

Matteo Pellegrini

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

361
papers

25,855
citations

73
h-index

153
g-index

403
ext. papers

31,264
ext. citations

10
avg, IF

6.83
L-index

#	Paper	IF	Citations
361	Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. <i>Nature</i> , 2008 , 452, 215-9	50.4	1704
360	Assigning protein functions by comparative genome analysis: protein phylogenetic profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 4285-8	11.5	1460
359	Detecting protein function and protein-protein interactions from genome sequences. <i>Science</i> , 1999 , 285, 751-3	33.3	1397
358	Genome-wide high-resolution mapping and functional analysis of DNA methylation in arabidopsis. <i>Cell</i> , 2006 , 126, 1189-201	56.2	1366
357	Conservation and divergence of methylation patterning in plants and animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 8689-94	11.5	884
356	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999 , 402, 83-6	50.4	773
355	Genome-wide erasure of DNA methylation in mouse primordial germ cells is affected by AID deficiency. <i>Nature</i> , 2010 , 463, 1101-5	50.4	697
354	Relationship between nucleosome positioning and DNA methylation. <i>Nature</i> , 2010 , 466, 388-92	50.4	555
353	Whole-genome analysis of histone H3 lysine 27 trimethylation in Arabidopsis. <i>PLoS Biology</i> , 2007 , 5, e1297	19.7	528
352	Pioneer transcription factors target partial DNA motifs on nucleosomes to initiate reprogramming. <i>Cell</i> , 2015 , 161, 555-568	56.2	430
351	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. <i>Genome Biology</i> , 2009 , 10, R62	18.3	381
350	Promoter CpG methylation contributes to ES cell gene regulation in parallel with Oct4/Nanog, PcG complex, and histone H3 K4/K27 trimethylation. <i>Cell Stem Cell</i> , 2008 , 2, 160-9	18	362
349	Three acyltransferases and nitrogen-responsive regulator are implicated in nitrogen starvation-induced triacylglycerol accumulation in Chlamydomonas. <i>Journal of Biological Chemistry</i> , 2012 , 287, 15811-25	5.4	317
348	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999 , 293, 151-60	6.5	313
347	Distinct Shifts in Microbiota Composition during Drosophila Aging Impair Intestinal Function and Drive Mortality. <i>Cell Reports</i> , 2015 , 12, 1656-67	10.6	258
346	BS-Seeker2: a versatile aligning pipeline for bisulfite sequencing data. <i>BMC Genomics</i> , 2013 , 14, 774	4.5	248
345	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, 4968-73	11.5	245

344	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	3.7	242
343	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018 , 8, 730-749	24.4	235
342	Nitrogen-Sparing Mechanisms in <i>Chlamydomonas</i> Affect the Transcriptome, the Proteome, and Photosynthetic Metabolism. <i>Plant Cell</i> , 2014 , 26, 1410-1435	11.6	231
341	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004 , 5, R35	18.3	230
340	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , 2012 , 336, 1448-51	33.3	220
339	ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 763-8	17.6	217
338	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	17.6	216
337	Evolution, genomic analysis, and reconstruction of isobutanol tolerance in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010 , 6, 449	12.2	216
336	Transcriptome sequencing identifies SPL7-regulated copper acquisition genes FRO4/FRO5 and the copper dependence of iron homeostasis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012 , 24, 738-61	11.6	215
335	RNA-seq analysis of sulfur-deprived <i>Chlamydomonas</i> cells reveals aspects of acclimation critical for cell survival. <i>Plant Cell</i> , 2010 , 22, 2058-84	11.6	214
334	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014 , 507, 124-128	50.4	199
333	A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016 , 29, 90-103	24.3	192
332	A revised mineral nutrient supplement increases biomass and growth rate in <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2011 , 66, 770-80	6.9	187
331	BS Seeker: precise mapping for bisulfite sequencing. <i>BMC Bioinformatics</i> , 2010 , 11, 203	3.6	181
330	Epigenetic reprogramming by adenovirus e1a. <i>Science</i> , 2008 , 321, 1086-8	33.3	179
329	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, 4709-14	11.5	173
328	Systems biology approach in <i>Chlamydomonas</i> reveals connections between copper nutrition and multiple metabolic steps. <i>Plant Cell</i> , 2011 , 23, 1273-92	11.6	170
327	Plants regenerated from tissue culture contain stable epigenome changes in rice. <i>ELife</i> , 2013 , 2, e003548.9		167

