

George M Church

List of Publications by Year in descending order

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544
papers

104,427
citations

143

157
h-index

265

298
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653
all docs

653
docs citations

653
times ranked

99638
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Guided Human Genome Engineering via Cas9. <i>Science</i> , 2013, 339, 823-826.	12.6	8,009
2	Systematic determination of genetic network architecture. <i>Nature Genetics</i> , 1999, 22, 281-285.	21.4	2,251
3	A Logic-Gated Nanorobot for Targeted Transport of Molecular Payloads. <i>Science</i> , 2012, 335, 831-834.	12.6	1,918
4	CAS9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering. <i>Nature Biotechnology</i> , 2013, 31, 833-838.	17.5	1,589
5	Genome engineering in <i>Saccharomyces cerevisiae</i> using CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2013, 41, 4336-4343.	14.5	1,374
6	Programming cells by multiplex genome engineering and accelerated evolution. <i>Nature</i> , 2009, 460, 894-898.	27.8	1,346
7	Multiplex and homologous recombination-mediated genome editing in <i>Arabidopsis</i> and <i>Nicotiana benthamiana</i> using guide RNA and Cas9. <i>Nature Biotechnology</i> , 2013, 31, 688-691.	17.5	1,280
8	Highly efficient Cas9-mediated transcriptional programming. <i>Nature Methods</i> , 2015, 12, 326-328.	19.0	1,245
9	Analysis of optimality in natural and perturbed metabolic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15112-15117.	7.1	1,244
10	Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. <i>Science</i> , 2005, 309, 1728-1732.	12.6	1,189
11	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
12	Human Genome Sequencing Using Unchained Base Reads on Self-Assembling DNA Nanoarrays. <i>Science</i> , 2010, 327, 78-81.	12.6	1,085
13	Cas9 as a versatile tool for engineering biology. <i>Nature Methods</i> , 2013, 10, 957-963.	19.0	1,073
14	Rapid prototyping of 3D DNA-origami shapes with caDNAno. <i>Nucleic Acids Research</i> , 2009, 37, 5001-5006.	14.5	1,054
15	CHOPCHOP: a CRISPR/Cas9 and TALEN web tool for genome editing. <i>Nucleic Acids Research</i> , 2014, 42, W401-W407.	14.5	997
16	Targeted and genome-scale strategies reveal gene-body methylation signatures in human cells. <i>Nature Biotechnology</i> , 2009, 27, 361-368.	17.5	985
17	A Deep Learning Approach to Antibiotic Discovery. <i>Cell</i> , 2020, 180, 688-702.e13.	28.9	978
18	Computational identification of Cis-regulatory elements associated with groups of functionally related genes in <i>Saccharomyces cerevisiae</i> 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 2000, 296, 1205-1214.	4.2	915

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19	Next-Generation Digital Information Storage in DNA. <i>Science</i> , 2012, 337, 1628-1628.	12.6	902
20	In vivo gene editing in dystrophic mouse muscle and muscle stem cells. <i>Science</i> , 2016, 351, 407-411.	12.6	889
21	Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation. <i>Nature Biotechnology</i> , 1998, 16, 939-945.	17.5	835
22	Heritable genome editing in <i>C. elegans</i> via a CRISPR-Cas9 system. <i>Nature Methods</i> , 2013, 10, 741-743.	19.0	825
23	Highly Multiplexed Subcellular RNA Sequencing in Situ. <i>Science</i> , 2014, 343, 1360-1363.	12.6	824
24	Cloning and sequencing of thiol-specific antioxidant from mammalian brain: alkyl hydroperoxide reductase and thiol-specific antioxidant define a large family of antioxidant enzymes.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 7017-7021.	7.1	768
25	Functional Characterization of the Antibiotic Resistance Reservoir in the Human Microflora. <i>Science</i> , 2009, 325, 1128-1131.	12.6	748
26	Orthogonal Cas9 proteins for RNA-guided gene regulation and editing. <i>Nature Methods</i> , 2013, 10, 1116-1121.	19.0	740
27	Optical control of mammalian endogenous transcription and epigenetic states. <i>Nature</i> , 2013, 500, 472-476.	27.8	733
28	Modeling the mitochondrial cardiomyopathy of Barth syndrome with induced pluripotent stem cell and heart-on-chip technologies. <i>Nature Medicine</i> , 2014, 20, 616-623.	30.7	733
29	DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017, 550, 345-353.	27.8	729
30	Genomically Recoded Organisms Expand Biological Functions. <i>Science</i> , 2013, 342, 357-360.	12.6	721
31	Efficient construction of sequence-specific TAL effectors for modulating mammalian transcription. <i>Nature Biotechnology</i> , 2011, 29, 149-153.	17.5	708
32	Unified rational protein engineering with sequence-based deep representation learning. <i>Nature Methods</i> , 2019, 16, 1315-1322.	19.0	680
33	Concerning RNA-guided gene drives for the alteration of wild populations. <i>ELife</i> , 2014, 3, .	6.0	653
34	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. <i>Bioinformatics</i> , 2009, 25, 875-881.	4.1	651
35	Large-scale de novo DNA synthesis: technologies and applications. <i>Nature Methods</i> , 2014, 11, 499-507.	19.0	644
36	Clinical assessment incorporating a personal genome. <i>Lancet, The</i> , 2010, 375, 1525-1535.	13.7	637

