

Matteo Pellegrini

List of Publications by Year in descending order

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Version: 2024-02-01

361
papers

34,745
citations

4955

84
h-index

4770

169
g-index

403
all docs

403
docs citations

403
times ranked

41791
citing authors

#	ARTICLE	IF	CITATIONS
1	Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. Nature, 2008, 452, 215-219.	13.7	2,039
2	Assigning protein functions by comparative genome analysis: Protein phylogenetic profiles. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 4285-4288.	3.3	1,653
3	Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. Cell, 2006, 126, 1189-1201.	13.5	1,647
4	Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. Science, 1999, 285, 751-753.	6.0	1,595
5	Conservation and divergence of methylation patterning in plants and animals. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8689-8694.	3.3	1,160
6	A combined algorithm for genome-wide prediction of protein function. Nature, 1999, 402, 83-86.	13.7	879
7	Genome-wide erasure of DNA methylation in mouse primordial germ cells is affected by AID deficiency. Nature, 2010, 463, 1101-1105.	13.7	777
8	Whole-Genome Analysis of Histone H3 Lysine 27 Trimethylation in Arabidopsis. PLoS Biology, 2007, 5, e129.	2.6	667
9	Pioneer Transcription Factors Target Partial DNA Motifs on Nucleosomes to Initiate Reprogramming. Cell, 2015, 161, 555-568.	13.5	643
10	Relationship between nucleosome positioning and DNA methylation. Nature, 2010, 466, 388-392.	13.7	625
11	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. Genome Biology, 2009, 10, R62.	13.9	504
12	Promoter CpG Methylation Contributes to ES Cell Gene Regulation in Parallel with Oct4/Nanog, PcG Complex, and Histone H3 K4/K27 Trimethylation. Cell Stem Cell, 2008, 2, 160-169.	5.2	395
13	A census of protein repeats. Journal of Molecular Biology, 1999, 293, 151-160.	2.0	385
14	Distinct Shifts in Microbiota Composition during Drosophila Aging Impair Intestinal Function and Drive Mortality. Cell Reports, 2015, 12, 1656-1667.	2.9	382
15	Three Acyltransferases and Nitrogen-responsive Regulator Are Implicated in Nitrogen Starvation-induced Triacylglycerol Accumulation in Chlamydomonas. Journal of Biological Chemistry, 2012, 287, 15811-15825.	1.6	379
16	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	7.7	367
17	BS-Seeker2: a versatile aligning pipeline for bisulfite sequencing data. BMC Genomics, 2013, 14, 774.	1.2	365
18	Nitrogen-Sparing Mechanisms in <i>Chlamydomonas</i> Affect the Transcriptome, the Proteome, and Photosynthetic Metabolism. Plant Cell, 2014, 26, 1410-1435.	3.1	314

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19	DNA methylation dynamics, metabolic fluxes, gene splicing, and alternative phenotypes in honey bees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4968-4973.	3.3	312
20	Genome-Wide Association of Histone H3 Lysine Nine Methylation with CHG DNA Methylation in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2008, 3, e3156.	1.1	293
21	Transcriptome Sequencing Identifies <i>SPL7</i> -Regulated Copper Acquisition Genes <i>FRO4</i> and <i>FRO5</i> and the Copper Dependence of Iron Homeostasis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 738-761.	3.1	286
22	Genome-wide Hi-C Analyses in Wild-Type and Mutants Reveal High-Resolution Chromatin Interactions in <i>Arabidopsis</i> . <i>Molecular Cell</i> , 2014, 55, 694-707.	4.5	283
23	A revised mineral nutrient supplement increases biomass and growth rate in <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2011, 66, 770-780.	2.8	282
24	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. <i>Science</i> , 2012, 336, 1448-1451.	6.0	279
25	ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 763-768.	3.6	278
26	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004, 5, R35.	13.9	276
27	A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016, 29, 90-103.	7.7	273
28	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014, 507, 124-128.	13.7	271
29	RNA-Seq Analysis of Sulfur-Deprived <i>Chlamydomonas</i> Cells Reveals Aspects of Acclimation Critical for Cell Survival. <i>Plant Cell</i> , 2010, 22, 2058-2084.	3.1	253
30	Evolution, genomic analysis, and reconstruction of isobutanol tolerance in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 449.	3.2	252
31	Plants regenerated from tissue culture contain stable epigenome changes in rice. <i>ELife</i> , 2013, 2, e00354.	2.8	225
32	BS Seeker: precise mapping for bisulfite sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 203.	1.2	212
33	Epigenetic Reprogramming by Adenovirus e1a. <i>Science</i> , 2008, 321, 1086-1088.	6.0	207
34	Proteomic and genomic approaches reveal critical functions of H3K9 methylation and heterochromatin protein-1 ³ in reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 872-882.	4.6	205
35	Systems Biology Approach in <i>Chlamydomonas</i> Reveals Connections between Copper Nutrition and Multiple Metabolic Steps. <i>Plant Cell</i> , 2011, 23, 1273-1292.	3.1	204
36	Transcriptome and methylome interactions in rice hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12040-12045.	3.3	203