326	Proteomic and genomic approaches reveal critical functions of H3K9 methylation and heterochromatin protein-1 in reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013 , 15, 872-82	23.4	164
325	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, 113-22	23.4	154
324	Transcriptome and methylome interactions in rice hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 12040-5	11.5	153
323	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, 4305-23	11.6	145
322	Transcriptome-wide changes in <i>Chlamydomonas reinhardtii</i> gene expression regulated by carbon dioxide and the CO ₂ -concentrating mechanism regulator CIA5/CCM1. <i>Plant Cell</i> , 2012 , 24, 1876-93	11.6	141
321	Stage-specific roles for tet1 and tet2 in DNA demethylation in primordial germ cells. <i>Cell Stem Cell</i> , 2013 , 12, 470-8	18	137
320	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	9.8	134
319	Molecular analyses of human induced pluripotent stem cells and embryonic stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 263-9	18	133
318	Scl represses cardiomyogenesis in prospective hemogenic endothelium and endocardium. <i>Cell</i> , 2012 , 150, 590-605	56.2	121
317	CRISPR/Cas9-Mediated Correction of the Sickle Mutation in Human CD34+ cells. <i>Molecular Therapy</i> , 2016 , 24, 1561-9	11.7	118
316	Evolution of an expanded sex-determining locus in <i>Volvox</i> . <i>Science</i> , 2010 , 328, 351-4	33.3	118
315	The path to triacylglyceride obesity in the sta6 strain of <i>Chlamydomonas reinhardtii</i> . <i>Eukaryotic Cell</i> , 2014 , 13, 591-613		114
314	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015 , 4, e06205	8.9	107
313	Novel stem/progenitor cell population from murine tracheal submucosal gland ducts with multipotent regenerative potential. <i>Stem Cells</i> , 2011 , 29, 1283-93	5.8	104
312	Systems and trans-system level analysis identifies conserved iron deficiency responses in the plant lineage. <i>Plant Cell</i> , 2012 , 24, 3921-48	11.6	104
311	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	4.5	102
310	Hybrid mouse diversity panel: a panel of inbred mouse strains suitable for analysis of complex genetic traits. <i>Mammalian Genome</i> , 2012 , 23, 680-92	3.2	101
309	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, 1013-22	50.5	100

308	Unraveling inflammatory responses using systems genetics and gene-environment interactions in macrophages. <i>Cell</i> , 2012 , 151, 658-70	56.2	96
307	Chromosome-level genome assembly and transcriptome of the green alga illuminates astaxanthin production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E4296-E4305	11.5	95
306	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	9.3	93
305	Conditional Depletion of the Chlamydomonas Chloroplast ClpP Protease Activates Nuclear Genes Involved in Autophagy and Plastid Protein Quality Control. <i>Plant Cell</i> , 2014 , 26, 2201-2222	11.6	90
304	Subunit asymmetry in the three-dimensional structure of a human CuZnSOD mutant found in familial amyotrophic lateral sclerosis. <i>Protein Science</i> , 1998 , 7, 545-55	6.3	90
303	Species-wide patterns of DNA methylation variation in <i>Quercus lobata</i> and their association with climate gradients. <i>Molecular Ecology</i> , 2016 , 25, 1665-80	5.7	88
302	IL-32 is a molecular marker of a host defense network in human tuberculosis. <i>Science Translational Medicine</i> , 2014 , 6, 250ra114	17.5	87
301	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017 , 9, 1055-1068	5.6	86
300	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018 , 10, 2832-2854	5.6	86
299	Glucose inhibits cardiac muscle maturation through nucleotide biosynthesis. <i>ELife</i> , 2017 , 6,	8.9	85
298	A large-scale zebrafish gene knockout resource for the genome-wide study of gene function. <i>Genome Research</i> , 2013 , 23, 727-35	9.7	84
297	Synaptic N-methyladenosine (mA) epitranscriptome reveals functional partitioning of localized transcripts. <i>Nature Neuroscience</i> , 2018 , 21, 1004-1014	25.5	83
296	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, 3621-6	11.5	81
295	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	11.5	81
294	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	16.7	80
293	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, 14234-45	5.4	80
292	Copy number variation influences gene expression and metabolic traits in mice. <i>Human Molecular Genetics</i> , 2009 , 18, 4118-29	5.6	79
291	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	18.3	79