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37	Identifying regulatory networks by combinatorial analysis of promoter elements. <i>Nature Genetics</i> , 2001, 29, 153-159.	21.4	585
38	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016, 3, 160025.	5.3	575
39	Correlation between transcriptome and interactome mapping data from <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 2001, 29, 482-486.	21.4	570
40	Inactivation of porcine endogenous retrovirus in pigs using CRISPR-Cas9. <i>Science</i> , 2017, 357, 1303-1307.	12.6	570
41	Modular epistasis in yeast metabolism. <i>Nature Genetics</i> , 2005, 37, 77-83.	21.4	552
42	A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015, 348, 36-38.	12.6	541
43	Identification of many microRNAs that copurify with polyribosomes in mammalian neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 360-365.	7.1	528
44	Synthetic Gene Networks That Count. <i>Science</i> , 2009, 324, 1199-1202.	12.6	528
45	Precise Manipulation of Chromosomes in Vivo Enables Genome-Wide Codon Replacement. <i>Science</i> , 2011, 333, 348-353.	12.6	512
46	The Brain Activity Map Project and the Challenge of Functional Connectomics. <i>Neuron</i> , 2012, 74, 970-974.	8.1	512
47	Genome-wide inactivation of porcine endogenous retroviruses (PERVs). <i>Science</i> , 2015, 350, 1101-1104.	12.6	511
48	Titin mutations in iPS cells define sarcomere insufficiency as a cause of dilated cardiomyopathy. <i>Science</i> , 2015, 349, 982-986.	12.6	508
49	A multifunctional AAV-CRISPR-Cas9 and its host response. <i>Nature Methods</i> , 2016, 13, 868-874.	19.0	506
50	Advanced sequencing technologies: methods and goals. <i>Nature Reviews Genetics</i> , 2004, 5, 335-344.	16.3	499
51	Bacteria Subsisting on Antibiotics. <i>Science</i> , 2008, 320, 100-103.	12.6	499
52	Syntrophic exchange in synthetic microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2149-56.	7.1	498
53	Causes and Effects of N-Terminal Codon Bias in Bacterial Genes. <i>Science</i> , 2013, 342, 475-479.	12.6	491
54	A computational analysis of whole-genome expression data reveals chromosomal domains of gene expression. <i>Nature Genetics</i> , 2000, 26, 183-186.	21.4	485

