# Shamil R Sunyaev

## 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.

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|---|---|---|---|
| 145 papers | 43,401 citations | 66 h-index | 161 g-index |
| 161 ext. papers | 51,345 ext. citations | 17.9 avg, IF | 6.83 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 145 | A method and server for predicting damaging missense mutations. *Nature Methods*, **2010**, 7, 248-9 | 21.6 | 9235 |
| 144 | Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816 | 50.4 | 4121 |
| 143 | Integrative analysis of 111 reference human epigenomes. *Nature*, **2015**, 518, 317-30 | 50.4 | 3849 |
| 142 | Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, **2013**, 499, 214-218 | 50.4 | 3616 |
| 141 | Systematic localization of common disease-associated variation in regulatory DNA. *Science*, **2012**, 337, 1190-5 | 33.3 | 2262 |
| 140 | The accessible chromatin landscape of the human genome. *Nature*, **2012**, 489, 75-82 | 50.4 | 1900 |
| 139 | Human non-synonymous SNPs: server and survey. *Nucleic Acids Research*, **2002**, 30, 3894-900 | 20.1 | 1767 |
| 138 | Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature*, **2012**, 485, 242-5 | 50.4 | 1300 |
| 137 | Evolution and functional impact of rare coding variation from deep sequencing of human exomes. *Science*, **2012**, 337, 64-9 | 33.3 | 1280 |
| 136 | The mystery of missing heritability: Genetic interactions create phantom heritability. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 1193-8 | 11.5 | 1064 |
| 135 | Pooled association tests for rare variants in exon-resequencing studies. *American Journal of Human Genetics*, **2010**, 86, 832-8 | 11 | 615 |
| 134 | Genomic variation landscape of the human gut microbiome. *Nature*, **2013**, 493, 45-50 | 50.4 | 571 |
| 133 | Charting the proteomes of organisms with unsequenced genomes by MALDI-quadrupole time-of-flight mass spectrometry and BLAST homology searching. *Analytical Chemistry*, **2001**, 73, 1917-26 | 7.8 | 530 |
| 132 | Assessing the evolutionary impact of amino acid mutations in the human genome. *PLoS Genetics*, **2008**, 4, e1000083 | 6 | 473 |
| 131 | Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. *Nature*, **2015**, 518, 102-6 | 50.4 | 463 |
| 130 | Most rare missense alleles are deleterious in humans: implications for complex disease and association studies. *American Journal of Human Genetics*, **2007**, 80, 727-39 | 11 | 461 |
| 129 | Searching for missing heritability: designing rare variant association studies. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E455-64 | 11.5 | 437 |

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|---|---|---|---|
| 128 | Genome sequencing reveals insights into physiology and longevity of the naked mole rat. *Nature*, **2011**, 479, 223-7 | 50.4 | 410 |
| 127 | Cell-of-origin chromatin organization shapes the mutational landscape of cancer. *Nature*, **2015**, 518, 360-364 | 50.4 | 344 |
| 126 | Widespread macromolecular interaction perturbations in human genetic disorders. *Cell*, **2015**, 161, 647-660 | 36.2 | 343 |
| 125 | Exome sequencing and the genetic basis of complex traits. *Nature Genetics*, **2012**, 44, 623-30 | 36.3 | 303 |
| 124 | Proportionally more deleterious genetic variation in European than in African populations. *Nature*, **2008**, 451, 994-7 | 50.4 | 299 |
| 123 | Towards a structural basis of human non-synonymous single nucleotide polymorphisms. *Trends in Genetics*, **2000**, 16, 198-200 | 8.5 | 293 |
| 122 | Human mutation rate associated with DNA replication timing. *Nature Genetics*, **2009**, 41, 393-5 | 36.3 | 288 |
| 121 | Genome-wide patterns and properties of de novo mutations in humans. *Nature Genetics*, **2015**, 47, 822-826 | 36.3 | 267 |
| 120 | Shifting paradigm of association studies: value of rare single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2008**, 82, 100-12 | 11 | 255 |
| 119 | Dobzhansky-Muller incompatibilities in protein evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 14878-83 | 11.5 | 229 |
| 118 | A universal trend of amino acid gain and loss in protein evolution. *Nature*, **2005**, 433, 633-8 | 50.4 | 212 |
| 117 | Impact of deleterious passenger mutations on cancer progression. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 2910-5 | 11.5 | 210 |
| 116 | Sequencing studies in human genetics: design and interpretation. *Nature Reviews Genetics*, **2013**, 14, 460-70 | 30.1 | 200 |
| 115 | Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genetics*, **2012**, 44, 631-5 | 36.3 | 184 |
| 114 | Medical sequencing at the extremes of human body mass. *American Journal of Human Genetics*, **2007**, 80, 779-91 | 11 | 180 |
| 113 | Differential relationship of DNA replication timing to different forms of human mutation and variation. *American Journal of Human Genetics*, **2012**, 91, 1033-40 | 11 | 172 |
| 112 | Increase of functional diversity by alternative splicing. *Trends in Genetics*, **2003**, 19, 124-8 | 8.5 | 171 |
| 111 | Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. *ELife*, **2019**, 8, | 8.9 | 166 |

