

CITATION REPORT

List of articles citing

Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing

DOI: 10.1038/nature12364

Nature, 2013, 500, 593-7.

Source: <https://exaly.com/paper-pdf/54809683/citation-report.pdf>

Version: 2024-04-25

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

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

#	Paper	IF	Citations
792	Single-cell genomics: An overview. 2013 , 8, 569-576		3
791	Ovary transcriptome profiling via artificial intelligence reveals a transcriptomic fingerprint predicting egg quality in striped bass, <i>Morone saxatilis</i> . 2014 , 9, e96818		46
790	Live pups from evaporatively dried mouse sperm stored at ambient temperature for up to 2 years. 2014 , 9, e99809		15
789	Differences in gene expression between mouse and human for dynamically regulated genes in early embryo. 2014 , 9, e102949		21
788	Insights into the next generation of cancer stem cell research. 2014 , 19, 1015-27		6
787	Reduced ability to recover from spindle disruption and loss of kinetochore spindle assembly checkpoint proteins in oocytes from aged mice. 2014 , 13, 1938-47		40
786	Characterizing heterogeneity in leukemic cells using single-cell gene expression analysis. 2014 , 15, 525		41
785	Characterizing human stem cell-derived sensory neurons at the single-cell level reveals their ion channel expression and utility in pain research. 2014 , 22, 1530-1543		78
784	Contribution of transcription to animal early development. 2014 , 5, e967602		4
783	All-trans retinoic acid-triggered antimicrobial activity against <i>Mycobacterium tuberculosis</i> is dependent on NPC2. 2014 , 192, 2280-2290		72
782	Freedom of expression: cell-type-specific gene profiling. 2014 , 3, 429-43		9
781	Defining midbrain dopaminergic neuron diversity by single-cell gene expression profiling. 2014 , 9, 930-43		179
780	Comparison of epigenetic mediator expression and function in mouse and human embryonic blastomeres. 2014 , 23, 4970-84		25
779	Genome-wide analysis of DNA methylation dynamics during early human development. <i>PLoS Genetics</i> , 2014 , 10, e1004868	6	167
778	Single cell genomics: advances and future perspectives. <i>PLoS Genetics</i> , 2014 , 10, e1004126	6	270
777	Genome-wide bisulfite sequencing in zygotes identifies demethylation targets and maps the contribution of TET3 oxidation. 2014 , 9, 1990-2000		95
776	The transcriptome of human pluripotent stem cells. <i>Current Opinion in Genetics and Development</i> , 2014 , 28, 71-7	4.9	13

775	Single-cell RNA-seq: advances and future challenges. 2014 , 42, 8845-60		478
774	Totipotency: what it is and what it is not. 2014 , 23, 796-812		66
773	A comprehensive transcriptomic analysis of infant and adult mouse ovary. 2014 , 12, 239-48		16
772	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. 2014 , 42, 9880-91		47
771	Irregular transcriptome reprogramming probably causes the developmental failure of embryos produced by interspecies somatic cell nuclear transfer between the Przewalski's gazelle and the bovine. 2014 , 15, 1113		17
770	Clinical outcome of preimplantation genetic diagnosis and screening using next generation sequencing. 2014 , 3, 30		77
769	The birth of embryonic pluripotency. 2014 , 369,		41
768	Transcriptional regulators of the trophoblast lineage in mammals with hemochorial placentation. 2014 , 148, R121-36		41
767	Integral proteomic analysis of blastocysts reveals key molecular machinery governing embryonic diapause and reactivation for implantation in mice. <i>Biology of Reproduction</i> , 2014 , 90, 52	3-9	33
766	Bifurcation analysis of single-cell gene expression data reveals epigenetic landscape. 2014 , 111, E5643-50		206
765	Current challenges in the bioinformatics of single cell genomics. <i>Frontiers in Oncology</i> , 2014 , 4, 7	5-3	35
764	Recent Advances in Studying of Copy Number Variation and Gene Expression. 2014 , 1		5
763	Transcriptional profiles of bovine in vivo pre-implantation development. 2014 , 15, 756		105
762	The earliest transcribed zygotic genes are short, newly evolved, and different across species. 2014 , 6, 285-92		121
761	Comparative gene expression signature of pig, human and mouse induced pluripotent stem cell lines reveals insight into pig pluripotency gene networks. 2014 , 10, 162-76		27
760	Improvement of mouse embryo quality by myo-inositol supplementation of IVF media. 2014 , 31, 463-9		36
759	PRDM14: a unique regulator for pluripotency and epigenetic reprogramming. 2014 , 39, 289-98		43
758	Single-cell sequencing technologies: current and future. 2014 , 41, 513-28		49

757	Decoding neural transcriptomes and epigenomes via high-throughput sequencing. 2014 , 17, 1463-75		42
756	Single cell sequencing approaches for complex biological systems. <i>Current Opinion in Genetics and Development</i> , 2014 , 26, 59-65	4.9	25
755	Microfluidic whole genome amplification device for single cell sequencing. 2014 , 86, 9386-90		48
754	Exonuclease-mediated degradation of nascent RNA silences genes linked to severe malaria. <i>Nature</i> , 2014 , 513, 431-5	50.4	58
753	Uniformity of nucleosome preservation pattern in Mammalian sperm and its connection to repetitive DNA elements. 2014 , 30, 23-35		107
752	Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. <i>Genome Research</i> , 2014 , 24, 1787-96	9.7	175
751	Single-cell analysis of the transcriptome and its application in the characterization of stem cells and early embryos. 2014 , 71, 2707-15		26
750	Singled out for sequencing. 2014 , 11, 13-7		20
749	Single molecule fluorescence approaches shed light on intracellular RNAs. 2014 , 114, 3224-65		65
748	Transcription in pronuclei and one- to four-cell embryos drives early development in a nematode. 2014 , 24, 124-133		31
747	The common ground of genomics and systems biology. 2014 , 8 Suppl 2, S1		21
746	Fine mapping of genome activation in bovine embryos by RNA sequencing. 2014 , 111, 4139-44		195
745	Role of Tet proteins in enhancer activity and telomere elongation. 2014 , 28, 2103-19		176
744	Zygotic genome activation during the maternal-to-zygotic transition. 2014 , 30, 581-613		320
743	The naive state of human pluripotent stem cells: a synthesis of stem cell and preimplantation embryo transcriptome analyses. <i>Cell Stem Cell</i> , 2014 , 15, 410-415	18	117
742	Chromatin dynamics in the regulation of cell fate allocation during early embryogenesis. 2014 , 15, 723-34		137
741	Single cell analysis of cancer genomes. <i>Current Opinion in Genetics and Development</i> , 2014 , 24, 82-91	4.9	99
740	Day-1 chick development. 2014 , 243, 357-67		22

739	Genomic profiling to improve embryogenesis in the pig. 2014 , 149, 39-45	6
738	Genome activation in bovine embryos: review of the literature and new insights from RNA sequencing experiments. 2014 , 149, 46-58	87
737	Current approaches to the diagnosis and treatment of white sponge nevus. 2015 , 17, e9	16
736	Transcriptome-wide variability in single embryonic development cells. 2014 , 4, 7137	52
735	Aberrant expression of maternal Plk1 and Dctn3 results in the developmental failure of human in-vivo- and in-vitro-matured oocytes. 2015 , 5, 8192	6
734	mRNA Levels of Imprinted Genes in Bovine In Vivo Oocytes, Embryos and Cross Species Comparisons with Humans, Mice and Pigs. 2015 , 5, 17898	21
733	Trichostatin A specifically improves the aberrant expression of transcription factor genes in embryos produced by somatic cell nuclear transfer. 2015 , 5, 10127	26
732	Imbalance between the expression dosages of X-chromosome and autosomal genes in mammalian oocytes. 2015 , 5, 14101	10
731	Expression profiling of white sponge nevus by RNA sequencing revealed pathological pathways. 2015 , 10, 72	3
730	Single-cell analysis for bioprocessing. 2015 , 15, 582-592	4
729	Improved detection of disease-associated variation by sex-specific characterization and prediction of genes required for fertility. 2015 , 3, 1140-9	1
728	Single-cell analysis of lung adenocarcinoma cell lines reveals diverse expression patterns of individual cells invoked by a molecular target drug treatment. 2015 , 16, 66	57
727	Dark RNA of the Early Embryo. <i>Biology of Reproduction</i> , 2015 , 92,	3.9
726	Evaluation of commercially available RNA amplification kits for RNA sequencing using very low input amounts of total RNA. 2015 , 26, 4-18	38
725	Digital Microfluidics for Manipulation and Analysis of a Single Cell. 2015 , 16, 22319-32	42
724	Potential role of lncRNA cyp2c91-protein interactions on diseases of the immune system. <i>Frontiers in Genetics</i> , 2015 , 6, 255	4.5 20
723	SINCERA: A Pipeline for Single-Cell RNA-Seq Profiling Analysis. 2015 , 11, e1004575	206
722	A Mouse Model for Imprinting of the Human Retinoblastoma Gene. 2015 , 10, e0134672	4

721	Comparative Transcriptomes and EVO-DEVO Studies Depending on Next Generation Sequencing. 2015 , 2015, 896176	3	
720	Gene Coexpression and Evolutionary Conservation Analysis of the Human Preimplantation Embryos. 2015 , 2015, 316735	4	
719	Mapping of Post-translational Modifications of Transition Proteins, TP1 and TP2, and Identification of Protein Arginine Methyltransferase 4 and Lysine Methyltransferase 7 as Methyltransferase for TP2. 2015 , 290, 12101-22	18	
718	Advances and applications of single-cell sequencing technologies. 2015 , 58, 598-609	341	
717	Single-cell transcriptome analyses reveal signals to activate dormant neural stem cells. 2015 , 161, 1175-1186	167	
716	The technology and biology of single-cell RNA sequencing. 2015 , 58, 610-20	650	
715	Significance of Single Cell Sequencing in Future Medicine. 2015 , 1-10		
714	Transcriptomics of mRNA and egg quality in farmed fish: Some recent developments and future directions. 2015 , 221, 23-30	33	
713	Metabolites involved in cellular communication among human cumulus-oocyte-complex and sperm during in vitro fertilization. 2015 , 13, 123	5	
712	Reference-based compression of short-read sequences using path encoding. 2015 , 31, 1920-8	32	
711	Discordant Growth of Monozygotic Twins Starts at the Blastocyst Stage: A Case Study. 2015 , 5, 946-953	38	
710	Finding Missing Proteins from the Epigenetically Manipulated Human Cell with Stringent Quality Criteria. 2015 , 14, 3645-57	18	
709	Decoding the regulatory network of early blood development from single-cell gene expression measurements. 2015 , 33, 269-276	268	
708	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. 2015 , 290, 685-97	20	
707	Introduction: nongenetic markers of oocyte and embryo competence. 2015 , 103, 301-2	4	
706	Dynamic transcription of distinct classes of endogenous retroviral elements marks specific populations of early human embryonic cells. <i>Cell Stem Cell</i> , 2015 , 16, 135-41	18	177
705	GATA family members as inducers for cellular reprogramming to pluripotency. <i>Cell Research</i> , 2015 , 25, 169-80	24.7	38
704	RNA-Seq profiling of single bovine oocyte transcript abundance and its modulation by cytoplasmic polyadenylation. 2015 , 82, 103-14		32

