Feng Zhang

List of Publications by Year
in descending order

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353 papers	90,625 citations	1099 112 h-index	394 279 g-index
387 all docs	387 docs citations	387 times ranked	77617 citing authors

#	Article	IF	Citations
1	Development and Applications of CRISPR-Cas9 for Genome Engineering. Cell, 2014, 157, 1262-1278.	28.9	4,607
2	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. Science, 2014, 343, 84-87.	12.6	4,210
3	Improved vectors and genome-wide libraries for CRISPR screening. Nature Methods, 2014, 11, 783-784.	19.0	4,032
4	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. Cell, 2015, 163, 759-771.	28.9	3,558
5	Nucleic acid detection with CRISPR-Cas13a/C2c2. Science, 2017, 356, 438-442.	12.6	2,275
6	Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. Nature, 2015, 517, 583-588.	27.8	2,272
7	In vivo genome editing using Staphylococcus aureus Cas9. Nature, 2015, 520, 186-191.	27.8	2,237
8	RNA-guided editing of bacterial genomes using CRISPR-Cas systems. Nature Biotechnology, 2013, 31, 233-239.	17.5	2,071
9	Rationally engineered Cas9 nucleases with improved specificity. Science, 2016, 351, 84-88.	12.6	1,948
10	Crystal Structure of Cas9 in Complex with Guide RNA and Target DNA. Cell, 2014, 156, 935-949.	28.9	1,690
11	Multiplexed and portable nucleic acid detection platform with Cas13, Cas12a, and Csm6. Science, 2018, 360, 439-444.	12.6	1,649
12	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science, 2016, 353, aaf5573.	12.6	1,647
13	MAGeCK enables robust identification of essential genes from genome-scale CRISPR/Cas9 knockout screens. Genome Biology, 2014, 15, 554.	8.8	1,614
14	CRISPR-Cas9 Knockin Mice for Genome Editing and Cancer Modeling. Cell, 2014, 159, 440-455.	28.9	1,566
15	RNA targeting with CRISPRâ€“Cas13. Nature, 2017, 550, 280-284.	27.8	1,442
16	Evolutionary classification of CRISPRâ€“Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	28.6	1,427
17	RNA editing with CRISPR-Cas13. Science, 2017, 358, 1019-1027.	12.6	1,301
18	Diversity, classification and evolution of CRISPR-Cas systems. Current Opinion in Microbiology, 2017, 37, 67-78.	5.1	1,076

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19	Therapeutic genome editing: prospects and challenges. Nature Medicine, 2015, 21, 121-131.	30.7	1,042
20	Copy Number Variation in Human Health, Disease, and Evolution. Annual Review of Genomics and Human Genetics, 2009, 10, 451-481.	6.2	1,026
21	High-throughput functional genomics using CRISPRâ€“Cas9. Nature Reviews Genetics, 2015, 16, 299-311.	16.3	998
22	Field-deployable viral diagnostics using CRISPR-Cas13. Science, 2018, 360, 444-448.	12.6	982
23	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5â€² Sites. Cell Reports, 2014, 8, 284-296.	6.4	972
24	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. Molecular Cell, 2015, 60, 385-397.	9.7	971
25	Programmable repression and activation of bacterial gene expression using an engineered CRISPR-Cas system. Nucleic Acids Research, 2013, 41, 7429-7437.	14.5	960
26	In vivo genome editing improves muscle function in a mouse model of Duchenne muscular dystrophy. Science, 2016, 351, 403-407.	12.6	957
27	Efficient genome editing in plants using a CRISPR/Cas system. Cell Research, 2013, 23, 1229-1232.	12.0	944
28	In vivo gene editing in dystrophic mouse muscle and muscle stem cells. Science, 2016, 351, 407-411.	12.6	889
29	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	19.0	859
30	Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening. Nature Protocols, 2017, 12, 828-863.	12.0	858
31	SHERLOCK: nucleic acid detection with CRISPR nucleases. Nature Protocols, 2019, 14, 2986-3012.	12.0	851
32	Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells. Nature Biotechnology, 2014, 32, 670-676.	17.5	829
33	Diversity and evolution of class 2 CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2017, 15, 169-182.	28.6	792
34	Engineered CRISPR-Cas9 nuclease with expanded targeting space. Science, 2018, 361, 1259-1262.	12.6	783
35	Genome-wide CRISPR Screen in a Mouse Model of Tumor Growth and Metastasis. Cell, 2015, 160, 1246-1260.	28.9	746
36	Multiplex gene editing by CRISPRâ€“Cpf1 using a single crRNA array. Nature Biotechnology, 2017, 35, 31-34.	17.5	736

