Axel Visel

List of Publications by Citations

133 papers	30,948 citations	60 h-index	166 g-index
166 ext. papers	39,293 ext. citations	20.7 avg, IF	8.16 L-index

#	Paper	IF	Citations
133	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
132	Genome-wide atlas of gene expression in the adult mouse brain. *Nature*, **2007**, 445, 168-76	50.4	3675
131	ChIP-seq accurately predicts tissue-specific activity of enhancers. *Nature*, **2009**, 457, 854-8	50.4	1301
130	Disruptions of topological chromatin domains cause pathogenic rewiring of gene-enhancer interactions. *Cell*, **2015**, 161, 1012-1025	56.2	1207
129	In vivo enhancer analysis of human conserved non-coding sequences. *Nature*, **2006**, 444, 499-502	50.4	911
128	Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. *Science*, **2011**, 331, 463-7	33.3	893
127	VISTA Enhancer Browser--a database of tissue-specific human enhancers. *Nucleic Acids Research*, **2007**, 35, D88-92	20.1	700
126	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, 17921-6	11.5	477
125	Genomic views of distant-acting enhancers. *Nature*, **2009**, 461, 199-205	50.4	451
124	GenePaint.org: an atlas of gene expression patterns in the mouse embryo. *Nucleic Acids Research*, **2004**, 32, D552-6	20.1	390
123	Plant compartment and biogeography affect microbiome composition in cultivated and native Agave species. *New Phytologist*, **2016**, 209, 798-811	9.8	380
122	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. *Nature*, **2010**, 464, 409-12	50.4	380
121	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
120	ChIP-Seq identification of weakly conserved heart enhancers. *Nature Genetics*, **2010**, 42, 806-10	36.3	343
119	Disruption of an AP-2alpha binding site in an IRF6 enhancer is associated with cleft lip. *Nature Genetics*, **2008**, 40, 1341-7	36.3	338
118	Enhancer redundancy provides phenotypic robustness in mammalian development. *Nature*, **2018**, 554, 239-243	50.4	275
117	Human-specific gain of function in a developmental enhancer. *Science*, **2008**, 321, 1346-50	33.3	260

116	Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. *Cell* , **2013**, 155, 1521-31	56.2	256
115	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. *Nature Genetics*, **2008**, 40, 158-60	36.3	253
114	Combinatorial regulation of endothelial gene expression by ets and forkhead transcription factors. *Cell*, **2008**, 135, 1053-64	56.2	245
113	Mutant phenotypes for thousands of bacterial genes of unknown function. *Nature*, **2018**, 557, 503-509	50.4	235
112	Deletion of ultraconserved elements yields viable mice. *PLoS Biology*, **2007**, 5, e234	9.7	217
111	The Epigenomic Landscape of Prokaryotes. *PLoS Genetics*, **2016**, 12, e1005854	6	198
110	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. *Genome Research*, **2014**, 24, 1517-25	9.7	197
109	Large-scale discovery of enhancers from human heart tissue. *Nature Genetics*, **2011**, 44, 89-93	36.3	197
108	Principles of regulatory information conservation between mouse and human. *Nature*, **2014**, 515, 371-375	50.4	190
107	A high-resolution enhancer atlas of the developing telencephalon. *Cell*, **2013**, 152, 895-908	56.2	189
106	Widespread adenine N6-methylation of active genes in fungi. *Nature Genetics*, **2017**, 49, 964-968	36.3	181
105	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. *Nature Neuroscience*, **2018**, 21, 432-439	25.5	172
104	Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. *Genome Research*, **2010**, 20, 565-77	9.7	167
103	1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life. *Nature Biotechnology*, **2017**, 35, 676-683	44.5	161
102	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. *Cell*, **2016**, 167, 633-642.e11	56.2	160
101	Fine tuning of craniofacial morphology by distant-acting enhancers. *Science*, **2013**, 342, 1241006	33.3	157
100	Germline Chd8 haploinsufficiency alters brain development in mouse. *Nature Neuroscience*, **2017**, 20, 1062-1073	25.5	136
99	Dlx1&2-dependent expression of Zfhx1b (Sip1, Zeb2) regulates the fate switch between cortical and striatal interneurons. *Neuron*, **2013**, 77, 83-98	13.9	122

