

# 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	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	6.5	89
2	Cardiomyocytes disrupt pyrimidine biosynthesis in nonmyocytes to regulate heart repair. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	16
3	Aortic intimal resident macrophages are essential for maintenance of the non-thrombogenic intravascular state. , 2022, 1, 67-84.		17
4	A complex network of interactions governs DNA methylation at telomeric regions. <i>Nucleic Acids Research</i> , 2022, 50, 1449-1464.	6.5	7
5	Heterogeneous <i>pdgfrb</i> cells regulate coronary vessel development and revascularization during heart regeneration. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	6
6	Tick tock, tick tock: Mouse culture and tissue aging captured by an epigenetic clock. <i>Aging Cell</i> , 2022, 21, e13553.	3.0	19
7	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	5.8	93
8	Abstract P2-11-06: Differential gene expression patterns in healthy breast tissue exhibiting epigenetic age acceleration. <i>Cancer Research</i> , 2022, 82, P2-11-06-P2-11-06.	0.4	0
9	Pseudotime Analysis Reveals Exponential Trends in DNA Methylation Aging with Mortality Associated Timescales. <i>Cells</i> , 2022, 11, 767.	1.8	1
10	Hibernation slows epigenetic ageing in yellow-bellied marmots. <i>Nature Ecology and Evolution</i> , 2022, 6, 418-426.	3.4	23
11	The transcription factor <i>Fli1</i> restricts the formation of memory precursor NK cells during viral infection. <i>Nature Immunology</i> , 2022, 23, 556-567.	7.0	13
12	Stem cell architecture drives myelodysplastic syndrome progression and predicts response to venetoclax-based therapy. <i>Nature Medicine</i> , 2022, 28, 557-567.	15.2	26
13	$\beta$ -cell-specific deletion of <i>PFKFB3</i> restores cell fitness competition and physiological replication under diabetogenic stress. <i>Communications Biology</i> , 2022, 5, 248.	2.0	1
14	DNA methylation profiles in pneumonia patients reflect changes in cell types and pneumonia severity. <i>Epigenetics</i> , 2022, 17, 1646-1660.	1.3	5
15	Canonical Wnt signaling induces focal adhesion and Integrin beta-1 endocytosis. <i>IScience</i> , 2022, 25, 104123.	1.9	13
16	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047.	5.8	30
17	Mapping human haematopoietic stem cells from haemogenic endothelium to birth. <i>Nature</i> , 2022, 604, 534-540.	13.7	88
18	Transcriptional Evaluation of the Ductus Arteriosus at the Single-Cell Level Uncovers a Requirement for <i>Vim</i> (Vimentin) for Complete Closure. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 732-742.	1.1	10

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19	DNA Methylation-Based Prediction of Post-operative Atrial Fibrillation. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, .	1.1	8
20	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
21	Cell-Free RNA as a Novel Biomarker for Response to Therapy in Head & Neck Cancer. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	6
22	Identification of Pediatric Septic Shock Subclasses Using the Whole Blood Transcriptome. , 2022, , .		0
23	The effects of age, sex, weight, and breed on canid methylomes. <i>Epigenetics</i> , 2022, 17, 1497-1512.	1.3	3
24	Integrated analysis of an in vivo model of intra-nasal exposure to instilled air pollutants reveals cell-type specific responses in the placenta. <i>Scientific Reports</i> , 2022, 12, 8438.	1.6	6
25	Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students. <i>PLoS ONE</i> , 2022, 17, e0268861.	1.1	0
26	Plasma contains ultrashort single-stranded DNA in addition to nucleosomal cell-free DNA. <i>IScience</i> , 2022, 25, 104554.	1.9	18
27	Targeted bisulfite sequencing for biomarker discovery. <i>Methods</i> , 2021, 187, 13-27.	1.9	30
28	Cell-free DNA Methylation and Transcriptomic Signature Prediction of Pregnancies with Adverse Outcomes. <i>Epigenetics</i> , 2021, 16, 642-661.	1.3	34
29	A High-Content Screen Identifies Drugs That Restrict Tumor Cell Extravasation across the Endothelial Barrier. <i>Cancer Research</i> , 2021, 81, 619-633.	0.4	8
30	Î²-Globin Lentiviral Vectors Have Reduced Titers due to Incomplete Vector RNA Genomes and Lowered Virion Production. <i>Stem Cell Reports</i> , 2021, 16, 198-211.	2.3	15
31	Genome-wide Association Analysis of Proinflammatory Cytokines and Geneâ€“lifestyle Interaction for Invasive Breast Cancer Risk: The WHI dbGaP Study. <i>Cancer Prevention Research</i> , 2021, 14, 41-54.	0.7	13
32	Metabolic reprogramming and epigenetic changes of vital organs in SARS-CoV-2â€“induced systemic toxicity. <i>JCI Insight</i> , 2021, 6, .	2.3	57
33	Extracellular traps released by antimicrobial TH17 cells contribute to host defense. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	30
34	Pro-inflammatory cytokine polymorphisms and interactions with dietary alcohol and estrogen, risk factors for invasive breast cancer using a post genome-wide analysis for geneâ€“gene and geneâ€“lifestyle interaction. <i>Scientific Reports</i> , 2021, 11, 1058.	1.6	6
35	The Gene Expression Deconvolution Interactive Tool (GEDIT): accurate cell type quantification from gene expression data. <i>GigaScience</i> , 2021, 10, .	3.3	33
36	Integrative analysis of chloroplast DNA methylation in a marine algaâ€“ <i>Saccharina japonica</i> . <i>Plant Molecular Biology</i> , 2021, 105, 611-623.	2.0	5