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55	Genome-Wide Identification of Human RNA Editing Sites by Parallel DNA Capturing and Sequencing. <i>Science</i> , 2009, 324, 1210-1213.	12.6	483
56	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. <i>Nature Medicine</i> , 2019, 25, 1104-1109.	30.7	477
57	Photosynthesis genes in marine viruses yield proteins during host infection. <i>Nature</i> , 2005, 438, 86-89.	27.8	470
58	Patterns and Implications of Gene Gain and Loss in the Evolution of <i>Prochlorococcus</i> . <i>PLoS Genetics</i> , 2007, 3, e231.	3.5	469
59	Tuberculosis Drug Resistance Mutation Database. <i>PLoS Medicine</i> , 2009, 6, e1000002.	8.4	458
60	Comparison of Cas9 activators in multiple species. <i>Nature Methods</i> , 2016, 13, 563-567.	19.0	438
61	Reprogramming to recover youthful epigenetic information and restore vision. <i>Nature</i> , 2020, 588, 124-129.	27.8	424
62	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. <i>Nature Protocols</i> , 2015, 10, 442-458.	12.0	422
63	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. <i>Science Translational Medicine</i> , 2014, 6, 248ra107.	12.4	394
64	Multiplex amplification of large sets of human exons. <i>Nature Methods</i> , 2007, 4, 931-936.	19.0	392
65	Generation of functional human hepatic endoderm from human induced pluripotent stem cells. <i>Hepatology</i> , 2010, 51, 329-335.	7.3	389
66	Sequencing genomes from single cells by polymerase cloning. <i>Nature Biotechnology</i> , 2006, 24, 680-686.	17.5	388
67	From genetic privacy to open consent. <i>Nature Reviews Genetics</i> , 2008, 9, 406-411.	16.3	385
68	pLogo: a probabilistic approach to visualizing sequence motifs. <i>Nature Methods</i> , 2013, 10, 1211-1212.	19.0	384
69	Accurate multiplex gene synthesis from programmable DNA microchips. <i>Nature</i> , 2004, 432, 1050-1054.	27.8	379
70	Crystal structure of yeast phenylalanine transfer RNA. <i>Journal of Molecular Biology</i> , 1978, 123, 607-630.	4.2	377
71	Composability of regulatory sequences controlling transcription and translation in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14024-14029.	7.1	377
72	Mature induced-pluripotent-stem-cell-derived human podocytes reconstitute kidney glomerular-capillary-wall function on a chip. <i>Nature Biomedical Engineering</i> , 2017, 1, .	22.5	376

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73	The promise of organ and tissue preservation to transform medicine. <i>Nature Biotechnology</i> , 2017, 35, 530-542.	17.5	371
74	Programmable transcriptional repression in mycobacteria using an orthogonal CRISPR interference platform. <i>Nature Microbiology</i> , 2017, 2, 16274.	13.3	368
75	Unraveling CRISPR-Cas9 genome engineering parameters via a library-on-library approach. <i>Nature Methods</i> , 2015, 12, 823-826.	19.0	361
76	An enhanced CRISPR repressor for targeted mammalian gene regulation. <i>Nature Methods</i> , 2018, 15, 611-616.	19.0	361
77	Towards synthesis of a minimal cell. <i>Molecular Systems Biology</i> , 2006, 2, 45.	7.2	360
78	Cell-type-specific contacts to immunoglobulin enhancers in nuclei. <i>Nature</i> , 1985, 313, 798-801.	27.8	358
79	Optimization of scarless human stem cell genome editing. <i>Nucleic Acids Research</i> , 2013, 41, 9049-9061.	14.5	358
80	Biocontainment of genetically modified organisms by synthetic protein design. <i>Nature</i> , 2015, 518, 55-60.	27.8	345
81	RNA expression analysis using a 30 base pair resolution Escherichia coli genome array. <i>Nature Biotechnology</i> , 2000, 18, 1262-1268.	17.5	340
82	Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12. <i>Electrophoresis</i> , 1997, 18, 1259-1313.	2.4	338
83	Regulatory Networks Revealed by Transcriptional Profiling of Damaged <i>Saccharomyces cerevisiae</i> Cells: Rpn4 Links Base Excision Repair with Proteasomes. <i>Molecular and Cellular Biology</i> , 2000, 20, 8157-8167.	2.3	329
84	Ethical and Practical Guidelines for Reporting Genetic Research Results to Study Participants. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 574-580.	5.1	328
85	Nanotools for Neuroscience and Brain Activity Mapping. <i>ACS Nano</i> , 2013, 7, 1850-1866.	14.6	323
86	A comprehensive library of DNA-binding site matrices for 55 proteins applied to the complete Escherichia coli K-12 genome 1 Edited by R. Ebright. <i>Journal of Molecular Biology</i> , 1998, 284, 241-254.	4.2	319
87	Global RNA Half-Life Analysis in Escherichia coli Reveals Positional Patterns of Transcript Degradation. <i>Genome Research</i> , 2003, 13, 216-223.	5.5	318
88	Preferred analysis methods for Affymetrix GeneChips revealed by a wholly defined control dataset. <i>Genome Biology</i> , 2005, 6, R16.	9.6	318
89	Genome-Scale Metabolic Model of <i>Helicobacter pylori</i> 26695. <i>Journal of Bacteriology</i> , 2002, 184, 4582-4593.	2.2	317
90	Genome-wide expression dynamics of a marine virus and host reveal features of co-evolution. <i>Nature</i> , 2007, 449, 83-86.	27.8	316