290	Intestinal subepithelial myofibroblasts support the growth of intestinal epithelial stem cells. <i>PLoS ONE</i> , 2014 , 9, e84651	3.7	75
289	A comparative analysis of DNA methylation across human embryonic stem cell lines. <i>Genome Biology</i> , 2011 , 12, R62	18.3	75
288	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017 , 18, 54-67	10.6	72
287	Similarity between soybean and 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	11.5	72
286	Adenovirus small E1A employs the lysine acetylases p300/CBP and tumor suppressor Rb to repress select host genes and promote productive virus infection. <i>Cell Host and Microbe</i> , 2014 , 16, 663-76	23.4	72
285	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	5.3	72
284	let-7 miRNAs can act through notch to regulate human gliogenesis. <i>Stem Cell Reports</i> , 2014 , 3, 758-73	8	72
283	Intrauterine calorie restriction affects placental DNA methylation and gene expression. <i>Physiological Genomics</i> , 2013 , 45, 565-76	3.6	72
282	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. <i>Genome Biology</i> , 2006 , 7, R93	18.3	71
281	Genome-wide signature of local adaptation linked to variable CpG methylation in oak populations. <i>Molecular Ecology</i> , 2015 , 24, 3823-30	5.7	70
280	Algal Functional Annotation Tool: a web-based analysis suite to functionally interpret large gene lists using integrated annotation and expression data. <i>BMC Bioinformatics</i> , 2011 , 12, 282	3.6	70
279	Crystal structure of a cross-reaction complex between Fab F9.13.7 and guinea fowl lysozyme. <i>Journal of Biological Chemistry</i> , 1995 , 270, 18067-76	5.4	70
278	Epigenome-wide association of liver methylation patterns and complex metabolic traits in mice. <i>Cell Metabolism</i> , 2015 , 21, 905-17	24.6	68
277	<i>Propionibacterium acnes</i> bacteriophages display limited genetic diversity and broad killing activity against bacterial skin isolates. <i>MBio</i> , 2012 , 3,	7.8	68
276	Targeted mutagenesis in a human-parasitic nematode. <i>PLoS Pathogens</i> , 2017 , 13, e1006675	7.6	68
275	Remodeling of membrane lipids in iron-starved <i>Chlamydomonas</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 30246-30258	5.4	67
274	Widespread use of non-productive alternative splice sites in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004249	6	67
273	Functional reprogramming of regulatory T cells in the absence of Foxp3. <i>Nature Immunology</i> , 2019 , 20, 1208-1219	19.1	66

272	Cardiac Fibroblasts Adopt Osteogenic Fates and Can Be Targeted to Attenuate Pathological Heart Calcification. <i>Cell Stem Cell</i> , 2017 , 20, 218-232.e5	18	65
271	The proteome of copper, iron, zinc, and manganese micronutrient deficiency in <i>Chlamydomonas reinhardtii</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 65-86	7.6	65
270	Reversible Regulation of Promoter and Enhancer Histone Landscape by DNA Methylation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2016 , 17, 289-302	10.6	65
269	<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, 2335-52	11.6	63
268	Copper response regulator1-dependent and -independent responses of the <i>Chlamydomonas reinhardtii</i> transcriptome to dark anoxia. <i>Plant Cell</i> , 2013 , 25, 3186-211	11.6	62
267	Genome and methylome of the oleaginous diatom reveal genetic flexibility toward a high lipid phenotype. <i>Biotechnology for Biofuels</i> , 2016 , 9, 258	7.8	61
266	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	7.2	60
265	Zinc deficiency impacts CO ₂ assimilation and disrupts copper homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 10672-83	5.4	59
264	AID-induced genotoxic stress promotes B cell differentiation in the germinal center via ATM and LKB1 signaling. <i>Molecular Cell</i> , 2010 , 39, 873-85	17.6	59
263	Inferring protein interactions from phylogenetic distance matrices. <i>Bioinformatics</i> , 2003 , 19, 2039-45	7.2	59
262	A fast algorithm for genome-wide analysis of proteins with repeated sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 35, 440-446	4.2	59
261	Molecular profiling of premalignant lesions in lung squamous cell carcinomas identifies mechanisms involved in stepwise carcinogenesis. <i>Cancer Prevention Research</i> , 2014 , 7, 487-95	3.2	57
260	Genome-wide evaluation of histone methylation changes associated with leaf senescence in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2012 , 7, e33151	3.7	57
259	First Draft Assembly and Annotation of the Genome of a California Endemic Oak N \bar{B} (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3485-3495	3.2	57
258	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016 , 17, 874	4.5	56
257	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Astrochloris glomerata</i> . <i>BMC Genomics</i> , 2019 , 20, 605	4.5	54
256	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	6	54
255	Identification of genes required for de novo DNA methylation in <i>Arabidopsis</i> . <i>Epigenetics</i> , 2011 , 6, 344-54.7	5.7	54