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37	Comparative analysis of embryo proper and suspensor transcriptomes in plant embryos with different morphologies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
38	Single-cell RNA sequencing of batch <i>Chlamydomonas</i> cultures reveals heterogeneity in their diurnal cycle phase. <i>Plant Cell</i> , 2021, 33, 1042-1057.	3.1	29
39	Human DNA methylation signatures differentiate persistent from resolving MRSA bacteremia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
40	GLUT1 overexpression enhances glucose metabolism and promotes neonatal heart regeneration. <i>Scientific Reports</i> , 2021, 11, 8669.	1.6	25
41	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
42	Species-Specific Relationships between DNA and Chromatin Properties of CpG Islands in Embryonic Stem Cells and Differentiated Cells. <i>Stem Cell Reports</i> , 2021, 16, 899-912.	2.3	4
43	Single Cell Transcriptomic Analyses Reveal the Impact of bHLH Factors on Human Retinal Organoid Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 653305.	1.8	9
44	Targeting monoamine oxidase A for T cell-based cancer immunotherapy. <i>Science Immunology</i> , 2021, 6, .	5.6	35
45	BiSulfite Bolt: A bisulfite sequencing analysis platform. <i>GigaScience</i> , 2021, 10, .	3.3	31
46	Targeting monoamine oxidase A-regulated tumor-associated macrophage polarization for cancer immunotherapy. <i>Nature Communications</i> , 2021, 12, 3530.	5.8	68
47	The cellular architecture of the antimicrobial response network in human leprosy granulomas. <i>Nature Immunology</i> , 2021, 22, 839-850.	7.0	60
48	Identification of Genes Encoding Antimicrobial Proteins in Langerhans Cells. <i>Frontiers in Immunology</i> , 2021, 12, 695373.	2.2	0
49	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
50	NOTUM promotes thermogenic capacity and protects against diet-induced obesity in male mice. <i>Scientific Reports</i> , 2021, 11, 16409.	1.6	3
51	Molecular Biology Networks and Key Gene Regulators for Inflammatory Biomarkers Shared by Breast Cancer Development: Multi-Omics Systems Analysis. <i>Biomolecules</i> , 2021, 11, 1379.	1.8	2
52	The induction of preterm labor in rhesus macaques is determined by the strength of immune response to intrauterine infection. <i>PLoS Biology</i> , 2021, 19, e3001385.	2.6	13
53	IRAK2 Has a Critical Role in Promoting Feed-Forward Amplification of Epidermal Inflammatory Responses. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2436-2448.	0.3	11
54	Early adaptive chromatin remodeling events precede pathologic phenotypes and are reinforced in the failing heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2021, 160, 73-86.	0.9	17

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55	Inhibition of microbiota-dependent TMAO production attenuates chronic kidney disease in mice. <i>Scientific Reports</i> , 2021, 11, 518.	1.6	70
56	Synergistic Effects of Genetic Variants of Glucose Homeostasis and Lifelong Exposures to Cigarette Smoking, Female Hormones, and Dietary Fat Intake on Primary Colorectal Cancer Development in African and Hispanic/Latino American Women. <i>Frontiers in Oncology</i> , 2021, 11, 760243.	1.3	1
57	Fasting-mimicking diet prevents high-fat diet effect on cardiometabolic risk and lifespan. <i>Nature Metabolism</i> , 2021, 3, 1342-1356.	5.1	34
58	Genetically determined elevated C-reactive protein associated with primary colorectal cancer risk: Mendelian randomization with lifestyle interactions. <i>American Journal of Cancer Research</i> , 2021, 11, 1733-1753.	1.4	1
59	Development of allogeneic HSC-engineered iNKT cells for off-the-shelf cancer immunotherapy. <i>Cell Reports Medicine</i> , 2021, 2, 100449.	3.3	39
60	Combining ReACp53 with Carboplatin to Target High-Grade Serous Ovarian Cancers. <i>Cancers</i> , 2021, 13, 5908.	1.7	11
61	Hematopoiesis under telomere attrition at the single-cell resolution. <i>Nature Communications</i> , 2021, 12, 6850.	5.8	15
62	Epigenetic models developed for plains zebras predict age in domestic horses and endangered equids. <i>Communications Biology</i> , 2021, 4, 1412.	2.0	23
63	ACTINN: automated identification of cell types in single cell RNA sequencing. <i>Bioinformatics</i> , 2020, 36, 533-538.	1.8	140
64	Single-cell base methylome profiling of the giant kelp <i>Saccharina japonica</i> reveals significant differences in DNA methylation to microalgae and plants. <i>New Phytologist</i> , 2020, 225, 234-249.	3.5	38
65	Interactions between core histone marks and DNA methyltransferases predict DNA methylation patterns observed in human cells and tissues. <i>Epigenetics</i> , 2020, 15, 272-282.	1.3	35
66	Activation of the HIF1 $\alpha$ /PFKFB3 stress response pathway in beta cells in type 1 diabetes. <i>Diabetologia</i> , 2020, 63, 149-161.	2.9	49
67	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.	1.8	50
68	Genome-wide DNA Methylation Profiling of Blood from Monozygotic Twins Discordant for Myocardial Infarction. <i>In Vivo</i> , 2020, 34, 361-367.	0.6	8
69	Transcriptome Profiling of Human Monocyte-Derived Macrophages Upon CCL2 Neutralization Reveals an Association Between Activation of Innate Immune Pathways and Restriction of HIV-1 Gene Expression. <i>Frontiers in Immunology</i> , 2020, 11, 2129.	2.2	7
70	Dysregulation of hsa-miR-34a and hsa-miR-449a leads to overexpression of PACS-1 and loss of DNA damage response (DDR) in cervical cancer. <i>Journal of Biological Chemistry</i> , 2020, 295, 17169-17186.	1.6	19
71	Creating New $\beta$ -Globin-Expressing Lentiviral Vectors by High-Resolution Mapping of Locus Control Region Enhancer Sequences. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 999-1013.	1.8	9
72	Dynamic changes in chromatin accessibility, altered adipogenic gene expression, and total versus de novo fatty acid synthesis in subcutaneous adipose stem cells of normal-weight polycystic ovary syndrome (PCOS) women during adipogenesis: evidence of cellular programming. <i>Clinical Epigenetics</i> , 2020, 12, 181.	1.8	17