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37	X-inactivation in female human embryonic stem cells is in a nonrandom pattern and prone to epigenetic alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4709-4714.	3.3	195
38	Transcriptome-Wide Changes in <i>Chlamydomonas reinhardtii</i> Gene Expression Regulated by Carbon Dioxide and the CO ₂ -Concentrating Mechanism Regulator <i>CIA5</i> / <i>CCM1</i> . <i>Plant Cell</i> , 2012, 24, 1876-1893.	3.1	180
39	The ontogeny of cKIT+ human primordial germ cells proves to be a resource for human germ line reprogramming, imprint erasure and in vitro differentiation. <i>Nature Cell Biology</i> , 2013, 15, 113-122.	4.6	177
40	Systems-Level Analysis of Nitrogen Starvation-Induced Modifications of Carbon Metabolism in a <i>Chlamydomonas reinhardtii</i> Starchless Mutant. <i>Plant Cell</i> , 2013, 25, 4305-4323.	3.1	176
41	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	3.5	173
42	Single-cell sequencing of human white adipose tissue identifies new cell states in health and obesity. <i>Nature Immunology</i> , 2021, 22, 639-653.	7.0	169
43	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	1.4	166
44	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . <i>Science</i> , 2010, 328, 351-354.	6.0	159
45	Species-wide patterns of DNA methylation variation in <i>Quercus lobata</i> and their association with climate gradients. <i>Molecular Ecology</i> , 2016, 25, 1665-1680.	2.0	159
46	CRISPR/Cas9-Mediated Correction of the Sickle Mutation in Human CD34+ cells. <i>Molecular Therapy</i> , 2016, 24, 1561-1569.	3.7	157
47	Molecular Analyses of Human Induced Pluripotent Stem Cells and Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 263-269.	5.2	155
48	Stage-Specific Roles for Tet1 and Tet2 in DNA Demethylation in Primordial Germ Cells. <i>Cell Stem Cell</i> , 2013, 12, 470-478.	5.2	153
49	Synaptic N6-methyladenosine (m6A) epitranscriptome reveals functional partitioning of localized transcripts. <i>Nature Neuroscience</i> , 2018, 21, 1004-1014.	7.1	153
50	CGmapTools improves the precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data. <i>Bioinformatics</i> , 2018, 34, 381-387.	1.8	152
51	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015, 4, e06205.	2.8	146
52	The Path to Triacylglyceride Obesity in the <i>sta6</i> Strain of <i>Chlamydomonas reinhardtii</i> . <i>Eukaryotic Cell</i> , 2014, 13, 591-613.	3.4	143
53	Systems and <i>Trans</i> -System Level Analysis Identifies Conserved Iron Deficiency Responses in the Plant Lineage. <i>Plant Cell</i> , 2012, 24, 3921-3948.	3.1	142
54	Scl Represses Cardiomyogenesis in Prospective Hemogenic Endothelium and Endocardium. <i>Cell</i> , 2012, 150, 590-605.	13.5	142

