George M Church

List of Publications by Year in Descending Order

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	Discovery and validation of human genomic safe harbor sites for gene and cell therapies.. *Cell Reports Methods*, **2022**, 2, 100154		1
589	Targeted intracellular delivery of Cas13 and Cas9 nucleases using bacterial toxin-based platforms.. *Cell Reports*, **2022**, 38, 110476	10.6	1
588	Orthogonally induced differentiation of stem cells for the programmatic patterning of vascularized organoids and bioprinted tissues.. *Nature Biomedical Engineering*, **2022**,	19	5
587	Thirty-Eight Special: George Church Pushes the Biotech Envelope **2022**, 1, 127-132		
586	Towards practical and robust DNA-based data archiving using the yin yang codec system. *Nature Computational Science*, **2022**, 2, 234-242		2
585	New intranasal and injectable gene therapy for healthy life extension.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2121499119	11.5	1
584	Framework for rapid comparison of extracellular vesicle isolation methods. *ELife*, **2021**, 10,	8.9	9
583	MegaGate: A toxin-less gateway molecular cloning tool. *STAR Protocols*, **2021**, 2, 100907	1.4	1
582	Multiplex Single-Molecule Kinetics of Nanopore-Coupled Polymerases. *ACS Nano*, **2021**, 15, 489-502	16.7	3
581	Ultrasensitive Measurement of Both SARS-CoV-2 RNA and Antibodies from Saliva. *Analytical Chemistry*, **2021**, 93, 5365-5370	7.8	9
580	Citizen-centered, auditable and privacy-preserving population genomics. *Nature Computational Science*, **2021**, 1, 192-198		3
579	Lineage barcoding in mice with homing CRISPR. *Nature Protocols*, **2021**, 16, 2088-2108	18.8	0
578	A computer-guided design tool to increase the efficiency of cellular conversions. *Nature Communications*, **2021**, 12, 1659	17.4	6
577	Barcoded oligonucleotides ligated on RNA amplified for multiplexed and parallel in situ analyses. *Nucleic Acids Research*, **2021**, 49, e58	20.1	3
576	High-throughput functional variant screens via in vivo production of single-stranded DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	15
575	Porcine germline genome engineering. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	4
574	Low-N protein engineering with data-efficient deep learning. *Nature Methods*, **2021**, 18, 389-396	21.6	50

573	Enhancing CRISPR-Cas9 gRNA efficiency prediction by data integration and deep learning. *Nature Communications*, **2021**, 12, 3238	17.4	13
572	Measurement of large serine integrase enzymatic characteristics in HEK293 cells reveals variability and influence on downstream reporter expression. *FEBS Journal*, **2021**, 288, 6410-6427	5.7	2
571	L1CAM is not associated with extracellular vesicles in human cerebrospinal fluid or plasma. *Nature Methods*, **2021**, 18, 631-634	21.6	30
570	ABLC Forum: Aspirations for a Fragile Planet. *Industrial Biotechnology*, **2021**, 17, 170-176	1.3	
569	Multisystem inflammatory syndrome in children is driven by zonulin-dependent loss of gut mucosal barrier. *Journal of Clinical Investigation*, **2021**, 131,	15.9	46
568	Porcine genome engineering for xenotransplantation. *Advanced Drug Delivery Reviews*, **2021**, 168, 229-245	13.5	10
567	A comprehensive library of human transcription factors for cell fate engineering. *Nature Biotechnology*, **2021**, 39, 510-519	44.5	40
566	Chromosome-scale, haplotype-resolved assembly of human genomes. *Nature Biotechnology*, **2021**, 39, 309-312	44.5	44
565	Extensive germline genome engineering in pigs. *Nature Biomedical Engineering*, **2021**, 5, 134-143	19	41
564	TBDB: a database of structurally annotated T-box riboswitch:tRNA pairs. *Nucleic Acids Research*, **2021**, 49, D229-D235	20.1	1
563	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. *Science*, **2021**, 371,	33.3	64
562	Characterizing the portability of phage-encoded homologous recombination proteins. *Nature Chemical Biology*, **2021**, 17, 394-402	11.7	10
561	Anomalous COVID-19 tests hinder researchers. *Science*, **2021**, 371, 244-245	33.3	8
560	Engineering adeno-associated viral vectors to evade innate immune and inflammatory responses. *Science Translational Medicine*, **2021**, 13,	17.5	38
559	Deep diversification of an AAV capsid protein by machine learning. *Nature Biotechnology*, **2021**, 39, 691-696	44.5	39
558	Regulation of host and virus genes by neuronal miR-138 favours herpes simplex virus 1 latency. *Nature Microbiology*, **2021**, 6, 682-696	26.6	13
557	In situ genome sequencing resolves DNA sequence and structure in intact biological samples. *Science*, **2021**, 371,	33.3	50
556	Synthetic auxotrophy remains stable after continuous evolution and in coculture with mammalian cells. *Science Advances*, **2021**, 7,	14.3	3