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73	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	5.8	49
74	Epigenetic Suppression of Transgenic T-cell Receptor Expression via Gamma-Retroviral Vector Methylation in Adoptive Cell Transfer Therapy. Cancer Discovery, 2020, 10, 1645-1653.	7.7	11
75	Omega-3 fatty acids increase OXPHOS energy for immune therapy of Alzheimer disease patients. FASEB Journal, 2020, 34, 9982-9994.	0.2	6
76	Impact of Soil Salinity on the Cowpea Nodule-Microbiome and the Isolation of Halotolerant PGPR Strains to Promote Plant Growth under Salinity Stress. Phytobiomes Journal, 2020, 4, 364-374.	1.4	14
77	Integrative Analysis of Glucometabolic Traits, Adipose Tissue DNA Methylation, and Gene Expression Identifies Epigenetic Regulatory Mechanisms of Insulin Resistance and Obesity in African Americans. Diabetes, 2020, 69, 2779-2793.	0.3	8
78	Differential Expression of the Whole Blood Transcriptome in Pediatric Septic Shock. , 2020, , .		0
79	Omega-3 Fatty Acids Increase Amyloid- $\beta$ Immunity, Energy, and Circadian Rhythm for Cognitive Protection of Alzheimer's Disease Patients Beyond Cholinesterase Inhibitors. Journal of Alzheimer's Disease, 2020, 75, 993-1002.	1.2	8
80	Phenotypic and functional characterization of corneal endothelial cells during in vitro expansion. Scientific Reports, 2020, 10, 7402.	1.6	41
81	EMP2 Is a Novel Regulator of Stemness in Breast Cancer Cells. Molecular Cancer Therapeutics, 2020, 19, 1682-1695.	1.9	11
82	Expression of Stromal Progesterone Receptor and Differential Methylation Patterns in the Endometrium May Correlate with Response to Progesterone Therapy in Endometrial Complex Atypical Hyperplasia. Reproductive Sciences, 2020, 27, 1778-1790.	1.1	7
83	Cellular, Molecular, and Immunological Characteristics of Langerhans Multinucleated Giant Cells Programmed by IL-15. Journal of Investigative Dermatology, 2020, 140, 1824-1836.e7.	0.3	8
84	Impacts of ciliary neurotrophic factor on the retinal transcriptome in a mouse model of photoreceptor degeneration. Scientific Reports, 2020, 10, 6593.	1.6	7
85	Type V Collagen in Scar Tissue Regulates the Size of Scar after Heart Injury. Cell, 2020, 182, 545-562.e23.	13.5	113
86	The Epigenetic Pacemaker: modeling epigenetic states under an evolutionary framework. Bioinformatics, 2020, 36, 4662-4663.	1.8	19
87	Effects of sulforaphane on the oxidative response, apoptosis, and the transcriptional profile of human stomach mucosa cells in vitro. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 854-855, 503201.	0.9	5
88	The dopamine receptor antagonist trifluoperazine prevents phenotype conversion and improves survival in mouse models of glioblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11085-11096.	3.3	33
89	Molecular signatures for inflammation vary across cancer types and correlate significantly with tumor stage, sex and vital status of patients. PLoS ONE, 2020, 15, e0221545.	1.1	9
90	ER Stress Regulates Immunosuppressive Function of Myeloid Derived Suppressor Cells in Leprosy that Can Be Overcome in the Presence of IFN- $\gamma$ . IScience, 2020, 23, 101050.	1.9	6

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91	TNF-Signaling Modulates Neutrophil-Mediated Immunity at the Feto-Maternal Interface During LPS-Induced Intrauterine Inflammation. <i>Frontiers in Immunology</i> , 2020, 11, 558.	2.2	33
92	Genetically Predicted C-Reactive Protein Associated With Postmenopausal Breast Cancer Risk: Interrelation With Estrogen and Cancer Molecular Subtypes Using Mendelian Randomization. <i>Frontiers in Oncology</i> , 2020, 10, 630994.	1.3	3
93	A randomized, phase 1, placebo-controlled trial of APC157 in oral cancer demonstrates systemic absorption and an inhibitory effect on cytokines and tumor-associated microbes. <i>Cancer</i> , 2020, 126, 1668-1682.	2.0	33
94	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	34
95	Cardiac fibroblast proliferation rates and collagen expression mature early and are unaltered with advancing age. <i>JCI Insight</i> , 2020, 5, .	2.3	14
96	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
97	A rat epigenetic clock recapitulates phenotypic aging and co-localizes with heterochromatin. <i>ELife</i> , 2020, 9, .	2.8	36
98	Telescope: an interactive tool for managing large-scale analysis from mobile devices. <i>GigaScience</i> , 2020, 9, .	3.3	0
99	Pro-inflammatory cytokine polymorphisms in ONECUT2 and HNF4A and primary colorectal carcinoma: a post genome-wide gene-lifestyle interaction study. <i>American Journal of Cancer Research</i> , 2020, 10, 2955-2976.	1.4	1
100	SF3B1-Mutant Myelodysplastic Syndrome with Ringed Sideroblasts (MDS-RS) at the Single-Cell Level. <i>Blood</i> , 2020, 136, 50-51.	0.6	2
101	Abstract 15945: Temporal Analyses of Chromatin Accessibility, Dna Methylation and Epigenomic Structure Identify Mechanisms of Locus-specific Regulation in the Heart. <i>Circulation</i> , 2020, 142, .	1.6	0
102	Functional reprogramming of regulatory T cells in the absence of Foxp3. <i>Nature Immunology</i> , 2019, 20, 1208-1219.	7.0	106
103	Alu RNA Modulates the Expression of Cell Cycle Genes in Human Fibroblasts. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3315.	1.8	10
104	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
105	The cell fate regulator NUPR1 is induced by <i>Mycobacterium leprae</i> via type I interferon in human leprosy. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007589.	1.3	7
106	IL-1 $\beta$ Induces the Rapid Secretion of the Antimicrobial Protein IL-26 from Th17 Cells. <i>Journal of Immunology</i> , 2019, 203, 911-921.	0.4	21
107	The size of cell-free mitochondrial DNA in blood is inversely correlated with tumor burden in cancer patients. <i>Precision Clinical Medicine</i> , 2019, 2, 131-139.	1.3	24
108	Identification of a systemic interferon- $\gamma$ inducible antimicrobial gene signature in leprosy patients undergoing reversal reaction. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007764.	1.3	21

