

George M Church

List of Publications by Citations

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

590 papers	80,334 citations	146 h-index	274 g-index
653 ext. papers	94,584 ext. citations	17.5 avg, IF	8.19 L-index

#	Paper	IF	Citations
590	RNA-guided human genome engineering via Cas9. <i>Science</i> , 2013 , 339, 823-6	33.3	6363
589	Systematic determination of genetic network architecture. <i>Nature Genetics</i> , 1999 , 22, 281-5	36.3	1911
588	A logic-gated nanorobot for targeted transport of molecular payloads. <i>Science</i> , 2012 , 335, 831-4	33.3	1563
587	CAS9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering. <i>Nature Biotechnology</i> , 2013 , 31, 833-8	44.5	1341
586	Programming cells by multiplex genome engineering and accelerated evolution. <i>Nature</i> , 2009 , 460, 894-898	39.4	1111
585	Genome engineering in <i>Saccharomyces cerevisiae</i> using CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2013 , 41, 4336-43	20.1	1094
584	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, 15112-7	11.5	1025
583	Accurate multiplex polony sequencing of an evolved bacterial genome. <i>Science</i> , 2005 , 309, 1728-32	33.3	1011
582	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, 688-91	44.5	1001
581	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005 , 23, 137-44	44.5	950
580	Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays. <i>Science</i> , 2010 , 327, 78-81	33.3	928
579	Cas9 as a versatile tool for engineering biology. <i>Nature Methods</i> , 2013 , 10, 957-63	21.6	897
578	Highly efficient Cas9-mediated transcriptional programming. <i>Nature Methods</i> , 2015 , 12, 326-8	21.6	856
577	Targeted and genome-scale strategies reveal gene-body methylation signatures in human cells. <i>Nature Biotechnology</i> , 2009 , 27, 361-8	44.5	830
576	Computational identification of cis-regulatory elements associated with groups of functionally related genes in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2000 , 296, 1205-14	6.5	806
575	Rapid prototyping of 3D DNA-origami shapes with caDNAno. <i>Nucleic Acids Research</i> , 2009 , 37, 5001-6	20.1	772
574	Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation. <i>Nature Biotechnology</i> , 1998 , 16, 939-45	44.5	732

573	In vivo gene editing in dystrophic mouse muscle and muscle stem cells. <i>Science</i> , 2016 , 351, 407-411	33.3	711
572	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, 7017-21	11.5	708
571	CHOPCHOP: a CRISPR/Cas9 and TALEN web tool for genome editing. <i>Nucleic Acids Research</i> , 2014 , 42, W401-7	20.1	707
570	Heritable genome editing in <i>C. elegans</i> via a CRISPR-Cas9 system. <i>Nature Methods</i> , 2013 , 10, 741-3	21.6	669
569	Optical control of mammalian endogenous transcription and epigenetic states. <i>Nature</i> , 2013 , 500, 472-476	36.4	635
568	Highly multiplexed subcellular RNA sequencing in situ. <i>Science</i> , 2014 , 343, 1360-3	33.3	631
567	Efficient construction of sequence-specific TAL effectors for modulating mammalian transcription. <i>Nature Biotechnology</i> , 2011 , 29, 149-53	44.5	620
566	Functional characterization of the antibiotic resistance reservoir in the human microflora. <i>Science</i> , 2009 , 325, 1128-1131	33.3	620
565	Orthogonal Cas9 proteins for RNA-guided gene regulation and editing. <i>Nature Methods</i> , 2013 , 10, 1116-1121	21.6	615
564	Modeling the mitochondrial cardiomyopathy of Barth syndrome with induced pluripotent stem cell and heart-on-chip technologies. <i>Nature Medicine</i> , 2014 , 20, 616-23	50.5	604
563	Next-generation digital information storage in DNA. <i>Science</i> , 2012 , 337, 1628	33.3	599
562	Clinical assessment incorporating a personal genome. <i>Lancet, The</i> , 2010 , 375, 1525-35	40	565
561	Genomically recoded organisms expand biological functions. <i>Science</i> , 2013 , 342, 357-60	33.3	553
560	Concerning RNA-guided gene drives for the alteration of wild populations. <i>ELife</i> , 2014 , 3,	8.9	525
559	Identifying regulatory networks by combinatorial analysis of promoter elements. <i>Nature Genetics</i> , 2001 , 29, 153-9	36.3	519
558	Correlation between transcriptome and interactome mapping data from <i>Saccharomyces cerevisiae</i> . <i>Nature Genetics</i> , 2001 , 29, 482-6	36.3	517
557	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. <i>Bioinformatics</i> , 2009 , 25, 875-81	7.2	496
556	DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017 , 550, 345-353	50.4	486