703	Integrated genome and transcriptome sequencing of the same cell. 2015 , 33, 285-289		326
702	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. 2015 , 33, 155-60		778
701	Differences in gene expression profiles between human preimplantation embryos cultured in two different IVF culture media. 2015 , 30, 2303-11		44
700	Sculpting the Transcriptome During the Oocyte-to-Embryo Transition in Mouse. 2015 , 113, 305-49		79
699	Prediction model for aneuploidy in early human embryo development revealed by single-cell analysis. 2015 , 6, 7601		72
698	Identification and Characterization of a PRDM14 Homolog in Japanese Flounder (<i>Paralichthys olivaceus</i>). 2015 , 16, 9097-118		4
697	New insights into the conserved mechanism of pluripotency maintenance. <i>Current Opinion in Genetics and Development</i> , 2015 , 34, 1-9	4.9	3
696	Application of single-cell genomics in cancer: promise and challenges. 2015 , 24, R74-84		51
695	Transcriptome Signature and Regulation in Human Somatic Cell Reprogramming. 2015 , 4, 1125-39		13
694	Intrinsic retroviral reactivation in human preimplantation embryos and pluripotent cells. <i>Nature</i> , 2015 , 522, 221-5	50.4	339
693	Calibrating genomic and allelic coverage bias in single-cell sequencing. 2015 , 6, 6822		57
692	How cells build totipotency and pluripotency: nuclear, chromatin and transcriptional architecture. 2015 , 34, 9-15		12
691	The first murine zygotic transcription is promiscuous and uncoupled from splicing and 3' processing. 2015 , 34, 1523-37		79
690	Single cell transcriptomics: methods and applications. <i>Frontiers in Oncology</i> , 2015 , 5, 53	5.3	42
689	Cellular analysis of cleavage-stage chick embryos reveals hidden conservation in vertebrate early development. 2015 , 142, 1279-86		18
688	Defining cell types and states with single-cell genomics. <i>Genome Research</i> , 2015 , 25, 1491-8	9.7	421
687	Cellular Deconstruction: Finding Meaning in Individual Cell Variation. 2015 , 25, 569-578		14
686	Single-Cell Analysis in Cancer Genomics. 2015 , 31, 576-586		128

685	Dynamic transcriptional symmetry-breaking in pre-implantation mammalian embryo development revealed by single-cell RNA-seq. 2015 , 142, 3468-77		67
684	Histone Demethylase Expression Enhances Human Somatic Cell Nuclear Transfer Efficiency and Promotes Derivation of Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2015 , 17, 758-766	18	119
683	Chromatin and extracellular vesicle associated sperm RNAs. 2015 , 43, 6847-59		44
682	Patterns of differential gene expression in adult rotation-resistant and wild-type western corn rootworm digestive tracts. 2015 , 8, 692-704		9
681	Spatiotemporal-specific lncRNAs in the brain, colon, liver and lung of macaque during development. 2015 , 11, 3253-63		26
680	Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape. 2015 , 16, 209		117
679	Single-cell messenger RNA sequencing reveals rare intestinal cell types. <i>Nature</i> , 2015 , 525, 251-5	50.4	762
678	Defining the three cell lineages of the human blastocyst by single-cell RNA-seq. 2015 , 142, 3151-65		223
677	Novel PRD-like homeodomain transcription factors and retrotransposon elements in early human development. 2015 , 6, 8207		57
676	Mammalian pre-implantation chromosomal instability: species comparison, evolutionary considerations, and pathological correlations. 2015 , 61, 321-35		19
675	Dynamic comparisons of high-resolution expression profiles highlighting mitochondria-related genes between in vivo and in vitro fertilized early mouse embryos. 2015 , 30, 2892-911		24
674	Lineage-Specific Profiling Delineates the Emergence and Progression of Naive Pluripotency in Mammalian Embryogenesis. 2015 , 35, 366-82		253
673	Angelman syndrome imprinting center encodes a transcriptional promoter. 2015 , 112, 6871-5		35
672	Pluripotency in the light of the developmental hourglass. 2015 , 90, 428-43		6
671	Reprogramming the genome to totipotency in mouse embryos. 2015 , 25, 82-91		73
670	Time-resolved ICP-MS analysis of mineral element contents and distribution patterns in single cells. 2015 , 140, 523-31		52
669	Comparative profiling of the sperm proteome. 2015 , 15, 632-48		25
668	Bioinformatics approaches to single-blastomere transcriptomics. 2015 , 21, 115-25		3

667	Gene network analysis reveals a novel 22-gene signature of carbon metabolism in hepatocellular carcinoma. 2016 , 7, 49232-49245		13
666	Transcriptional Regulation During Zygotic Genome Activation in Zebrafish and Other Anamniote Embryos. 2016 , 95, 161-94		11
665	Maternal LSD1/KDM1A is an essential regulator of chromatin and transcription landscapes during zygotic genome activation. 2016 , 5,		80
664	Single-cell transcriptome sequencing: recent advances and remaining challenges. 2016 , 5,		149
663	A transcriptional blueprint for a spiral-cleaving embryo. 2016 , 17, 552		12
662	Human Oocyte-Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. <i>PLoS Genetics</i> , 2016 , 12, e1006427	6	61
661	Exploring timing activation of functional pathway based on differential co-expression analysis in preimplantation embryogenesis. 2016 , 7, 74120-74131		19
660	Spatiotemporal Reconstruction of the Human Blastocyst by Single-Cell Gene-Expression Analysis Informs Induction of Naive Pluripotency. 2016 , 38, 100-15		24
659	Transcriptome activity of isochores during preimplantation process in human and mouse. 2016 , 590, 2297-306		1
658	Transcriptome analysis of bovine oocytes from distinct follicle sizes: Insights from correlation network analysis. 2016 , 83, 558-69		20
657	Identifying and annotating human bifunctional RNAs reveals their versatile functions. 2016 , 59, 981-992		8
656	Identification of key factors conquering developmental arrest of somatic cell cloned embryos by combining embryo biopsy and single-cell sequencing. 2016 , 2, 16010		111
655	Single-cell analysis of differences in transcriptomic profiles of oocytes and cumulus cells at GV, MI, MII stages from PCOS patients. 2016 , 6, 39638		31
654	The human PRD-like homeobox gene LEUTX has a central role in embryo genome activation. 2016 , 143, 3459-3469		21
653	Systems analysis uncovers inflammatory Th/Tc17-driven modules during acute GVHD in monkey and human T cells. 2016 , 128, 2568-2579		32
652	ECAT1 is essential for human oocyte maturation and pre-implantation development of the resulting embryos. 2016 , 6, 38192		9
651	Exploiting single-cell expression to characterize co-expression replicability. 2016 , 17, 101		43
650	Heterogeneity of Mesp1+ mesoderm revealed by single-cell RNA-seq. 2016 , 474, 469-475		11

649	Design and computational analysis of single-cell RNA-sequencing experiments. 2016 , 17, 63	301
648	Activation of endogenous human stem cell-associated retroviruses (SCARs) and therapy-resistant phenotypes of malignant tumors. 2016 , 376, 347-59	15
647	Single-cell sequencing in stem cell biology. 2016 , 17, 71	97
646	Simultaneous profiling of transcriptome and DNA methylome from a single cell. 2016 , 17, 88	169
645	TET enzymes are successively expressed during human spermatogenesis and their expression level is pivotal for male fertility. 2016 , 31, 1411-24	26
644	Dissecting stem cell differentiation using single cell expression profiling. 2016 , 43, 78-86	18
643	Single-cell RNA sequencing reveals dynamic changes in A-to-I RNA editome during early human embryogenesis. 2016 , 17, 766	17
642	Pediatric Biomedical Informatics. 2016 ,	1
641	Inhibition of P-TEFb disrupts global transcription, oocyte maturation, and embryo development in the mouse. 2016 , 54, 470-82	6
640	Epigenetic Control of Early Mouse Development. 2016 , 120, 311-60	17
639	Species-Specific Variation Among Mammals. 2016 , 120, 401-20	4
638	Single cell genomics reveals activation signatures of endogenous SCAR's networks in aneuploid human embryos and clinically intractable malignant tumors. 2016 , 381, 176-93	12
637	Single-cell RNA sequencing: revealing human pre-implantation development, pluripotency and germline development. 2016 , 280, 252-64	8
636	Advances, practice, and clinical perspectives in high-throughput sequencing. 2016 , 22, 353-64	7
635	Disentangling neural cell diversity using single-cell transcriptomics. 2016 , 19, 1131-41	213
634	At the interface of stem cell research and new technologies. 2016 , 280, 232-5	
633	Modeling heterogeneity in the pluripotent state: A promising strategy for improving the efficiency and fidelity of stem cell differentiation. 2016 , 38, 758-68	7
632	A Transcriptional Lineage of the Early <i>C. elegans</i> Embryo. 2016 , 38, 430-44	54

631	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. <i>Nature</i> , 2016 , 537, 548-552	50.4	311
630	Genetics and immunity in the era of single-cell genomics. 2016 , 25, R141-R148		18
629	CellTree: an R/bioconductor package to infer the hierarchical structure of cell populations from single-cell RNA-seq data. 2016 , 17, 363		54
628	Assay of Genome-Wide Transcriptome and Secreted Proteins on the Same Single Immune Cells by Microfluidics and RNA Sequencing. 2016 , 88, 10309-10315		19
627	Long non-coding RNAs in human early embryonic development and their potential in ART. 2016 , 23, 19-40		70
626	Single-Cell Molecular Profiles and Biophysical Assessment of Circulating Tumor Cells. 2016 , 329-350		
625	Transcriptome analyses of inner cell mass and trophectoderm cells isolated by magnetic-activated cell sorting from bovine blastocysts using single cell RNA-seq. 2016 , 51, 726-35		15
624	CTRL+INSERT: retrotransposons and their contribution to regulation and innovation of the transcriptome. 2016 , 17, 1131-44		46
623	Single-cell genome-wide studies give new insight into nongenetic cell-to-cell variability in animals. 2016 , 146, 239-54		4
622	Genome-Wide Analysis of Single Cells and the Role of Microfluidics. 2016 , 29-56		1
621	Massive and parallel expression profiling using microarrayed single-cell sequencing. 2016 , 7, 13182		33
620	A cross-species bi-clustering approach to identifying conserved co-regulated genes. 2016 , 32, i137-i146		4
619	Epipolymorphisms associated with the clinical outcome of autoimmune arthritis affect CD4+ T cell activation pathways. 2016 , 113, 13845-13850		19
618	Human oocyte developmental potential is predicted by mechanical properties within hours after fertilization. 2016 , 7, 10809		100
617	Transcriptomic Profiling Maps Anatomically Patterned Subpopulations among Single Embryonic Cardiac Cells. 2016 , 39, 491-507		129
616	SCOUP: a probabilistic model based on the Ornstein-Uhlenbeck process to analyze single-cell expression data during differentiation. 2016 , 17, 232		38
615	Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. 2016 , 14, 45		19
614	HIPSTR and thousands of lncRNAs are heterogeneously expressed in human embryos, primordial germ cells and stable cell lines. 2016 , 6, 32753		26

613	A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. 2016 , 17, 222	133
612	Revealing the vectors of cellular identity with single-cell genomics. 2016 , 34, 1145-1160	382
611	Nuclease Footprints in Sperm Project Past and Future Chromatin Regulatory Events. 2016 , 6, 25864	16
610	Diversity of human and mouse homeobox gene expression in development and adult tissues. 2016 , 16, 40	20
609	Recent advances in preimplantation genetic diagnosis and screening. 2016 , 33, 1129-34	18
608	Using Dicationic Ion-Pairing Compounds To Enhance the Single Cell Mass Spectrometry Analysis Using the Single-Probe: A Microscale Sampling and Ionization Device. 2016 , 88, 6812-9	45
607	Cell death is involved in sexual dimorphism during preimplantation development. 2016 , 139, 42-50	10
606	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. 2016 , 165, 1375-1388	158
605	Stem Cells: A Renaissance in Human Biology Research. 2016 , 165, 1572-1585	67
604	Classification of low quality cells from single-cell RNA-seq data. 2016 , 17, 29	329
603	Single-Cell Genomics and Epigenomics. 2016 , 257-301	2
602	Serum-Based Culture Conditions Provoke Gene Expression Variability in Mouse Embryonic Stem Cells as Revealed by Single-Cell Analysis. 2016 , 14, 956-965	56
601	Essentials of Single-Cell Analysis. 2016 ,	23
600	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. 2016 , 165, 61-74	240
599	Spatial Transcriptome for the Molecular Annotation of Lineage Fates and Cell Identity in Mid-gastrula Mouse Embryo. 2016 , 36, 681-97	147
598	Cytoplasmic polyadenylation in mammalian oocyte maturation. 2016 , 7, 71-89	48
597	Emerging Imaging and Genomic Tools for Developmental Systems Biology. 2016 , 36, 597-610	37
596	A maternal deletion upstream of the imprint control region 2 in 11p15 causes loss of methylation and familial Beckwith-Wiedemann syndrome. 2016 , 24, 1280-6	18