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91	Nanoscale imaging of RNA with expansion microscopy. <i>Nature Methods</i> , 2016, 13, 679-684.	19.0	314
92	Proteogenomic mapping as a complementary method to perform genome annotation. <i>Proteomics</i> , 2004, 4, 59-77.	2.2	305
93	Immuno-SABER enables highly multiplexed and amplified protein imaging in tissues. <i>Nature Biotechnology</i> , 2019, 37, 1080-1090.	17.5	301
94	A highly annotated whole-genome sequence of a Korean individual. <i>Nature</i> , 2009, 460, 1011-1015.	27.8	295
95	An Analysis of the Relationship Between Metabolism, Developmental Schedules, and Longevity Using Phylogenetic Independent Contrasts. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2007, 62, 149-160.	3.6	293
96	Safeguarding CRISPR-Cas9 gene drives in yeast. <i>Nature Biotechnology</i> , 2015, 33, 1250-1255.	17.5	291
97	Computational and Experimental Identification of <i>C. elegans</i> microRNAs. <i>Molecular Cell</i> , 2003, 11, 1253-1263.	9.7	289
98	Reprogramming of T Cells from Human Peripheral Blood. <i>Cell Stem Cell</i> , 2010, 7, 15-19.	11.1	288
99	Regulating gene drives. <i>Science</i> , 2014, 345, 626-628.	12.6	287
100	Quantitative Morphological Signatures Define Local Signaling Networks Regulating Cell Morphology. <i>Science</i> , 2007, 316, 1753-1756.	12.6	286
101	Nucleotides of transcription factor binding sites exert interdependent effects on the binding affinities of transcription factors. <i>Nucleic Acids Research</i> , 2002, 30, 1255-1261.	14.5	282
102	The Isw2 Chromatin Remodeling Complex Represses Early Meiotic Genes upon Recruitment by Ume6p. <i>Cell</i> , 2000, 103, 423-433.	28.9	280
103	Insights into the Evolution of Longevity from the Bowhead Whale Genome. <i>Cell Reports</i> , 2015, 10, 112-122.	6.4	280
104	Improving molecular cancer class discovery through sparse non-negative matrix factorization. <i>Bioinformatics</i> , 2005, 21, 3970-3975.	4.1	278
105	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016, 13, 177-183.	19.0	274
106	Cas9 gRNA engineering for genome editing, activation and repression. <i>Nature Methods</i> , 2015, 12, 1051-1054.	19.0	272
107	Autoantigen discovery with a synthetic human peptidome. <i>Nature Biotechnology</i> , 2011, 29, 535-541.	17.5	267
108	The role of replicates for error mitigation in next-generation sequencing. <i>Nature Reviews Genetics</i> , 2014, 15, 56-62.	16.3	267

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109	Exploring the DNA-binding specificities of zinc fingers with DNA microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 7158-7163.	7.1	263
110	Developmental barcoding of whole mouse via homing CRISPR. Science, 2018, 361, .	12.6	263
111	Identification of a Novel cis-Regulatory Element Involved in the Heat Shock Response in <i>Caenorhabditis elegans</i> Using Microarray Gene Expression and Computational Methods. Genome Research, 2002, 12, 701-712.	5.5	262
112	Nucleic acid memory. Nature Materials, 2016, 15, 366-370.	27.5	261
113	Safeguarding gene drive experiments in the laboratory. Science, 2015, 349, 927-929.	12.6	254
114	CRISPR-Cas encoding of a digital movie into the genomes of a population of living bacteria. Nature, 2017, 547, 345-349.	27.8	254
115	Microarray analysis of the transcriptional network controlled by the photoreceptor homeobox gene <i>Crx</i> . Current Biology, 2000, 10, 301-310.	3.9	252
116	Submicrometre geometrically encoded fluorescent barcodes self-assembled from DNA. Nature Chemistry, 2012, 4, 832-839.	13.6	252
117	Design, synthesis, and testing toward a 57-codon genome. Science, 2016, 353, 819-822.	12.6	251
118	Regulatory network of acid resistance genes in <i>Escherichia coli</i> . Molecular Microbiology, 2003, 48, 699-712.	2.5	250
119	The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation. Molecular Cell, 2011, 44, 252-264.	9.7	249
120	Measuring absolute expression with microarrays with a calibrated reference sample and an extended signal intensity range. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7554-7559.	7.1	248
121	Relationships between p63 Binding, DNA Sequence, Transcription Activity, and Biological Function in Human Cells. Molecular Cell, 2006, 24, 593-602.	9.7	248
122	Extensive phosphorylation with overlapping specificity by <i>Mycobacterium tuberculosis</i> serine/threonine protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7521-7526.	7.1	245
123	Evolution-guided optimization of biosynthetic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17803-17808.	7.1	242
124	RNA - ligand interactions:(I) magnesium binding sites in yeast tRNAPhe. Nucleic Acids Research, 1977, 4, 2811-2820.	14.5	238
125	An Integrated Genome-wide CRISPR Approach to Functionalize lncRNAs in Drug Resistance. Cell, 2018, 173, 649-664.e20.	28.9	238
126	Scalable gene synthesis by selective amplification of DNA pools from high-fidelity microchips. Nature Biotechnology, 2010, 28, 1295-1299.	17.5	235