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55	Glucose inhibits cardiac muscle maturation through nucleotide biosynthesis. <i>ELife</i> , 2017, 6, .	2.8	142
56	ACTINN: automated identification of cell types in single cell RNA sequencing. <i>Bioinformatics</i> , 2020, 36, 533-538.	1.8	140
57	An asthma-associated IL4R variant exacerbates airway inflammation by promoting conversion of regulatory T cells to TH17-like cells. <i>Nature Medicine</i> , 2016, 22, 1013-1022.	15.2	138
58	Dynamic DNA cytosine methylation in the <i>Populus trichocarpa</i> genome: tissue-level variation and relationship to gene expression. <i>BMC Genomics</i> , 2012, 13, 27.	1.2	136
59	High-Resolution Mapping of Chromatin Conformation in Cardiac Myocytes Reveals Structural Remodeling of the Epigenome in Heart Failure. <i>Circulation</i> , 2017, 136, 1613-1625.	1.6	135
60	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. <i>Mammalian Genome</i> , 2012, 23, 680-692.	1.0	134
61	Unraveling Inflammatory Responses using Systems Genetics and Gene-Environment Interactions in Macrophages. <i>Cell</i> , 2012, 151, 658-670.	13.5	134
62	Chromosome-level genome assembly and transcriptome of the green alga <i>Chromochloris zofingiensis</i> illuminates astaxanthin production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4296-E4305.	3.3	131
63	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017, 9, 1055-1068.	1.4	125
64	Novel Stem/Progenitor Cell Population from Murine Tracheal Submucosal Gland Ducts with Multipotent Regenerative Potential. <i>Stem Cells</i> , 2011, 29, 1283-1293.	1.4	124
65	Conditional Depletion of the <i>Chlamydomonas</i> Chloroplast ClpP Protease Activates Nuclear Genes Involved in Autophagy and Plastid Protein Quality Control. <i>Plant Cell</i> , 2014, 26, 2201-2222.	3.1	122
66	Type V Collagen in Scar Tissue Regulates the Size of Scar after Heart Injury. <i>Cell</i> , 2020, 182, 545-562.e23.	13.5	113
67	A Genome-Wide Chronological Study of Gene Expression and Two Histone Modifications, H3K4me3 and H3K9ac, during Developmental Leaf Senescence. <i>Plant Physiology</i> , 2015, 168, 1246-1261.	2.3	111
68	Similarity between soybean and <i>Arabidopsis</i> seed methylomes and loss of non-CG methylation does not affect seed development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9730-E9739.	3.3	111
69	IL-32 is a molecular marker of a host defense network in human tuberculosis. <i>Science Translational Medicine</i> , 2014, 6, 250ra114.	5.8	110
70	Copy number variation influences gene expression and metabolic traits in mice. <i>Human Molecular Genetics</i> , 2009, 18, 4118-4129.	1.4	107
71	Retrograde bilin signaling enables <i>Chlamydomonas</i> greening and phototrophic survival. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3621-3626.	3.3	107
72	Genome-wide signature of local adaptation linked to variable CpG methylation in oak populations. <i>Molecular Ecology</i> , 2015, 24, 3823-3830.	2.0	107