555	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, 360-5	11.5	483
554	Modular epistasis in yeast metabolism. <i>Nature Genetics</i> , 2005 , 37, 77-83	36.3	463
553	Large-scale de novo DNA synthesis: technologies and applications. <i>Nature Methods</i> , 2014 , 11, 499-507	21.6	457
552	Synthetic gene networks that count. <i>Science</i> , 2009 , 324, 1199-202	33.3	449
551	Advanced sequencing technologies: methods and goals. <i>Nature Reviews Genetics</i> , 2004 , 5, 335-44	30.1	440
550	A Deep Learning Approach to Antibiotic Discovery. <i>Cell</i> , 2020 , 180, 688-702.e13	56.2	430
549	Precise manipulation of chromosomes in vivo enables genome-wide codon replacement. <i>Science</i> , 2011 , 333, 348-53	33.3	424
548	A computational analysis of whole-genome expression data reveals chromosomal domains of gene expression. <i>Nature Genetics</i> , 2000 , 26, 183-6	36.3	424
547	Genome-wide identification of human RNA editing sites by parallel DNA capturing and sequencing. <i>Science</i> , 2009 , 324, 1210-3	33.3	415
546	Biotechnology. A prudent path forward for genomic engineering and germline gene modification. <i>Science</i> , 2015 , 348, 36-8	33.3	413
545	Bacteria subsisting on antibiotics. <i>Science</i> , 2008 , 320, 100-3	33.3	398
544	Patterns and implications of gene gain and loss in the evolution of <i>Prochlorococcus</i> . <i>PLoS Genetics</i> , 2007 , 3, e231	6	397
543	Tuberculosis drug resistance mutation database. <i>PLoS Medicine</i> , 2009 , 6, e2	11.6	396
542	Inactivation of porcine endogenous retrovirus in pigs using CRISPR-Cas9. <i>Science</i> , 2017 , 357, 1303-1307	33.3	395
541	Genome-wide inactivation of porcine endogenous retroviruses (PERVs). <i>Science</i> , 2015 , 350, 1101-4	33.3	394
540	The brain activity map project and the challenge of functional connectomics. <i>Neuron</i> , 2012 , 74, 970-4	13.9	383
539	Causes and effects of N-terminal codon bias in bacterial genes. <i>Science</i> , 2013 , 342, 475-9	33.3	381
538	HEART DISEASE. Titin mutations in iPS cells define sarcomere insufficiency as a cause of dilated cardiomyopathy. <i>Science</i> , 2015 , 349, 982-6	33.3	379

