Luca Pinello

List of Publications by Year
in descending order

87 papers	10,067 citations	71061 41 h-index	49868 87 g-index
115 all docs	115 docs citations	115 times ranked	15929 citing authors

#	Article	IF	Citations
1	CRISPR prime editing with ribonucleoprotein complexes in zebrafish and primary human cells. Nature Biotechnology, 2022, 40, 189-193.	9.4	118
2	Targeting leukemia-specific dependence on the de novo purine synthesis pathway. Leukemia, 2022, 36, 383-393.	3.3	11
3	Epigenetic Alterations in Keratinocyte Carcinoma. Journal of Investigative Dermatology, 2021, 141, 1207-1218.	0.3	9
4	PrimeDesign software for rapid and simplified design of prime editing guide RNAs. Nature Communications, 2021, 12, 1034.	5.8	105
5	Motif-Raptor: a cell type-specific and transcription factor centric approach for post-GWAS prioritization of causal regulators. Bioinformatics, 2021, 37, 2103-2111.	1.8	5
6	Transcription factor competition at the Î³-globin promoters controls hemoglobin switching. Nature Genetics, 2021, 53, 511-520.	9.4	43
7	ZNF410 represses fetal globin by singular control of CHD4. Nature Genetics, 2021, 53, 719-728.	9.4	35
8	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. Cell Stem Cell, 2021, 28, 833-845.e5.	5.2	23
9	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. Current Opinion in Systems Biology, 2021, 26, 1-11.	1.3	8
10	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	9.0	17
11	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5
12	Hedgehog interacting proteinâ€"expressing lung fibroblasts suppress lymphocytic inflammation in mice. JCI Insight, 2021, 6, .	2.3	9
13	Three subtypes of lung cancer fibroblasts define distinct therapeutic paradigms. Cancer Cell, 2021, 39, 1531-1547.e10.	7.7	106
14	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. Frontiers in Genetics, 2021, 12, 764170.	1.1	14
15	Human Genetic Diversity Alters Therapeutic Gene Editing Off-Target Outcomes. Blood, 2021, 138, 3993-3993.	0.6	0
16	CRISPRitz: rapid, high-throughput and variant-aware *in silico* off-target site identification for CRISPR genome editing. Bioinformatics, 2020, 36, 2001-2008.	1.8	41
17	Parallel Single-Cell RNA-Seq and Genetic Recording Reveals Lineage Decisions in Developing Embryoid Bodies. Cell Reports, 2020, 33, 108222.	2.9	16
18	High throughput single-cell detection of multiplex CRISPR-edited gene modifications. Genome Biology, 2020, 21, 266.	3.8	23

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19	Therapeutic base editing of human hematopoietic stem cells. Nature Medicine, 2020, 26, 535-541.	15.2	196
20	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ElPiGraph. Entropy, 2020, 22, 296.	1.1	45
21	Technologies and Computational Analysis Strategies for CRISPR Applications. Molecular Cell, 2020, 79, 11-29.	4.5	28
22	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
23	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. Cell Reports, 2020, 33, 108566.	2.9	75
24	A saturating mutagenesis CRISPR-Cas9–mediated functional genomic screen identifies cis- and trans-regulatory elements of Oct4 in murine ESCs. Journal of Biological Chemistry, 2020, 295, 15797-15809.	1.6	6
25	LSD1 suppresses invasion, migration and metastasis of luminal breast cancer cells via activation of GATA3 and repression of TRIM37 expression. Oncogene, 2019, 38, 7017-7034.	2.6	48
26	Rational targeting of a NuRD subcomplex guided by comprehensive in situ mutagenesis. Nature Genetics, 2019, 51, 1149-1159.	9.4	83
27	Editing aberrant splice sites efficiently restores Î²-globin expression in Î²-thalassemia. Blood, 2019, 133, 2255-2262.	0.6	57
28	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	5.8	198
29	TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. Molecular Cell, 2019, 74, 1148-1163.e7.	4.5	36
30	CRISPR-suppressor scanning reveals a nonenzymatic role of LSD1 in AML. Nature Chemical Biology, 2019, 15, 529-539.	3.9	71
31	Highly efficient therapeutic gene editing of human hematopoietic stem cells. Nature Medicine, 2019, 25, 776-783.	15.2	344
32	Engineered CRISPR–Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	9.4	439
33	CRISPResso2 provides accurate and rapid genome editing sequence analysis. Nature Biotechnology, 2019, 37, 224-226.	9.4	891
34	Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241.	3.8	225
35	DrugThatGene: integrative analysis to streamline the identification of druggable genes, pathways and protein complexes from CRISPR screens. Bioinformatics, 2019, 35, 1981-1984.	1.8	3
36	Genome-wide CRISPR-Cas9 Screen Identifies Leukemia-Specific Dependence on a Pre-mRNA Metabolic Pathway Regulated by DCPS. Cancer Cell, 2018, 33, 386-400.e5.	7.7	99