555 Cell therapy strategies for COVID-19: Current approaches and potential applications. *Science Advances*, **2021**, 7, 14.3 3

554 Designing efficient genetic code expansion in Bacillus subtilis to gain biological insights. *Nature Communications*, **2021**, 12, 5429 17.4 0

553 Neuronal Cell-type Engineering by Transcriptional Activation. *Frontiers in Genome Editing*, **2021**, 3, 715697 7.5 1

552 Laboratory-Generated DNA Can Cause Anomalous Pathogen Diagnostic Test Results. *Microbiology Spectrum*, **2021**, 9, e0031321 8.9 3

551 Recording Temporal Signals with Minutes Resolution Using Enzymatic DNA Synthesis. *Journal of the American Chemical Society*, **2021**, 143, 16630-16640 16.4 2

550 An integrated pipeline for mammalian genetic screening.. *Cell Reports Methods*, **2021**, 1, 100082   2

549 Recombineering and MAGE.. *Nature Reviews Methods Primers*, **2021**, 1,   13

548 Algorithms for the selection of fluorescent reporters. *Communications Biology*, **2021**, 4, 118 6.7 2

547 A machine learning toolkit for genetic engineering attribution to facilitate biosecurity. *Nature Communications*, **2020**, 11, 6293 17.4 4

546 Improved bacterial recombineering by parallelized protein discovery. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 13689-13698 11.5 25

545 Korean Genome Project: 1094 Korean personal genomes with clinical information. *Science Advances*, **2020**, 6, eaaz7835 14.3 23

544 A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355 44.5 98

543 Implications of antibody-dependent enhancement of infection for SARS-CoV-2 countermeasures. *Nature Biotechnology*, **2020**, 38, 789-791 44.5 80

542 Release Factor Inhibiting Antimicrobial Peptides Improve Nonstandard Amino Acid Incorporation in Wild-type Bacterial Cells. *ACS Chemical Biology*, **2020**, 15, 1852-1861 4.9 8

541 A Deep Learning Approach to Antibiotic Discovery. *Cell*, **2020**, 180, 688-702.e13 56.2 430

540 KLOTHO and sTGFßR2 treatment counteract the osteoarthritic phenotype developed in a rat model. *Protein and Cell*, **2020**, 11, 219-226 7.2 6

539 The Role of Synthetic Biology in Atmospheric Greenhouse Gas Reduction: Prospects and Challenges. *Biodesign Research*, **2020**, 2020, 1-8 3.1 7