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127	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
128	Quantifying DNA-protein interactions by double-stranded DNA arrays. <i>Nature Biotechnology</i> , 1999, 17, 573-577.	17.5	232
129	The challenges of sequencing by synthesis. <i>Nature Biotechnology</i> , 2009, 27, 1013-1023.	17.5	232
130	Accurate whole-genome sequencing and haplotyping from 10 to 20 human cells. <i>Nature</i> , 2012, 487, 190-195.	27.8	226
131	The Complete Genome and Proteome of <i>Mycoplasma mobile</i> . <i>Genome Research</i> , 2004, 14, 1447-1461.	5.5	224
132	Comprehensive AAV capsid fitness landscape reveals a viral gene and enables machine-guided design. <i>Science</i> , 2019, 366, 1139-1143.	12.6	217
133	A Dynamic Programming Approach to De Novo Peptide Sequencing via Tandem Mass Spectrometry. <i>Journal of Computational Biology</i> , 2001, 8, 325-337.	1.6	215
134	Genome engineering. <i>Nature Biotechnology</i> , 2009, 27, 1151-1162.	17.5	215
135	Physical principles for scalable neural recording. <i>Frontiers in Computational Neuroscience</i> , 2013, 7, 137.	2.1	215
136	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. <i>Nature Neuroscience</i> , 2017, 20, 1217-1224.	14.8	212
137	Low-N protein engineering with data-efficient deep learning. <i>Nature Methods</i> , 2021, 18, 389-396.	19.0	212
138	The Scientific Foundation for Personal Genomics: Recommendations from a National Institutes of Health Centers for Disease Control and Prevention Multidisciplinary Workshop. <i>Genetics in Medicine</i> , 2009, 11, 559-567.	2.4	207
139	Genome-scale promoter engineering by coselection MAGE. <i>Nature Methods</i> , 2012, 9, 591-593.	19.0	207
140	Forward Error Correction for DNA Data Storage. <i>Procedia Computer Science</i> , 2016, 80, 1011-1022.	2.0	203
141	In situ localized amplification and contact replication of many individual DNA molecules. <i>Nucleic Acids Research</i> , 1999, 27, 34e-34.	14.5	202
142	Automated modelling of signal transduction networks. <i>BMC Bioinformatics</i> , 2002, 3, 34.	2.6	198
143	Biosensor-based engineering of biosynthetic pathways. <i>Current Opinion in Biotechnology</i> , 2016, 42, 84-91.	6.6	198
144	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	12.6	197