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109	Identification of Bridging Centrality in Complex Networks. <i>IEEE Access</i> , 2019, 7, 93123-93130.	2.6	14
110	An in situ high-throughput screen identifies inhibitors of intracellular <i>Burkholderia pseudomallei</i> with therapeutic efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18597-18606.	3.3	13
111	H3K36 Methylation and the Chromodomain Protein Eaf3 Are Required for Proper Cotranscriptional Spliceosome Assembly. <i>Cell Reports</i> , 2019, 27, 3760-3769.e4.	2.9	37
112	Human epigenetic ageing is logarithmic with time across the entire lifespan. <i>Epigenetics</i> , 2019, 14, 912-926.	1.3	47
113	ZEB1 insufficiency causes corneal endothelial cell state transition and altered cellular processing. <i>PLoS ONE</i> , 2019, 14, e0218279.	1.1	20
114	Dual RNA-Seq of Human Leprosy Lesions Identifies Bacterial Determinants Linked to Host Immune Response. <i>Cell Reports</i> , 2019, 26, 3574-3585.e3.	2.9	38
115	DNA methylation estimation using methylation-sensitive restriction enzyme bisulfite sequencing (MREBS). <i>PLoS ONE</i> , 2019, 14, e0214368.	1.1	14
116	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
117	Endocardially Derived Macrophages Are Essential for Valvular Remodeling. <i>Developmental Cell</i> , 2019, 48, 617-630.e3.	3.1	61
118	DNA Methylation Changes More Slowly Than Physiological States in Response to Weight Loss in Genetically Diverse Mouse Strains. <i>Frontiers in Endocrinology</i> , 2019, 10, 882.	1.5	7
119	Plasticity of antimicrobial and phagocytic programs in human macrophages. <i>Immunology</i> , 2019, 156, 164-173.	2.0	20
120	Single-Cell RNA Sequencing Reveals Distinct Hematopoietic Stem Cell Hierarchies in MDS. <i>Blood</i> , 2019, 134, 771-771.	0.6	2
121	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	7.7	367
122	Topological Arrangement of Cardiac Fibroblasts Regulates Cellular Plasticity. <i>Circulation Research</i> , 2018, 123, 73-85.	2.0	42
123	<i>Mycobacterium tuberculosis</i> Transfer RNA Induces IL-12p70 via Synergistic Activation of Pattern Recognition Receptors within a Cell Network. <i>Journal of Immunology</i> , 2018, 200, 3244-3258.	0.4	18
124	Complete genomic sequences of <i>Propionibacterium freudenreichii</i> phages from Swiss cheese reveal greater diversity than <i>Cutibacterium</i> (formerly <i>Propionibacterium</i> ) <i>acnes</i> phages. <i>BMC Microbiology</i> , 2018, 18, 19.	1.3	13
125	Epigenome-wide association in adipose tissue from the METSIM cohort. <i>Human Molecular Genetics</i> , 2018, 27, 1830-1846.	1.4	38
126	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

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127	Prenatal Growth Patterns and Birthweight Are Associated With Differential DNA Methylation and Gene Expression of Cardiometabolic Risk Genes in Human Placentas: A Discovery-Based Approach. <i>Reproductive Sciences</i> , 2018, 25, 523-539.	1.1	41
128	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. <i>Plant Journal</i> , 2018, 93, 545-565.	2.8	90
129	Immunotherapy of Mild Cognitive Impairment by $\gamma$ -3 Supplementation: Why Are Amyloid- $\beta$ Antibodies and $\gamma$ -3 Not Working in Clinical Trials?. <i>Journal of Alzheimer's Disease</i> , 2018, 62, 1013-1022.	1.2	11
130	Comparison of reprogramming factor targets reveals both species-specific and conserved mechanisms in early iPSC reprogramming. <i>BMC Genomics</i> , 2018, 19, 956.	1.2	15
131	A temporal transcriptome and methylome in human embryonic stem cell-derived cardiomyocytes identifies novel regulators of early cardiac development. <i>Epigenetics</i> , 2018, 13, 1013-1026.	1.3	35
132	A phylogenomic study quantifies competing mechanisms for pseudogenization in prokaryotes—The <i>Mycobacterium leprae</i> case. <i>PLoS ONE</i> , 2018, 13, e0204322.	1.1	3
133	Metabolic repair through emergence of new pathways in <i>Escherichia coli</i> . <i>Nature Chemical Biology</i> , 2018, 14, 1005-1009.	3.9	20
134	Human antimicrobial cytotoxic T lymphocytes, defined by NK receptors and antimicrobial proteins, kill intracellular bacteria. <i>Science Immunology</i> , 2018, 3, .	5.6	59
135	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.	2.9	53
136	Synaptic N6-methyladenosine (m6A) epitranscriptome reveals functional partitioning of localized transcripts. <i>Nature Neuroscience</i> , 2018, 21, 1004-1014.	7.1	153
137	CRACR2A-Mediated TCR Signaling Promotes Local Effector Th1 and Th17 Responses. <i>Journal of Immunology</i> , 2018, 201, 1174-1185.	0.4	18
138	An epigenetic pacemaker is detected via a fast conditional expectation maximization algorithm. <i>Epigenomics</i> , 2018, 10, 695-706.	1.0	14
139	Loss of MECP2 Leads to Activation of P53 and Neuronal Senescence. <i>Stem Cell Reports</i> , 2018, 10, 1453-1463.	2.3	56
140	Transposon-associated epigenetic silencing during <i>Pleurotus ostreatus</i> life cycle. <i>DNA Research</i> , 2018, 25, 451-464.	1.5	17
141	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. <i>Metabolic Engineering</i> , 2018, 49, 153-163.	3.6	22
142	Seed genome hypomethylated regions are enriched in transcription factor genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8315-E8322.	3.3	19
143	Vav3-induced cytoskeletal dynamics contribute to heterotypic properties of endothelial barriers. <i>Journal of Cell Biology</i> , 2018, 217, 2813-2830.	2.3	22
144	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	1.4	166

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145	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
146	Astrocytes Can Adopt Endothelial Cell Fates in a p53-Dependent Manner. <i>Molecular Neurobiology</i> , 2017, 54, 4584-4596.	1.9	14
147	Altered methylation of specific DNA loci in the liver of <i>Bhmt</i> <sup>Δ</sup> mice results in repression of <i>Iqgap2</i> and <i>F2r2</i> and is associated with development of preneoplastic foci. <i>FASEB Journal</i> , 2017, 31, 2090-2103.	0.2	12
148	Modulation of innate immunity of patients with Alzheimer's disease by omega-3 fatty acids. <i>FASEB Journal</i> , 2017, 31, 3229-3239.	0.2	37
149	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
150	Abf1 and other general regulatory factors control ribosome biogenesis gene expression in budding yeast. <i>Nucleic Acids Research</i> , 2017, 45, 4493-4506.	6.5	41
151	Omega-3 fatty acids increase the unfolded protein response and improve amyloid $\beta$ phagocytosis by macrophages of patients with mild cognitive impairment. <i>FASEB Journal</i> , 2017, 31, 4359-4369.	0.2	22
152	Cytoreductive conditioning intensity predicts clonal diversity in ADA-SCID retroviral gene therapy patients. <i>Blood</i> , 2017, 129, 2624-2635.	0.6	27
153	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017, 18, 54-67.	2.9	100
154	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
155	Addressing the Digital Divide in Contemporary Biology: Lessons from Teaching UNIX. <i>Trends in Biotechnology</i> , 2017, 35, 901-903.	4.9	22
156	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
157	Cardiac Fibroblasts Adopt Osteogenic Fates and Can Be Targeted to Attenuate Pathological Heart Calcification. <i>Cell Stem Cell</i> , 2017, 20, 218-232.e5.	5.2	86
158	Increased intermediate M1-M2 macrophage polarization and improved cognition in mild cognitive impairment patients on DHA supplementation. <i>FASEB Journal</i> , 2017, 31, 148-160.	0.2	72
159	Regulation of Marginal Zone B-Cell Differentiation by MicroRNA-146a. <i>Frontiers in Immunology</i> , 2017, 7, 670.	2.2	25
160	Divergence in Morris Water Maze-Based Cognitive Performance under Chronic Stress Is Associated with the Hippocampal Whole Transcriptomic Modification in Mice. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 275.	1.4	26
161	Glucose inhibits cardiac muscle maturation through nucleotide biosynthesis. <i>ELife</i> , 2017, 6, .	2.8	142
162	SaVanT: a web-based tool for the sample-level visualization of molecular signatures in gene expression profiles. <i>BMC Genomics</i> , 2017, 18, 824.	1.2	32