537	A multifunctional AAV-CRISPR-Cas9 and its host response. <i>Nature Methods</i> , 2016 , 13, 868-74	21.6	359
536	Multiplex amplification of large sets of human exons. <i>Nature Methods</i> , 2007 , 4, 931-6	21.6	357
535	Sequencing genomes from single cells by polymerase cloning. <i>Nature Biotechnology</i> , 2006 , 24, 680-6	44.5	353
534	Photosynthesis genes in marine viruses yield proteins during host infection. <i>Nature</i> , 2005 , 438, 86-9	50.4	348
533	Generation of functional human hepatic endoderm from human induced pluripotent stem cells. <i>Hepatology</i> , 2010 , 51, 329-35	11.2	347
532	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016 , 3, 160025	8.2	345
531	Crystal structure of yeast phenylalanine transfer RNA. I. Crystallographic refinement. <i>Journal of Molecular Biology</i> , 1978 , 123, 607-30	6.5	344
530	Cell-type-specific contacts to immunoglobulin enhancers in nuclei. <i>Nature</i> , 1985 , 313, 798-801	50.4	336
529	Accurate multiplex gene synthesis from programmable DNA microchips. <i>Nature</i> , 2004 , 432, 1050-4	50.4	325
528	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	11.5	322
527	From genetic privacy to open consent. <i>Nature Reviews Genetics</i> , 2008 , 9, 406-11	30.1	313
526	RNA expression analysis using a 30 base pair resolution Escherichia coli genome array. <i>Nature Biotechnology</i> , 2000 , 18, 1262-8	44.5	309
525	Comparison of Cas9 activators in multiple species. <i>Nature Methods</i> , 2016 , 13, 563-567	21.6	308
524	Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12. <i>Electrophoresis</i> , 1997 , 18, 1259-313	3.6	305
523	Towards synthesis of a minimal cell. <i>Molecular Systems Biology</i> , 2006 , 2, 45	12.2	305
522	Regulatory networks revealed by transcriptional profiling of damaged Saccharomyces cerevisiae cells: Rpn4 links base excision repair with proteasomes. <i>Molecular and Cellular Biology</i> , 2000 , 20, 8157-67	4.8	304
521	Optimization of scarless human stem cell genome editing. <i>Nucleic Acids Research</i> , 2013 , 41, 9049-61	20.1	302
520	Ethical and practical guidelines for reporting genetic research results to study participants: updated guidelines from a National Heart, Lung, and Blood Institute working group. <i>Circulation: Cardiovascular Genetics</i> , 2010 , 3, 574-80		297

519	Preferred analysis methods for Affymetrix GeneChips revealed by a wholly defined control dataset. <i>Genome Biology</i> , 2005 , 6, R16	18.3	293
518	A comprehensive library of DNA-binding site matrices for 55 proteins applied to the complete Escherichia coli K-12 genome. <i>Journal of Molecular Biology</i> , 1998 , 284, 241-54	6.5	287
517	B cells populating the multiple sclerosis brain mature in the draining cervical lymph nodes. <i>Science Translational Medicine</i> , 2014 , 6, 248ra107	17.5	285
516	Genome-scale metabolic model of Helicobacter pylori 26695. <i>Journal of Bacteriology</i> , 2002 , 184, 4582-93	3.5	285
515	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. <i>Nature Protocols</i> , 2015 , 10, 442-58	18.8	280
514	Composability of regulatory sequences controlling transcription and translation in Escherichia coli. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14024-9	11.5	274
513	Global RNA half-life analysis in Escherichia coli reveals positional patterns of transcript degradation. <i>Genome Research</i> , 2003 , 13, 216-23	9.7	274
512	Unraveling CRISPR-Cas9 genome engineering parameters via a library-on-library approach. <i>Nature Methods</i> , 2015 , 12, 823-6	21.6	265
511	A highly annotated whole-genome sequence of a Korean individual. <i>Nature</i> , 2009 , 460, 1011-5	50.4	265
510	Computational and experimental identification of C. elegans microRNAs. <i>Molecular Cell</i> , 2003 , 11, 1253-63	3.6	265
509	Biocontainment of genetically modified organisms by synthetic protein design. <i>Nature</i> , 2015 , 518, 55-60	50.4	255
508	The Isw2 chromatin remodeling complex represses early meiotic genes upon recruitment by Ume6p. <i>Cell</i> , 2000 , 103, 423-33	56.2	255
507	Proteogenomic mapping as a complementary method to perform genome annotation. <i>Proteomics</i> , 2004 , 4, 59-77	4.8	254
506	Mature induced-pluripotent-stem-cell-derived human podocytes reconstitute kidney glomerular-capillary-wall function on a chip. <i>Nature Biomedical Engineering</i> , 2017 , 1,	19	253
505	Reprogramming of T cells from human peripheral blood. <i>Cell Stem Cell</i> , 2010 , 7, 15-9	18	251
504	Nanotools for neuroscience and brain activity mapping. <i>ACS Nano</i> , 2013 , 7, 1850-66	16.7	248
503	Genome-wide expression dynamics of a marine virus and host reveal features of co-evolution. <i>Nature</i> , 2007 , 449, 83-6	50.4	248
502	The promise of organ and tissue preservation to transform medicine. <i>Nature Biotechnology</i> , 2017 , 35, 530-542	44.5	246