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73	The effects of perinatal testosterone exposure on the DNA methylome of the mouse brain are late-emerging. <i>Biology of Sex Differences</i> , 2014, 5, 8.	1.8	106
74	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	1.2	106
75	Functional reprogramming of regulatory T cells in the absence of Foxp3. <i>Nature Immunology</i> , 2019, 20, 1208-1219.	7.0	106
76	A large-scale zebrafish gene knockout resource for the genome-wide study of gene function. <i>Genome Research</i> , 2013, 23, 727-735.	2.4	105
77	Targeted mutagenesis in a human-parasitic nematode. <i>PLoS Pathogens</i> , 2017, 13, e1006675.	2.1	104
78	Inference of protein function and protein linkages in <i>Mycobacterium tuberculosis</i> based on prokaryotic genome organization: a combined computational approach. <i>Genome Biology</i> , 2003, 4, R59.	13.9	103
79	<i>Chlamydomonas</i> Genome Resource for Laboratory Strains Reveals a Mosaic of Sequence Variation, Identifies True Strain Histories, and Enables Strain-Specific Studies. <i>Plant Cell</i> , 2015, 27, 2335-2352.	3.1	102
80	Subunit asymmetry in the three-dimensional structure of a human CuZnSOD mutant found in familial amyotrophic lateral sclerosis. <i>Protein Science</i> , 1998, 7, 545-555.	3.1	101
81	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017, 18, 54-67.	2.9	100
82	Epigenome-Wide Association of Liver Methylation Patterns and Complex Metabolic Traits in Mice. <i>Cell Metabolism</i> , 2015, 21, 905-917.	7.2	98
83	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>BMC Genomics</i> , 2019, 20, 605.	1.2	98
84	SINGLET OXYGEN RESISTANT 1 links reactive electrophile signaling to singlet oxygen acclimation in <i>Chlamydomonas reinhardtii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1302-11.	3.3	95
85	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95
86	All-Trans Retinoic Acid-Triggered Antimicrobial Activity against <i>Mycobacterium tuberculosis</i> Is Dependent on NPC2. <i>Journal of Immunology</i> , 2014, 192, 2280-2290.	0.4	94
87	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. <i>Genome Biology</i> , 2006, 7, R93.	13.9	93
88	Impact of Oxidative Stress on Ascorbate Biosynthesis in <i>Chlamydomonas</i> via Regulation of the VTC2 Gene Encoding a GDP-l-galactose Phosphorylase. <i>Journal of Biological Chemistry</i> , 2012, 287, 14234-14245.	1.6	93
89	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	5.8	93
90	Reversible Regulation of Promoter and Enhancer Histone Landscape by DNA Methylation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2016, 17, 289-302.	2.9	92

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91	Intestinal Subepithelial Myofibroblasts Support the Growth of Intestinal Epithelial Stem Cells. PLoS ONE, 2014, 9, e84651.	1.1	91
92	let-7 miRNAs Can Act through Notch to Regulate Human Gliogenesis. Stem Cell Reports, 2014, 3, 758-773.	2.3	90
93	High-throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved <i>de novo</i> assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. Plant Journal, 2018, 93, 545-565.	2.8	90
94	Propionibacterium acnes Bacteriophages Display Limited Genetic Diversity and Broad Killing Activity against Bacterial Skin Isolates. MBio, 2012, 3, .	1.8	89
95	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	6.5	89
96	Adenovirus Small E1A Employs the Lysine Acetylases p300/CBP and Tumor Suppressor Rb to Repress Select Host Genes and Promote Productive Virus Infection. Cell Host and Microbe, 2014, 16, 663-676.	5.1	88
97	Mapping human haematopoietic stem cells from haemogenic endothelium to birth. Nature, 2022, 604, 534-540.	13.7	88
98	Genome and methylome of the oleaginous diatom Cyclotella cryptica reveal genetic flexibility toward a high lipid phenotype. Biotechnology for Biofuels, 2016, 9, 258.	6.2	87
99	A comparative analysis of DNA methylation across human embryonic stem cell lines. Genome Biology, 2011, 12, R62.	13.9	86
100	Cardiac Fibroblasts Adopt Osteogenic Fates and Can Be Targeted to Attenuate Pathological Heart Calcification. Cell Stem Cell, 2017, 20, 218-232.e5.	5.2	86
101	The Proteome of Copper, Iron, Zinc, and Manganese Micronutrient Deficiency in Chlamydomonas reinhardtii. Molecular and Cellular Proteomics, 2013, 12, 65-86.	2.5	85
102	Widespread Use of Non-productive Alternative Splice Sites in Saccharomyces cerevisiae. PLoS Genetics, 2014, 10, e1004249.	1.5	85
103	Algal Functional Annotation Tool: a web-based analysis suite to functionally interpret large gene lists using integrated annotation and expression data. BMC Bioinformatics, 2011, 12, 282.	1.2	84
104	Intrauterine calorie restriction affects placental DNA methylation and gene expression. Physiological Genomics, 2013, 45, 565-576.	1.0	84
105	Genome-Wide Evaluation of Histone Methylation Changes Associated with Leaf Senescence in Arabidopsis. PLoS ONE, 2012, 7, e33151.	1.1	83
106	Crystal Structure of a Cross-reaction Complex between Fab F9.13.7 and Guinea Fowl Lysozyme. Journal of Biological Chemistry, 1995, 270, 18067-18076.	1.6	79
107	Protein Interaction Networks. Expert Review of Proteomics, 2004, 1, 239-249.	1.3	79
108	Remodeling of Membrane Lipids in Iron-starved Chlamydomonas. Journal of Biological Chemistry, 2013, 288, 30246-30258.	1.6	77