538 Spatial Sequencing: A Perspective. *Journal of Biomolecular Techniques*, **2020**, 31, 44-46 1.1 6

#	Reference		
537	Transparency is key to ethical vaccine research. *Science*, **2020**, 370, 1422-1423	33.3	0
536	Synthetic genomes with altered genetic codes. *Current Opinion in Systems Biology*, **2020**, 24, 32-40	3.2	0
535	Characterization of porcine endogenous retrovirus particles released by the CRISPR/Cas9 inactivated cell line PK15 clone 15. *Xenotransplantation*, **2020**, 27, e12563	2.8	8
534	A haplotype-aware de novo assembly of related individuals using pedigree sequence graph. *Bioinformatics*, **2020**, 36, 2385-2392	7.2	9
533	A deep learning approach to programmable RNA switches. *Nature Communications*, **2020**, 11, 5057	17.4	27
532	Photon-directed multiplexed enzymatic DNA synthesis for molecular digital data storage. *Nature Communications*, **2020**, 11, 5246	17.4	20
531	Targeted intracellular degradation of SARS-CoV-2 via computationally optimized peptide fusions. *Communications Biology*, **2020**, 3, 715	6.7	8
530	Reprogramming to recover youthful epigenetic information and restore vision. *Nature*, **2020**, 588, 124-129	39.4	128
529	Pluripotent stem cell-derived CAR-macrophage cells with antigen-dependent anti-cancer cell functions. *Journal of Hematology and Oncology*, **2020**, 13, 153	22.4	50
528	Robust differentiation of human pluripotent stem cells into endothelial cells via temporal modulation of ETV2 with modified mRNA. *Science Advances*, **2020**, 6, eaba7606	14.3	20
527	The whale shark genome reveals how genomic and physiological properties scale with body size. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 20662-20671	11.5	13
526	3D mapping and accelerated super-resolution imaging of the human genome using in situ sequencing. *Nature Methods*, **2020**, 17, 822-832	21.6	39
525	Benchmarking evolutionary tinkering underlying human-viral molecular mimicry shows multiple host pulmonary-arterial peptides mimicked by SARS-CoV-2. *Cell Death Discovery*, **2020**, 6, 96	6.9	22
524	Reactions to the National Academies/Royal Society Report on. *CRISPR Journal*, **2020**, 3, 332-349	2.5	10
523	Global citizen deliberation on genome editing. *Science*, **2020**, 369, 1435-1437	33.3	27
522	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. *Nature Biotechnology*, **2020**, 38, 1021-1024	44.5	45
521	Core commitments for field trials of gene drive organisms. *Science*, **2020**, 370, 1417-1419	33.3	35
520	Enabling large-scale genome editing at repetitive elements by reducing DNA nicking. *Nucleic Acids Research*, **2020**, 48, 5183-5195	20.1	15

519	Data privacy in the age of personal genomics. *Nature Biotechnology*, **2019**, 37, 1115-1117	44.5	19
518	REST and Neural Gene Network Dysregulation in iPSC Models of Alzheimer's Disease. *Cell Reports*, **2019**, 26, 1112-1127.e9	10.6	96
517	Significant abundance of cis configurations of coding variants in diploid human genomes. *Nucleic Acids Research*, **2019**, 47, 2981-2995	20.1	4
516	Meta-omics analysis of elite athletes identifies a performance-enhancing microbe that functions via lactate metabolism. *Nature Medicine*, **2019**, 25, 1104-1109	50.5	242
515	The Advent of Human Life Data Economics. *Trends in Molecular Medicine*, **2019**, 25, 566-570	11.5	4
514	Terminator-free template-independent enzymatic DNA synthesis for digital information storage. *Nature Communications*, **2019**, 10, 2383	17.4	68
513	'Fit-for-purpose?' - challenges and opportunities for applications of blockchain technology in the future of healthcare. *BMC Medicine*, **2019**, 17, 68	11.4	121
512	Accurate analysis of genuine CRISPR editing events with ampliCan. *Genome Research*, **2019**, 29, 843-847	9.7	25
511	Functional genomics of the rapidly replicating bacterium Vibrio natriegens by CRISPRi. *Nature Microbiology*, **2019**, 4, 1105-1113	26.6	75
510	Evolthon: A community endeavor to evolve lab evolution. *PLoS Biology*, **2019**, 17, e3000182	9.7	8
509	Cell-free Protein Expression Using the Rapidly Growing Bacterium Vibrio natriegens. *Journal of Visualized Experiments*, **2019**,	1.6	8
508	Daisy-chain gene drives for the alteration of local populations. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 8275-8282	11.5	93
507	Review of Scientific Self-Experimentation: Ethics History, Regulation, Scenarios, and Views Among Ethics Committees and Prominent Scientists. *Rejuvenation Research*, **2019**, 22, 31-42	2.6	14
506	Immuno-SABER enables highly multiplexed and amplified protein imaging in tissues. *Nature Biotechnology*, **2019**, 37, 1080-1090	44.5	141
505	Technological challenges and milestones for writing genomes. *Science*, **2019**, 366, 310-312	33.3	22
504	To help aging populations, classify organismal senescence. *Science*, **2019**, 366, 576-578	33.3	24
503	Rapid in vitro production of single-stranded DNA. *Nucleic Acids Research*, **2019**, 47, 11956-11962	20.1	12
502	A single combination gene therapy treats multiple age-related diseases. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 23505-23511	11.5	26