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37	Optical control of mammalian endogenous transcription and epigenetic states. Nature, 2013, 500, 472-476.	27.8	733
38	BCL11A enhancer dissection by Cas9-mediated in situ saturating mutagenesis. Nature, 2015, 527, 192-197.	27.8	726
39	Whole-Genome Sequencing in a Patient with Charcotâ€“Marieâ€“Tooth Neuropathy. New England Journal of Medicine, 2010, 362, 1181-1191.	27.0	698
40	In vivo interrogation of gene function in the mammalian brain using CRISPR-Cas9. Nature Biotechnology, 2015, 33, 102-106.	17.5	675
41	CRISPR-mediated direct mutation of cancer genes in the mouse liver. Nature, 2014, 514, 380-384.	27.8	673
42	Identification of essential genes for cancer immunotherapy. Nature, 2017, 548, 537-542.	27.8	668
43	A split-Cas9 architecture for inducible genome editing and transcription modulation. Nature Biotechnology, 2015, 33, 139-142.	17.5	603
44	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. Cell, 2016, 165, 949-962.	28.9	552
45	Mechanisms for human genomic rearrangements. PathoGenetics, 2008, 1, 4.	5.7	523
46	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. Science, 2016, 353, aad5147.	12.6	523
47	Sequence determinants of improved CRISPR sgRNA design. Genome Research, 2015, 25, 1147-1157.	5.5	514
48	Detection of SARS-CoV-2 with SHERLOCK One-Pot Testing. New England Journal of Medicine, 2020, 383, 1492-1494.	27.0	506
49	CRISPR-based diagnostics. Nature Biomedical Engineering, 2021, 5, 643-656.	22.5	492
50	Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. Science, 2019, 364, 292-295.	12.6	491
51	CRISPR/Cas9 for genome editing: progress, implications and challenges. Human Molecular Genetics, 2014, 23, R40-R46.	2.9	487
52	Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. Science, 2016, 353, 925-928.	12.6	482
53	Non-coding genetic variants in human disease: Figure 1.. Human Molecular Genetics, 2015, 24, R102-R110.	2.9	466
54	RNA-guided DNA insertion with CRISPR-associated transposases. Science, 2019, 365, 48-53.	12.6	448

