

Axel Visel

List of Publications by Year in descending order

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Version: 2024-02-01

127
papers

43,817
citations

14644

66
h-index

13365

130
g-index

166
all docs

166
docs citations

166
times ranked

63562
citing authors

#	ARTICLE	IF	CITATIONS
1	Perfect and imperfect views of ultraconserved sequences. <i>Nature Reviews Genetics</i> , 2022, 23, 182-194.	7.7	16
2	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
3	MusMorph, a database of standardized mouse morphology data for morphometric meta-analyses. <i>Scientific Data</i> , 2022, 9, .	2.4	3
4	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
5	Ultraconserved enhancer function does not require perfect sequence conservation. <i>Nature Genetics</i> , 2021, 53, 521-528.	9.4	39
6	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.	3.6	15
7	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, .	0.2	0
8	Plant single-cell solutions for energy and the environment. <i>Communications Biology</i> , 2021, 4, 962.	2.0	23
9	Bi-fated tendon-to-bone attachment cells are regulated by shared enhancers and KLF transcription factors. <i>ELife</i> , 2021, 10, .	2.8	36
10	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. <i>Communications Biology</i> , 2021, 4, 1302.	2.0	21
11	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, .	1.2	4
12	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
13	Interrogating the Grainyhead-like 2 (<i>Grhl2</i>) genomic locus identifies an enhancer element that regulates palatogenesis in mouse. <i>Developmental Biology</i> , 2020, 459, 194-203.	0.9	7
14	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	25
15	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. <i>Cell Stem Cell</i> , 2020, 27, 765-783.e14.	5.2	101
16	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. <i>Science</i> , 2020, 370, 208-214.	6.0	41
17	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
18	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84

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19	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
20	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
21	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767.	13.7	131
22	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	9.0	71
23	Power in isolation: insights from single cells. Nature Reviews Microbiology, 2020, 18, 364-364.	13.6	2
24	Comprehensive In Vivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. Cell, 2020, 180, 1262-1271.e15.	13.5	100
25	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. ELife, 2020, 9, .	2.8	23
26	Regulatory Dynamics of Midfacial Growth in Evolution and Disease. FASEB Journal, 2020, 34, 1-1.	0.2	0
27	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68
28	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. Genome Biology, 2019, 20, 140.	3.8	11
29	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. Nature Microbiology, 2019, 4, 1895-1906.	5.9	206
30	Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111.	13.7	24
31	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. Cell Stem Cell, 2019, 25, 69-86.e5.	5.2	72
32	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. Cell, 2019, 177, 32-37.	13.5	113
33	Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 27124-27132.	3.3	129
34	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. Nature Microbiology, 2019, 4, 2498-2510.	5.9	85
35	Multilab EcoFAB study shows highly reproducible physiology and depletion of soil metabolites by a model grass. New Phytologist, 2019, 222, 1149-1160.	3.5	55
36	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

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37	Enhancer redundancy provides phenotypic robustness in mammalian development. <i>Nature</i> , 2018, 554, 239-243.	13.7	514
38	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	13.5	169
39	<i>Dlx1</i> and <i>Dlx2</i> Promote Interneuron GABA Synthesis, Synaptogenesis, and Dendritogenesis. <i>Cerebral Cortex</i> , 2018, 28, 3797-3815.	1.6	72
40	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
41	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. <i>Nature Genetics</i> , 2018, 50, 1463-1473.	9.4	147
42	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
43	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in <i>Agave</i> . <i>BMC Genomics</i> , 2018, 19, 588.	1.2	64
44	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
45	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	9.4	292
46	HAND2 Target Gene Regulatory Networks Control Atrioventricular Canal and Cardiac Valve Development. <i>Cell Reports</i> , 2017, 19, 1602-1613.	2.9	50
47	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. <i>Nature Biotechnology</i> , 2017, 35, 676-683.	9.4	222
48	Germline <i>Chd8</i> haploinsufficiency alters brain development in mouse. <i>Nature Neuroscience</i> , 2017, 20, 1062-1073.	7.1	210
49	Composition and dosage of a multipartite enhancer cluster control developmental expression of <i>lh</i> (Indian hedgehog). <i>Nature Genetics</i> , 2017, 49, 1539-1545.	9.4	107
50	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
51	Genome-wide identification of bacterial plant colonization genes. <i>PLoS Biology</i> , 2017, 15, e2002860.	2.6	173
52	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. <i>Frontiers in Microbiology</i> , 2016, 7, 150.	1.5	219
53	Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by <i>HOX13</i> . <i>Cell Reports</i> , 2016, 17, 2913-2926.	2.9	72
54	Fishing for Function in the Human Gene Pool. <i>Trends in Genetics</i> , 2016, 32, 392-394.	2.9	0