501	Circumventing cellular immunity by miR142-mediated regulation sufficiently supports rAAV-delivered OVA expression without activating humoral immunity. *JCI Insight*, **2019**, 5,	9.9	14
500	Challenges and opportunities of machine-guided capsid engineering for gene therapy. *Cell & Gene Therapy Insights*, **2019**, 5, 523-536	2.3	4
499	Comprehensive AAV capsid fitness landscape reveals a viral gene and enables machine-guided design. *Science*, **2019**, 366, 1139-1143	33.3	101
498	Regulation of lifespan by neural excitation and REST. *Nature*, **2019**, 574, 359-364	50.4	71
497	Unified rational protein engineering with sequence-based deep representation learning. *Nature Methods*, **2019**, 16, 1315-1322	21.6	234
496	Crystal structure of the RedβC-terminal domain in complex with λExonuclease reveals an unexpected homology with λOrf and an interaction with Escherichia coli single stranded DNA binding protein. *Nucleic Acids Research*, **2019**, 47, 1950-1963	20.1	12
495	Material solutions for delivery of CRISPR/Cas-based genome editing tools: Current status and future outlook. *Materials Today*, **2019**, 26, 40-66	21.8	58
494	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. *Cell*, **2018**, 173, 649-664.e20	56.2	157
493	Adaptive evolution of genomically recoded. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 3090-3095	11.5	53
492	Spontaneous CRISPR loci generation in vivo by non-canonical spacer integration. *Nature Microbiology*, **2018**, 3, 310-318	26.6	15
491	Vom Design der Moleküle des Lebens zum Design von Leben: Zukünftige Anwendungen von DNA-Technologien. *Angewandte Chemie*, **2018**, 130, 4395-4411	3.6	5
490	From Designing the Molecules of Life to Designing Life: Future Applications Derived from Advances in DNA Technologies. *Angewandte Chemie - International Edition*, **2018**, 57, 4313-4328	16.4	21
489	Efficient in situ barcode sequencing using padlock probe-based BaristaSeq. *Nucleic Acids Research*, **2018**, 46, e22	20.1	53
488	Engineering posttranslational proofreading to discriminate nonstandard amino acids. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 619-624	11.5	26
487	Simultaneous Discovery of Cell-Free DNA and the Nucleosome Ladder. *Genetics*, **2018**, 209, 27-29	4	6
486	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nature Methods*, **2018**, 15, 236-237	27.6	23
485	Precise Cas9 targeting enables genomic mutation prevention. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 3669-3673	11.5	18
484	A CRISPR-Cas9-based gene drive platform for genetic interaction analysis in Candida albicans. *Nature Microbiology*, **2018**, 3, 73-82	26.6	95