595	What we can learn from single-cell analysis in development. 2016 , 22, 160-71	2
594	Gene expression variability in mammalian embryonic stem cells using single cell RNA-seq data. 2016 , 63, 52-61	21
593	Use of the Fluidigm C1 platform for RNA sequencing of single mouse pancreatic islet cells. 2016 , 113, 3293-8	104
592	Gene expression variability in clonal populations: Causes and consequences. 2016 , 42, 969-84	17
591	The double-edged sword of the mammalian oocyte--advantages, drawbacks and approaches for basic and clinical analysis at the single cell level. 2016 , 22, 200-7	10
590	Bioinformatics approaches to single-cell analysis in developmental biology. 2016 , 22, 182-92	15
589	Significant variations in alternative splicing patterns and expression profiles between human-mouse orthologs in early embryos. 2017 , 60, 178-188	5
588	Regulation of heat-inducible HSPA1A gene expression during maternal-to-embryo transition and in response to heat in in vitro-produced bovine embryos. 2017 , 29, 1868-1881	9
587	Primate embryogenesis predicts the hallmarks of human naïve pluripotency. 2017 , 144, 175-186	77
586	Dysregulation of long noncoding RNAs in mouse testes and spermatozoa after exposure to cadmium. 2017 , 484, 8-14	20
585	Towards a CRISPR view of early human development: applications, limitations and ethical concerns of genome editing in human embryos. 2017 , 144, 3-7	30
584	Gene co-expression analysis for functional classification and gene-disease predictions. 2018 , 19, 575-592	377
583	Nuclear Localization of Mitochondrial TCA Cycle Enzymes as a Critical Step in Mammalian Zygotic Genome Activation. 2017 , 168, 210-223.e11	123
582	Deficiency of microRNA expands cell fate potential in pluripotent stem cells. 2017 , 355,	96
581	Studying hematopoiesis using single-cell technologies. 2017 , 10, 27	26
580	Transcriptome analyses of rhesus monkey preimplantation embryos reveal a reduced capacity for DNA double-strand break repair in primate oocytes and early embryos. <i>Genome Research</i> , 2017 , 27, 567-579	40
579	MR-seq: measuring a single cell's transcriptome repeatedly by RNA-seq. 2017 , 62, 391-398	7
578	Spatial transcriptomic analysis of cryosectioned tissue samples with Geo-seq. 2017 , 12, 566-580	118

577	Exploratory bioinformatics investigation reveals importance of "junk" DNA in early embryo development. 2017 , 18, 200	33
576	Oocyte Developmental Competence: Insights from Cross-Species Differential Gene Expression and Human Oocyte-Specific Functional Gene Networks. 2017 , 21, 156-168	16
575	Placental transcriptome co-expression analysis reveals conserved regulatory programs across gestation. 2017 , 18, 10	16
574	Single-Cell Transcriptome Analysis of Neural Stem Cells. 2017 , 3, 68-76	0
573	Differential regulation of H3S10 phosphorylation, mitosis progression and cell fate by Aurora Kinase B and C in mouse preimplantation embryos. 2017 , 8, 662-674	11
572	Recent Technical Breakthroughs for ARTs in Mice. 2017 , 34, 13-21	2
571	Comparative transcriptomics in human and mouse. 2017 , 18, 425-440	99
570	Using scale and feather traits for module construction provides a functional approach to chicken epidermal development. 2017 , 17, 641-651	2
569	Conserved roles of mouse DUX and human DUX4 in activating cleavage-stage genes and MERVL/HERVL retrotransposons. 2017 , 49, 925-934	314
568	Obesity Modulates Inflammation and Lipid Metabolism Oocyte Gene Expression: A Single-Cell Transcriptome Perspective. 2017 , 102, 2029-2038	36
567	Dysregulation of the SIRT1/OCT6 Axis Contributes to Environmental Stress-Induced Neural Induction Defects. 2017 , 8, 1270-1286	10
566	Computational approaches for interpreting scRNA-seq data. 2017 , 591, 2213-2225	75
565	New insights into human primordial germ cells and early embryonic development from single-cell analysis. 2017 , 591, 2226-2240	4
564	The transcriptome of human oocytes is related to age and ovarian reserve. 2017 , 23, 535-548	26
563	Single-cell RNA-sequencing of the brain. 2017 , 6, 20	28
562	Derivation of Pluripotent Stem Cells with In Vivo Embryonic and Extraembryonic Potency. 2017 , 169, 243-257.e25	237
561	Single-Cell 5-Formylcytosine Landscapes of Mammalian Early Embryos and ESCs at Single-Base Resolution. <i>Cell Stem Cell</i> , 2017 , 20, 720-731.e5	18 93
560	Single-cell analysis reveals lineage segregation in early post-implantation mouse embryos. 2017 , 292, 9840-9854	18

559	Understanding development and stem cells using single cell-based analyses of gene expression. 2017 , 144, 17-32		87
558	New genes from old: asymmetric divergence of gene duplicates and the evolution of development. 2017 , 372,		55
557	Cell Cycle Remodeling and Zygotic Gene Activation at the Midblastula Transition. 2017 , 953, 441-487		12
556	XACT Noncoding RNA Competes with XIST in the Control of X Chromosome Activity during Human Early Development. <i>Cell Stem Cell</i> , 2017 , 20, 102-111	18	114
555	Clearance of Parental Products. 2017 , 953, 489-535		5
554	Controlling for Confounding Effects in Single Cell RNA Sequencing Studies Using both Control and Target Genes. 2017 , 7, 13587		24
553	Transcriptome analysis reveals determinant stages controlling human embryonic stem cell commitment to neuronal cells. 2017 , 292, 19590-19604		20
552	Treatment donor cells with UNC0638 modify the abnormal histone H3K9 dimethylation and gene expression in cloned goat embryos. 2017 , 156, 27-32		4
551	Human embryos from induced pluripotent stem cell-derived gametes: ethical and quality considerations. 2017 , 12, 681-691		4
550	A short review of variants calling for single-cell-sequencing data with applications. 2017 , 92, 218-226		4
549	Alternative Polyadenylation: Methods, Findings, and Impacts. 2017 , 15, 287-300		50
548	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. 2017 , 45, 12723-12738		28
547	Differing molecular response of young and advanced maternal age human oocytes to IVM. 2017 , 32, 2199-2208		26
546	Lineage specification of early embryos and embryonic stem cells at the dawn of enabling technologies. 2017 , 4, 533-542		3
545	Human imprinting disorders: Principles, practice, problems and progress. 2017 , 60, 618-626		35
544	Potential sperm contributions to the murine zygote predicted by analysis. 2017 , 154, 777-788		14
543	Regulation of ERVs in pluripotent stem cells and reprogramming. <i>Current Opinion in Genetics and Development</i> , 2017 , 46, 194-201	4-9	8
542	HEMO, an ancestral endogenous retroviral envelope protein shed in the blood of pregnant women and expressed in pluripotent stem cells and tumors. 2017 , 114, E6642-E6651		36

541	KRAB zinc finger proteins. 2017 , 144, 2719-2729		141
540	Parallel embryonic transcriptional programs evolve under distinct constraints and may enable morphological conservation amidst adaptation. 2017 , 430, 202-213		10
539	The Zygotic Transition Is Initiated in Unicellular Plant Zygotes with Asymmetric Activation of Parental Genomes. 2017 , 43, 349-358.e4		44
538	Identification of miRNAs involved in DRG neurite outgrowth and their putative targets. 2017 , 591, 2091-2105		16
537	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017 , 46, 66-76	4-9	14
536	Transcriptomics analysis and human preimplantation development. 2017 , 162, 135-140		2
535	Peromyscus transcriptomics: Understanding adaptation and gene expression plasticity within and between species of deer mice. 2017 , 61, 131-139		8
534	Single-cell RNA-seq reveals lincRNA expression differences in Hela-S3 cells. 2017 , 39, 359-366		6
533	Mechanisms of gene regulation in human embryos and pluripotent stem cells. 2017 , 144, 4496-4509		45
532	Transcriptome profiling of individual rhesus macaque oocytes and preimplantation embryos. <i>Biology of Reproduction</i> , 2017 , 97, 353-364	3-9	10
531	The landscape of human mutually exclusive splicing. 2017 , 13, 959		36
530	Protein Expression Landscape of Mouse Embryos during Pre-implantation Development. 2017 , 21, 3957-3969		62
529	Bibliography. 311-356		
528	A unique mechanism regulating gene expression in 1-cell embryos. 2017 , 63, 9-11		7
527	Perspective: Is Random Monoallelic Expression a Contributor to Phenotypic Variability of Autosomal Dominant Disorders?. <i>Frontiers in Genetics</i> , 2017 , 8, 191	4-5	7
526	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. 2017 , 6,		57
525	Comparative analysis of weighted gene co-expression networks in human and mouse. 2017 , 12, e0187611		8
524	Evidence of reduced recombination rate in human regulatory domains. 2017 , 18, 193		23

523	Granatum: a graphical single-cell RNA-Seq analysis pipeline for genomics scientists. 2017 , 9, 108		50
522	Long non-coding RNA exchange during the oocyte-to-embryo transition in mice. 2017 , 24, 129-141		18
521	The transcriptome of early chicken embryos reveals signaling pathways governing rapid asymmetric cellularization and lineage segregation. 2018 , 145,		12
520	Chromatin Accessibility Landscape in Human Early Embryos and Its Association with Evolution. 2018 , 173, 248-259.e15		97
519	The Human Cell Atlas: Technical approaches and challenges. <i>Briefings in Functional Genomics</i> , 2018 , 17, 283-294	4.9	22
518	The oocyte-to-embryo transition in mouse: past, present, and future. <i>Biology of Reproduction</i> , 2018 , 99, 160-174	3.9	37
517	Introduction to Single-Cell RNA Sequencing. 2018 , 122, e57		47
516	Dynamics of the epigenetic landscape during the maternal-to-zygotic transition. 2018 , 19, 436-450		160
515	The Use of the Fluidigm C1 for RNA Expression Analyses of Single Cells. 2018 , 122, e55		7
514	Single-cell transcriptional profiling: a window into embryonic cell-type specification. 2018 , 19, 399-412		32
513	Defining Cell Identity with Single-Cell Omics. 2018 , 18, e1700312		34
512	Follicle capacitation: a meta-analysis to investigate the transcriptome dynamics following follicle-stimulating hormone decline in bovine granulosa cells. <i>Biology of Reproduction</i> , 2018 , 99, 877-887.9		6
511	H3K9 demethylase KDM4E is an epigenetic regulator for bovine embryonic development and a defective factor for nuclear reprogramming. 2018 , 145,		67
510	Differential long non-coding RNA expression profiles in human oocytes and cumulus cells. 2018 , 8, 2202		36
509	Inertial-ordering-assisted droplet microfluidics for high-throughput single-cell RNA-sequencing. <i>Lab on A Chip</i> , 2018 , 18, 775-784	7.2	60
508	Global and targeted approaches to single-cell transcriptome characterization. <i>Briefings in Functional Genomics</i> , 2018 , 17, 209-219	4.9	17
507	Parental age and gene expression profiles in individual human blastocysts. 2018 , 8, 2380		21
506	Mapping human development at single-cell resolution. 2018 , 145,		24