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145	Realizing the potential of synthetic biology. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 289-294.	37.0	196
146	The Transition between Transcriptional Initiation and Elongation in <i>E. coli</i> Is Highly Variable and Often Rate Limiting. <i>Molecular Cell</i> , 2006, 24, 747-757.	9.7	194
147	A public resource facilitating clinical use of genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11920-11927.	7.1	194
148	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	12.6	194
149	Synthetic biosensors for precise gene control and real-time monitoring of metabolites. <i>Nucleic Acids Research</i> , 2015, 43, 7648-7660.	14.5	193
150	“Fit-for-purpose” challenges and opportunities for applications of blockchain technology in the future of healthcare. <i>BMC Medicine</i> , 2019, 17, 68.	5.5	193
151	sgRNA Scorer 2.0: A Species-Independent Model To Predict CRISPR/Cas9 Activity. <i>ACS Synthetic Biology</i> , 2017, 6, 902-904.	3.8	189
152	Rapid neurogenesis through transcriptional activation in human stem cells. <i>Molecular Systems Biology</i> , 2014, 10, 760.	7.2	187
153	High-resolution antibody dynamics of vaccine-induced immune responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4928-4933.	7.1	186
154	Iterative capped assembly: rapid and scalable synthesis of repeat-module DNA such as TAL effectors from individual monomers. <i>Nucleic Acids Research</i> , 2012, 40, e117-e117.	14.5	185
155	Polony Multiplex Analysis of Gene Expression (PMAGE) in Mouse Hypertrophic Cardiomyopathy. <i>Science</i> , 2007, 316, 1481-1484.	12.6	182
156	The Brain Activity Map. <i>Science</i> , 2013, 339, 1284-1285.	12.6	181
157	Conservation of DNA Regulatory Motifs and Discovery of New Motifs in Microbial Genomes. <i>Genome Research</i> , 2000, 10, 744-757.	5.5	180
158	Molecular recordings by directed CRISPR spacer acquisition. <i>Science</i> , 2016, 353, aaf1175.	12.6	179
159	Rapidly evolving homing CRISPR barcodes. <i>Nature Methods</i> , 2017, 14, 195-200.	19.0	179
160	Codon usage of highly expressed genes affects proteome-wide translation efficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4940-E4949.	7.1	177
161	The amino-acid mutational spectrum of human genetic disease. <i>Genome Biology</i> , 2003, 4, R72.	9.6	176
162	The Effects of Somatic Hypermutation on Neutralization and Binding in the PGT121 Family of Broadly Neutralizing HIV Antibodies. <i>PLoS Pathogens</i> , 2013, 9, e1003754.	4.7	175

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163	The Human Ageing Genomic Resources: online databases and tools for biogerontologists. <i>Aging Cell</i> , 2009, 8, 65-72.	6.7	173
164	A Microarray-Based Antibiotic Screen Identifies a Regulatory Role for Supercoiling in the Osmotic Stress Response of <i>Escherichia coli</i> . <i>Genome Research</i> , 2003, 13, 206-215.	5.5	172
165	Elevated Coding Mutation Rate During the Reprogramming of Human Somatic Cells into Induced Pluripotent Stem Cells. <i>Stem Cells</i> , 2012, 30, 435-440.	3.2	172
166	Evolutionary dynamics of CRISPR gene drives. <i>Science Advances</i> , 2017, 3, e1601964.	10.3	172
167	Pluripotent stem cell-derived CAR-macrophage cells with antigen-dependent anti-cancer cell functions. <i>Journal of Hematology and Oncology</i> , 2020, 13, 153.	17.0	172
168	Multisystem inflammatory syndrome in children is driven by zonulin-dependent loss of gut mucosal barrier. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	170
169	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. <i>Virulence</i> , 2010, 1, 299-303.	4.4	166
170	Engineering Life: Building a FAB for Biology. <i>Scientific American</i> , 2006, 294, 44-51.	1.0	165
171	Deep diversification of an AAV capsid protein by machine learning. <i>Nature Biotechnology</i> , 2021, 39, 691-696.	17.5	165
172	Systematic identification of edited microRNAs in the human brain. <i>Genome Research</i> , 2012, 22, 1533-1540.	5.5	163
173	Lambda Red Recombineering in <i>Escherichia coli</i> Occurs Through a Fully Single-Stranded Intermediate. <i>Genetics</i> , 2010, 186, 791-799.	2.9	161
174	Alignment and structure prediction of divergent protein families: periplasmic and outer membrane proteins of bacterial efflux pumps. <i>Journal of Molecular Biology</i> , 1999, 287, 695-715.	4.2	159
175	<i>Escherichia coli</i> Gene Expression Responsive to Levels of the Response Regulator EvgA. <i>Journal of Bacteriology</i> , 2002, 184, 6225-6234.	2.2	159
176	Fluorescent in situ sequencing on polymerase colonies. <i>Analytical Biochemistry</i> , 2003, 320, 55-65.	2.4	159
177	Genetically encoded sensors enable real-time observation of metabolite production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2388-2393.	7.1	155
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