

Axel Visel

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4373633/publications.pdf>

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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Genome-wide atlas of gene expression in the adult mouse brain. <i>Nature</i> , 2007, 445, 168-176.	13.7	4,863
3	Disruptions of Topological Chromatin Domains Cause Pathogenic Rewiring of Gene-Enhancer Interactions. <i>Cell</i> , 2015, 161, 1012-1025.	13.5	1,725
4	ChIP-seq accurately predicts tissue-specific activity of enhancers. <i>Nature</i> , 2009, 457, 854-858.	13.7	1,526
5	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
6	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	6.0	1,135
7	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	13.7	1,072
8	VISTA Enhancer Browser--a database of tissue-specific human enhancers. <i>Nucleic Acids Research</i> , 2007, 35, D88-D92.	6.5	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.	3.5	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.	3.3	606
11	Genomic views of distant-acting enhancers. <i>Nature</i> , 2009, 461, 199-205.	13.7	549
12	Enhancer redundancy provides phenotypic robustness in mammalian development. <i>Nature</i> , 2018, 554, 239-243.	13.7	514
13	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
14	GenePaint.org: an atlas of gene expression patterns in the mouse embryo. <i>Nucleic Acids Research</i> , 2004, 32, 552D-556.	6.5	455
15	Mutant phenotypes for thousands of bacterial genes of unknown function. <i>Nature</i> , 2018, 557, 503-509.	13.7	433
16	Targeted deletion of the 9p21 non-coding coronary artery disease risk interval in mice. <i>Nature</i> , 2010, 464, 409-412.	13.7	425
17	ChIP-Seq identification of weakly conserved heart enhancers. <i>Nature Genetics</i> , 2010, 42, 806-810.	9.4	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.	9.4	382

#	ARTICLE	IF	CITATIONS
19	The Epigenomic Landscape of Prokaryotes. <i>PLoS Genetics</i> , 2016, 12, e1005854.	1.5	348
20	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. <i>Cell</i> , 2013, 155, 1521-1531.	13.5	342
21	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332
22	Human-Specific Gain of Function in a Developmental Enhancer. <i>Science</i> , 2008, 321, 1346-1350.	6.0	330
23	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. <i>Cell</i> , 2008, 135, 1053-1064.	13.5	306
24	Ultraconservation identifies a small subset of extremely constrained developmental enhancers. <i>Nature Genetics</i> , 2008, 40, 158-160.	9.4	299
25	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	9.4	292
26	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. <i>Nature Neuroscience</i> , 2018, 21, 432-439.	7.1	290
27	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. <i>Cell</i> , 2016, 167, 633-642.e11.	13.5	275
28	Principles of regulatory information conservation between mouse and human. <i>Nature</i> , 2014, 515, 371-375.	13.7	259
29	Large-scale discovery of enhancers from human heart tissue. <i>Nature Genetics</i> , 2012, 44, 89-93.	9.4	257
30	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
31	Deletion of Ultraconserved Elements Yields Viable Mice. <i>PLoS Biology</i> , 2007, 5, e234.	2.6	255
32	A High-Resolution Enhancer Atlas of the Developing Telencephalon. <i>Cell</i> , 2013, 152, 895-908.	13.5	241
33	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
34	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. <i>Frontiers in Microbiology</i> , 2016, 7, 150.	1.5	219
35	Germline Chd8 haploinsufficiency alters brain development in mouse. <i>Nature Neuroscience</i> , 2017, 20, 1062-1073.	7.1	210
36	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. <i>Science</i> , 2013, 342, 1241006.	6.0	209