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55	Cas13b Is a Type VI-B CRISPR-Associated RNA-Guided RNase Differentially Regulated by Accessory Proteins Csx27 and Csx28. Molecular Cell, 2017, 65, 618-630.e7.	9.7	445
56	Clinical validation of a Cas13-based assay for the detection of SARS-CoV-2 RNA. Nature Biomedical Engineering, 2020, 4, 1140-1149.	22.5	442
57	Transcription Activator-Like Effector Nucleases Enable Efficient Plant Genome Engineering Â Â. Plant Physiology, 2012, 161, 20-27.	4.8	407
58	A single mutation in the prM protein of Zika virus contributes to fetal microcephaly. Science, 2017, 358, 933-936.	12.6	399
59	Genetic evidence supports demic diffusion of Han culture. Nature, 2004, 431, 302-305.	27.8	398
60	Chromosome Catastrophes Involve Replication Mechanisms Generating Complex Genomic Rearrangements. Cell, 2011, 146, 889-903.	28.9	391
61	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	12.6	391
62	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	28.9	383
63	The DNA replication FoSTeS/MMBIR mechanism can generate genomic, genic and exonic complex rearrangements in humans. Nature Genetics, 2009, 41, 849-853.	21.4	382
64	Crystal Structure of Staphylococcus aureus Cas9. Cell, 2015, 162, 1113-1126.	28.9	357
65	m6A facilitates hippocampus-dependent learning and memory through YTHDF1. Nature, 2018, 563, 249-253.	27.8	354
66	Engineered Cpf1 variants with altered PAM specificities. Nature Biotechnology, 2017, 35, 789-792.	17.5	351
67	High frequency targeted mutagenesis in Arabidopsis thaliana using zinc finger nucleases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12028-12033.	7.1	347
68	Hypoxia as a therapy for mitochondrial disease. Science, 2016, 352, 54-61.	12.6	339
69	Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood. Nature, 2017, 548, 343-346.	27.8	336
70	A cytosine deaminase for programmable single-base RNA editing. Science, 2019, 365, 382-386.	12.6	322
71	Human Pluripotent Stem Cell-Derived Neural Cells and Brain Organoids Reveal SARS-CoV-2 Neurotropism Predominates in Choroid Plexus Epithelium. Cell Stem Cell, 2020, 27, 937-950.e9.	11.1	314
72	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. Science, 2020, 369, 1077-1084.	12.6	302

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73	BLISS is a versatile and quantitative method for genome-wide profiling of DNA double-strand breaks. Nature Communications, 2017, 8, 15058.	12.8	298
74	Structure and Engineering of Francisella novicida Cas9. Cell, 2016, 164, 950-961.	28.9	296
75	Comprehensive interrogation of natural TALE DNA-binding modules and transcriptional repressor domains. Nature Communications, 2012, 3, 968.	12.8	291
76	CRISPR-Based Therapeutic Genome Editing: Strategies and InÂVivo Delivery by AAV Vectors. Cell, 2020, 181, 136-150.	28.9	289
77	Programmable Inhibition and Detection of RNA Viruses Using Cas13. Molecular Cell, 2019, 76, 826-837.e11.	9.7	286
78	Mice with Shank3 Mutations Associated with ASD and Schizophrenia Display Both Shared and Distinct Defects. Neuron, 2016, 89, 147-162.	8.1	279
79	Autism and other neuropsychiatric symptoms are prevalent in individuals with MeCP2 duplication syndrome. Annals of Neurology, 2009, 66, 771-782.	5.3	271
80	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
81	Autism-like behaviours and germline transmission in transgenic monkeys overexpressing MeCP2. Nature, 2016, 530, 98-102.	27.8	260
82	High-resolution interrogation of functional elements in the noncoding genome. Science, 2016, 353, 1545-1549.	12.6	251
83	Engineering of CRISPR-Cas12b for human genome editing. Nature Communications, 2019, 10, 212.	12.8	249
84	Transcription control by the ENL YEATS domain in acute leukaemia. Nature, 2017, 543, 270-274.	27.8	248
85	CRISPR/Cas9 cleavage of viral DNA efficiently suppresses hepatitis B virus. Scientific Reports, 2015, 5, 10833.	3.3	245
86	Complex human chromosomal and genomic rearrangements. Trends in Genetics, 2009, 25, 298-307.	6.7	239
87	TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. New England Journal of Medicine, 2015, 372, 341-350.	27.0	239
88	Brains, Genes, and Primates. Neuron, 2015, 86, 617-631.	8.1	231
89	Orthogonal gene knockout and activation with a catalytically active Cas9 nuclease. Nature Biotechnology, 2015, 33, 1159-1161.	17.5	231
90	Biallelic Mutations in CFAP43 and CFAP44 Cause Male Infertility with Multiple Morphological Abnormalities of the Sperm Flagella. American Journal of Human Genetics, 2017, 100, 854-864.	6.2	220