254	High-throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved de novo assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. <i>Plant Journal</i> , 2018 , 93, 545-565	6.9	54
253	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, 1246-61	6.6	53
252	Increased intermediate M1-M2 macrophage polarization and improved cognition in mild cognitive impairment patients on EB supplementation. <i>FASEB Journal</i> , 2017 , 31, 148-160	0.9	53
251	Global phosphoproteomics reveals crosstalk between Bcr-Abl and negative feedback mechanisms controlling Src signaling. <i>Science Signaling</i> , 2011 , 4, ra18	8.8	52
250	Protein interaction networks. <i>Expert Review of Proteomics</i> , 2004 , 1, 239-49	4.2	52
249	The concerted impact of domestication and transposon insertions on methylation patterns between dogs and grey wolves. <i>Molecular Ecology</i> , 2016 , 25, 1838-55	5.7	52
248	Reorganization of the host epigenome by a viral oncogene. <i>Genome Research</i> , 2012 , 22, 1212-21	9.7	51
247	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , 2017 , 22, 187-215	5	50
246	Scl binds to primed enhancers in mesoderm to regulate hematopoietic and cardiac fate divergence. <i>EMBO Journal</i> , 2015 , 34, 759-77	13	50
245	An apoptosis-enhancing drug overcomes platinum resistance in a tumour-initiating subpopulation of ovarian cancer. <i>Nature Communications</i> , 2015 , 6, 7956	17.4	49
244	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	18.3	47
243	Methylome reorganization during in vitro dedifferentiation and regeneration of <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2013 , 13, 92	5.3	46
242	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, 7099-109	20.1	46
241	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016 , 7, 157-66	8.8	46
240	Identification of RNA polymerase III-transcribed Alu loci by computational screening of RNA-Seq data. <i>Nucleic Acids Research</i> , 2015 , 43, 817-35	20.1	45
239	ACTINN: automated identification of cell types in single cell RNA sequencing. <i>Bioinformatics</i> , 2020 , 36, 533-538	7.2	44
238	Characterizing the strand-specific distribution of non-CpG methylation in human pluripotent cells. <i>Nucleic Acids Research</i> , 2014 , 42, 3009-16	20.1	44
237	Epigenetic differences between shoots and roots in <i>Arabidopsis</i> reveals tissue-specific regulation. <i>Epigenetics</i> , 2014 , 9, 236-42	5.7	44