505	Metabolism in Pluripotent Stem Cells and Early Mammalian Development. 2018 , 27, 332-338	58
504	Integrated analysis of single-cell embryo data yields a unified transcriptome signature for the human pre-implantation epiblast. 2018 , 145,	93
503	Characterization of H3.3 and HIRA expression and function in bovine early embryos. 2018 , 85, 106-116	5
502	Capturing Totipotent Stem Cells. <i>Cell Stem Cell</i> , 2018 , 22, 25-34	18 44
501	Extraction of total RNA from single-oocytes and single-cell mRNA sequencing of swine oocytes. 2018 , 11, 155	3
500	Chromatin analysis in human early development reveals epigenetic transition during ZGA. <i>Nature</i> , 2018 , 557, 256-260	504 135
499	Discovery of Blood Transcriptional Endotypes in Women with Pelvic Inflammatory Disease. 2018 , 200, 2941-2956	13
498	EpiDenovo: a platform for linking regulatory de novo mutations to developmental epigenetics and diseases. 2018 , 46, D92-D99	11
497	Are blastocyst aneuploidy rates different between fertile and infertile populations?. 2018 , 35, 403-408	20
496	Esrrb, an estrogen-related receptor involved in early development, pluripotency, and reprogramming. 2018 , 592, 852-877	30
495	Lessons from single-cell transcriptome analysis of oxygen-sensing cells. 2018 , 372, 403-415	3
494	Single-cell transcriptome sequencing reveals that cell division cycle 5-like protein is essential for porcine oocyte maturation. 2018 , 293, 1767-1780	15
493	Mammalian zygotic genome activation. 2018 , 84, 118-126	37
492	Transcriptional and translational dynamics during maternal-to-zygotic transition in early chicken development. 2018 , 32, 2004-2011	7
491	Single-cell RNA sequencing: Technical advancements and biological applications. 2018 , 59, 36-46	120
490	Identifying cell populations with scRNASeq. 2018 , 59, 114-122	138
489	Regulatory network characterization in development: challenges and opportunities. 2018 , 7,	2
488	VIPER: variability-preserving imputation for accurate gene expression recovery in single-cell RNA sequencing studies. 2018 , 19, 196	53

487	Transcriptional and epigenetic control of cell fate decisions in early embryos. 2017 , 30, 73-84		5
486	Transcriptome profiling of human oocytes experiencing recurrent total fertilization failure. 2018 , 8, 17890		9
485	Zygotic gene activation in the chicken occurs in two waves, the first involving only maternally derived genes. 2018 , 7,		8
484	Global, Survival, and Apoptotic Transcriptome during Mouse and Human Early Embryonic Development. 2018 , 2018, 5895628		6
483	The Transcriptomic Landscape of Yaks Reveals Molecular Pathways for High Altitude Adaptation. 2019 , 11, 72-85		24
482	Essential requirement of mammalian Pumilio family in embryonic development. 2018 , 29, 2922-2932		14
481	Transcriptional defects and reprogramming barriers in somatic cell nuclear reprogramming as revealed by single-embryo RNA sequencing. 2018 , 19, 734		12
480	Effects of PRDM14 Silencing on Parthenogenetically Activated Porcine Embryos. 2018 , 20, 382-388		1
479	Single-cell RNA-sequencing reveals the existence of naive and primed pluripotency in pre-implantation rhesus monkey embryos. <i>Genome Research</i> , 2018 , 28, 1481-1493	9:7	16
478	A Mutant p53-Dependent Embryonic Stem Cell Gene Signature Is Associated with Augmented Tumorigenesis of Stem Cells. 2018 , 78, 5833-5847		17
477	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. 2018 , 1, 29-51		59
476	Reprogramming of Chromatin Accessibility in Somatic Cell Nuclear Transfer Is DNA Replication Independent. 2018 , 23, 1939-1947		19
475	Single-cell RNA sequencing for the study of development, physiology and disease. 2018 , 14, 479-492		172
474	Using Single Molecule mRNA Fluorescent in Situ Hybridization (RNA-FISH) to Quantify mRNAs in Individual Murine Oocytes and Embryos. 2018 , 8, 7930		15
473	States and Origins of Mammalian Embryonic Pluripotency In Vivo and in a Dish. 2018 , 128, 151-179		7
472	The Potential Roles and Advantages of Single Cell Sequencing in the Diagnosis and Treatment of Hematological Malignancies. 2018 , 1068, 119-133		2
471	Single-Cell Non-coding RNA in Embryonic Development. 2018 , 1068, 19-32		10
470	High Throughput Single Cell RNA Sequencing, Bioinformatics Analysis and Applications. 2018 , 1068, 33-43		25

469	Single Cell Genetics and Epigenetics in Early Embryo: From Oocyte to Blastocyst. 2018 , 1068, 103-117		5
468	Single Cell Biomedicine. 2018 ,		0
467	Single cell expression analysis of primate-specific retroviruses-derived HPAT lincRNAs in viable human blastocysts identifies embryonic cells co-expressing genetic markers of multiple lineages. 2018 , 4, e00667		14
466	SRSF3 maintains transcriptome integrity in oocytes by regulation of alternative splicing and transposable elements. 2018 , 4, 33		24
465	Deconstructing and reconstructing the mouse and human early embryo. 2018 , 20, 878-887		93
464	Unbiased classification of mosquito blood cells by single-cell genomics and high-content imaging. 2018 , 115, E7568-E7577		28
463	Transcriptional profiles of crossbred embryos derived from yak oocytes in vitro fertilized with cattle sperm. 2018 , 8, 11571		2
462	Determination of Oocyte-Manipulation, Zygote-Manipulation, and Genome-Reprogramming Effects on the Transcriptomes of Bovine Blastocysts. <i>Frontiers in Genetics</i> , 2018 , 9, 143	4-5	4
461	The Role of Systems Biologic Approach in Cell Signaling and Drug Development Responses-A Mini Review. 2018 , 6,		3
460	Sea Anemones: Quiet Achievers in the Field of Peptide Toxins. 2018 , 10,		55
459	Single Cell Multi-Omics Technology: Methodology and Application. 2018 , 6, 28		97
458	Analysis of protein-protein interaction network based on transcriptome profiling of ovine granulosa cells identifies candidate genes in cyclic recruitment of ovarian follicles. 2018 , 60, 11		7
457	Mouse and modulate preimplantation transcriptional profiles revealing similarity between paralogous mouse and human homeobox genes. 2018 , 9, 2		6
456	Functional genetics of early human development. <i>Current Opinion in Genetics and Development</i> , 2018 , 52, 1-6	4-9	11
455	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. 2018 , 12, 59		28
454	Building Principles for Constructing a Mammalian Blastocyst Embryo. 2018 , 7,		20
453	Inhibition of Aberrant DNA Re-methylation Improves Post-implantation Development of Somatic Cell Nuclear Transfer Embryos. <i>Cell Stem Cell</i> , 2018 , 23, 426-435.e5	18	43
452	Long non-coding RNAs potentially function synergistically in the cellular reprogramming of SCNT embryos. 2018 , 19, 631		9

451	Age-related gene expression profiles of immature human oocytes. 2018 , 24, 469-477	7
450	DCAF13 promotes pluripotency by negatively regulating SUV39H1 stability during early embryonic development. 2018 , 37,	16
449	Human Pre-gastrulation Development. 2018 , 128, 295-338	35
448	A single-cell chromatin map of human embryos. 2018 , 20, 742-744	1
447	Single-cell RNA sequencing reveals distinct gene expression patterns in glucose metabolism of human preimplantation embryos. 2019 , 31, 237-247	9
446	FoxO transcription factors 1 regulate mouse preimplantation embryo development. 2019 , 36, 2121-2133	6
445	Comprehensive Analysis of LncRNA Reveals the Temporal-Specific Module of Goat Skeletal Muscle Development. 2019 , 20,	11
444	Embryonic self-fracking. 2019 , 365, 442-443	1
443	Single-cell reconstruction of follicular remodeling in the human adult ovary. 2019 , 10, 3164	56
442	Recent Progress in Single-Cell Sequencing. 2019 , 21-34	
441	Cellular Heterogeneity and Single-Cell Omics. 2019 , 35-44	1
440	Systems-Level Understanding of Single-Cell Omics. 2019 , 433-456	
439	Light-Sheet Microscopy and Its Potential for Understanding Developmental Processes. 2019 , 35, 655-681	48
438	Inosine RNA modifications are enriched at the codon wobble position in mouse oocytes and eggs□ <i>Biology of Reproduction</i> , 2019 , 101, 938-949	3-9 4
437	SCDevDB: A Database for Insights Into Single-Cell Gene Expression Profiles During Human Developmental Processes. <i>Frontiers in Genetics</i> , 2019 , 10, 903	4-5 7
436	Single-cell RNA sequencing reveals regulatory mechanism for trophoblast cell-fate divergence in human peri-implantation conceptuses. 2019 , 17, e3000187	23
435	Identification of lncRNAs by RNA Sequencing Analysis During Pre-Implantation Developmental Transformation in the Goat. <i>Frontiers in Genetics</i> , 2019 , 10, 1040	4-5 7
434	Voltage-gated proton channels exist in the plasma membrane of human oocytes. 2019 , 34, 1974-1983	2

433	Biological process activity transformation of single cell gene expression for cross-species alignment. 2019 , 10, 4899		11
432	Sin3a regulates the developmental progression through morula-to-blastocyst transition Hdac1. 2019 , 33, 12541-12553		7
431	Integrated Analysis of Oncogenic Networks in Colorectal Cancer Identifies GUCA2A as a Molecular Marker. 2019 , 2019, 6469420		13
430	Light-induced injury in mouse embryos revealed by single-cell RNA sequencing. 2019 , 52, 48		5
429	Regulation of Genomic Output and (Pluri)potency in Regeneration. 2019 , 53, 327-346		6
428	A Chemically Defined Feeder-free System for the Establishment and Maintenance of the Human Naive Pluripotent State. 2019 , 13, 612-626		9
427	RNA-seq as a tool for evaluating human embryo competence. <i>Genome Research</i> , 2019 , 29, 1705-1718	9.7	9
426	Human Germline Cell Development: from the Perspective of Single-Cell Sequencing. 2019 , 76, 320-328		27
425	Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development. <i>Cell Stem Cell</i> , 2019 , 25, 697-712.e6	18	24
424	Microbiome Multi-Omics Network Analysis: Statistical Considerations, Limitations, and Opportunities. <i>Frontiers in Genetics</i> , 2019 , 10, 995	4.5	42
423	An integrated chromatin accessibility and transcriptome landscape of human pre-implantation embryos. 2019 , 10, 364		36
422	The Lupus Susceptibility Locus Sgp3 Encodes the Suppressor of Endogenous Retrovirus Expression SNERV. 2019 , 50, 334-347.e9		43
421	Dppa2 and Dppa4 directly regulate the Dux-driven zygotic transcriptional program. 2019 , 33, 194-208		81
420	H3K27me3 is an epigenetic barrier while KDM6A overexpression improves nuclear reprogramming efficiency. 2019 , 33, 4638-4652		28
419	Single-Cell RNA Sequencing-Based Computational Analysis to Describe Disease Heterogeneity. <i>Frontiers in Genetics</i> , 2019 , 10, 629	4.5	12
418	Pleomorphic Adenoma Gene 1 Is Needed For Timely Zygotic Genome Activation and Early Embryo Development. 2019 , 9, 8411		6
417	EmExplorer: a database for exploring time activation of gene expression in mammalian embryos. 2019 , 9, 190054		25
416	Genetic basis for primordial germ cells specification in mouse and human: Conserved and divergent roles of PRDM and SOX transcription factors. 2019 , 135, 35-89		20

