 2016, 32, 392-394.	6.7	0
125	Identification of a non-coding SNP associated with risk for non-syndromic orofacial clefting with allele-specific effects on <i>IRF6</i> expression in vitro. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
126	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

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127	Regulatory Dynamics of Midfacial Growth in Evolution and Disease. FASEB Journal, 2020, 34, 1-1.	0.5	0