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| 110 | Gain-of-function mutations in the mechanically activated ion channel PIEZO2 cause a subtype of Distal Arthrogryposis. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 4667-72 | 11.5 | 151 |
| 109 | Power of deep, all-exon resequencing for discovery of human trait genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 3871-6 | 11.5 | 139 |
| 108 | Large-scale identification and evolution indexing of tyrosine phosphorylation sites from murine brain. *Journal of Proteome Research*, **2008**, 7, 311-8 | 5.6 | 139 |
| 107 | A model for statistical significance of local similarities in structure. *Journal of Molecular Biology*, **2003**, 326, 1307-16 | 6.5 | 139 |
| 106 | The interface of protein structure, protein biophysics, and molecular evolution. *Protein Science*, **2012**, 21, 769-85 | 6.3 | 136 |
| 105 | The power and the limitations of cross-species protein identification by mass spectrometry-driven sequence similarity searches. *Molecular and Cellular Proteomics*, **2004**, 3, 238-49 | 7.6 | 133 |
| 104 | No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. *Nature Genetics*, **2015**, 47, 126-31 | 36.3 | 129 |
| 103 | Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. *Nature Genetics*, **2017**, 49, 600-605 | 36.3 | 124 |
| 102 | Evaluating empirical bounds on complex disease genetic architecture. *Nature Genetics*, **2013**, 45, 1418-27 | 36.3 | 120 |
| 101 | Metabolites: a helping hand for pathway evolution?. *Trends in Biochemical Sciences*, **2003**, 28, 336-41 | 10.3 | 117 |
| 100 | Progressive multifocal leukoencephalopathy (PML) development is associated with mutations in JC virus capsid protein VP1 that change its receptor specificity. *Journal of Infectious Diseases*, **2011**, 204, 103-14 | 7 | 113 |
| 99 | Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. *Nature Genetics*, **2015**, 47, 1085-90 | 36.3 | 112 |
| 98 | Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. *American Journal of Human Genetics*, **2016**, 98, 1051-1066 | 11 | 107 |
| 97 | MultiTag: multiple error-tolerant sequence tag search for the sequence-similarity identification of proteins by mass spectrometry. *Analytical Chemistry*, **2003**, 75, 1307-15 | 7.8 | 106 |
| 96 | Computational and statistical approaches to analyzing variants identified by exome sequencing. *Genome Biology*, **2011**, 12, 227 | 18.3 | 104 |
| 95 | Mutation mapping and identification by whole-genome sequencing. *Genome Research*, **2012**, 22, 1541-8 | 9.7 | 101 |
| 94 | Homology-based fold predictions for Mycoplasma genitalium proteins. *Journal of Molecular Biology* , **1998**, 280, 323-6 | 6.5 | 100 |
| 93 | Adaptive mutations in the JC virus protein capsid are associated with progressive multifocal leukoencephalopathy (PML). *PLoS Genetics*, **2009**, 5, e1000368 | 6 | 99 |