415	Expression dynamics of repetitive DNA in early human embryonic development. 2019 , 20, 439		22
414	High-throughput single-cell whole-genome amplification through centrifugal emulsification and eMDA. 2019 , 2, 147		22
413	High-Order Correlation Integration for Single-Cell or Bulk RNA-seq Data Analysis. <i>Frontiers in Genetics</i> , 2019 , 10, 371	4-5	5
412	Big Data to the Bench: Transcriptome Analysis for Undergraduates. 2019 , 18, ar19		1
411	VPAC: Variational projection for accurate clustering of single-cell transcriptomic data. 2019 , 20, 0		3
410	Single-cell RNA-seq reveals distinct dynamic behavior of sex chromosomes during early human embryogenesis. 2019 , 86, 871-882		11
409	The evolution of Great Apes has shaped the functional enhancers' landscape in human embryonic stem cells. 2019 , 37, 101456		10
408	Single-cell transcriptomes of the regenerating intestine reveal a revival stem cell. <i>Nature</i> , 2019 , 569, 121-125	50-4	164
407	Dynamic Transcriptome Analysis Reveals Potential Long Non-coding RNAs Governing Postnatal Pineal Development in Pig. <i>Frontiers in Genetics</i> , 2019 , 10, 409	4-5	6
406	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. 2019 , 116, 9775-9784		67
405	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. 2019 , 14, 260-276		14
404	Maternal-biased H3K27me3 correlates with paternal-specific gene expression in the human morula. 2019 , 33, 382-387		24
403	Epigenetic Regulation and Risk Factors During the Development of Human Gametes and Early Embryos. 2019 , 20, 21-40		11
402	The KRAB-zinc-finger protein ZFP708 mediates epigenetic repression at RMER19B retrotransposons. 2019 , 146,		12
401	Systems based analysis of human embryos and gene networks involved in cell lineage allocation. 2019 , 20, 171		11
400	Mechanosensing and Mechanoregulation of Endothelial Cell Functions. 2019 , 9, 873-904		55
399	Characterization and comparative analyses of transcriptomes of cloned and fertilized porcine pre-implantation embryos. 2019 , 8,		3
398	Individual assessment of bovine embryo development using a homemade chamber reveals kinetic patterns of success and failure to reach blastocyst stage. 2019 , 65, 301-311		3

397	Transcriptome Comparisons of Multi-Species Identify Differential Genome Activation of Mammals Embryogenesis. 2019 , 7, 7794-7802		28
396	Adventitial Cell Atlas of wt (Wild Type) and ApoE (Apolipoprotein E)-Deficient Mice Defined by Single-Cell RNA Sequencing. 2019 , 39, 1055-1071		49
395	Proteotyping pluripotency with mass spectrometry. 2019 , 16, 391-400		
394	scRNAss: a single-cell RNA-seq assembler via imputing dropouts and combing junctions. 2019 , 35, 4264-4271		4
393	Translational activation of maternally derived mRNAs in oocytes and early embryos and the role of embryonic poly(A) binding protein (EPAB). <i>Biology of Reproduction</i> , 2019 , 100, 1147-1157	3.9	6
392	Quality Control of Single-Cell RNA-seq. 2019 , 1935, 1-9		5
391	Inference of Gene Co-expression Networks from Single-Cell RNA-Sequencing Data. 2019 , 1935, 141-153		8
390	PsyMuKB: An Integrative De Novo Variant Knowledge Base for Developmental Disorders. 2019 , 17, 453-464		3
389	A KHDC3L mutation resulting in recurrent hydatidiform mole causes genome-wide DNA methylation loss in oocytes and persistent imprinting defects post-fertilisation. 2019 , 11, 84		23
388	A primate-specific retroviral enhancer wires the XACT lncRNA into the core pluripotency network in humans. 2019 , 10, 5652		13
387	Analyzing the Effects of Intrauterine Hypoxia on Gene Expression in Oocytes of Rat Offspring by Single Cell Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 2019 , 10, 1102	4.5	2
386	Key role for CTCF in establishing chromatin structure in human embryos. <i>Nature</i> , 2019 , 576, 306-310	50.4	51
385	RNA element discovery from germ cell to blastocyst. 2019 , 47, 2263-2275		13
384	Single-cell transcriptomic analysis of pancreatic islets in health and type 2 diabetes. 2019 , 11, 105-118		0
383	A test metric for assessing single-cell RNA-seq batch correction. 2019 , 16, 43-49		140
382	(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. 2020 , 17, 1154-1173		20
381	On the Regulatory Evolution of New Genes Throughout Their Life History. 2019 , 36, 15-27		9
380	Translational Regulation of Gene Expression During Oogenesis and Preimplantation Embryo Development. 2019 , 221-239		1

379	Histone supply: Multitiered regulation ensures chromatin dynamics throughout the cell cycle. 2019 , 218, 39-54		34
378	Methionine adenosyltransferase 2A regulates mouse zygotic genome activation and morula to blastocyst transition <i>Biology of Reproduction</i> , 2019 , 100, 601-617	3.9	15
377	Single-Cell Transcriptomics of Human Oocytes: Environment-Driven Metabolic Competition and Compensatory Mechanisms During Oocyte Maturation. 2019 , 30, 542-559		27
376	Essential roles of HDAC1 and 2 in lineage development and genome-wide DNA methylation during mouse preimplantation development. 2020 , 15, 369-385		11
375	Single Cell Metabolism. 2020 ,		5
374	Evolutionary History of GLIS Genes Illuminates Their Roles in Cell Reprogramming and Ciliogenesis. 2020 , 37, 100-109		4
373	scRCMF: Identification of Cell Subpopulations and Transition States From Single-Cell Transcriptomes. 2020 , 67, 1418-1428		11
372	Zygotic genome activation in the chicken: a comparative review. 2020 , 77, 1879-1891		6
371	Tumor Functional Heterogeneity Unraveled by scRNA-seq Technologies. 2020 , 6, 13-19		54
370	Recent advances in mammalian reproductive biology. 2020 , 63, 18-58		10
369	An Experiment on Discovery of Biological Knowledge from scRNA-Seq Data Using Machine Learning. 2020 , 1, 100071		1
368	Dusp4 Contributes to Anesthesia Neurotoxicity via Mediated Neural Differentiation in Primates. 2020 , 8, 786		2
367	Proteomic analysis demonstrates that parthenogenetically activated swamp buffalo embryos have dysregulated energy metabolism. 2020 , 55, 1764-1773		2
366	EpiMogrify Models H3K4me3 Data to Identify Signaling Molecules that Improve Cell Fate Control and Maintenance. 2020 , 11, 509-522.e10		6
365	Phytochemical and antimicrobial investigation of the leaves of five Egyptian mango cultivars and evaluation of their essential oils as preservatives materials. 2021 , 58, 3130-3142		2
364	IsoXpressor: A Tool to Assess Transcriptional Activity within Isochores. 2020 , 12, 1573-1578		1
363	Untangling early embryo development using single cell genomics. 2020 , 150, 55-58		0
362	Analysis of accessible chromatin landscape in the inner cell mass and trophectoderm of human blastocysts. 2020 , 26, 702-711		2

361	Single cell RNA-seq reveals molecular pathways altered by 7, 12-dimethylbenz[a]anthracene treatment on pig oocytes. 2020 , 157, 449-457	6
360	STRAP regulates alternative splicing fidelity during lineage commitment of mouse embryonic stem cells. 2020 , 11, 5941	5
359	Single-cell network biology for resolving cellular heterogeneity in human diseases. 2020 , 52, 1798-1808	26
358	A DNA methylation state transition model reveals the programmed epigenetic heterogeneity in human pre-implantation embryos. 2020 , 21, 277	1
357	Aberrant spliceosome expression and altered alternative splicing events correlate with maturation deficiency in human oocytes. 2020 , 19, 2182-2194	8
356	Sharing of Genetic Association Signals by Age-Related Macular Degeneration and Alzheimer's Disease at Multiple Levels. 2020 , 57, 4488-4499	2
355	Deep Transcriptomic Analysis Reveals the Dynamic Developmental Progression during Early Development of Channel Catfish (). 2020 , 21,	2
354	Comparison of Human Antral Follicles of Xenograft versus Ovarian Origin Reveals Disparate Molecular Signatures. 2020 , 32, 108027	7
353	Developmental Gene Expression Differences between Humans and Mammalian Models. 2020 , 33, 108308	11
352	Coordinated analysis of exon and intron data reveals novel differential gene expression changes. 2020 , 10, 15669	3
351	Loss of POLR1D results in embryonic lethality prior to blastocyst formation in mice. 2020 , 87, 1152-1158	1
350	Unsupervised Inference of Developmental Directions for Single Cells Using VECTOR. 2020 , 32, 108069	2
349	EnClasC: a novel ensemble approach for accurate and robust cell-type classification of single-cell transcriptomes. 2020 , 21, 392	1
348	Single-cell Sequencing and Methylation. 2020 ,	3
347	Single-Cell Transcriptome Analysis Reveals Six Subpopulations Reflecting Distinct Cellular Fates in Senescent Mouse Embryonic Fibroblasts. <i>Frontiers in Genetics</i> , 2020 , 11, 867	4-5 7
346	Single-cell RNA sequencing in Drosophila: Technologies and applications. 2021 , 10, e396	16
345	PABPN1L mediates cytoplasmic mRNA decay as a placeholder during the maternal-to-zygotic transition. 2020 , 21, e49956	16
344	Dynamic pattern of histone H3 core acetylation in human early embryos. 2020 , 19, 2226-2234	1

343	Single-Cell RNA-Sequencing Data Clustering via Locality Preserving Kernel Matrix Alignment. 2020 , 8, 201577-201594	0
342	A Comparative View on the Oviductal Environment during the Periconception Period. 2020 , 10,	6
341	Dppa2/4 as a trigger of signaling pathways to promote zygote genome activation by binding to CG-rich region. 2021 , 22,	4
340	Whole-Transcriptome Sequencing-Based Analysis of and Its Interacting Genes during Germ Cells Specification and Zygotic Genome Activation in Chickens. 2020 , 21,	3
339	scDoc: correcting drop-out events in single-cell RNA-seq data. 2020 , 36, 4233-4239	7
338	Single-cell sequencing of miRNAs: A modified technology. 2020 , 44, 1773-1780	5
337	DNA methylation changes during preimplantation development reveal inter-species differences and reprogramming events at imprinted genes. 2020 , 12, 64	19
336	Single-Cell RNA Sequencing and Its Combination with Protein and DNA Analyses. 2020 , 9,	22
335	High-resolution annotation of the mouse preimplantation embryo transcriptome using long-read sequencing. 2020 , 11, 2653	7
334	Does growth hormone supplementation improve oocyte competence and IVF outcomes in patients with poor embryonic development? A randomized controlled trial. 2020 , 20, 310	8
333	Abiotic-stress tolerance in plants-system biology approach. 2020 , 577-609	4
332	Toxicity and mechanism of mesoporous silica nanoparticles in eyes. 2020 , 12, 13637-13653	15
331	Early cleavage of preimplantation embryos is regulated by tRNA-derived small RNAs present in mature spermatozoa. 2020 , 295, 10885-10900	12
330	A transcriptional roadmap for 2C-like-to-pluripotent state transition. 2020 , 6, eaay5181	13
329	Long non-coding RNAs in ovarian granulosa cells. 2020 , 13, 63	13
328	Epigenetic regulation of mouse preimplantation embryo development. <i>Current Opinion in Genetics and Development</i> , 2020 , 64, 13-20	4-9 7
327	Alternative splicing signatures in preimplantation embryo development. 2020 , 10, 33	3
326	Proteomics Analysis Reveals that Warburg Effect along with Modification in Lipid Metabolism Improves In Vitro Embryo Development under Low Oxygen. 2020 , 21,	8