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37	Impact of Genetic Variation on CRISPR-Cas Targeting. CRISPR Journal, 2018, 1, 159-170.	1.4	24
38	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986.	5.5	70
39	Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. Bioinformatics, 2018, 34, 1930-1933.	1.8	16
40	Response to "Unexpected mutations after CRISPR–Cas9 editing in vivo" Nature Methods, 2018, 15, 238-239.	9.0	25
41	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. Nature Methods, 2018, 15, 992-993.	9.0	33
42	CRISPRO: identification of functional protein coding sequences based on genome editing dense mutagenesis. Genome Biology, 2018, 19, 169.	3.8	34
43	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	13.7	274
44	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
45	AmpUMI: design and analysis of unique molecular identifiers for deep amplicon sequencing. Bioinformatics, 2018, 34, i202-i210.	1.8	28
46	An APOBEC3A-Cas9 base editor with minimized bystander and off-target activities. Nature Biotechnology, 2018, 36, 977-982.	9.4	328
47	A molecular roadmap for induced multi-lineage trans-differentiation of fibroblasts by chemical combinations. Cell Research, 2017, 27, 386-401.	5.7	20
48	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. Nature Genetics, 2017, 49, 625-634.	9.4	96
49	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. Nature Communications, 2017, 8, 15011.	5.8	40
50	The histone demethylase UTX regulates the lineage-specific epigenetic program of invariant natural killer T cells. Nature Immunology, 2017, 18, 184-195.	7.0	56
51	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. Journal of Experimental Medicine, 2017, 214, 2875-2887.	4.2	168
52	Identification of Transcribed Enhancers by Genome-Wide Chromatin Immunoprecipitation Sequencing. Methods in Molecular Biology, 2017, 1468, 91-109.	0.4	15
53	The role of Cdx2 as a lineage specific transcriptional repressor for pluripotent network during the first developmental cell lineage segregation. Scientific Reports, 2017, 7, 17156.	1.6	58
54	Gene regulatory pattern analysis reveals essential role of core transcriptional factors' activation in triple-negative breast cancer. Oncotarget, 2017, 8, 21938-21953.	0.8	13