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55	Subpallial Enhancer Transgenic Lines: a Data and Tool Resource to Study Transcriptional Regulation of GABAergic Cell Fate. <i>Neuron</i> , 2016, 92, 59-74.	3.8	62
56	Transcriptional Networks Controlled by NKX2-1 in the Development of Forebrain GABAergic Neurons. <i>Neuron</i> , 2016, 91, 1260-1275.	3.8	120
57	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
58	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. <i>Cell</i> , 2016, 167, 1163-1166.	13.5	27
59	Genome-wide compendium and functional assessment of in vivo heart enhancers. <i>Nature Communications</i> , 2016, 7, 12923.	5.8	83
60	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. <i>Cell</i> , 2016, 167, 633-642.e11.	13.5	275
61	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. <i>Development (Cambridge)</i> , 2016, 143, 2677-88.	1.2	62
62	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.	1.2	13
63	A unique stylopod patterning mechanism by <i>Shox2</i> controlled osteogenesis. <i>Development (Cambridge)</i> , 2016, 143, 2548-60.	1.2	15
64	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	3.5	663
65	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348
66	Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae. <i>Nature Plants</i> , 2015, 1, 15107.	4.7	89
67	The Joint Genome Institute's synthetic biology internal review process. <i>Journal of Responsible Innovation</i> , 2015, 2, 133-136.	2.3	0
68	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
69	Pbx Regulates Patterning of the Cerebral Cortex in Progenitors and Postmitotic Neurons. <i>Neuron</i> , 2015, 88, 1192-1207.	3.8	58
70	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. <i>Neuron</i> , 2015, 85, 27-47.	3.8	136
71	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. <i>Human Molecular Genetics</i> , 2015, 24, 3895-3907.	1.4	36
72	Disruptions of Topological Chromatin Domains Cause Pathogenic Rewiring of Gene-Enhancer Interactions. <i>Cell</i> , 2015, 161, 1012-1025.	13.5	1,725

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73	Fuzzy <scp>GIS</scp>â€based multiâ€criteria evaluation for US <i>Agave</i> production as a bioenergy feedstock. GCB Bioenergy, 2015, 7, 84-99.	2.5	25
74	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. PLoS Genetics, 2014, 10, e1004610.	1.5	105
75	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. Neuron, 2014, 82, 989-1003.	3.8	99
76	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	9.0	71
77	An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. Human Molecular Genetics, 2014, 23, 2711-2720.	1.4	55
78	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	2.4	63
79	Stop codon reassignments in the wild. Science, 2014, 344, 909-913.	6.0	124
80	Principles of regulatory information conservation between mouse and human. Nature, 2014, 515, 371-375.	13.7	259
81	HAND2 Targets Define a Network of Transcriptional Regulators that Compartmentalize the Early Limb Bud Mesenchyme. Developmental Cell, 2014, 31, 345-357.	3.1	98
82	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.	1.1	69
83	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. Nature Communications, 2014, 5, 4907.	5.8	142
84	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. Genome Research, 2014, 24, 1517-1525.	2.4	332
85	Multiple conserved regulatory domains promote Fezf2 expression in the developing cerebral cortex. Neural Development, 2014, 9, 6.	1.1	21
86	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531.	13.5	342
87	De novo transcriptome assembly of drought tolerant CAM plants, Agave deserti and Agave tequilana. BMC Genomics, 2013, 14, 563.	1.2	115
88	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
89	A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908.	13.5	241
90	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	6.0	209