483	Heterologous erythromycin production across strain and plasmid construction. *Biotechnology Progress*, **2018**, 34, 271-276	2.8	24
482	Characterizing Protein Kinase Substrate Specificity Using the Proteomic Peptide Library (ProPeL) Approach. *Current Protocols in Chemical Biology*, **2018**, 10, e38	1.8	9
481	An enhanced CRISPR repressor for targeted mammalian gene regulation. *Nature Methods*, **2018**, 15, 611-616	2.6	192
480	Directed differentiation of human induced pluripotent stem cells into mature kidney podocytes and establishment of a Glomerulus Chip. *Nature Protocols*, **2018**, 13, 1662-1685	18.8	72
479	Enabling multiplexed testing of pooled donor cells through whole-genome sequencing. *Genome Medicine*, **2018**, 10, 31	14.4	4
478	Codon usage of highly expressed genes affects proteome-wide translation efficiency. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E4940-E4949	11.5	81
477	High-resolution mapping of DNA polymerase fidelity using nucleotide imbalances and next-generation sequencing. *Nucleic Acids Research*, **2018**, 46, e78	20.1	9
476	Biosensor libraries harness large classes of binding domains for construction of allosteric transcriptional regulators. *Nature Communications*, **2018**, 9, 3101	17.4	32
475	Inter-homologue repair in fertilized human eggs?. *Nature*, **2018**, 560, E5-E7	50.4	55
474	Developmental barcoding of whole mouse via homing CRISPR. *Science*, **2018**, 361,	33.3	168
473	Building Capacity for a Global Genome Editing Observatory: Conceptual Challenges. *Trends in Biotechnology*, **2018**, 36, 639-641	15.1	18
472	Building Capacity for a Global Genome Editing Observatory: Institutional Design. *Trends in Biotechnology*, **2018**, 36, 741-743	15.1	16
471	The Future of Multiplexed Eukaryotic Genome Engineering. *ACS Chemical Biology*, **2018**, 13, 313-325	4.9	27
470	CRISPR Guide RNA Cloning for Mammalian Systems. *Journal of Visualized Experiments*, **2018**,	1.6	3
469	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 11096-11101	11.5	28
468	CRISPR-C: circularization of genes and chromosome by CRISPR in human cells. *Nucleic Acids Research*, **2018**, 46, e131	20.1	23
467	Establishing a Cell-Free Vibrio natriegens Expression System. *ACS Synthetic Biology*, **2018**, 7, 2475-2479	5.7	44
466	High-throughput creation and functional profiling of DNA sequence variant libraries using CRISPR-Cas9 in yeast. *Nature Biotechnology*, **2018**, 36, 540-546	44.5	53

465	Enhanced Bacterial Immunity and Mammalian Genome Editing via RNA-Polymerase-Mediated Dislodging of Cas9 from Double-Strand DNA Breaks. *Molecular Cell*, **2018**, 71, 42-55.e8	17.6	62
464	Current CRISPR gene drive systems are likely to be highly invasive in wild populations. *ELife*, **2018**, 7,	8.9	96
463	Cushing's syndrome mutant PKA exhibits altered substrate specificity. *FEBS Letters*, **2017**, 591, 459-467	3.8	11
462	sgRNA Scorer 2.0: A Species-Independent Model To Predict CRISPR/Cas9 Activity. *ACS Synthetic Biology*, **2017**, 6, 902-904	5.7	124
461	Programmable transcriptional repression in mycobacteria using an orthogonal CRISPR interference platform. *Nature Microbiology*, **2017**, 2, 16274	26.6	204
460	Mature induced-pluripotent-stem-cell-derived human podocytes reconstitute kidney glomerular-capillary-wall function on a chip. *Nature Biomedical Engineering*, **2017**, 1,	19	253
459	Rapidly evolving homing CRISPR barcodes. *Nature Methods*, **2017**, 14, 195-200	21.6	125
458	Towards in situ sequencing for life detection **2017**,		7
457	Dissecting limiting factors of the Protein synthesis Using Recombinant Elements (PURE) system. *Translation*, **2017**, 5, e1327006		16
456	An unbiased index to quantify participant's phenotypic contribution to an open-access cohort. *Scientific Reports*, **2017**, 7, 46148	4.9	1
455	The promise of organ and tissue preservation to transform medicine. *Nature Biotechnology*, **2017**, 35, 530-542	44.5	246
454	Optimizing complex phenotypes through model-guided multiplex genome engineering. *Genome Biology*, **2017**, 18, 100	18.3	18
453	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. *Human Mutation*, **2017**, 38, 1266-1276	4.7	9
452	Cogenerating Synthetic Parts toward a Self-Replicating System. *ACS Synthetic Biology*, **2017**, 6, 1327-1336	5.7	31
451	Evolutionary dynamics of CRISPR gene drives. *Science Advances*, **2017**, 3, e1601964	14.3	134
450	Efficient, footprint-free human iPSC genome editing by consolidation of Cas9/CRISPR and piggyBac technologies. *Nature Protocols*, **2017**, 12, 88-103	18.8	68
449	Editing the Human Genome: Progress and Controversies **2017**, 1, 4-11	0.9	
448	DNA sequencing at 40: past, present and future. *Nature*, **2017**, 550, 345-353	50.4	486