501	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. <i>Nature Medicine</i> , 2019 , 25, 1104-1109	50.5	242
500	Quantitative morphological signatures define local signaling networks regulating cell morphology. <i>Science</i> , 2007 , 316, 1753-6	33.3	238
499	Microarray analysis of the transcriptional network controlled by the photoreceptor homeobox gene Crx. <i>Current Biology</i> , 2000 , 10, 301-10	6.3	238
498	Nucleotides of transcription factor binding sites exert interdependent effects on the binding affinities of transcription factors. <i>Nucleic Acids Research</i> , 2002 , 30, 1255-61	20.1	234
497	Unified rational protein engineering with sequence-based deep representation learning. <i>Nature Methods</i> , 2019 , 16, 1315-1322	21.6	234
496	pLogo: a probabilistic approach to visualizing sequence motifs. <i>Nature Methods</i> , 2013 , 10, 1211-2	21.6	233
495	Biotechnology. Regulating gene drives. <i>Science</i> , 2014 , 345, 626-8	33.3	232
494	Safeguarding CRISPR-Cas9 gene drives in yeast. <i>Nature Biotechnology</i> , 2015 , 33, 1250-1255	44.5	231
493	Exploring the DNA-binding specificities of zinc fingers with DNA microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 7158-63	11.5	229
492	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, 149-60	6.4	227
491	Relationships between p63 binding, DNA sequence, transcription activity, and biological function in human cells. <i>Molecular Cell</i> , 2006 , 24, 593-602	17.6	227
490	Regulatory network of acid resistance genes in Escherichia coli. <i>Molecular Microbiology</i> , 2003 , 48, 699-712	12.1	220
489	Nanoscale imaging of RNA with expansion microscopy. <i>Nature Methods</i> , 2016 , 13, 679-84	21.6	220
488	Improving molecular cancer class discovery through sparse non-negative matrix factorization. <i>Bioinformatics</i> , 2005 , 21, 3970-5	7.2	218
487	Measuring absolute expression with microarrays with a calibrated reference sample and an extended signal intensity range. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 7554-9	11.5	217
486	BIOSAFETY. Safeguarding gene drive experiments in the laboratory. <i>Science</i> , 2015 , 349, 927-9	33.3	215
485	Extensive phosphorylation with overlapping specificity by Mycobacterium tuberculosis serine/threonine protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7521-6	11.5	213
484	RNA-ligand interactions. (I) Magnesium binding sites in yeast tRNAPhe. <i>Nucleic Acids Research</i> , 1977 , 4, 2811-20	20.1	212