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91	Functional anatomy of distant-acting mammalian enhancers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120359.	1.8	40
92	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
93	Congenital Heart Defects in Patients with Deletions Upstream of <i>SOX9</i> . <i>Human Mutation</i> , 2013, 34, 1628-1631.	1.1	33
94	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
95	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
96	Large-scale discovery of enhancers from human heart tissue. <i>Nature Genetics</i> , 2012, 44, 89-93.	9.4	257
97	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
98	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	6.0	1,135
99	The FaceBase Consortium: A comprehensive program to facilitate craniofacial research. <i>Developmental Biology</i> , 2011, 355, 175-182.	0.9	72
100	A liver enhancer in the fibrinogen gene cluster. <i>Blood</i> , 2011, 117, 276-282.	0.6	17
101	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. <i>Nature</i> , 2010, 464, 409-412.	13.7	425
102	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	9.4	395
103	Limits of sequence and functional conservation. <i>Nature Genetics</i> , 2010, 42, 557-558.	9.4	15
104	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
105	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.	1.1	79
106	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	13.7	1,526
107	Genomic views of distant-acting enhancers. <i>Nature</i> , 2009, 461, 199-205.	13.7	549
108	Functional autonomy of distant-acting human enhancers. <i>Genomics</i> , 2009, 93, 509-513.	1.3	56

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109	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. <i>Nature Genetics</i> , 2008, 40, 158-160.	9.4	299
110	Disruption of an AP-2 β binding site in an IRF6 enhancer is associated with cleft lip. <i>Nature Genetics</i> , 2008, 40, 1341-1347.	9.4	382
111	Human-Specific Gain of Function in a Developmental Enhancer. <i>Science</i> , 2008, 321, 1346-1350.	6.0	330
112	Transmembrane protein 50b (C21orf4), a candidate for Down syndrome neurophenotypes, encodes an intracellular membrane protein expressed in the rodent brain. <i>Neuroscience</i> , 2008, 154, 1255-1266.	1.1	30
113	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. <i>Cell</i> , 2008, 135, 1053-1064.	13.5	306
114	VISTA Enhancer Browser--a database of tissue-specific human enhancers. <i>Nucleic Acids Research</i> , 2007, 35, D88-D92.	6.5	950
115	Regulatory Pathway Analysis by High-Throughput In Situ Hybridization. <i>PLoS Genetics</i> , 2007, 3, e178.	1.5	55
116	Deletion of Ultraconserved Elements Yields Viable Mice. <i>PLoS Biology</i> , 2007, 5, e234.	2.6	255
117	Enhancer identification through comparative genomics. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 140-152.	2.3	97
118	Genome-wide atlas of gene expression in the adult mouse brain. <i>Nature</i> , 2007, 445, 168-176.	13.7	4,863
119	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	13.7	1,072
120	Comprehensive analysis of the expression patterns of the adenylate cyclase gene family in the developing and adult mouse brain. <i>Journal of Comparative Neurology</i> , 2006, 496, 684-697.	0.9	56
121	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.	0.8	142
122	GenePaint.org: an atlas of gene expression patterns in the mouse embryo. <i>Nucleic Acids Research</i> , 2004, 32, 552D-556.	6.5	455
123	Scaffolding by ERK3 regulates MK5 in development. <i>EMBO Journal</i> , 2004, 23, 4770-4779.	3.5	124
124	Expression of the winged helix/forkhead gene, foxn4, during zebrafish development. <i>Developmental Brain Research</i> , 2004, 153, 115-119.	2.1	17
125	Adenylate Cyclase 1 dependent refinement of retinotopic maps in the mouse. <i>Vision Research</i> , 2004, 44, 3357-3364.	0.7	19
126	A Gene Expression Map of the Mouse Brain. , 2003, , 19-35.		3

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127	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0