325	Finding cell-specific expression patterns in the early Ciona embryo with single-cell RNA-seq. 2020 , 10, 4961	3
324	Probe Signal Values in mRNA Arrays Imply an Excessive Involvement of Neutrophil FCGR1 in Tuberculosis. 2020 , 7, 19	1
323	Germline nuclear transfer in mice may rescue poor embryo development associated with advanced maternal age and early embryo arrest. 2020 , 35, 1562-1577	5
322	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. 2020 , 11, 25-41.e9	27
321	Comparative analysis of single-cell transcriptomics in human and Zebrafish oocytes. 2020 , 21, 471	4
320	Single-cell RNA sequencing in breast cancer: Understanding tumor heterogeneity and paving roads to individualized therapy. 2020 , 40, 329-344	28
319	-Cre-Mediated Global Knockout. 2020 , 4, bvaa001	10
318	CMF-Impute: an accurate imputation tool for single-cell RNA-seq data. 2020 , 36, 3139-3147	28
317	Adapting the 14-day rule for embryo research to encompass evolving technologies. 2020 , 10, 1-9	13
316	Methionine Adenosyltransferase 2 β Participates in Mouse Oocyte Maturation by Regulating the MAPK Pathway. 2020 , 27, 163-171	5
315	Progress and applications of single-cell sequencing techniques. 2020 , 80, 104198	14
314	Biophysical principles of choanoflagellate self-organization. 2020 , 117, 1303-1311	15
313	MLL1 combined with GSK3 and MAP2K inhibition improves the development of in vitro-fertilized embryos. 2020 , 146, 58-70	0
312	DUX-miR-344-ZMYM2-Mediated Activation of MERVL LTRs Induces a Totipotent 2C-like State. <i>Cell Stem Cell</i> , 2020 , 26, 234-250.e7	18 32
311	Fatty acid metabolism as an indicator for the maternal-to-zygotic transition in porcine IVF embryos revealed by RNA sequencing. 2020 , 151, 128-136	2
310	Revealing cell fate decisions during reprogramming by scRNA-seq. 2020 , 145, 01033	
309	Transcription profiles of oocytes during maturation and embryos during preimplantation development in vivo in the goat. 2020 , 32, 714-725	2
308	Loss of RBBP4 results in defective inner cell mass, severe apoptosis, hyperacetylated histones and preimplantation lethality in mice <i>Biology of Reproduction</i> , 2020 , 103, 13-23	3.9 8

307	Dimension Reduction and Clustering Models for Single-Cell RNA Sequencing Data: A Comparative Study. 2020 , 21,	18
306	Ptk2b deletion improves mice folliculogenesis and fecundity via inhibiting follicle loss mediated by Erk pathway. 2021 , 236, 1043-1053	2
305	Dux facilitates post-implantation development, but is not essential for zygotic genome activation \square <i>Biology of Reproduction</i> , 2021 , 104, 83-93	3.9 9
304	ZC3H4-a novel Cys-Cys-Cys-His-type zinc finger protein-is essential for early embryogenesis in mice \square <i>Biology of Reproduction</i> , 2021 , 104, 325-335	3.9 4
303	Nanophotonics in Biomedical Engineering. 2021 ,	1
302	Polyphenism of a Novel Trait Integrated Rapidly Evolving Genes into Ancestrally Plastic Networks. 2021 , 38, 331-343	9
301	Five multicopy gene family genes expressed during the maternal-to-zygotic transition are not essential for mouse development. 2021 , 534, 752-757	1
300	Effects of Cigarette Smoking on Preimplantation Embryo Development. 2021 , 1300, 137-150	0
299	SCSIt: A high-efficiency preprocessing tool for single-cell sequencing data from SPLiT-seq. 2021 , 19, 4574-4580	0
298	Large field of view-spatially resolved transcriptomics at nanoscale resolution.	24
297	Independent component analysis based gene co-expression network inference (ICAnet) to decipher functional modules for better single-cell clustering and batch integration. 2021 , 49, e54	6
296	Maternal UHRF1 Is Essential for Transcription Landscapes and Repression of Repetitive Elements During the Maternal-to-Zygotic Transition. 2020 , 8, 610773	1
295	Cross-species single-cell transcriptomic analysis reveals pre-gastrulation developmental differences among pigs, monkeys, and humans. 2021 , 7, 8	5
294	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. 2021 , 19, 282-291	2
293	Single-cell analysis of nonhuman primate preimplantation development in comparison to humans and mice. 2021 , 250, 974-985	3
292	SIN3A Regulates Porcine Early Embryonic Development by Modulating Expression. 2021 , 9, 604232	0
291	Single-cell RNA-seq reveals mRNAs and lncRNAs important for oocytes in vitro matured in pigs. 2021 , 56, 642-657	5
290	Identification of hub genes and key pathways in the emphysema phenotype of COPD. 2021 , 13, 5120-5135	3

289	Tracing cell-type evolution by cross-species comparison of cell atlases. 2021 , 34, 108803		4
288	A Novel Method to Identify the Differences Between Two Single Cell Groups at Single Gene, Gene Pair, and Gene Module Levels. <i>Frontiers in Genetics</i> , 2021 , 12, 648898	4.5	1
287	The Transcriptome in Transition: Global Gene Expression Profiles of Young Adult Fruit Flies Depend More Strongly on Developmental Than Adult Diet. 2021 , 9,		0
286	High-Throughput Methods in the Discovery and Study of Biomaterials and Materiobiology. 2021 , 121, 4561-4677		45
285	Genomics-Guided Drawing of Molecular and Pathophysiological Components of Malignant Regulatory Signatures Reveals a Pivotal Role in Human Diseases of Stem Cell-Associated Retroviral Sequences and Functionally-Active hESC Enhancers. <i>Frontiers in Oncology</i> , 2021 , 11, 638363	5.3	0
284	NOTCH signaling pathway is required for bovine early embryonic development \square <i>Biology of Reproduction</i> , 2021 , 105, 332-344	3.9	3
283	Herpesviral induction of germline transcription factor DUX4 is critical for viral gene expression.		2
282	An improved method for specific-target preamplification PCR analysis of single blastocysts useful for embryo sexing and high-throughput gene expression analysis. 2021 , 104, 3722-3735		1
281	WEDGE: imputation of gene expression values from single-cell RNA-seq datasets using biased matrix decomposition. 2021 , 22,		2
280	Multiply restimulated human thymic regulatory T cells express distinct signature regulatory T-cell transcription factors without evidence of exhaustion. 2021 , 23, 704-714		0
279	Uncovering transcriptional dark matter via gene annotation independent single-cell RNA sequencing analysis. 2021 , 12, 2158		0
278	Activation of Blood Vessel Development in Endometrial Stromal Cells In Vitro Cocultured with Human Peri-Implantation Embryos Revealed by Single-Cell RNA-Seq. 2021 , 11,		0
277	Benchmarking scRNA-seq imputation tools with respect to network inference highlights deficits in performance at high levels of sparsity.		0
276	Functional roles of the chromatin remodeler SMARCA5 in mouse and bovine preimplantation embryos \square <i>Biology of Reproduction</i> , 2021 , 105, 359-370	3.9	2
275	Between Fate Choice and Self-Renewal-Heterogeneity of Adult Neural Crest-Derived Stem Cells. 2021 , 9, 662754		6
274	Mitochondrial proteome of mouse oocytes and cisplatin-induced shifts in protein profile. 2021 , 42, 2144-2154		
273	Integrating Spatial Transcriptomics and Single-Cell RNA-seq Reveals the Gene Expression Profiling of the Human Embryonic Liver. 2021 , 9, 652408		7
272	All models are wrong, but some are useful: Establishing standards for stem cell-based embryo models. 2021 , 16, 1117-1141		7

271	SUMO2, a small ubiquitin-like modifier, is essential for development of murine preimplantation embryos. 2021 , 166, 29-37	
270	Control of DUX4 Expression in Facioscapulohumeral Muscular Dystrophy and Cancer. 2021 , 27, 588-601	1
269	DevOmics: an integrated multi-omics database of human and mouse early embryo. 2021 , 22,	3
268	Absolute Quantification of MicroRNAs in a Single Cell with Chemiluminescence Detection Based on Rolling Circle Amplification on a Microchip Platform. 2021 , 93, 9218-9225	8
267	Single-Cell Transcriptome Analysis as a Promising Tool to Study Pluripotent Stem Cell Reprogramming. 2021 , 22,	0
266	Post-Translational Modifications in Oocyte Maturation and Embryo Development. 2021 , 9, 645318	2
265	Contextualizing Autophagy during Gametogenesis and Preimplantation Embryonic Development. 2021 , 22,	3
264	Exploring the role of autophagy during early human embryonic development through single-cell transcriptome and methylome analyses. 2021 , 1	0
263	Comparative Transcriptomics Reveals Distinct Patterns of Gene Expression Conservation through Vertebrate Embryogenesis. 2021 , 13,	0
262	scSGL: Signed Graph Learning for Single-Cell Gene Regulatory Network Inference.	0
261	Single cell RNA-seq reveals genes vital to in vitro fertilized embryos and parthenotes in pigs. 2021 , 11, 14393	4
260	Impact of Global Transcriptional Silencing on Cell Cycle Regulation and Chromosome Segregation in Early Mammalian Embryos. 2021 , 22,	0
259	Two mutations in TUBB8 cause developmental arrest in human oocytes and early embryos. 2021 , 43, 891-898	2
258	Cyclin D1 gene expression is essential for cell cycle progression from the maternal-to-zygotic transition during blastoderm development in Japanese quail. 2021 , 476, 249-258	2
257	Systematic Identification and Validation of Housekeeping and Tissue-Specific Genes in Allotetraploid <i>Chenopodium quinoa</i> . 2021 , 7, 235	1
256	Knockdown of Dnmt1 and Dnmt3a gene expression disrupts preimplantation embryo development through global DNA methylation. 2021 , 1	4
255	Maternal Dppa2 and Dppa4 are dispensable for zygotic genome activation but important for offspring survival.	
254	Genome activation in equine in vitro-produced embryos. <i>Biology of Reproduction</i> , 2021 ,	3.9 0

253	Molecular Profiling of Spermatozoa Reveals Correlations between Morphology and Gene Expression: A Novel Biomarker Panel for Male Infertility. 2021 , 2021, 1434546	0
252	scDEA: differential expression analysis in single-cell RNA-sequencing data via ensemble learning. 2021 ,	0
251	Allele-specific expression analysis reveals conserved and unique features of preimplantation development in equine ICSI embryos. <i>Biology of Reproduction</i> , 2021 ,	3.9 0
250	Construction of heparin-based hydrogel incorporated with Cu5.4O ultrasmall nanozymes for wound healing and inflammation inhibition. 2021 , 6, 3109-3124	26
249	Modularity and hierarchy in biological systems: Using gene regulatory networks to understand evolutionary change. 2021 , 141, 39-73	3
248	A Gene Expression Signature Predicting Colorectal Cancer Relapse Reveals LEMD1 as an Oncogenic Gene That Promotes CRC Cells Migration by RhoA/ROCK1 Signaling Pathway.	
247	Methods for Single-Cell Isolation and Preparation. 2020 , 1255, 7-27	4
246	Imaging nascent transcription in wholemount vertebrate embryos to characterize zygotic genome activation. 2020 , 638, 139-165	1
245	Global hyperactivation of enhancers stabilizes human and mouse naive pluripotency through inhibition of CDK8/19 Mediator kinases. 2020 , 22, 1223-1238	17
244	scDD: A statistical approach for identifying differential distributions in single-cell RNA-seq experiments.	5
243	Dropout-based feature selection for scRNASeq.	13
242	SOMSC: Self-Organization-Map for High-Dimensional Single-Cell Data of Cellular States and Their Transitions.	1
241	A non-catalytic role of TET3 promotes open chromatin and enhances global transcription.	1
240	A probabilistic model-based bi-clustering method for single-cell transcriptomic data analysis.	2
239	Assessment of batch-correction methods for scRNA-seq data with a new test metric.	15
238	Imputing Single-cell RNA-seq data by combining Graph Convolution and Autoencoder Neural Networks.	5
237	X-chromosome dosage compensation dynamics in human early embryos.	2
236	Network analysis of mass spectrometry imaging data from colorectal cancer identifies key metabolites common to metastatic development.	2