98	A genomic catalog of Earth's microbiomes. *Nature Biotechnology*, **2021**, 39, 499-509	44.5	120
97	Comprehensive expression atlas of fibroblast growth factors and their receptors generated by a novel robotic in situ hybridization platform. *Developmental Dynamics*, **2005**, 234, 371-86	2.9	118
96	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. *Frontiers in Microbiology*, **2016**, 7, 150	5.7	112
95	Genomic perspectives of transcriptional regulation in forebrain development. *Neuron*, **2015**, 85, 27-47	13.9	109
94	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. *Nature Communications*, **2014**, 5, 4907	17.4	102
93	Ultraconserved Enhancers Are Required for Normal Development. *Cell*, **2018**, 172, 491-499.e15	56.2	101
92	Genome-wide identification of bacterial plant colonization genes. *PLoS Biology*, **2017**, 15, e2002860	9.7	101
91	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. *Nature Microbiology*, **2019**, 4, 1895-1906	26.6	99
90	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. *Nature Genetics*, **2018**, 50, 1463-1473	36.3	95
89	Scaffolding by ERK3 regulates MK5 in development. *EMBO Journal*, **2004**, 23, 4770-9	13	93
88	Stop codon reassignments in the wild. *Science*, **2014**, 344, 909-13	33.3	83
87	Enhancer identification through comparative genomics. *Seminars in Cell and Developmental Biology*, **2007**, 18, 140-52	7.5	81
86	Tissue-specific RNA expression marks distant-acting developmental enhancers. *PLoS Genetics*, **2014** , 10, e1004610	6	80
85	De novo transcriptome assembly of drought tolerant CAM plants, Agave deserti and Agave tequilana. *BMC Genomics*, **2013**, 14, 563	4.5	79
84	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
83	An atlas of dynamic chromatin landscapes in mouse fetal development. *Nature*, **2020**, 583, 744-751	50.4	76
82	Transcriptional regulation of enhancers active in protodomains of the developing cerebral cortex. *Neuron*, **2014**, 82, 989-1003	13.9	73
81	Transcriptional Networks Controlled by NKX2-1 in the Development of Forebrain GABAergic Neurons. *Neuron*, **2016**, 91, 1260-1275	13.9	71

80	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	5.8	71
79	Composition and dosage of a multipartite enhancer cluster control developmental expression of Ihh (Indian hedgehog). *Nature Genetics*, **2017**, 49, 1539-1545	36.3	70
78	HAND2 targets define a network of transcriptional regulators that compartmentalize the early limb bud mesenchyme. *Developmental Cell*, **2014**, 31, 345-357	10.2	69
77	Transcriptional control of axonal guidance and sorting in dorsal interneurons by the Lim-HD proteins Lhx9 and Lhx1. *Neural Development*, **2009**, 4, 21	3.9	68
76	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**,	11.5	68
75	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
74	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	11.5	60
73	Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae. *Nature Plants*, **2015**, 1, 15107	11.5	60
72	Function-based identification of mammalian enhancers using site-specific integration. *Nature Methods*, **2014**, 11, 566-71	21.6	59
71	The FaceBase Consortium: a comprehensive program to facilitate craniofacial research. *Developmental Biology*, **2011**, 355, 175-82	3.1	59
70	Identification of novel craniofacial regulatory domains located far upstream of SOX9 and disrupted in Pierre Robin sequence. *Human Mutation*, **2014**, 35, 1011-20	4.7	54
69	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. *Cell*, **2019**, 177, 32-37	56.2	53
68	Genome-wide compendium and functional assessment of in vivo heart enhancers. *Nature Communications*, **2016**, 7, 12923	17.4	51
67	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, 684-97	3.4	51
66	Regulatory pathway analysis by high-throughput in situ hybridization. *PLoS Genetics*, **2007**, 3, 1867-83	6	50
65	Functional autonomy of distant-acting human enhancers. *Genomics*, **2009**, 93, 509-13	4.3	49
64	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. *Nature Microbiology*, **2019**, 4, 2498-2510	26.6	48
63	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. *Genome Research*, **2014**, 24, 920-9	9.7	47