#	ARTICLE	IF	CITATIONS
163	Targeted mutagenesis in a human-parasitic nematode. <i>PLoS Pathogens</i> , 2017, 13, e1006675.	2.1	104
164	An epigenetic aging clock for dogs and wolves. <i>Aging</i> , 2017, 9, 1055-1068.	1.4	125
165	Sequencing of cancer cell subpopulations identifies micrometastases in a bladder cancer patient. <i>Oncotarget</i> , 2017, 8, 45619-45625.	0.8	8
166	Identification and Characterization of a cis-Regulatory Element for Zygotic Gene Expression in <i>Chlamydomonas reinhardtii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1541-1548.	0.8	11
167	Transcriptomic Modification in the Cerebral Cortex following Noninvasive Brain Stimulation: RNA-Sequencing Approach. <i>Neural Plasticity</i> , 2016, 2016, 1-15.	1.0	9
168	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
169	Genetic Tagging During Human Mesoderm Differentiation Reveals Tripotent Lateral Plate Mesodermal Progenitors. <i>Stem Cells</i> , 2016, 34, 1239-1250.	1.4	10
170	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
171	Epigenetic changes in T cell and monocyte signatures and production of neurotoxic cytokines in ALS patients. <i>FASEB Journal</i> , 2016, 30, 3461-3473.	0.2	41
172	A naïve Bayesian classifier for identifying plant microRNAs. <i>Plant Journal</i> , 2016, 86, 481-492.	2.8	13
173	Whole-genome expression analysis of mammalian-wide interspersed repeat elements in human cell lines. <i>DNA Research</i> , 2016, 24, dsw048.	1.5	16
174	CRISPR-Mediated VHL Knockout Generates an Improved Model for Metastatic Renal Cell Carcinoma. <i>Scientific Reports</i> , 2016, 6, 29032.	1.6	51
175	Genome and methylome of the oleaginous diatom <i>Cyclotella cryptica</i> reveal genetic flexibility toward a high lipid phenotype. <i>Biotechnology for Biofuels</i> , 2016, 9, 258.	6.2	87
176	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
177	Imatinib Triggers Phagolysosome Acidification and Antimicrobial Activity against <i>Mycobacterium bovis</i> Bacille Calmette-Guérin in Glucocorticoid-Treated Human Macrophages. <i>Journal of Immunology</i> , 2016, 197, 222-232.	0.4	37
178	Biased Expression of the FOXP3 <sup>3</sup> Isoform in Aggressive Bladder Cancer Mediates Differentiation and Cisplatin Chemotherapy Resistance. <i>Clinical Cancer Research</i> , 2016, 22, 5349-5361.	3.2	21
179	Small molecule inhibition of cAMP response element binding protein in human acute myeloid leukemia cells. <i>Leukemia</i> , 2016, 30, 2302-2311.	3.3	37
180	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	2.7	59

#	ARTICLE	IF	CITATIONS
181	Epigenetic changes mediated by polycomb repressive complex 2 and E2a are associated with drug resistance in a mouse model of lymphoma. <i>Genome Medicine</i> , 2016, 8, 54.	3.6	12
182	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
183	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
184	Gestational food restriction decreases placental interleukin-10 expression and markers of autophagy and endoplasmic reticulum stress in murine intrauterine growth restriction. <i>Nutrition Research</i> , 2016, 36, 1055-1067.	1.3	20
185	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	1.2	106
186	Novel features of telomere biology revealed by the absence of telomeric DNA methylation. <i>Genome Research</i> , 2016, 26, 1047-1056.	2.4	18
187	CRISPR/Cas9-Mediated Correction of the Sickle Mutation in Human CD34+ cells. <i>Molecular Therapy</i> , 2016, 24, 1561-1569.	3.7	157
188	Cutaneous wound healing through paradoxical MAPK activation by BRAF inhibitors. <i>Nature Communications</i> , 2016, 7, 12348.	5.8	52
189	Discovering communities in complex networks by edge label propagation. <i>Scientific Reports</i> , 2016, 6, 22470.	1.6	37
190	DNA Methylation Indicates Susceptibility to Isoproterenol-Induced Cardiac Pathology and Is Associated With Chromatin States. <i>Circulation Research</i> , 2016, 118, 786-797.	2.0	40
191	Rapid Changes in the Transcriptome during the Conversion of Growth Cones to Synaptic Terminals. <i>Cell Reports</i> , 2016, 14, 1258-1271.	2.9	40
192	A Designed Inhibitor of p53 Aggregation Rescues p53 Tumor Suppression in Ovarian Carcinomas. <i>Cancer Cell</i> , 2016, 29, 90-103.	7.7	273
193	Cell-type deconvolution with immune pathways identifies gene networks of host defense and immunopathology in leprosy. <i>JCI Insight</i> , 2016, 1, e88843.	2.3	29
194	A Statistical Framework to Identify Deviation from Time Linearity in Epigenetic Aging. <i>PLoS Computational Biology</i> , 2016, 12, e1005183.	1.5	24
195	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
196	Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes. <i>ELife</i> , 2016, 5, .	2.8	35
197	Regulation of Marginal Zone B Cell Differentiation By microRNA-146a Via the Numb-Notch Pathway. <i>Blood</i> , 2016, 128, 3701-3701.	0.6	0
198	Preservation of Gene Edited Hematopoietic Stem Cells By Transient Overexpression of BCL-2 mRNA. <i>Blood</i> , 2016, 128, 3636-3636.	0.6	0