235	iterativeWGCNA: iterative refinement to improve module detection from WGCNA co-expression networks.	7
234	Embryonic gene transcription in the spiny mouse (<i>Acomys cahirinus</i>): an investigation into the embryonic genome activation.	1
233	scMerge: Integration of multiple single-cell transcriptomics datasets leveraging stable expression and pseudo-replication.	8
232	Dppa2 and Dppa4 directly regulate the Dux driven zygotic transcriptional programme.	1
231	Deep learning does not outperform classical machine learning for cell-type annotation.	11
230	Biophysical principles of choanoflagellate self-organization.	1
229	A primate-specific retroviral enhancer wires the XACT lncRNA into the core pluripotency network in human.	1
228	DUX4 regulates oocyte to embryo transition in human.	2
227	A single-cell transcriptomics CRISPR-activation screen identifies new epigenetic regulators of zygotic genome activation.	0
226	Developmental gene expression differences between humans and mammalian models.	2
225	WIPI1 is a conserved mediator of right ventricular failure. 2019 , 5,	8
224	Human Embryo Development and Assessment of Viability. 2017 , 181-204	0
223	RNA-seq Using Next Generation Sequencing. 3,	15
222	Comparative Developmental Transcriptomics Reveals Rewiring of a Highly Conserved Gene Regulatory Network during a Major Life History Switch in the Sea Urchin Genus <i>Heliocidaris</i> . 2016 , 14, e1002391	58
221	Four simple rules that are sufficient to generate the mammalian blastocyst. 2017 , 15, e2000737	29
220	Chromosome Y centromere array deletion leads to impaired centromere function. 2014 , 9, e86875	1
219	Transcriptome Dynamics and Potential Roles of Sox6 in the Postnatal Heart. 2016 , 11, e0166574	6
218	Systematic identification and characterization of long non-coding RNAs in mouse mature sperm. 2017 , 12, e0173402	32

217	Viruses, stemness, embryogenesis, and cancer: a miracle leap toward molecular definition of novel oncotargets for therapy-resistant malignant tumors?. 2015 , 2, 751-4	8
216	Identification and functional analysis of long non-coding RNAs in human and mouse early embryos based on single-cell transcriptome data. 2016 , 7, 61215-61228	23
215	Coexpression analysis identifies nuclear reprogramming barriers of somatic cell nuclear transfer embryos. 2017 , 8, 65847-65859	18
214	Role of in maternal mRNA turnover. 2018 , 1, e201800084	23
213	Searching for naïve human pluripotent stem cells. 2015 , 7, 649-56	9
212	Maternally provided LSD1/KDM1A enables the maternal-to-zygotic transition and prevents defects that manifest postnatally. 2016 , 5,	54
211	Haplotyping-based preimplantation genetic testing reveals parent-of-origin specific mechanisms of aneuploidy formation. 2021 , 6, 81	2
210	A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. 2021 , 184, 5541-5558.e22	5
209	EXOSC10/Rrp6 is essential for the eight-cell embryo/morula transition.	
208	Metabolic remodelling during early mouse embryo development. 2021 , 3, 1372-1384	2
207	RNA-seq Using Next Generation Sequencing. 2,	
206	Oocyte-associated transcription factors in reprogramming after somatic cell nuclear transfer: a review. 2014 , 1, 104	
205	Developing a Comprehensive Taxonomy for Human Cell Types. 2015 , 123-151	
204	Systems Biology Approaches for Elucidation of the Transcriptional Regulation of Pulmonary Maturation. 2016 , 385-419	
203	Protein-Protein Functional Linkage Predictions: Bringing Regulation to Context. 2016 , 159-177	
202	Evidence of a recombination rate valley in human regulatory domains.	1
201	A Transcriptional Lineage of the Early <i>C. elegans</i> Embryo.	1
200	Single cell analysis of lincRNA expression during human blastocyst differentiation identifies TERT(+) multi-lineage precursor cells.	

- 199 Exploratory bioinformatics analysis reveals importance of junkDNA in early embryo development.
- 198 SOMSC: Self-Organization-Map for High-Dimensional Single-Cell Data of Cellular States and Their Transitions. 2
- 197 The landscape of human mutually exclusive splicing.
- 196 Finding cell-specific expression patterns in the early Ciona embryo with single-cell RNA-seq.
- 195 Integrated analysis of single-cell embryo data yields a unified transcriptome signature for the human preimplantation epiblast. 0
- 194 Unbiased classification of mosquito blood cells by single-cell genomics and high-content imaging.
- 193 ADAR1 A-to-I RNA editing alters codon usage.
- 192 Machine learning methods to reverse engineer dynamic gene regulatory networks governing cell state transitions. 2
- 191 On the regulatory evolution of new genes throughout their life history. 1
- 190 Pleomorphic Adenoma Gene 1 Is Needed For Timely Zygotic Genome Activation and Early Embryo Development.
- 189 Single-embryo and single-blastomere immunoblotting reports protein expression heterogeneity in early-stage preimplantation embryos.
- 188 Role of Cnot6l in maternal mRNA turnover.
- 187 Single-cell RNA-seq reveals distinct dynamic behavior of sex chromosomes during early human embryogenesis.
- 186 VPAC: Variational projection for accurate clustering of single-cell transcriptomic data.
- 185 Application of a Modified Smart-seq2 Sample Preparation Protocol for Rare Cell Full-length Single-cell mRNA Sequencing to Mouse Oocytes. **2019**, 9, e3345 0
- 184 Biological Process Activity Transformation of Single Cell Gene Expression for Cross-Species Alignment.
- 183 Single-Cell RNA Sequencing Reveals Regulatory Mechanism for Trophoblast Cell-Fate Divergence in Human Peri-Implantation Embryo. 1
- 182 Single cell multi-omics analysis reveals novel roles for DNA methylation in sensory neuron injury responses.

- 181 Putting (single-cell) data into orbit. **2019**,
- 180 Essential roles of Hdac1 and 2 in lineage development and genome-wide DNA methylation during mouse preimplantation development.
- 179 PsyMuKB: A De Novo Variant Knowledge Base Integrating Transcriptional and Translational Information to Identify Isoform-specific Mutations in Developmental Disorders.
- 178 scDoc: Correcting Drop-out Events in Single-cell RNA-seq Data. 0
- 177 Compact Quantum Dots for Quantitative Cytology. **2020**, 2064, 147-158
- 176 EnClasC: A novel ensemble approach for accurate and robust cell-type classification of single-cell transcriptomes.
- 175 Comparative transcriptomics reveal distinct patterns of gene expression conservation through vertebrate embryogenesis.
- 174 Quality assessment of single-cell RNA sequencing data by coverage skewness analysis. 1
- 173 WEDGE: imputation of gene expression values from single-cell RNA-seq datasets using biased matrix decomposition.
- 172 Dppa2/4 promotes zygotic genome activation by binding to GC-rich region in signaling pathways.
- 171 Functional modules from variable genes: Leveraging percolation to analyze noisy, high-dimensional data.
- 170 Developmentally Programmed Tankyrase Activity Upregulates β -Catenin and Licenses Progression of Embryonic Genome Activation. **2020**, 53, 545-560.e7 6
- 169 Uncovering Transcriptional Dark Matter via Gene Annotation Independent Single-Cell RNA Sequencing Analysis.
- 168 Comparing transcriptome profiles of human embryo cultured in closed and standard incubators. **2020**, 8, e9738 1
- 167 Modelling human zygotic genome activation in 8C-like cells in vitro. 1
- 166 Identification of defense related gene families and their response against powdery and downy mildew infections in *Vitis vinifera*. **2021**, 22, 776 2
- 165 Epigenetic and Transcriptional Regulation of the Reproductive Hypothalamus. **2020**, 207-235
- 164 Single-cell Sequencing in the Field of Stem Cells. **2020**, 21, 576-584 1

- 163 Values of Single-Cell RNA Sequencing in Development of Cerebral Cortex. **2020**, 1255, 231-247 ○
- 162 Bioinformatics Advancements for Detecting Epidemic Disease Using Machine Learning Approaches. **2020**, 1051-1060 1
- 161 Oocytes, a single cell and a tissue.
- 160 SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. ○
- 159 Computational Inference of Gene Regulation from Whole-Transcriptome Analysis of Early Embryos. 241-279
- 158 Nanophotonic Techniques for Single-Cell Analysis. **2021**, 79-109
- 157 Derivation of human extended pluripotent stem cells in feeder-free condition.
- 156 Mouse fertilization triggers a conserved transcription program in one-cell embryos.
- 155 A developmentally programmed splicing failure attenuates the DNA damage response during mammalian zygotic genome activation.
- 154 [Research Progress of PR Domain Zinc Finger Protein 14]. **2016**, 19, 93-7
- 153 [Research progress of single cell sequencing in the diagnosis and treatment of hematological diseases]. **2019**, 40, 443-446
- 152 GDF9 concentration in embryo culture medium is linked to human embryo quality and viability. **2021**, 1 ○
- 151 Paternal factors in recurrent pregnancy loss: an insight through analysis of non-synonymous single-nucleotide polymorphism in human testis-specific chaperone HSPA2 gene. **2021**, 1 ○
- 150 Gene biomarker prediction in glioma by integrating scRNA-seq data and gene regulatory network. **2021**, 14, 287 ○
- 149 RNA editing regulates lncRNA splicing in human early embryo development. **2021**, 17, e1009630 ○
- 148 Expression and function of PDGF-C in development and stem cells. **2021**, 11, 210268 ○
- 147 SCNMLRR: Single Cell Clustering Based on Low-rank Non-negative Matrix Factorization. **2020**,
- 146 CHAF1b, chromatin assembly factor-1 subunit b, is essential for mouse preimplantation embryos.. **2021**, 195, 547-557 ○

145	Zygotic gene activation in mice: profile and regulation.. 2022 ,		1
144	Discoveries in Pancreatic Physiology and Disease Biology Using Single-Cell RNA Sequencing.. 2021 , 9, 732776		0
143	FSCAM: CAM-Based Feature Selection for Clustering scRNA-seq.. 2022 , 1		
142	Photo-Assisted Robust Anti-Interference Self-Powered Biosensing of MicroRNA Based on Pt-S Bonds and the Inorganic-Organic Hybridization Strategy.. 2022 ,		6
141	The Transcriptional Cell Atlas of Testis Development in Sheep at Pre-Sexual Maturity. 2022 , 44, 483-497		1
140	SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data.. 2022 , 25, 103777		0
139	Long-Term Storage Does Not Affect the Expression Profiles of mRNA and Long Non-Coding RNA in Vitrified-Warmed Human Embryos.. <i>Frontiers in Genetics</i> , 2021 , 12, 751467	4.5	0
138	Protein Expression Landscape Defines the Formation Potential of Mouse Blastoids From EPSCs.. 2022 , 10, 840492		0
137	An investigation of mechanisms underlying mouse blastocyst hatching: a ribonucleic acid sequencing study.. 2022 , 3, 35-48		0
136	Human embryonic genome activation initiates at the one-cell stage.. <i>Cell Stem Cell</i> , 2021 ,	18	6
135	Mining RNAseq data reveals dynamic metaboloepigenetic profiles in human, mouse and bovine pre-implantation embryos.. 2022 , 25, 103904		0
134	Mechanism of spindle pole organization and instability in human oocytes.. 2022 , 375, eabj3944		7
133	Big data: Historic advances and emerging trends in biomedical research. 2022 , 4, 138-151		2
132	The non-coding genome in early human development - Recent advancements.. 2022 ,		0
131	Rolling back of human pluripotent stem cells to an 8-cell embryo-like stage.. <i>Nature</i> , 2022 ,	50.4	3
130	Comparative developmental genomics of sex-biased gene expression in early embryogenesis across mammals.		
129	Mouse Oocytes, A Complex Single Cell Transcriptome.. 2022 , 10, 827937		
128	8C-like cells capture the human zygotic genome activation program in vitro.. <i>Cell Stem Cell</i> , 2022 , 29, 449-459.e6	18	3