#	ARTICLE	IF	CITATIONS
37	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	5.9	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.	2.4	203
39	Genome-wide identification of bacterial plant colonization genes. <i>PLoS Biology</i> , 2017, 15, e2002860.	2.6	173
40	Ultraconserved Enhancers Are Required for Normal Development. <i>Cell</i> , 2018, 172, 491-499.e15.	13.5	169
41	Dynamic 3D chromatin architecture contributes to enhancer specificity and limb morphogenesis. <i>Nature Genetics</i> , 2018, 50, 1463-1473.	9.4	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.	0.8	142
43	Dynamic GATA4 enhancers shape the chromatin landscape central to heart development and disease. <i>Nature Communications</i> , 2014, 5, 4907.	5.8	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.	3.8	140
45	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. <i>Neuron</i> , 2015, 85, 27-47.	3.8	136
46	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. <i>Nature</i> , 2020, 583, 760-767.	13.7	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.	3.3	129
48	Scaffolding by ERK3 regulates MK5 in development. <i>EMBO Journal</i> , 2004, 23, 4770-4779.	3.5	124
49	Stop codon reassignments in the wild. <i>Science</i> , 2014, 344, 909-913.	6.0	124
50	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
51	Transcriptional Networks Controlled by NKX2-1 in the Development of Forebrain GABAergic Neurons. <i>Neuron</i> , 2016, 91, 1260-1275.	3.8	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.	1.2	115
53	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
54	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. <i>Cell</i> , 2019, 177, 32-37.	13.5	113

#	ARTICLE	IF	CITATIONS
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.	9.4	107
56	Tissue-Specific RNA Expression Marks Distant-Acting Developmental Enhancers. <i>PLoS Genetics</i> , 2014, 10, e1004610.	1.5	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.	5.2	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.	1.8	100
59	Comprehensive In Vivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. <i>Cell</i> , 2020, 180, 1262-1271.e15.	13.5	100
60	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. <i>Neuron</i> , 2014, 82, 989-1003.	3.8	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.	3.1	98
62	Enhancer identification through comparative genomics. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 140-152.	2.3	97
63	Lineage-specific chromatin signatures reveal a regulator of lipid metabolism in microalgae. <i>Nature Plants</i> , 2015, 1, 15107.	4.7	89
64	CRAGE enables rapid activation of biosynthetic gene clusters in undomesticated bacteria. <i>Nature Microbiology</i> , 2019, 4, 2498-2510.	5.9	85
65	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
66	Genome-wide compendium and functional assessment of in vivo heart enhancers. <i>Nature Communications</i> , 2016, 7, 12923.	5.8	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.	1.1	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.	3.3	78
69	The FaceBase Consortium: A comprehensive program to facilitate craniofacial research. <i>Developmental Biology</i> , 2011, 355, 175-182.	0.9	72
70	Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by <i>HOX13</i> . <i>Cell Reports</i> , 2016, 17, 2913-2926.	2.9	72
71	<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
72	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. <i>Cell Stem Cell</i> , 2019, 25, 69-86.e5.	5.2	72

#	ARTICLE	IF	CITATIONS
73	Function-based identification of mammalian enhancers using site-specific integration. <i>Nature Methods</i> , 2014, 11, 566-571.	9.0	71
74	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. <i>Nature Methods</i> , 2020, 17, 807-814.	9.0	71
75	Identification of Novel Craniofacial Regulatory Domains Located far Upstream of <i>SOX9</i> and Disrupted in Pierre Robin Sequence. <i>Human Mutation</i> , 2014, 35, 1011-1020.	1.1	69
76	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>Cell Reports</i> , 2019, 28, 2048-2063.e8.	2.9	68
77	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
78	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014, 24, 920-929.	2.4	63
79	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
80	The FaceBase Consortium: A comprehensive resource for craniofacial researchers. <i>Development (Cambridge)</i> , 2016, 143, 2677-88.	1.2	62
81	Pbx Regulates Patterning of the Cerebral Cortex in Progenitors and Postmitotic Neurons. <i>Neuron</i> , 2015, 88, 1192-1207.	3.8	58
82	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
83	Functional autonomy of distant-acting human enhancers. <i>Genomics</i> , 2009, 93, 509-513.	1.3	56
84	Regulatory Pathway Analysis by High-Throughput In Situ Hybridization. <i>PLoS Genetics</i> , 2007, 3, e178.	1.5	55
85	An etiologic regulatory mutation in <i>IRF6</i> with loss- and gain-of-function effects. <i>Human Molecular Genetics</i> , 2014, 23, 2711-2720.	1.4	55
86	Multilab EcoFAB study shows highly reproducible physiology and depletion of soil metabolites by a model grass. <i>New Phytologist</i> , 2019, 222, 1149-1160.	3.5	55
87	HAND2 Target Gene Regulatory Networks Control Atrioventricular Canal and Cardiac Valve Development. <i>Cell Reports</i> , 2017, 19, 1602-1613.	2.9	50
88	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. <i>Science</i> , 2020, 370, 208-214.	6.0	41
89	Functional anatomy of distant-acting mammalian enhancers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120359.	1.8	40
90	Ultraconserved enhancer function does not require perfect sequence conservation. <i>Nature Genetics</i> , 2021, 53, 521-528.	9.4	39