483	Cas9 gRNA engineering for genome editing, activation and repression. <i>Nature Methods</i> , 2015 , 12, 1051-4	21.6	210
482	Quantifying DNA-protein interactions by double-stranded DNA arrays. <i>Nature Biotechnology</i> , 1999 , 17, 573-7	44.5	209
481	Programmable transcriptional repression in mycobacteria using an orthogonal CRISPR interference platform. <i>Nature Microbiology</i> , 2017 , 2, 16274	26.6	204
480	Insights into the evolution of longevity from the bowhead whale genome. <i>Cell Reports</i> , 2015 , 10, 112-22	10.6	203
479	The three-dimensional architecture of a bacterial genome and its alteration by genetic perturbation. <i>Molecular Cell</i> , 2011 , 44, 252-64	17.6	203
478	Submicrometre geometrically encoded fluorescent barcodes self-assembled from DNA. <i>Nature Chemistry</i> , 2012 , 4, 832-9	17.6	202
477	Evolution-guided optimization of biosynthetic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17803-8	11.5	197
476	The complete genome and proteome of <i>Mycoplasma mobile</i> . <i>Genome Research</i> , 2004 , 14, 1447-61	9.7	193
475	An enhanced CRISPR repressor for targeted mammalian gene regulation. <i>Nature Methods</i> , 2018 , 15, 611-6	21.6	192
474	The role of replicates for error mitigation in next-generation sequencing. <i>Nature Reviews Genetics</i> , 2014 , 15, 56-62	30.1	192
473	Accurate whole-genome sequencing and haplotyping from 10 to 20 human cells. <i>Nature</i> , 2012 , 487, 190-5	50.4	191
472	The challenges of sequencing by synthesis. <i>Nature Biotechnology</i> , 2009 , 27, 1013-23	44.5	189
471	Scalable gene synthesis by selective amplification of DNA pools from high-fidelity microchips. <i>Nature Biotechnology</i> , 2010 , 28, 1295-9	44.5	188
470	Genome engineering. <i>Nature Biotechnology</i> , 2009 , 27, 1151-62	44.5	188
469	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, 559-67	8.1	186
468	Engineering an allosteric transcription factor to respond to new ligands. <i>Nature Methods</i> , 2016 , 13, 177-83	21.6	184
467	A dynamic programming approach to de novo peptide sequencing via tandem mass spectrometry. <i>Journal of Computational Biology</i> , 2001 , 8, 325-37	1.7	180
466	Genome-scale promoter engineering by coselection MAGE. <i>Nature Methods</i> , 2012 , 9, 591-3	21.6	177

465	Autoantigen discovery with a synthetic human peptidome. <i>Nature Biotechnology</i> , 2011 , 29, 535-41	44.5	172
464	Design, synthesis, and testing toward a 57-codon genome. <i>Science</i> , 2016 , 353, 819-22	33.3	169
463	CRISPR-Cas encoding of a digital movie into the genomes of a population of living bacteria. <i>Nature</i> , 2017 , 547, 345-349	50.4	169
462	Developmental barcoding of whole mouse via homing CRISPR. <i>Science</i> , 2018 , 361,	33.3	168
461	The transition between transcriptional initiation and elongation in E. coli is highly variable and often rate limiting. <i>Molecular Cell</i> , 2006 , 24, 747-757	17.6	168
460	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. <i>Genome Research</i> , 2002 , 12, 701-12	9.7	166
459	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	20.1	160
458	Automated modelling of signal transduction networks. <i>BMC Bioinformatics</i> , 2002 , 3, 34	3.6	159
457	In situ localized amplification and contact replication of many individual DNA molecules. <i>Nucleic Acids Research</i> , 1999 , 27, e34	20.1	159
456	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018 , 173, 649-664.e20	56.2	157
455	Physical principles for scalable neural recording. <i>Frontiers in Computational Neuroscience</i> , 2013 , 7, 137	3.5	155
454	Polony multiplex analysis of gene expression (PMAGE) in mouse hypertrophic cardiomyopathy. <i>Science</i> , 2007 , 316, 1481-4	33.3	155
453	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, 11920-7	11.5	154
452	The Human Ageing Genomic Resources: online databases and tools for biogerontologists. <i>Aging Cell</i> , 2009 , 8, 65-72	9.9	152
451	Synthetic biosensors for precise gene control and real-time monitoring of metabolites. <i>Nucleic Acids Research</i> , 2015 , 43, 7648-60	20.1	151
450	Realizing the potential of synthetic biology. <i>Nature Reviews Molecular Cell Biology</i> , 2014 , 15, 289-94	48.7	151
449	Biosensor-based engineering of biosynthetic pathways. <i>Current Opinion in Biotechnology</i> , 2016 , 42, 84-91	11.4	150
448	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, 4928-33	11.5	148