127	is a multifunctional factor priming human embryonic genome activation.. 2022 , 25, 104137	1
126	Single-cell RNA sequencing identifies a migratory keratinocyte subpopulation expressing THBS1 in epidermal wound healing.. 2022 , 25, 104130	0
125	KLF17 promotes human naive pluripotency through repressing MAPK3 and ZIC2.. 2022 ,	0
124	DNA repair and response to sperm DNA damage in oocytes and embryos, and the potential consequences in ART: a systematic review.. 2021 ,	0
123	Maternal Dppa2 and Dppa4 are dispensable for zygotic genome activation but important for offspring survival.. 2021 , 148,	2
122	Cortical Cartography: Mapping Arealization Using Single-Cell Omics Technology.. 2021 , 15, 788560	1
121	Dynamics of Known Long Non-Coding RNAs during the Maternal-to-Zygotic Transition in Rabbit.. 2021 , 11,	1
120	Single-Cell Sequencing to Unveil the Mystery of Embryonic Development.. 2021 , e2101151	1
119	scSGL: Kernelized Signed Graph Learning for Single-Cell Gene Regulatory Network Inference.. 2022 ,	1
118	A developmentally programmed splicing failure contributes to DNA damage response attenuation during mammalian zygotic genome activation.. 2022 , 8, eabn4935	1
117	Polygenic and Network-Based Studies in Risk Identification and Demystification of cancer.. 2022 ,	0
116	Image_1.jpeg. 2019 ,	
115	Image_2.jpeg. 2019 ,	
114	Image_3.jpeg. 2019 ,	
113	Table_1.xlsx. 2019 ,	
112	Table_10.xlsx. 2019 ,	
111	Table_11.xlsx. 2019 ,	
110	Table_2.xlsx. 2019 ,	

109 Table_3.xlsx. 2019,

108 Table_4.xlsx. 2019,

107 Table_5.xlsx. 2019,

106 Table_6.xlsx. 2019,

105 Table_7.xlsx. 2019,

104 Table_8.xlsx. 2019,

103 Table_9.xlsx. 2019,

102 Table_2.xlsx. 2019,

101 Data_Sheet_1.XLSX. 2018,

100 Data_Sheet_2.XLSX. 2018,

99 Data_Sheet_3.XLSX. 2018,

98 Image_1.pdf. 2018,

97 Table_1.docx. 2019,

96 Table_2.XLSX. 2019,

95 Table_3.XLS. 2019,

94 Table_4.XLSX. 2019,

93 Table_5.XLSX. 2019,

92 Image_1.TIF. 2019,

91 Table_1.DOCX. 2019,

90 Table_2.XLSX. 2019,

89 Table_3.XLSX. 2019,

88 Table_4.XLSX. 2019,

87 Data_Sheet_1.pdf. 2020,

86 Table_1.docx. 2019,

85 Table_2.xlsx. 2019,

84 Table_3.docx. 2019,

83 Table_4.docx. 2019,

82 Image_1.pdf. 2020,

81 Table_1.xls. 2020,

80 Table_1.xlsx. 2019,

79 MicroRNA-21 expression in single living cells revealed by fluorescence and SERS dual-response microfluidic droplet platform.. *Lab on A Chip*, 2022, 7.2 0

78 Epigenetic regulation of cell fate transition: learning from early embryo development and somatic cell reprogramming.. *Biology of Reproduction*, 2022, 3.9 2

77 Derivation of totipotent-like stem cells with blastocyst-like structure forming potential.. *Cell Research*, 2022, 24.7 3

76 A hominoid-specific endogenous retrovirus may have rewired the gene regulatory network shared between primordial germ cells and naïve pluripotent cells.. *PLoS Genetics*, 2022, 18, e1009846 6 0

75 A Three-Genes Signature Predicting Colorectal Cancer Relapse Reveals LEMD1 Promoting CRC Cells Migration by RhoA/ROCK1 Signaling Pathway. *Frontiers in Oncology*, 2022, 12, 5.3 0

74 DAE-TPGM: A deep autoencoder network based on a two-part-gamma model for analyzing single-cell RNA-seq data.. *Computers in Biology and Medicine*, 2022, 146, 105578 7 0

73	Genome-Wide Identification and Characterization of Long Non-Coding RNAs in Longissimus dorsi Skeletal Muscle of Shandong Black Cattle and Luxi Cattle. <i>Frontiers in Genetics</i> , 2022 , 13,	4.5	0
72	CDSImpute: An ensemble similarity imputation method for single-cell RNA sequence dropouts. <i>Computers in Biology and Medicine</i> , 2022 , 146, 105658	7	
71	Transcriptome analysis of human preimplantation embryo reveals expressed waves associated with blastulation failure based on embryonic grade and age.		
70	Hierarchical Accumulation of Histone Variant H2A.Z Regulates Transcriptional States and Histone Modifications in Early Mammalian Embryos. <i>Advanced Science</i> , 2200057	13.6	0
69	Activation of Inc-ALVE1-AS1 inhibited ALV-J replication through triggering the TLR3 pathway in chicken macrophage like cell line. <i>Veterinary Research Communications</i> ,	2.9	
68	Pathogenesis of Choledochal Cyst: Insights from Genomics and Transcriptomics. <i>Genes</i> , 2022 , 13, 1030	4.2	0
67	Single-cell sequencing: expansion, integration and translation. <i>Briefings in Functional Genomics</i> ,	4.9	0
66	Missing Value Imputation With Low-Rank Matrix Completion in Single-Cell RNA-Seq Data by Considering Cell Heterogeneity. <i>Frontiers in Genetics</i> , 13,	4.5	0
65	Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. <i>Cell Stem Cell</i> , 2022 , 29, 1031-1050.e12	18	1
64	Single-cell technologies: a new lens into epigenetic regulation in development. <i>Current Opinion in Genetics and Development</i> , 2022 , 76, 101947	4.9	1
63	Coordination of zygotic genome activation entry and exit by H3K4me3 and H3K27me3 in porcine early embryos. <i>Genome Research</i> , gr.276207.121	9.7	
62	Advances in Single-Cell Toxicogenomics in Environmental Toxicology. <i>Environmental Science & Technology</i> ,	10.3	1
61	Chromatin dynamics through mouse preimplantation development revealed by single molecule localisation microscopy. 2022 , 11,		0
60	Integration of computational analysis and spatial transcriptomics in single-cell study. 2022 ,		1
59	Hand2os1 Regulates the Secretion of Progesterone in Mice Corpus Luteum. 2022 , 9, 404		
58	Krppel-like factor 5 rewires NANOG regulatory network to activate human naive pluripotency specific LTR7Ys and promote naive pluripotency. 2022 , 40, 111240		
57	Replication stress impairs chromosome segregation and preimplantation development in human embryos. 2022 , 185, 2988-3007.e20		2
56	Comparative Functional RNA Editomes of Neural Differentiation from Human PSCs.		1

- 55 Decoding the Spermatogenesis Program: New Insights from Transcriptomic Analyses. **2022**, 56, ○
- 54 Heterozygosity and homozygosity regions affect reproductive success and the loss of reproduction: A case study with litter traits in pigs. **2022**, 20, 4060-4071 ○
- 53 Interspecies Chimeric Barriers for Generating Exogenic Organs and Cells for Transplantation. **2022**, 31, 096368972211105 ○
- 52 Comparative maternal protein profiling of mouse biparental and uniparental embryos. **2022**, 11, 1
- 51 DNA Technologies in Precision Medicine and Pharmacogenetics. **2022**, 129-149 ○
- 50 Inferring structural and dynamical properties of gene networks from data with deep learning. **2022**, 4, ○
- 49 AHNAK2 is a biomarker and a potential therapeutic target of adenocarcinomas. **2022**, ○
- 48 Transcriptome dynamics uncovers long non-coding RNAs response to salinity stress in *Chenopodium quinoa*. 13, ○
- 47 Aneuploidy in mammalian oocytes and the impact of maternal ageing. 1
- 46 Dynamic and aberrant patterns of H3K4me3, H3K9me3, and H3K27me3 during early zygotic genome activation in cloned mouse embryos. 1-7 ○
- 45 The initiation of mammalian embryonic transcription: to begin at the beginning. **2022**, ○
- 44 Assessing the influence of distinct IVF culture media on human pre-implantation development using single-embryo transcriptomics. ○
- 43 An FGF Timer for Zygotic Genome Activation. ○
- 42 Chromatin as a sensor of metabolic changes during early development. 10, ○
- 41 Single-cell technologies: From research to application. **2022**, 3, 100342 ○
- 40 The single-cell expression profile of transposable elements and transcription factors in human early biparental and uniparental embryonic development. 10, ○
- 39 CHK1-CDC25A-CDK1 regulate cell cycle progression in early mouse embryos to protect genome integrity. ○
- 38 KRAB family is involved in network shifts in response to osmotic stress in camels. 1-10 ○

- 37 Pre-processing, Dimension Reduction, and Clustering for Single-Cell RNA-seq Data. **2022**, 37-51 ○
- 36 Biological Sequence Classification: A Review on Data and General Methods. **2022**, 2022, 2 ○
- 35 Anesthesia and developing brain: What have we learned from recent studies. 15, ○
- 34 Comparative developmental genomics of sex-biased gene expression in early embryogenesis across mammals. ○
- 33 Comparative analysis of sperm DNA methylation supports evolutionary acquired epigenetic plasticity for organ speciation. ○
- 32 Coexpression Network Construction and Visualization from Transcriptomes Underlying ER Stress Responses. **2023**, 385-401 ○
- 31 Recurrent RNA edits in human preimplantation potentially enhance maternal mRNA clearance. **2022**, 5, ○
- 30 Single-nucleus co-expression networks of dopaminergic neurons support iron accumulation as a plausible explanation to their vulnerability in Parkinson's disease. ○
- 29 Comparative single-cell transcriptomic profiles of human androgenotes and parthenogenotes during early development.. **2022**, ○
- 28 Effect of paternal age on assisted reproductive outcomes in ICSI donor cycles. ○
- 27 Early embryonic lethality of mice lacking POLD2. ○
- 26 Proteomic profiling reveals the molecular control of oocyte maturation. **2022**, 100481 ○
- 25 CFIm-mediated alternative polyadenylation safeguards the development of mammalian pre-implantation embryos. **2022**, ○
- 24 Remodeling of maternal mRNA through poly(A) tail orchestrates human oocyte-to-embryo transition. ○
- 23 Ultrasensitive Proteomics Depicted an In-depth Landscape for Mouse Embryo. ○
- 22 Scd1 Deficiency in Early Embryos Affects Blastocyst ICM Formation through RPs-Mdm2-p53 Pathway. **2023**, 24, 1750 ○
- 21 Human zygotic genome activation is initiated from paternal genome. **2023**, 9, ○
- 20 Actin-driven chromosome clustering facilitates fast and complete chromosome capture in mammalian oocytes. ○

- 19 Comprehensive characterization of the embryonic factor LEUTX. **2023**, 26, 106172
- 18 Metabolism-based cardiomyocytes production for regenerative therapy. **2023**, 176, 11-20
- 17 A program of successive gene expression in mouse one-cell embryos. **2023**, 42, 112023
- 16 An FGF timer for zygotic genome activation. **2023**, 37, 80-85
- 15 The genetic architecture of behavioral canalization. **2023**,
- 14 Complex Analysis of Single-Cell RNA Sequencing Data. **2023**, 88, 231-252
- 13 A multi-omics genome-and-transcriptome single-cell atlas of human preimplantation embryogenesis reveals the cellular and molecular impact of chromosome instability.
- 12 Exploring the noncanonical translome using massively integrated coexpression analysis.
- 11 multiWGCNA: an R package for deep mining gene co-expression networks in multi-trait expression data. **2023**, 24,
- 10 An extended wave of global mRNA deadenylation sets up a switch in translation regulation across the mammalian oocyte-to-embryo transition.
- 9 Dynamics of histone acetylation during human early embryogenesis. **2023**, 9,
- 8 Large-scale analysis of de novo mutations identifies risk genes for female infertility characterized by oocyte and early embryo defects. **2023**, 24,
- 7 Genetic variation associated with human longevity and Alzheimer's disease risk act through microglia and oligodendrocyte cross-talk.
- 6 A single-cell transcriptional timelapse of mouse embryonic development, from gastrula to pup.
- 5 Mosaic results after preimplantation genetic testing for aneuploidy may be accompanied by changes in global gene expression. 10,
- 4 Omics Views of Mechanisms for Cell Fate Determination in Early Mammalian Development. **2023**,
- 3 R-loop landscape in mature human sperm: Regulatory and evolutionary implications. 14,
- 2 Spatiotemporal transcriptome atlas of human embryos after gastrulation.

- 1 Sperm-borne microRNA-34c regulates maternal mRNA degradation and preimplantation embryonic development in mice. **2023**, 21,

o