#	ARTICLE	IF	CITATIONS
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. <i>Human Molecular Genetics</i> , 2015, 24, 3895-3907.	1.4	36
92	Bi-fated tendon-to-bone attachment cells are regulated by shared enhancers and KLF transcription factors. <i>ELife</i> , 2021, 10, .	2.8	36
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	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
95	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
96	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
97	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. <i>Cell</i> , 2016, 167, 1163-1166.	13.5	27
98	Fuzzy GIS-based multi-criteria evaluation for US <i>Agave</i> production as a bioenergy feedstock. <i>GCB Bioenergy</i> , 2015, 7, 84-99.	2.5	25
99	FaceBase 3: analytical tools and FAIR resources for craniofacial and dental research. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	25
100	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
101	Noncoding deletions reveal a gene that is critical for intestinal function. <i>Nature</i> , 2019, 571, 107-111.	13.7	24
102	Plant single-cell solutions for energy and the environment. <i>Communications Biology</i> , 2021, 4, 962.	2.0	23
103	Analysis of zebrafish periderm enhancers facilitates identification of a regulatory variant near human KRT8/18. <i>ELife</i> , 2020, 9, .	2.8	23
104	Multiple conserved regulatory domains promote Fezf2 expression in the developing cerebral cortex. <i>Neural Development</i> , 2014, 9, 6.	1.1	21
105	Long-read metagenomics of soil communities reveals phylum-specific secondary metabolite dynamics. <i>Communications Biology</i> , 2021, 4, 1302.	2.0	21
106	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
107	Adenylate Cyclase 1 dependent refinement of retinotopic maps in the mouse. <i>Vision Research</i> , 2004, 44, 3357-3364.	0.7	19
108	Expression of the winged helix/forkhead gene, foxn4, during zebrafish development. <i>Developmental Brain Research</i> , 2004, 153, 115-119.	2.1	17

#	ARTICLE	IF	CITATIONS
109	A liver enhancer in the fibrinogen gene cluster. <i>Blood</i> , 2011, 117, 276-282.	0.6	17
110	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
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.	1.2	16
112	Perfect and imperfect views of ultraconserved sequences. <i>Nature Reviews Genetics</i> , 2022, 23, 182-194.	7.7	16
113	Limits of sequence and functional conservation. <i>Nature Genetics</i> , 2010, 42, 557-558.	9.4	15
114	A unique stylopod patterning mechanism by <i>Shox2</i> controlled osteogenesis. <i>Development (Cambridge)</i> , 2016, 143, 2548-60.	1.2	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.	3.6	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.	1.2	13
117	Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. <i>Genome Biology</i> , 2019, 20, 140.	3.8	11
118	Interrogating the Grainyhead-like 2 (<i>Grl2</i>) genomic locus identifies an enhancer element that regulates palatogenesis in mouse. <i>Developmental Biology</i> , 2020, 459, 194-203.	0.9	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, .	1.2	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, .	2.4	3
122	Power in isolation: insights from single cells. <i>Nature Reviews Microbiology</i> , 2020, 18, 364-364.	13.6	2
123	The Joint Genome Institute's synthetic biology internal review process. <i>Journal of Responsible Innovation</i> , 2015, 2, 133-136.	2.3	0
124	Fishing for Function in the Human Gene Pool. <i>Trends in Genetics</i> , 2016, 32, 392-394.	2.9	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, .	0.2	0
126	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
127	Regulatory Dynamics of Midfacial Growth in Evolution and Disease. FASEB Journal, 2020, 34, 1-1.	0.2	0