447	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	6.5	148
446	Neuroscience. The brain activity map. <i>Science</i> , 2013 , 339, 1284-5	33.3	147
445	Nucleic acid memory. <i>Nature Materials</i> , 2016 , 15, 366-70	27	145
444	Conservation of DNA regulatory motifs and discovery of new motifs in microbial genomes. <i>Genome Research</i> , 2000 , 10, 744-57	9.7	145
443	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. <i>Nature Neuroscience</i> , 2017 , 20, 1217-1224	25.5	144
442	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	7.6	144
441	Fluorescent in situ sequencing on polymerase colonies. <i>Analytical Biochemistry</i> , 2003 , 320, 55-65	3.1	144
440	Immuno-SABER enables highly multiplexed and amplified protein imaging in tissues. <i>Nature Biotechnology</i> , 2019 , 37, 1080-1090	44.5	141
439	A microarray-based antibiotic screen identifies a regulatory role for supercoiling in the osmotic stress response of Escherichia coli. <i>Genome Research</i> , 2003 , 13, 206-15	9.7	141
438	Elevated coding mutation rate during the reprogramming of human somatic cells into induced pluripotent stem cells. <i>Stem Cells</i> , 2012 , 30, 435-40	5.8	140
437	GENOME ENGINEERING. The Genome Project-Write. <i>Science</i> , 2016 , 353, 126-7	33.3	138
436	Engineering life: building a fab for biology. <i>Scientific American</i> , 2006 , 294, 44-51	0.5	138
435	Systematic identification of edited microRNAs in the human brain. <i>Genome Research</i> , 2012 , 22, 1533-40	9.7	136
434	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. <i>Nature Methods</i> , 2009 , 6, 613-8	21.6	136
433	The amino-acid mutational spectrum of human genetic disease. <i>Genome Biology</i> , 2003 , 4, R72	18.3	136
432	Evolutionary dynamics of CRISPR gene drives. <i>Science Advances</i> , 2017 , 3, e1601964	14.3	134
431	Selection analyses of insertional mutants using subgenic-resolution arrays. <i>Nature Biotechnology</i> , 2001 , 19, 1060-5	44.5	134
430	Synthetic biology projects in vitro. <i>Genome Research</i> , 2007 , 17, 1-6	9.7	133

429	A sequence-oriented comparison of gene expression measurements across different hybridization-based technologies. <i>Nature Biotechnology</i> , 2006 , 24, 832-40	44.5	133
428	Escherichia coli gene expression responsive to levels of the response regulator EvgA. <i>Journal of Bacteriology</i> , 2002 , 184, 6225-34	3.5	132
427	Rapid neurogenesis through transcriptional activation in human stem cells. <i>Molecular Systems Biology</i> , 2014 , 10, 760	12.2	130
426	Digital genotyping and haplotyping with polymerase colonies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 5926-31	11.5	130
425	Molecular recordings by directed CRISPR spacer acquisition. <i>Science</i> , 2016 , 353, aaf1175	33.3	129
424	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. <i>Virulence</i> , 2010 , 1, 299-303	4.7	128
423	Reprogramming to recover youthful epigenetic information and restore vision. <i>Nature</i> , 2020 , 588, 124-129	39.4	128
422	Computational discovery of sense-antisense transcription in the human and mouse genomes. <i>Genome Biology</i> , 2002 , 3, RESEARCH0044	18.3	127
421	Lambda red recombineering in Escherichia coli occurs through a fully single-stranded intermediate. <i>Genetics</i> , 2010 , 186, 791-9	4	126
420	Rapidly evolving homing CRISPR barcodes. <i>Nature Methods</i> , 2017 , 14, 195-200	21.6	125
419	sgRNA Scorer 2.0: A Species-Independent Model To Predict CRISPR/Cas9 Activity. <i>ACS Synthetic Biology</i> , 2017 , 6, 902-904	5.7	124
418	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, 2388-93	11.5	124
417	Titelbild: Umkodierung des genetischen Codes mit Selenocystein (Angew. Chem. 1/2014). <i>Angewandte Chemie</i> , 2014 , 126, 1-1	3.6	124
416	Genomic analysis of LexA binding reveals the permissive nature of the Escherichia coli genome and identifies unconventional target sites. <i>Genes and Development</i> , 2005 , 19, 2619-30	12.6	122
415	'Fit-for-purpose?' - challenges and opportunities for applications of blockchain technology in the future of healthcare. <i>BMC Medicine</i> , 2019 , 17, 68	11.4	121
414	PEPPeR, a platform for experimental proteomic pattern recognition. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1927-41	7.6	119
413	Yeast oligo-mediated genome engineering (YOGI). <i>ACS Synthetic Biology</i> , 2013 , 2, 741-9	5.7	116
412	Identifying regulatory mechanisms using individual variation reveals key role for chromatin modification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14062-7	11.5	115