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91	Mammalian retrovirus-like protein PEG10 packages its own mRNA and can be pseudotyped for mRNA delivery. Science, 2021, 373, 882-889.	12.6	214
92	Structural Basis for the Canonical and Non-canonical PAM Recognition by CRISPR-Cpf1. Molecular Cell, 2017, 67, 633-645.e3.	9.7	206
93	Efficient CRISPR-Cas9â€“mediated genome editing in Plasmodium falciparum. Nature Methods, 2014, 11, 915-918.	19.0	205
94	Increased LIS1 expression affects human and mouse brain development. Nature Genetics, 2009, 41, 168-177.	21.4	199
95	Ongoing global and regional adaptive evolution of SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	196
96	Lipid nanoparticle-mediated codelivery of Cas9 mRNA and single-guide RNA achieves liver-specific in vivo genome editing ofAngptl3. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	192
97	AAV-mediated direct in vivo CRISPR screen identifies functional suppressors in glioblastoma. Nature Neuroscience, 2017, 20, 1329-1341.	14.8	179
98	Chd8 Mutation Leads to Autistic-like Behaviors and Impaired Striatal Circuits. Cell Reports, 2017, 19, 335-350.	6.4	177
99	Optical Pooled Screens in Human Cells. Cell, 2019, 179, 787-799.e17.	28.9	170
100	Complex rearrangements in patients with duplications of MECP2 can occur by fork stalling and template switching. Human Molecular Genetics, 2009, 18, 2188-2203.	2.9	165
101	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. Science, 2020, 370, .	12.6	155
102	Assessing structural variation in a personal genomeâ€”towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	2.8	153
103	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. Science, 2021, 374, 57-65.	12.6	152
104	A cellular and spatial map of the choroid plexus across brain ventricles and ages. Cell, 2021, 184, 3056-3074.e21.	28.9	150
105	Multidimensional chemical control of CRISPRâ€“Cas9. Nature Chemical Biology, 2017, 13, 9-11.	8.0	146
106	Crystal Structure of the Minimal Cas9 from Campylobacter jejuni Reveals the Molecular Diversity in the CRISPR-Cas9 Systems. Molecular Cell, 2017, 65, 1109-1121.e3.	9.7	145
107	Single-Cell Transcriptomics Uncovers Glial Progenitor Diversity and Cell Fate Determinants during Development and Gliomagenesis. Cell Stem Cell, 2019, 24, 707-723.e8.	11.1	145
108	The copy number variation landscape of congenital anomalies of the kidney and urinary tract. Nature Genetics, 2019, 51, 117-127.	21.4	144