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|---|---|---|---|
| 92 | Sequence similarity-driven proteomics in organisms with unknown genomes by LC-MS/MS and automated de novo sequencing. *Proteomics*, **2007**, 7, 2318-29 | 4.8 | 93 |
| 91 | Reduced local mutation density in regulatory DNA of cancer genomes is linked to DNA repair. *Nature Biotechnology*, **2014**, 32, 71-5 | 44.5 | 92 |
| 90 | A limited role for balancing selection. *Trends in Genetics*, **2005**, 21, 30-2 | 8.5 | 92 |
| 89 | Estimating the selective effects of heterozygous protein-truncating variants from human exome data. *Nature Genetics*, **2017**, 49, 806-810 | 36.3 | 84 |
| 88 | Identification of cis-suppression of human disease mutations by comparative genomics. *Nature*, **2015**, 524, 225-9 | 50.4 | 84 |
| 87 | Widely distributed noncoding purifying selection in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12410-5 | 11.5 | 75 |
| 86 | Rare, low-frequency, and common variants in the protein-coding sequence of biological candidate genes from GWASs contribute to risk of rheumatoid arthritis. *American Journal of Human Genetics*, **2013**, 92, 15-27 | 11 | 72 |
| 85 | SNP frequencies in human genes an excess of rare alleles and differing modes of selection. *Trends in Genetics*, **2000**, 16, 335-7 | 8.5 | 72 |
| 84 | Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. *Nature Genetics*, **2018**, 50, 1600-1607 | 36.3 | 72 |
| 83 | Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 194, 886-897 | 10.2 | 70 |
| 82 | Calibration of multiple in silico tools for predicting pathogenicity of mismatch repair gene missense substitutions. *Human Mutation*, **2013**, 34, 255-65 | 4.7 | 70 |
| 81 | Protein identification pipeline for the homology-driven proteomics. *Journal of Proteomics*, **2008**, 71, 346-56 | 3.9 | 70 |
| 80 | Small fitness effect of mutations in highly conserved non-coding regions. *Human Molecular Genetics* , **2005**, 14, 2221-9 | 5.6 | 67 |
| 79 | Homology-based functional proteomics by mass spectrometry: application to the Xenopus microtubule-associated proteome. *Proteomics*, **2004**, 4, 2707-21 | 4.8 | 64 |
| 78 | Identification of cancer driver genes based on nucleotide context. *Nature Genetics*, **2020**, 52, 208-218 | 36.3 | 64 |
| 77 | Development and validation of a computational method for assessment of missense variants in hypertrophic cardiomyopathy. *American Journal of Human Genetics*, **2011**, 88, 183-92 | 11 | 60 |
| 76 | Multiplex padlock targeted sequencing reveals human hypermutable CpG variations. *Genome Research*, **2009**, 19, 1606-15 | 9.7 | 59 |
| 75 | Positive selection at sites of multiple amino acid replacements since rat-mouse divergence. *Nature*, **2004**, 429, 558-62 | 50.4 | 58 |