#	ARTICLE	IF	CITATIONS
199	Integrative analysis of human protein, function and disease networks. <i>Scientific Reports</i> , 2015, 5, 14344.	1.6	32
200	A high-throughput screen of inactive X chromosome reactivation identifies the enhancement of DNA demethylation by 5-aza-2- $\beta$ -dC upon inhibition of ribonucleotide reductase. <i>Epigenetics and Chromatin</i> , 2015, 8, 42.	1.8	38
201	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
202	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.	1.3	44
203	Pancreatic Cancer Patient Survival Correlates with DNA Methylation of Pancreas Development Genes. <i>PLoS ONE</i> , 2015, 10, e0128814.	1.1	57
204	Epigenome-Wide Association of Liver Methylation Patterns and Complex Metabolic Traits in Mice. <i>Cell Metabolism</i> , 2015, 21, 905-917.	7.2	98
205	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
206	Genome-wide gene order distances support clustering the gram-positive bacteria. <i>Frontiers in Microbiology</i> , 2015, 5, 785.	1.5	2
207	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
208	Development of effective therapy for sporadic ALS. <i>Expert Opinion on Biological Therapy</i> , 2015, 15, 1249-1249.	1.4	1
209	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
210	Pioneer Transcription Factors Target Partial DNA Motifs on Nucleosomes to Initiate Reprogramming. <i>Cell</i> , 2015, 161, 555-568.	13.5	643
211	Endogenous CCL2 neutralization restricts HIV-1 replication in primary human macrophages by inhibiting viral DNA accumulation. <i>Retrovirology</i> , 2015, 12, 4.	0.9	35
212	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
213	<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
214	Distinct Shifts in Microbiota Composition during <i>Drosophila</i> Aging Impair Intestinal Function and Drive Mortality. <i>Cell Reports</i> , 2015, 12, 1656-1667.	2.9	382
215	Comparison of Molecular Signatures from Multiple Skin Diseases Identifies Mechanisms of Immunopathogenesis. <i>Journal of Investigative Dermatology</i> , 2015, 135, 151-159.	0.3	35
216	In vivo targeting of de novo DNA methylation by histone modifications in yeast and mouse. <i>ELife</i> , 2015, 4, e06205.	2.8	146

#	ARTICLE	IF	CITATIONS
217	Interpretation of the Genome in Synchronized Chlamydomonas Cells. <i>FASEB Journal</i> , 2015, 29, 485.1.	0.2	0
218	Anti-inflammatory therapies of amyotrophic lateral sclerosis guided by immune pathways. <i>American Journal of Neurodegenerative Disease</i> , 2015, 4, 28-39.	0.1	6
219	Intestinal Subepithelial Myofibroblasts Support the Growth of Intestinal Epithelial Stem Cells. <i>PLoS ONE</i> , 2014, 9, e84651.	1.1	91
220	Selective demethylation and altered gene expression are associated with ICF syndrome in human-induced pluripotent stem cells and mesenchymal stem cells. <i>Human Molecular Genetics</i> , 2014, 23, 6448-6457.	1.4	26
221	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
222	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
223	All- <i>Trans</i> 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
224	Epigenetic differences between shoots and roots in <i>Arabidopsis</i> reveals tissue-specific regulation. <i>Epigenetics</i> , 2014, 9, 236-242.	1.3	54
225	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
226	Widespread Use of Non-productive Alternative Splice Sites in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2014, 10, e1004249.	1.5	85
227	Nrx2-5 Suppresses the Proliferation of Atrial Myocytes and Conduction System. <i>Circulation Research</i> , 2014, 114, 1103-1113.	2.0	50
228	let-7 miRNAs Can Act through Notch to Regulate Human Gliogenesis. <i>Stem Cell Reports</i> , 2014, 3, 758-773.	2.3	90
229	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
230	A comprehensive resource of genomic, epigenomic and transcriptomic sequencing data for the black truffle <i>Tuber melanosporum</i> . <i>GigaScience</i> , 2014, 3, 25.	3.3	10
231	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
232	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
233	Gene expression and nucleotide composition are associated with genic methylation level in <i>Oryza sativa</i> . <i>BMC Bioinformatics</i> , 2014, 15, 23.	1.2	17
234	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014, 507, 124-128.	13.7	271

#	ARTICLE	IF	CITATIONS
235	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, 663-676.	5.1	88
236	FamAnn: an automated variant annotation pipeline to facilitate target discovery for family-based sequencing studies. <i>Bioinformatics</i> , 2014, 30, 1175-1176.	1.8	7
237	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
238	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
239	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
240	Intergenerational genomic DNA methylation patterns in mouse hybrid strains. <i>Genome Biology</i> , 2014, 15, R68.	13.9	30
241	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
242	Nitrogen-Sparing Mechanisms in <i>Chlamydomonas</i> Affect the Transcriptome, the Proteome, and Photosynthetic Metabolism. <i>Plant Cell</i> , 2014, 26, 1410-1435.	3.1	314
243	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.	2.3	37
244	Detecting Communities Based on Network Topology. <i>Scientific Reports</i> , 2014, 4, 5739.	1.6	53
245	Phosphoprotein SAK1 is a regulator of acclimation to singlet oxygen in <i>Chlamydomonas reinhardtii</i> . <i>ELife</i> , 2014, 3, e02286.	2.8	45
246	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
247	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
248	Remodeling of Membrane Lipids in Iron-starved <i>Chlamydomonas</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 30246-30258.	1.6	77
249	Methylome reorganization during in vitro dedifferentiation and regeneration of <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2013, 13, 92.	1.6	51
250	BS-Seeker2: a versatile aligning pipeline for bisulfite sequencing data. <i>BMC Genomics</i> , 2013, 14, 774.	1.2	365
251	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
252	Proteomic and genomic approaches reveal critical functions of H3K9 methylation and heterochromatin protein-1 <sup>3</sup> in reprogramming to pluripotency. <i>Nature Cell Biology</i> , 2013, 15, 872-882.	4.6	205