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109	COPPER RESPONSE REGULATOR1â€‘Dependent and â€‘Independent Responses of the <i>Chlamydomonas reinhardtii</i> Transcriptome to Dark Anoxia. <i>Plant Cell</i> , 2013, 25, 3186-3211.	3.1	77
110	S100A12 Is Part of the Antimicrobial Network against <i>Mycobacterium leprae</i> in Human Macrophages. <i>PLoS Pathogens</i> , 2016, 12, e1005705.	2.1	77
111	AID-Induced Genotoxic Stress Promotes B Cell Differentiation in the Germinal Center via ATM and LKB1 Signaling. <i>Molecular Cell</i> , 2010, 39, 873-885.	4.5	74
112	Molecular Profiling of Premalignant Lesions in Lung Squamous Cell Carcinomas Identifies Mechanisms Involved in Stepwise Carcinogenesis. <i>Cancer Prevention Research</i> , 2014, 7, 487-495.	0.7	74
113	The concerted impact of domestication and transposon insertions on methylation patterns between dogs and grey wolves. <i>Molecular Ecology</i> , 2016, 25, 1838-1855.	2.0	73
114	Zinc Deficiency Impacts CO2 Assimilation and Disrupts Copper Homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 10672-10683.	1.6	72
115	Increased intermediate M1â€‘M2 macrophage polarization and improved cognition in mild cognitive impairment patients on Î³ supplementations. <i>FASEB Journal</i> , 2017, 31, 148-160.	0.2	72
116	A fast algorithm for genome-wide analysis of proteins with repeated sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 440-446.	1.5	71
117	Inhibition of microbiota-dependent TMAO production attenuates chronic kidney disease in mice. <i>Scientific Reports</i> , 2021, 11, 518.	1.6	70
118	Inferring protein interactions from phylogenetic distance matrices. <i>Bioinformatics</i> , 2003, 19, 2039-2045.	1.8	69
119	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , 2017, 22, 187-215.	2.4	69
120	Targeting monoamine oxidase A-regulated tumor-associated macrophage polarization for cancer immunotherapy. <i>Nature Communications</i> , 2021, 12, 3530.	5.8	68
121	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. <i>Genome Biology</i> , 2014, 15, 411.	3.8	67
122	A comparison between whole transcript and 3â€‘ RNA sequencing methods using Kapa and Lexogen library preparation methods. <i>BMC Genomics</i> , 2019, 20, 9.	1.2	66
123	Repression of Sox9 by Jag1 Is Continuously Required to Suppress the Default Chondrogenic Fate of Vascular Smooth Muscle Cells. <i>Developmental Cell</i> , 2014, 31, 707-721.	3.1	65
124	An Epigenetic Signature in Peripheral Blood Associated with the Haplotype on 17q21.31, a Risk Factor for Neurodegenerative Tauopathy. <i>PLoS Genetics</i> , 2014, 10, e1004211.	1.5	65
125	Identification of genes required for de novo DNA methylation in <i>Arabidopsis</i> . <i>Epigenetics</i> , 2011, 6, 344-354.	1.3	64
126	New transgenic reporters identify somatosensory neuron subtypes in larval zebrafish. <i>Developmental Neurobiology</i> , 2013, 73, 152-167.	1.5	64