62	Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by HOX13. *Cell Reports*, **2016**, 17, 2913-2926	10.6	46
61	Subpallial Enhancer Transgenic Lines: a Data and Tool Resource to Study Transcriptional Regulation of GABAergic Cell Fate. *Neuron*, **2016**, 92, 59-74	13.9	46
60	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. *Cell Stem Cell*, **2019**, 25, 69-86.e5	18	45
59	Dlx1 and Dlx2 Promote Interneuron GABA Synthesis, Synaptogenesis, and Dendritogenesis. *Cerebral Cortex*, **2018**, 28, 3797-3815	5.1	42
58	An etiologic regulatory mutation in IRF6 with loss- and gain-of-function effects. *Human Molecular Genetics*, **2014**, 23, 2711-20	5.6	39
57	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. *Nature*, **2020**, 583, 760-767	50.4	39
56	Pbx Regulates Patterning of the Cerebral Cortex in Progenitors and Postmitotic Neurons. *Neuron*, **2015**, 88, 1192-1207	13.9	37
55	The FaceBase Consortium: a comprehensive resource for craniofacial researchers. *Development (Cambridge)*, **2016**, 143, 2677-88	6.6	35
54	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. *Nature*, **2020**, 583, 752-759	50.4	35
53	Comprehensive In Vivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. *Cell*, **2020**, 180, 1262-1271.e15	56.2	34
52	HAND2 Target Gene Regulatory Networks Control Atrioventricular Canal and Cardiac Valve Development. *Cell Reports*, **2017**, 19, 1602-1613	10.6	30
51	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, 3895-907	5.6	30
50	Functional anatomy of distant-acting mammalian enhancers. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2013**, 368, 20120359	5.8	30
49	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. *Cell Reports*, **2019**, 28, 2048-2063.e8	10.6	29
48	Congenital heart defects in patients with deletions upstream of SOX9. *Human Mutation*, **2013**, 34, 1628-31	4.7	27
47	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. *BMC Genomics*, **2018**, 19, 588	4.5	25
46	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	3.7	25
45	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. *Cell Stem Cell*, **2020**, 27, 765-783.e14	18	24

44	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. *Nature Methods*, **2020**, 17, 807-814	21.6	24
43	Multilab EcoFAB study shows highly reproducible physiology and depletion of soil metabolites by a model grass. *New Phytologist*, **2019**, 222, 1149-1160	9.8	22
42	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. *Cell*, **2016**, 167, 1163-1166	56.2	19
41	Adenylate Cyclase 1 dependent refinement of retinotopic maps in the mouse. *Vision Research*, **2004** , 44, 3357-64	2.1	19
40	Fuzzy GIS-based multi-criteria evaluation for US Agave production as a bioenergy feedstock. *GCB Bioenergy*, **2015**, 7, 84-99	5.6	17
39	Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression. *BMC Genomics*, **2012**, 13, 713	4.5	16
38	A liver enhancer in the fibrinogen gene cluster. *Blood*, **2011**, 117, 276-82	2.2	16
37	Expression of the winged helix/forkhead gene, foxn4, during zebrafish development. *Developmental Brain Research*, **2004**, 153, 115-9		15
36	Systematic mapping of chromatin state landscapes during mouse development		15
35	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. *American Journal of Human Genetics*, **2018**, 103, 874-892	11	15
34	Bi-fated tendon-to-bone attachment cells are regulated by shared enhancers and KLF transcription factors. *ELife*, **2021**, 10,	8.9	15
33	Multiple conserved regulatory domains promote Fezf2 expression in the developing cerebral cortex. *Neural Development*, **2014**, 9, 6	3.9	14
32	Noncoding deletions reveal a gene that is critical for intestinal function. *Nature*, **2019**, 571, 107-111	50.4	12
31	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. *PLoS Computational Biology*, **2017**, 13, e1005720	5	12
30	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human. *ELife*, **2020**, 9,	8.9	11
29	Spatiotemporal DNA Methylome Dynamics of the Developing Mammalian Fetus		11
28	A unique stylopod patterning mechanism by Shox2-controlled osteogenesis. *Development (Cambridge)*, **2016**, 143, 2548-60	6.6	10
27	Transmembrane protein 50b (C21orf4), a candidate for Down syndrome neurophenotypes, encodes an intracellular membrane protein expressed in the rodent brain. *Neuroscience*, **2008**, 154, 1255-66	3.9	10