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109	Increasing frequencies of site-specific mutagenesis and gene targeting in Arabidopsis by manipulating DNA repair pathways. Genome Research, 2013, 23, 547-554.	5.5	142
110	SnapShot: Class 2 CRISPR-Cas Systems. Cell, 2017, 168, 328-328.e1.	28.9	138
111	Highly Parallel Profiling of Cas9 Variant Specificity. Molecular Cell, 2020, 78, 794-800.e8.	9.7	134
112	Discovery of proteins associated with a predefined genomic locus via dCas9â€“APEX-mediated proximity labeling. Nature Methods, 2018, 15, 437-439.	19.0	133
113	Y chromosome evidence of earliest modern human settlement in East Asia and multiple origins of Tibetan and Japanese populations. BMC Biology, 2008, 6, 45.	3.8	129
114	Clinical characteristics of recovered COVID-19 patients with re-detectable positive RNA test. Annals of Translational Medicine, 2020, 8, 1084-1084.	1.7	128
115	Mechanisms for Nonrecurrent Genomic Rearrangements Associated with CMT1A or HNPP: Rare CNVs as a Cause for Missing Heritability. American Journal of Human Genetics, 2010, 86, 892-903.	6.2	125
116	LGR5, a novel functional glioma stem cell marker, promotes EMT by activating the Wnt/Î²-catenin pathway and predicts poor survival of glioma patients. Journal of Experimental and Clinical Cancer Research, 2018, 37, 225.	8.6	122
117	Opportunities and challenges in modeling human brain disorders in transgenic primates. Nature Neuroscience, 2016, 19, 1123-1130.	14.8	115
118	Bi-allelic Mutations in ARMC2 Lead to Severe Astheno-Teratozoospermia Due to Sperm Flagellum Malformations in Humans and Mice. American Journal of Human Genetics, 2019, 104, 331-340.	6.2	113
119	Dual Requirement of CHD8 for Chromatin Landscape Establishment and Histone Methyltransferase Recruitment to Promote CNS Myelination and Repair. Developmental Cell, 2018, 45, 753-768.e8.	7.0	112
120	Bi-allelic DNAH8 Variants Lead to Multiple Morphological Abnormalities of the Sperm Flagella and Primary Male Infertility. American Journal of Human Genetics, 2020, 107, 330-341.	6.2	111
121	Loss-of-function mutations in QRICH2 cause male infertility with multiple morphological abnormalities of the sperm flagella. Nature Communications, 2019, 10, 433.	12.8	108
122	Genetic Structure of Hmong-Mien Speaking Populations in East Asia as Revealed by mtDNA Lineages. Molecular Biology and Evolution, 2005, 22, 725-734.	8.9	105
123	Implications of human genetic variation in CRISPR-based therapeutic genome editing. Nature Medicine, 2017, 23, 1095-1101.	30.7	105
124	Frequency of Nonallelic Homologous Recombination Is Correlated with Length of Homology: Evidence that Ectopic Synapsis Precedes Ectopic Crossing-Over. American Journal of Human Genetics, 2011, 89, 580-588.	6.2	104
125	The Nuclear Matrix Protein SAFB Cooperates with Major Satellite RNAs to Stabilize Heterochromatin Architecture Partially through Phase Separation. Molecular Cell, 2020, 77, 368-383.e7.	9.7	104
126	Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. Molecular Cell, 2020, 79, 728-740.e6.	9.7	104

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127	Bi-allelic Mutations in TTC21A Induce Asthenoteratospermia in Humans and Mice. American Journal of Human Genetics, 2019, 104, 738-748.	6.2	103
128	High-Resolution Structure of Cas13b and Biochemical Characterization of RNA Targeting and Cleavage. Cell Reports, 2019, 26, 3741-3751.e5.	6.4	102
129	Single-Cell Transcriptomics in Medulloblastoma Reveals Tumor-Initiating Progenitors and Oncogenic Cascades during Tumorigenesis and Relapse. Cancer Cell, 2019, 36, 302-318.e7.	16.8	96
130	Multiplexed, targeted gene editing in Nicotiana benthamiana for glycoâ€engineering and monoclonal antibody production. Plant Biotechnology Journal, 2016, 14, 533-542.	8.3	95
131	Nucleic Acid Detection of Plant Genes Using CRISPR-Cas13. CRISPR Journal, 2019, 2, 165-171.	2.9	92
132	The nuclear matrix protein HNRNPU maintains 3D genome architecture globally in mouse hepatocytes. Genome Research, 2018, 28, 192-202.	5.5	91
133	An RNA-aptamer-based two-color CRISPR labeling system. Scientific Reports, 2016, 6, 26857.	3.3	88
134	Structural Basis for the Altered PAM Recognition by Engineered CRISPR-Cpf1. Molecular Cell, 2017, 67, 139-147.e2.	9.7	88
135	A DNAH17 missense variant causes flagella destabilization and asthenozoospermia. Journal of Experimental Medicine, 2020, 217, .	8.5	88
136	X-Linked Congenital Hypertrichosis Syndrome Is Associated with Interchromosomal Insertions Mediated by a Human-Specific Palindrome near SOX3. American Journal of Human Genetics, 2011, 88, 819-826.	6.2	87
137	The b2/b3 subdeletion shows higher risk of spermatogenic failure and higher frequency of complete AZFc deletion than the gr/gr subdeletion in a Chinese population. Human Molecular Genetics, 2009, 18, 1122-1130.	2.9	86
138	Dual modes of CRISPR-associated transposon homing. Cell, 2021, 184, 2441-2453.e18.	28.9	86
139	Compact RNA editors with small Cas13 proteins. Nature Biotechnology, 2022, 40, 194-197.	17.5	86
140	Partial deletions are associated with an increased risk of complete deletion in AZFc: a new insight into the role of partial AZFc deletions in male infertility. Journal of Medical Genetics, 2007, 44, 437-444.	3.2	82
141	Identification of Uncommon Recurrent Potocki-Lupski Syndrome-Associated Duplications and the Distribution of Rearrangement Types and Mechanisms in PTLS. American Journal of Human Genetics, 2010, 86, 462-470.	6.2	79
142	Genome Editing Using Cas9 Nickases. Methods in Enzymology, 2014, 546, 161-174.	1.0	78
143	Coupling immunity and programmed cell suicide in prokaryotes: Lifeâ€orâ€death choices. BioEssays, 2017, 39, 1-9.	2.5	78
144	Effects of 3D culturing conditions on the transcriptomic profile of stem-cell-derived neurons. Nature Biomedical Engineering, 2018, 2, 540-554.	22.5	78