447	Extracellular Vesicle Isolation and Analysis by Western Blotting. *Methods in Molecular Biology*, **2017**, 1660, 143-152	1.4	48
446	Imaging of Isolated Extracellular Vesicles Using Fluorescence Microscopy. *Methods in Molecular Biology*, **2017**, 1660, 233-241	1.4	14
445	Beyond editing to writing large genomes. *Nature Reviews Genetics*, **2017**, 18, 749-760	30.1	35
444	Rapid Sequential in Situ Multiplexing with DNA Exchange Imaging in Neuronal Cells and Tissues. *Nano Letters*, **2017**, 17, 6131-6139	11.5	85
443	Rates, distribution and implications of postzygotic mosaic mutations in autism spectrum disorder. *Nature Neuroscience*, **2017**, 20, 1217-1224	25.5	144
442	Inactivation of porcine endogenous retrovirus in pigs using CRISPR-Cas9. *Science*, **2017**, 357, 1303-1307	33.3	395
441	Challenges and recommendations for epigenomics in precision health. *Nature Biotechnology*, **2017**, 35, 1128-1132	44.5	16
440	Compelling Reasons for Repairing Human Germlines. *New England Journal of Medicine*, **2017**, 377, 1909-1911	59.1	25
439	CRISPR-Cas encoding of a digital movie into the genomes of a population of living bacteria. *Nature*, **2017**, 547, 345-349	50.4	169
438	Millstone: software for multiplex microbial genome analysis and engineering. *Genome Biology*, **2017**, 18, 101	18.3	5
437	Scalable Device for Automated Microbial Electroporation in a Digital Microfluidic Platform. *ACS Synthetic Biology*, **2017**, 6, 1701-1709	5.7	25
436	A systematic comparison of error correction enzymes by next-generation sequencing. *Nucleic Acids Research*, **2017**, 45, 9206-9217	20.1	15
435	PERV inactivation is necessary to guarantee absence of pig-to-patient PERVs transmission in xenotransplantation. *Xenotransplantation*, **2017**, 24, e12366	2.8	17
434	Décrypter le cerveau **2017**, N° 93, 14-21		
433	Addressing the ethical issues raised by synthetic human entities with embryo-like features. *ELife*, **2017**, 6,	8.9	55
432	Nucleotide-time alignment for molecular recorders. *PLoS Computational Biology*, **2017**, 13, e1005483	5	
431	Overcoming Challenges in Engineering the Genetic Code. *Journal of Molecular Biology*, **2016**, 428, 1004-21	5.5	40
430	CRISPR-Cas9 System: Opportunities and Concerns. *Clinical Chemistry*, **2016**, 62, 1304-11	5.5	5

429	Design, synthesis, and testing toward a 57-codon genome. *Science*, **2016**, 353, 819-22	33.3	169
428	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. *Nature Communications*, **2016**, 7, 13637	17.4	38
427	**2016**,		6
426	Extensive sequencing of seven human genomes to characterize benchmark reference materials. *Scientific Data*, **2016**, 3, 160025	8.2	345
425	Engineering and optimising deaminase fusions for genome editing. *Nature Communications*, **2016**, 7, 13330	17.4	46
424	Molecular recordings by directed CRISPR spacer acquisition. *Science*, **2016**, 353, aaf1175	33.3	129
423	GENOME ENGINEERING. The Genome Project-Write. *Science*, **2016**, 353, 126-7	33.3	138
422	Biosensor-based engineering of biosynthetic pathways. *Current Opinion in Biotechnology*, **2016**, 42, 84-91	11.4	150
421	Nucleic acid memory. *Nature Materials*, **2016**, 15, 366-70	27	145
420	Multiplexed Engineering in Biology. *Trends in Biotechnology*, **2016**, 34, 198-206	15.1	34
419	Genetically encoded sensors enable real-time observation of metabolite production. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 2388-93	11.5	124
418	In vivo gene editing in dystrophic mouse muscle and muscle stem cells. *Science*, **2016**, 351, 407-411	33.3	711
417	Engineering an allosteric transcription factor to respond to new ligands. *Nature Methods*, **2016**, 13, 177-83	21.6	184
416	Tools for the Microbiome: Nano and Beyond. *ACS Nano*, **2016**, 10, 6-37	16.7	99
415	Efficient Reassignment of a Frequent Serine Codon in Wild-Type Escherichia coli. *ACS Synthetic Biology*, **2016**, 5, 163-71	5.7	30
414	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. *PLoS ONE*, **2016**, 11, e0147651	3.7	10
413	Forward Error Correction for DNA Data Storage. *Procedia Computer Science*, **2016**, 80, 1011-1022	1.6	114
412	Next stop for the CRISPR revolution: RNA-guided epigenetic regulators. *FEBS Journal*, **2016**, 283, 3181-93	5.7	52