236	Bio-crude transcriptomics: gene discovery and metabolic network reconstruction for the biosynthesis of the terpene of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa). <i>BMC Genomics</i> , 2012 , 13, 576	4.5	44
235	S100A12 Is Part of the Antimicrobial Network against <i>Mycobacterium leprae</i> in Human Macrophages. <i>PLoS Pathogens</i> , 2016 , 12, e1005705	7.6	43
234	Cross-species analysis of genic GC3 content and DNA methylation patterns. <i>Genome Biology and Evolution</i> , 2013 , 5, 1443-56	3.9	42
233	Pancreatic cancer patient survival correlates with DNA methylation of pancreas development genes. <i>PLoS ONE</i> , 2015 , 10, e0128814	3.7	41
232	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, 707-21	10.2	41
231	New transgenic reporters identify somatosensory neuron subtypes in larval zebrafish. <i>Developmental Neurobiology</i> , 2013 , 73, 152-67	3.2	41
230	Mef2C is a lineage-restricted target of Scl/Tal1 and regulates megakaryopoiesis and B-cell homeostasis. <i>Blood</i> , 2009 , 113, 3461-71	2.2	40
229	An improved method for identifying functionally linked proteins using phylogenetic profiles. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 4, S7	3.6	39
228	Epigenetic changes in T-cell and monocyte signatures and production of neurotoxic cytokines in ALS patients. <i>FASEB Journal</i> , 2016 , 30, 3461-3473	0.9	39
227	Detecting communities based on network topology. <i>Scientific Reports</i> , 2014 , 4, 5739	4.9	38
226	Protein flexibility in solution and in crystals. <i>Journal of Chemical Physics</i> , 1999 , 110, 10141-10152	3.9	38
225	Rapid Changes in the Transcriptome during the Conversion of Growth Cones to Synaptic Terminals. <i>Cell Reports</i> , 2016 , 14, 1258-1271	10.6	36
224	Nkx2-5 suppresses the proliferation of atrial myocytes and conduction system. <i>Circulation Research</i> , 2014 , 114, 1103-13	15.7	36
223	Estrogen and progesterone together expand murine endometrial epithelial progenitor cells. <i>Stem Cells</i> , 2013 , 31, 808-22	5.8	36
222	Determining DNA methylation profiles using sequencing. <i>Methods in Molecular Biology</i> , 2011 , 733, 223-384	3.4	36
221	Type V Collagen in Scar Tissue Regulates the Size of Scar after Heart Injury. <i>Cell</i> , 2020 , 182, 545-562.e23	56.2	35
220	Cutaneous wound healing through paradoxical MAPK activation by BRAF inhibitors. <i>Nature Communications</i> , 2016 , 7, 12348	17.4	35
219	Dynamic Changes in the Transcriptome and Methylome of <i>Chlamydomonas reinhardtii</i> throughout Its Life Cycle. <i>Plant Physiology</i> , 2015 , 169, 2730-43	6.6	34

218	Identification of novel targets of CSL-dependent Notch signaling in hematopoiesis. <i>PLoS ONE</i> , 2011 , 6, e20022	3.7	34
217	Human antimicrobial cytotoxic T lymphocytes, defined by NK receptors and antimicrobial proteins, kill intracellular bacteria. <i>Science Immunology</i> , 2018 , 3,	2.8	34
216	Comparison of the Mitochondrial Genomes and Steady State Transcriptomes of Two Strains of the Trypanosomatid Parasite, <i>Leishmania tarentolae</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003841	4.8	32
215	Phosphoprotein SAK1 is a regulator of acclimation to singlet oxygen in <i>Chlamydomonas reinhardtii</i> . <i>ELife</i> , 2014 , 3, e02286	8.9	32
214	CRISPR-Mediated VHL Knockout Generates an Improved Model for Metastatic Renal Cell Carcinoma. <i>Scientific Reports</i> , 2016 , 6, 29032	4.9	32
213	The Memory of Environmental Chemical Exposure in <i>C. elegans</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	10.6	32
212	A comparison between whole transcript and 3RRNA sequencing methods using Kapa and Lexogen library preparation methods. <i>BMC Genomics</i> , 2019 , 20, 9	4.5	31
211	Transcriptome and DNA methylation changes modulated by sulforaphane induce cell cycle arrest, apoptosis, DNA damage, and suppression of proliferation in human liver cancer cells. <i>Food and Chemical Toxicology</i> , 2020 , 136, 111047	4.7	31
210	Single-cell sequencing of human white adipose tissue identifies new cell states in health and obesity. <i>Nature Immunology</i> , 2021 , 22, 639-653	19.1	31
209	A mammalian methylation array for profiling methylation levels at conserved sequences		31
208	Discovering communities in complex networks by edge label propagation. <i>Scientific Reports</i> , 2016 , 6, 22470	4.9	30
207	A panel of CpG methylation sites distinguishes human embryonic stem cells and induced pluripotent stem cells. <i>Stem Cell Reports</i> , 2014 , 2, 36-43	8	30
206	Topological Arrangement of Cardiac Fibroblasts Regulates Cellular Plasticity. <i>Circulation Research</i> , 2018 , 123, 73-85	15.7	29
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