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127	Scl binds to primed enhancers in mesoderm to regulate hematopoietic and cardiac fate divergence. <i>EMBO Journal</i> , 2015, 34, 759-777.	3.5	64
128	X chromosome dosage of histone demethylase KDM5C determines sex differences in adiposity. <i>Journal of Clinical Investigation</i> , 2020, 130, 5688-5702.	3.9	62
129	Reorganization of the host epigenome by a viral oncogene. <i>Genome Research</i> , 2012, 22, 1212-1221.	2.4	61
130	Endocardially Derived Macrophages Are Essential for Valvular Remodeling. <i>Developmental Cell</i> , 2019, 48, 617-630.e3.	3.1	61
131	The cellular architecture of the antimicrobial response network in human leprosy granulomas. <i>Nature Immunology</i> , 2021, 22, 839-850.	7.0	60
132	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	2.7	59
133	Human antimicrobial cytotoxic T lymphocytes, defined by NK receptors and antimicrobial proteins, kill intracellular bacteria. <i>Science Immunology</i> , 2018, 3, .	5.6	59
134	Cross-Species Analysis of Genic GC3 Content and DNA Methylation Patterns. <i>Genome Biology and Evolution</i> , 2013, 5, 1443-1456.	1.1	57
135	Pancreatic Cancer Patient Survival Correlates with DNA Methylation of Pancreas Development Genes. <i>PLoS ONE</i> , 2015, 10, e0128814.	1.1	57
136	Metabolic reprogramming and epigenetic changes of vital organs in SARS-CoV-2-induced systemic toxicity. <i>JCI Insight</i> , 2021, 6, .	2.3	57
137	Global Phosphoproteomics Reveals Crosstalk Between Bcr-Abl and Negative Feedback Mechanisms Controlling Src Signaling. <i>Science Signaling</i> , 2011, 4, ra18.	1.6	56
138	Loss of MECP2 Leads to Activation of P53 and Neuronal Senescence. <i>Stem Cell Reports</i> , 2018, 10, 1453-1463.	2.3	56
139	Visualization and interpretation of protein networks in <i>Mycobacterium tuberculosis</i> based on hierarchical clustering of genome-wide functional linkage maps. <i>Nucleic Acids Research</i> , 2003, 31, 7099-7109.	6.5	55
140	Identification of RNA polymerase III-transcribed Alu loci by computational screening of RNA-Seq data. <i>Nucleic Acids Research</i> , 2015, 43, 817-835.	6.5	55
141	Characterizing the strand-specific distribution of non-CpG methylation in human pluripotent cells. <i>Nucleic Acids Research</i> , 2014, 42, 3009-3016.	6.5	54
142	Epigenetic differences between shoots and roots in <i>Arabidopsis</i> reveals tissue-specific regulation. <i>Epigenetics</i> , 2014, 9, 236-242.	1.3	54
143	Detecting Communities Based on Network Topology. <i>Scientific Reports</i> , 2014, 4, 5739.	1.6	53
144	The Memory of Environmental Chemical Exposure in <i>C.Âelegans</i> Is Dependent on the Jumonji Demethylases <i>jmjd-2</i> and <i>jmjd-3/utx-1</i> . <i>Cell Reports</i> , 2018, 23, 2392-2404.	2.9	53

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145	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	1.2	52
146	Cutaneous wound healing through paradoxical MAPK activation by BRAF inhibitors. <i>Nature Communications</i> , 2016, 7, 12348.	5.8	52
147	Nonlesional lupus skin contributes to inflammatory education of myeloid cells and primes for cutaneous inflammation. <i>Science Translational Medicine</i> , 2022, 14, eabn2263.	5.8	52
148	Mef2C is a lineage-restricted target of Scl/Tal1 and regulates megakaryopoiesis and B-cell homeostasis. <i>Blood</i> , 2009, 113, 3461-3471.	0.6	51
149	Methylome reorganization during in vitro dedifferentiation and regeneration of <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2013, 13, 92.	1.6	51
150	Dynamic changes in the transcriptome and methylome of <i>Chlamydomonas reinhardtii</i> throughout its life cycle. <i>Plant Physiology</i> , 2015, 169, pp.00861.2015.	2.3	51
151	CRISPR-Mediated VHL Knockout Generates an Improved Model for Metastatic Renal Cell Carcinoma. <i>Scientific Reports</i> , 2016, 6, 29032.	1.6	51
152	Nkx2-5 Suppresses the Proliferation of Atrial Myocytes and Conduction System. <i>Circulation Research</i> , 2014, 114, 1103-1113.	2.0	50
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