411	Nanoscale imaging of RNA with expansion microscopy. *Nature Methods*, **2016**, 13, 679-84	21.6	220
410	Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. *BMC Evolutionary Biology*, **2016**, 16, 230	3	25
409	Comparison of Cas9 activators in multiple species. *Nature Methods*, **2016**, 13, 563-567	21.6	308
408	Real-time single-molecule electronic DNA sequencing by synthesis using polymer-tagged nucleotides on a nanopore array. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 5233-8	11.5	86
407	Performance of optimized noncanonical amino acid mutagenesis systems in the absence of release factor 1. *Molecular BioSystems*, **2016**, 12, 1746-9		26
406	Characterizing Cas9 Protospacer-Adjacent Motifs with High-Throughput Sequencing of Library Depletion Experiments. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	2
405	Characterization of Cas9-Guide RNA Orthologs. *Cold Spring Harbor Protocols*, **2016**, 2016,	1.2	10
404	A multifunctional AAV-CRISPR-Cas9 and its host response. *Nature Methods*, **2016**, 13, 868-74	21.6	359
403	Emergent rules for codon choice elucidated by editing rare arginine codons in Escherichia coli. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E5588-97	11.5	30
402	Design and characterization of a nanopore-coupled polymerase for single-molecule DNA sequencing by synthesis on an electrode array. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E6749-E6756	11.5	37
401	The whole genome sequences and experimentally phased haplotypes of over 100 personal genomes. *GigaScience*, **2016**, 5, 42	7.6	15
400	Biocontainment of genetically modified organisms by synthetic protein design. *Nature*, **2015**, 518, 55-60	50.4	255
399	BIOSAFETY. Safeguarding gene drive experiments in the laboratory. *Science*, **2015**, 349, 927-9	33.3	215
398	Preserved DNA Damage Checkpoint Pathway Protects against Complications in Long-Standing Type 1 Diabetes. *Cell Metabolism*, **2015**, 22, 239-52	24.6	34
397	Unraveling CRISPR-Cas9 genome engineering parameters via a library-on-library approach. *Nature Methods*, **2015**, 12, 823-6	21.6	265
396	Complete Genome Sequences of T4-Like Bacteriophages RB3, RB5, RB6, RB7, RB9, RB10, RB27, RB33, RB55, RB59, and RB68. *Genome Announcements*, **2015**, 3,		8
395	Biotechnology. A prudent path forward for genomic engineering and germline gene modification. *Science*, **2015**, 348, 36-8	33.3	413
394	Highly efficient Cas9-mediated transcriptional programming. *Nature Methods*, **2015**, 12, 326-8	21.6	856

393	Neutralizing antibodies against West Nile virus identified directly from human B cells by single-cell analysis and next generation sequencing. *Integrative Biology (United Kingdom)*, **2015**, 7, 1587-97	3.7	57
392	A National Network of Neurotechnology Centers for the BRAIN Initiative. *Neuron*, **2015**, 88, 445-8	13.9	12
391	Improving microbial fitness in the mammalian gut by in vivo temporal functional metagenomics. *Molecular Systems Biology*, **2015**, 11, 788	12.2	22
390	Genome-wide inactivation of porcine endogenous retroviruses (PERVs). *Science*, **2015**, 350, 1101-4	33.3	394
389	HEART DISEASE. Titin mutations in iPS cells define sarcomere insufficiency as a cause of dilated cardiomyopathy. *Science*, **2015**, 349, 982-6	33.3	379
388	Synthetic biosensors for precise gene control and real-time monitoring of metabolites. *Nucleic Acids Research*, **2015**, 43, 7648-60	20.1	151
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