411	Global gene expression of <i>Prochlorococcus</i> ecotypes in response to changes in nitrogen availability. <i>Molecular Systems Biology</i> , 2006 , 2, 53	12.2	115
410	A general strategy to construct small molecule biosensors in eukaryotes. <i>ELife</i> , 2015 , 4,	8.9	114
409	Forward Error Correction for DNA Data Storage. <i>Procedia Computer Science</i> , 2016 , 80, 1011-1022	1.6	114
408	Large-scale identification of genetic design strategies using local search. <i>Molecular Systems Biology</i> , 2009 , 5, 296	12.2	113
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67	Photon-directed Multiplexed Enzymatic DNA Synthesis for Molecular Digital Data Storage		2
66	Induced Pluripotent Stem Cell-derived CAR-Macrophage Cells with Antigen-dependent Anti-Cancer Cell Functions for Liquid and Solid Tumors		2
65	Fluorescent in situ sequencing of DNA barcoded antibodies		2
64	Significant abundance of cis configurations of mutations in diploid human genomes		2
63	Highly multiplexed in situ protein imaging with signal amplification by Immuno-SABER		2
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42	An orthogonal differentiation platform for genomically programming stem cells, organoids, and bioprinted tissues		1
41	A DNA nanoscope that identifies and precisely localizes over a hundred unique molecular features with nanometer accuracy		1
40	Enhanced bacterial immunity and mammalian genome editing via RNA polymerase-mediated dislodging of Cas9 from double strand DNA breaks		1
39	Genetic design automation for autonomous formation of multicellular shapes from a single cell progenitor		1
38	Physiological assembly of functionally active 30S ribosomal subunits from in vitro synthesized parts		1
37	Engineering post-translational proofreading to discriminate non-standard amino acids		1
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23	Genome Editing with Desired Mutations (Knockin) with CRISPR in Model Organisms97-109		
22	Genetically Engineered Pig Models for Human Diseases using ZFNs, TALENs and CRISPR/Cas9110-131		
21	Gene Editing to Create Agricultural and Biomedical Swine Models132-149		
20	Generation of New Model Cell Lines using ssODN Knockin Donors and FACS-based Genome Editing150-162		
19	CRISPR Genome Editing in Mice165-180		
18	Genome Engineering Using Sleeping Beauty Transposition in Vertebrates249-269		
17	Application of CRISPR for Pooled, Vector-based Functional Genomic Screening in Mammalian Cell Lines209-222		
16	Targeted Genome Editing Using Nuclease-assisted Vector Integration237-248		

- 15 Inducible CRISPR-based Genome Editing for the Characterization of Cancer Genes 337-357
- 14 Use of the CRISPR/Cas9 System for Genome Editing of Immune System Cells, Defense Against HIV-1 and Cancer Therapies 401-413
- 13 Regulating Human Genome Editing: Negotiating Ethical Concerns Through Science and Policy 454-463
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