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55	Forward genetic screen of human transposase genomic rearrangements. BMC Genomics, 2016, 17, 548.	1.2	13
56	Analyzing CRISPR genome-editing experiments with CRISPResso. Nature Biotechnology, 2016, 34, 695-697.	9.4	410
57	GiniClust: detecting rare cell types from single-cell gene expression data with Gini index. Genome Biology, 2016, 17, 144.	3.8	238
58	Acquired Tissue-Specific Promoter Bivalency Is a Basis for PRC2 Necessity in Adult Cells. Cell, 2016, 165, 1389-1400.	13.5	101
59	High-fat diet enhances stemness and tumorigenicity of intestinal progenitors. Nature, 2016, 531, 53-58.	13.7	602
60	The cohesin-associated protein Wapal is required for proper Polycomb-mediated gene silencing. Epigenetics and Chromatin, 2016, 9, 14.	1.8	10
61	Serum-Based Culture Conditions Provoke Gene Expression Variability in Mouse Embryonic Stem Cells as Revealed by Single-Cell Analysis. Cell Reports, 2016, 14, 956-965.	2.9	73
62	Functionally distinct patterns of nucleosome remodeling at enhancers in glucocorticoid-treated acute lymphoblastic leukemia. Epigenetics and Chromatin, 2015, 8, 53.	1.8	22
63	Predicting chromatin organization using histone marks. Genome Biology, 2015, 16, 162.	3.8	98
64	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. Molecular Cell, 2015, 57, 636-647.	4.5	363
65	Developmental Control of Polycomb Subunit Composition by GATA Factors Mediates a Switch to Non-Canonical Functions. Molecular Cell, 2015, 57, 304-316.	4.5	119
66	Impact of the N-Terminal Domain of STAT3 in STAT3-Dependent Transcriptional Activity. Molecular and Cellular Biology, 2015, 35, 3284-3300.	1.1	44
67	A New Feature Selection Methodology for K-mers Representation of DNA Sequences. Lecture Notes in Computer Science, 2015, , 99-108.	1.0	9
68	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. Nature, 2015, 527, 192-197.	13.7	726
69	Analysis of chromatin-state plasticity identifies cell-type-specific regulators of H3K27me3 patterns. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E344-53.	3.3	66
70	Applications of alignment-free methods in epigenomics. Briefings in Bioinformatics, 2014, 15, 419-430.	3.2	40
71	Distinct and Combinatorial Functions of Jmjd2b/Kdm4b and Jmjd2c/Kdm4c in Mouse Embryonic Stem Cell Identity. Molecular Cell, 2014, 53, 32-48.	4.5	112
72	LincRNA-p21 Regulates Neointima Formation, Vascular Smooth Muscle Cell Proliferation, Apoptosis, and Atherosclerosis by Enhancing p53 Activity. Circulation, 2014, 130, 1452-1465.	1.6	425

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73	A methodology to assess the intrinsic discriminative ability of a distance function and its interplay with clustering algorithms for microarray data analysis. BMC Bioinformatics, 2013, 14, S6.	1.2	7
74	An Erythroid Enhancer of *BCL11A* Subject to Genetic Variation Determines Fetal Hemoglobin Level. Science, 2013, 342, 253-257.	6.0	518
75	Enhancer transcribed RNAs arise from hypomethylated, Tet-occupied genomic regions. Epigenetics, 2013, 8, 1303-1320.	1.3	55
76	STAT5 Outcompetes STAT3 To Regulate the Expression of the Oncogenic Transcriptional Modulator BCL6. Molecular and Cellular Biology, 2013, 33, 2879-2890.	1.1	77
77	Combinatorial Assembly of Developmental Stage-Specific Enhancers Controls Gene Expression Programs during Human Erythropoiesis. Developmental Cell, 2012, 23, 796-811.	3.1	183
78	Genome-wide characterization of chromatin binding and nucleosome spacing activity of the nucleosome remodelling ATPase ISWI. EMBO Journal, 2011, 30, 1766-1777.	3.5	54
79	A motif-independent metric for DNA sequence specificity. BMC Bioinformatics, 2011, 12, 408.	1.2	18
80	A New Dissimilarity Measure for Clustering Seismic Signals. Lecture Notes in Computer Science, 2011, , 434-443.	1.0	2
81	Distance Functions, Clustering Algorithms and Microarray Data Analysis. Lecture Notes in Computer Science, 2010, , 125-138.	1.0	21
82	A multi-layer method to study genome-scale positions of nucleosomes. Genomics, 2009, 93, 140-145.	1.3	18
83	A Fuzzy One Class Classifier for Multi Layer Model. Lecture Notes in Computer Science, 2009, , 124-131.	1.0	5
84	Interval Length Analysis in Multi Layer Model. Lecture Notes in Computer Science, 2009, , 114-122.	1.0	0
85	A One Class Classifier for Signal Identification: A Biological Case Study. Lecture Notes in Computer Science, 2008, , 747-754.	1.0	5
86	A New Multi-Layers Method to Analyze Gene Expression. Lecture Notes in Computer Science, 2007, , 862-869.	1.0	4
87	A MULTI-LAYER MODEL TO STUDY GENOME-SCALE POSITIONS OF NUCLEOSOMES. , 2007, , .		1