26	Ultraconserved enhancer function does not require perfect sequence conservation. *Nature Genetics* , **2021**, 53, 521-528	36.3	10
25	A distal 594 bp ECR specifies Hmx1 expression in pinna and lateral facial morphogenesis and is regulated by the Hox-Pbx-Meis complex. *Development (Cambridge)*, **2016**, 143, 2582-92	6.6	9
24	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. *Science*, **2020**, 370, 208-214	33.3	9
23	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. *Development (Cambridge)*, **2020**, 147,	6.6	8
22	Genome-Wide Fetalization of Enhancer Architecture in Heart Disease		6
21	A cross-organism framework for supervised enhancer prediction with epigenetic pattern recognition and targeted validation		5
20	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. *Genome Medicine*, **2021**, 13, 69	14.4	5
19	Plant single-cell solutions for energy and the environment. *Communications Biology*, **2021**, 4, 962	6.7	5
18	Interrogating the Grainyhead-like 2 (Grhl2) genomic locus identifies an enhancer element that regulates palatogenesis in mouse. *Developmental Biology*, **2020**, 459, 194-203	3.1	4
17	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. *Genome Biology*, **2019**, 20, 140	18.3	3
16	Multi-lab EcoFAB study shows highly reproducible physiology and depletion of soil metabolites by a model grass		3
15	A Gene Expression Map of the Mouse Brain **2003**, 19-35		3
14	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. *Communications Biology*, **2021**, 4, 1302	6.7	2
13	Single nucleus analysis of the chromatin landscape in mouse forebrain development		2
12	Transcriptional Network Orchestrating Regional Patterning of Cortical Progenitors		2
11	Cryptic inoviruses are pervasive in bacteria and archaea across Earth biomes		2
10	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics		2
9	Transcriptional network orchestrating regional patterning of cortical progenitors.. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2

8	Perfect and imperfect views of ultraconserved sequences. *Nature Reviews Genetics*, **2021**,	30.1	1
7	SMAD4 target genes are part of a transcriptional network that integrates the response to BMP and SHH signaling during early limb bud patterning. *Development (Cambridge)*, **2021**, 148,	6.6	1
6	Heterozygous mutation to Chd8 causes macrocephaly and widespread alteration of neurodevelopmental transcriptional networks in mouse		1
5	Power in isolation: insights from single cells. *Nature Reviews Microbiology*, **2020**, 18, 364	22.2	0
4	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing.. *Methods in Molecular Biology*, **2022**, 2403, 147-186	1.4	0
3	The Joint Genome Institute's synthetic biology internal review process. *Journal of Responsible Innovation*, **2015**, 2, 133-136	2.1	
2	Regulatory Dynamics of Midfacial Growth in Evolution and Disease. *FASEB Journal*, **2020**, 34, 1-1	0.9	
1	Fishing for Function in the Human Gene Pool. *Trends in Genetics*, **2016**, 32, 392-394	8.5	