#	ARTICLE	IF	CITATIONS
253	Insights into the mechanism of cell death induced by saporin delivered into cancer cells by an antibody fusion protein targeting the transferrin receptor 1. <i>Toxicology in Vitro</i> , 2013, 27, 220-231.	1.1	32
254	Evolutionary dynamics and information hierarchies in biological systems. <i>Annals of the New York Academy of Sciences</i> , 2013, 1305, 1-17.	1.8	6
255	Intrauterine calorie restriction affects placental DNA methylation and gene expression. <i>Physiological Genomics</i> , 2013, 45, 565-576.	1.0	84
256	COPPER RESPONSE REGULATOR1-Dependent and -Independent Responses of the <i>Chlamydomonas reinhardtii</i> Transcriptome to Dark Anoxia. <i>Plant Cell</i> , 2013, 25, 3186-3211.	3.1	77
257	New transgenic reporters identify somatosensory neuron subtypes in larval zebrafish. <i>Developmental Neurobiology</i> , 2013, 73, 152-167.	1.5	64
258	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.	2.5	85
259	Estrogen and progesterone together expand murine endometrial epithelial progenitor cells. <i>Stem Cells</i> , 2013, 31, 808-822.	1.4	47
260	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
261	Cross-Species Analysis of Genic GC3 Content and DNA Methylation Patterns. <i>Genome Biology and Evolution</i> , 2013, 5, 1443-1456.	1.1	57
262	Zinc Deficiency Impacts CO <sub>2</sub> Assimilation and Disrupts Copper Homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 10672-10683.	1.6	72
263	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
264	Plants regenerated from tissue culture contain stable epigenome changes in rice. <i>ELife</i> , 2013, 2, e00354.	2.8	225
265	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
266	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
267	Systems and Trans-System Level Analysis Identifies Conserved Iron Deficiency Responses in the Plant Lineage. <i>Plant Cell</i> , 2012, 24, 3921-3948.	3.1	142
268	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
269	Transcriptome Sequencing Identifies SPL7-Regulated Copper Acquisition Genes FRO4 and FRO5 and the Copper Dependence of Iron Homeostasis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 738-761.	3.1	286
270	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

#	ARTICLE	IF	CITATIONS
271	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
272	Scl Represses Cardiomyogenesis in Prospective Hemogenic Endothelium and Endocardium. <i>Cell</i> , 2012, 150, 590-605.	13.5	142
273	Unraveling Inflammatory Responses using Systems Genetics and Gene-Environment Interactions in Macrophages. <i>Cell</i> , 2012, 151, 658-670.	13.5	134
274	Transcriptome-Wide Changes in <i>Chlamydomonas reinhardtii</i> Gene Expression Regulated by Carbon Dioxide and the CO <sub>2</sub> -Concentrating Mechanism Regulator <i>CIA5</i> / <i>CCM1</i> . <i>Plant Cell</i> , 2012, 24, 1876-1893.	3.1	180
275	Three Acyltransferases and Nitrogen-responsive Regulator Are Implicated in Nitrogen Starvation-induced Triacylglycerol Accumulation in <i>Chlamydomonas</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 15811-15825.	1.6	379
276	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
277	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
278	Epigenetic Analysis: CHIP-chip and CHIP-seq. <i>Methods in Molecular Biology</i> , 2012, 802, 377-387.	0.4	28
279	<i>Propionibacterium acnes</i> Bacteriophages Display Limited Genetic Diversity and Broad Killing Activity against Bacterial Skin Isolates. <i>MBio</i> , 2012, 3, .	1.8	89
280	Genome-Wide Evaluation of Histone Methylation Changes Associated with Leaf Senescence in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2012, 7, e33151.	1.1	83
281	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
282	Reorganization of the host epigenome by a viral oncogene. <i>Genome Research</i> , 2012, 22, 1212-1221.	2.4	61
283	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. <i>Science</i> , 2012, 336, 1448-1451.	6.0	279
284	Using Phylogenetic Profiles to Predict Functional Relationships. <i>Methods in Molecular Biology</i> , 2012, 804, 167-177.	0.4	48
285	Lethal iron deprivation induced by non-neutralizing antibodies targeting transferrin receptor 1 in malignant B cells. <i>Leukemia and Lymphoma</i> , 2011, 52, 2169-2178.	0.6	20
286	Determining DNA Methylation Profiles Using Sequencing. <i>Methods in Molecular Biology</i> , 2011, 733, 223-238.	0.4	40
287	A comparative analysis of DNA methylation across human embryonic stem cell lines. <i>Genome Biology</i> , 2011, 12, R62.	13.9	86
288	Genome-Wide Binding Map of the HIV-1 Tat Protein to the Human Genome. <i>PLoS ONE</i> , 2011, 6, e26894.	1.1	40

#	ARTICLE	IF	CITATIONS
289	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
290	Regulation of the yeast metabolic cycle by transcription factors with periodic activities. <i>BMC Systems Biology</i> , 2011, 5, 160.	3.0	14
291	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.	1.2	84
292	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
293	Identification of genes required for de novo DNA methylation in <i>Arabidopsis</i> . <i>Epigenetics</i> , 2011, 6, 344-354.	1.3	64
294	Global Phosphoproteomics Reveals Crosstalk Between Bcr-Abl and Negative Feedback Mechanisms Controlling Src Signaling. <i>Science Signaling</i> , 2011, 4, ra18.	1.6	56
295	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
296	Identification of Novel Targets of CSL-Dependent Notch Signaling in Hematopoiesis. <i>PLoS ONE</i> , 2011, 6, e20022.	1.1	36
297	BS Seeker: precise mapping for bisulfite sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 203.	1.2	212
298	Genome-wide erasure of DNA methylation in mouse primordial germ cells is affected by AID deficiency. <i>Nature</i> , 2010, 463, 1101-1105.	18.7	777
299	Evolution, genomic analysis, and reconstruction of isobutanol tolerance in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 449.	3.2	252
300	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
301	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
302	Molecular Analyses of Human Induced Pluripotent Stem Cells and Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 263-269.	5.2	155
303	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . <i>Science</i> , 2010, 328, 351-354.	6.0	159
304	Relationship between nucleosome positioning and DNA methylation. <i>Nature</i> , 2010, 466, 388-392.	18.7	625
305	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, 8689-8694.	3.3	1,160
306	Determining the conservation of DNA methylation in <i>Arabidopsis</i> . <i>Epigenetics</i> , 2009, 4, 119-124.	1.3	22