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145	DNA Microscopy: Optics-free Spatio-genetic Imaging by a Stand-Alone Chemical Reaction. Cell, 2019, 178, 229-241.e16.	28.9	77
146	Deleterious variants in X-linked CFAP47 induce asthenoteratozoospermia and primary male infertility. American Journal of Human Genetics, 2021, 108, 309-323.	6.2	74
147	Generation of hypothalamic arcuate organoids from human induced pluripotent stem cells. Cell Stem Cell, 2021, 28, 1657-1670.e10.	11.1	72
148	Microcephaly-Associated Protein WDR62 Regulates Neurogenesis through JNK1 in the Developing Neocortex. Cell Reports, 2014, 6, 104-116.	6.4	71
149	Bi-allelic Loss-of-function Variants in CFAP58 Cause Flagellar Axoneme and Mitochondrial Sheath Defects and Asthenoteratozoospermia in Humans and Mice. American Journal of Human Genetics, 2020, 107, 514-526.	6.2	71
150	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	17.5	71
151	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986.	12.0	70
152	Novel homozygousCFAP69mutations in humans and mice cause severe asthenoteratospermia with multiple morphological abnormalities of the sperm flagella. Journal of Medical Genetics, 2019, 56, 96-103.	3.2	70
153	Global microRNA depletion suppresses tumor angiogenesis. Genes and Development, 2014, 28, 1054-1067.	5.9	66
154	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
155	Genome-Wide Identification of Regulatory Sequences Undergoing Accelerated Evolution in the Human Genome. Molecular Biology and Evolution, 2016, 33, 2565-2575.	8.9	64
156	Mapping a functional cancer genome atlas of tumor suppressors in mouse liver using AAV-CRISPRâ€“mediated direct in vivo screening. Science Advances, 2018, 4, eaao5508.	10.3	64
157	Efficient typing of copy number variations in a segmental duplication-mediated rearrangement hotspot using multiplex competitive amplification. Journal of Human Genetics, 2012, 57, 545-551.	2.3	63
158	POSH Localizes Activated Rac1 to Control the Formation of Cytoplasmic Dilation of the Leading Process and Neuronal Migration. Cell Reports, 2012, 2, 640-651.	6.4	63
159	Bi-allelic Mutations in TTC29 Cause Male Subfertility with Asthenoteratospermia in Humans and Mice. American Journal of Human Genetics, 2019, 105, 1168-1181.	6.2	62
160	Genetic studies of human diversity in East Asia. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 987-996.	4.0	61
161	Genomic disorders: A window into human gene and genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1765-1771.	7.1	60
162	TBX6-associated congenital scoliosis (TACS) as a clinically distinguishable subtype of congenital scoliosis: further evidence supporting the compound inheritance and TBX6 gene dosage model. Genetics in Medicine, 2019, 21, 1548-1558.	2.4	60

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163	Conferring DNA virus resistance with high specificity in plants using virus-inducible genome-editing system. Genome Biology, 2018, 19, 197.	8.8	59
164	Î²-Sitosterol-loaded solid lipid nanoparticles ameliorate complete Freundâ€™s adjuvant-induced arthritis in rats: involvement of NF-ÐºB and HO-1/Nrf-2 pathway. Drug Delivery, 2020, 27, 1329-1341.	5.7	59
165	Rapid SARS-CoV-2 testing in primary material based on a novel multiplex RT-LAMP assay. PLoS ONE, 2020, 15, e0238612.	2.5	58
166	The coexistence of copy number variations (CNVs) and single nucleotide polymorphisms (SNPs) at a locus can result in distorted calculations of the significance in associating SNPs to disease. Human Genetics, 2018, 137, 553-567.	3.8	57
167	Homozygous mutations inSPEF2induce multiple morphological abnormalities of the sperm flagella and male infertility. Journal of Medical Genetics, 2020, 57, 31-37.	3.2	57
168	Homozygous mutations in DZIP1 can induce asthenoteratospermia with severe MMAF. Journal of Medical Genetics, 2020, 57, 445-453.	3.2	57
169	Rare variants in FANCA induce premature ovarian insufficiency. Human Genetics, 2019, 138, 1227-1236.	3.8	56
170	Biallelic mutations of CFAP251 cause sperm flagellar defects and human male infertility. Journal of Human Genetics, 2019, 64, 49-54.	2.3	56
171	Biallelic mutations inCFAP65cause male infertility with multiple morphological abnormalities of the sperm flagella in humans and mice. Journal of Medical Genetics, 2020, 57, 89-95.	3.2	55
172	Alu-specific microhomology-mediated deletion of the final exon of SPAST in three unrelated subjects with hereditary spastic paraplegia. Genetics in Medicine, 2011, 13, 582-592.	2.4	53
173	Non-transgenic Plant Genome Editing Using Purified Sequence-Specific Nucleases. Molecular Plant, 2015, 8, 1425-1427.	8.3	52
174	Curing hemophilia A by NHEJ-mediated ectopic F8 insertion in the mouse. Genome Biology, 2019, 20, 276.	8.8	50
175	Disruption in ACTL7A causes acrosomal ultrastructural defects in human and mouse sperm as a novel male factor inducing early embryonic arrest. Science Advances, 2020, 6, eaaz4796.	10.3	50
176	Bi-allelic mutations of DNAH10 cause primary male infertility with asthenoteratozoospermia in humans and mice. American Journal of Human Genetics, 2021, 108, 1466-1477.	6.2	50
177	The Suppression of CRMP2 Expression by Bone Morphogenetic Protein (BMP)-SMAD Gradient Signaling Controls Multiple Stages of Neuronal Development. Journal of Biological Chemistry, 2010, 285, 39039-39050.	3.4	49
178	Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in Setaria viridis. Plant Journal, 2020, 104, 828-838.	5.7	48
179	American Strain of Zika Virus Causes More Severe Microcephaly Than an Old Asian Strain in Neonatal Mice. EBioMedicine, 2017, 25, 95-105.	6.1	47
180	Epigenetic regulation of Atrophin1 by lysine-specific demethylase 1 is required for cortical progenitor maintenance. Nature Communications, 2014, 5, 5815.	12.8	46

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181	TBX6 compound inheritance leads to congenital vertebral malformations in humans and mice. Human Molecular Genetics, 2019, 28, 539-547.	2.9	46
182	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562.	17.5	46
183	A spatial analysis of genetic structure of human populations in China reveals distinct difference between maternal and paternal lineages. European Journal of Human Genetics, 2008, 16, 705-717.	2.8	45
184	MacroH2A1 associates with nuclear lamina and maintains chromatin architecture in mouse liver cells. Scientific Reports, 2015, 5, 17186.	3.3	44
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