#	ARTICLE	IF	CITATIONS
307	A Primer on Regression Methods for Decoding cis-Regulatory Logic. PLoS Computational Biology, 2009, 5, e1000269.	1.5	14
308	Copy number variation influences gene expression and metabolic traits in mice. Human Molecular Genetics, 2009, 18, 4118-4129.	1.4	107
309	Nonsense-mediated mRNA decay mutes the splicing defects of spliceosome component mutations. Rna, 2009, 15, 2236-2247.	1.6	30
310	Detecting coordinated regulation of multi-protein complexes using logic analysis of gene expression. BMC Systems Biology, 2009, 3, 115.	3.0	15
311	ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. Nature Structural and Molecular Biology, 2009, 16, 763-768.	3.6	278
312	Genome-wide analysis of mono-, di- and trimethylation of histone H3 lysine 4 in Arabidopsis thaliana. Genome Biology, 2009, 10, R62.	13.9	504
313	Mef2C is a lineage-restricted target of Scl/Tal1 and regulates megakaryopoiesis and B-cell homeostasis. Blood, 2009, 113, 3461-3471.	0.6	51
314	Specification and Maintenance of the Scl Induced Hematopoietic Stem Cell Fate.. Blood, 2009, 114, 1504-1504.	0.6	0
315	Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. Nature, 2008, 452, 215-219.	13.7	2,039
316	Expression profile of CREB knockdown in myeloid leukemia cells. BMC Cancer, 2008, 8, 264.	1.1	30
317	Genome-Wide Association of Histone H3 Lysine Nine Methylation with CHG DNA Methylation in Arabidopsis thaliana. PLoS ONE, 2008, 3, e3156.	1.1	293
318	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
319	X-inactivation in female human embryonic stem cells is in a nonrandom pattern and prone to epigenetic alterations. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4709-4714.	3.3	195
320	Identifying Cognate Binding Pairs among a Large Set of Paralogs: The Case of PE/PPE Proteins of Mycobacterium tuberculosis. PLoS Computational Biology, 2008, 4, e1000174.	1.5	37
321	Epigenetic Reprogramming by Adenovirus e1a. Science, 2008, 321, 1086-1088.	6.0	207
322	Cellular and Molecular Mechanisms of Sensitivity and Resistance of Hematopoietic Malignant Cells to Treatment with ch128.1Av, An Antibody-Avidin Fusion Protein Specific for Human Transferrin Receptor 1 (CD71).. Blood, 2008, 112, 1608-1608.	0.6	0
323	Genomewide Clonal Analysis of Lethal Mutations in the <i>Drosophila melanogaster</i> Eye: Comparison of the X Chromosome and Autosomes. Genetics, 2007, 177, 689-697.	1.2	37
324	Modeling the regulatory network of histone acetylation in <i>Saccharomyces cerevisiae</i> . Molecular Systems Biology, 2007, 3, 153.	3.2	32

#	ARTICLE	IF	CITATIONS
325	Whole-Genome Analysis of Histone H3 Lysine 27 Trimethylation in Arabidopsis. <i>PLoS Biology</i> , 2007, 5, e129.	2.6	667
326	An improved method for identifying functionally linked proteins using phylogenetic profiles. <i>BMC Bioinformatics</i> , 2007, 8, S7.	1.2	44
327	Insights into the Genetic Signature Associated with Cell Death Induced by an Antibody-Avidin Fusion Protein Specific for Transferrin Receptor.. <i>Blood</i> , 2007, 110, 3476-3476.	0.6	0
328	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
329	Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. <i>Cell</i> , 2006, 126, 1189-1201.	13.5	1,647
330	Modelling the network of cell cycle transcription factors in the yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Bioinformatics</i> , 2006, 7, 381.	1.2	31
331	Bioinformatic challenges for the next decade(s). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 525-527.	1.8	10
332	Phylogenetic profiling. , 2005, , .		0
333	Detection of parallel functional modules by comparative analysis of genome sequences. <i>Nature Biotechnology</i> , 2005, 23, 253-260.	9.4	30
334	Protein Interaction Networks. <i>Expert Review of Proteomics</i> , 2004, 1, 239-249.	1.3	79
335	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004, 5, R35.	13.9	276
336	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
337	Defining interacting partners for drug discovery. <i>Expert Opinion on Therapeutic Targets</i> , 2003, 7, 287-297.	1.5	4
338	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
339	Inferring protein interactions from phylogenetic distance matrices. <i>Bioinformatics</i> , 2003, 19, 2039-2045.	1.8	69
340	Computational methods for protein function analysis. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 46-50.	2.8	27
341	Computational method to assign microbial genes to pathways. <i>Journal of Cellular Biochemistry</i> , 2001, 84, 106-109.	1.2	19
342	Protein flexibility in solution and in crystals. <i>Journal of Chemical Physics</i> , 1999, 110, 10141-10152.	1.2	42

#	ARTICLE	IF	CITATIONS
343	A combined algorithm for genome-wide prediction of protein function. <i>Nature</i> , 1999, 402, 83-86.	13.7	879
344	Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. <i>Science</i> , 1999, 285, 751-753.	6.0	1,595
345	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
346	Searching for frameshift evolutionary relationships between protein sequence families. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 278-283.	1.5	11
347	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, 4285-4288.	3.3	1,653
348	A census of protein repeats. <i>Journal of Molecular Biology</i> , 1999, 293, 151-160.	2.0	385
349	A fast algorithm for genome-wide analysis of proteins with repeated sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 440-6.	1.5	34
350	Searching for frameshift evolutionary relationships between protein sequence families. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 278-83.	1.5	4
351	A new constrained Langevin method: application to protein crystallographic refinement. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1998, 261, 224-231.	1.2	1
352	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
353	Simulations of the thermodynamic properties of a short polyaniline peptide using potentials of mean force. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1997, 239, 244-254.	1.2	9
354	Simulation of protein crystal nucleation. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 515-521.	1.5	14
355	Highly constrained multiple-copy refinement of protein crystal structures. , 1997, 29, 426-432.		31
356	Simulation of protein crystal nucleation. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 515-21.	1.5	4
357	Potentials of mean force for biomolecular simulations: Theory and test on alanine dipeptide. <i>Journal of Chemical Physics</i> , 1996, 104, 8639-8648.	1.2	26
358	Modeling solvation contributions to conformational free energy changes of biomolecules using a potential of mean force expansion. <i>Journal of Chemical Physics</i> , 1995, 103, 2696-2702.	1.2	18
359	Crystal Structure of a Cross-reaction Complex between Fab F9.13.7 and Guinea Fowl Lysozyme. <i>Journal of Biological Chemistry</i> , 1995, 270, 18067-18076.	1.6	79
360	Computer simulation of antibody binding specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 436-444.	1.5	29

#	ARTICLE	IF	CITATIONS
361	Medicago root nodule microbiomes: insights into a complex ecosystem with potential candidates for plant growth promotion. <i>Plant and Soil</i> , 0, , 1.	1.8	4