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| 74 | APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. *Cell Reports*, **2015**, 13, 1103-1109 | 10.6 | 57 |
| 73 | Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. *American Journal of Human Genetics*, **2015**, 97, 775-89 | 11 | 56 |
| 72 | Human allelic variation: perspective from protein function, structure, and evolution. *Current Opinion in Structural Biology*, **2010**, 20, 342-50 | 8.1 | 56 |
| 71 | Analysis of sequence conservation at nucleotide resolution. *PLoS Computational Biology*, **2007**, 3, e254 | 5 | 55 |
| 70 | Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. *Nature Communications*, **2019**, 10, 790 | 17.4 | 55 |
| 69 | Negative selection in humans and fruit flies involves synergistic epistasis. *Science*, **2017**, 356, 539-542 | 33.3 | 53 |
| 68 | Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. *PLoS Genetics*, **2015**, 11, e1005436 | 6 | 53 |
| 67 | GWAS for quantitative resistance phenotypes in Mycobacterium tuberculosis reveals resistance genes and regulatory regions. *Nature Communications*, **2019**, 10, 2128 | 17.4 | 52 |
| 66 | Deleterious alleles in the human genome are on average younger than neutral alleles of the same frequency. *PLoS Genetics*, **2013**, 9, e1003301 | 6 | 49 |
| 65 | Genes with monoallelic expression contribute disproportionately to genetic diversity in humans. *Nature Genetics*, **2016**, 48, 231-237 | 36.3 | 47 |
| 64 | Bayesian inference of negative and positive selection in human cancers. *Nature Genetics*, **2017**, 49, 1785-1788 | 36.3 | 46 |
| 63 | Inferring causality and functional significance of human coding DNA variants. *Human Molecular Genetics*, **2012**, 21, R10-7 | 5.6 | 46 |
| 62 | Evolutionary constraints in conserved nongenic sequences of mammals. *Genome Research*, **2005**, 15, 1373-8 | 9.7 | 44 |
| 61 | Indel-based evolutionary distance and mouse-human divergence. *Genome Research*, **2004**, 14, 1610-6 | 9.7 | 42 |
| 60 | Prediction of nonsynonymous single nucleotide polymorphisms in human disease-associated genes. *Journal of Molecular Medicine*, **1999**, 77, 754-60 | 5.5 | 38 |
| 59 | Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. *American Journal of Respiratory Cell and Molecular Biology*, **2018**, 58, 391-401 | 5.7 | 37 |
| 58 | Separating the wheat from the chaff: unbiased filtering of background tandem mass spectra improves protein identification. *Journal of Proteome Research*, **2008**, 7, 3382-95 | 5.6 | 35 |
| 57 | Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. *Lancet Haematology,the*, **2018**, 5, e241-e251 | 14.6 | 35 |

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| 56 | Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nature Genetics*, **2020**, 52, 969-983 | 36.3 | 33 |
| 55 | Common single-nucleotide polymorphisms act in concert to affect plasma levels of high-density lipoprotein cholesterol. *American Journal of Human Genetics*, **2007**, 81, 1298-303 | 11 | 32 |
| 54 | Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. *Nature Genetics*, **2019**, 51, 1308-1314 | 36.3 | 31 |
| 53 | Excess of Deleterious Mutations around HLA Genes Reveals Evolutionary Cost of Balancing Selection. *Molecular Biology and Evolution*, **2016**, 33, 2555-64 | 8.3 | 29 |
| 52 | Triplet repeat length bias and variation in the human transcriptome. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 17095-100 | 11.5 | 27 |
| 51 | Hypermutable non-synonymous sites are under stronger negative selection. *PLoS Genetics*, **2008**, 4, e1000281 | 6 | 26 |
| 50 | Impact of selection, mutation rate and genetic drift on human genetic variation. *Human Molecular Genetics*, **2003**, 12, 3325-30 | 5.6 | 23 |
| 49 | Balancing selection on a regulatory region exhibiting ancient variation that predates human-neandertal divergence. *PLoS Genetics*, **2013**, 9, e1003404 | 6 | 21 |
| 48 | Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. *Human Molecular Genetics*, **2019**, 28, 675-687 | 5.6 | 20 |
| 47 | Error-tolerant EST database searches by tandem mass spectrometry and multiTag software. *Proteomics*, **2005**, 5, 4118-22 | 4.8 | 19 |
| 46 | Signals of polygenic adaptation on height have been overestimated due to uncorrected population structure in genome-wide association studies | | 19 |
| 45 | Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits | | 18 |
| 44 | Error-prone bypass of DNA lesions during lagging-strand replication is a common source of germline and cancer mutations. *Nature Genetics*, **2019**, 51, 36-41 | 36.3 | 17 |
| 43 | Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. *American Journal of Human Genetics*, **2020**, 107, 46-59 | 11 | 16 |
| 42 | Population-specific causal disease effect sizes in functionally important regions impacted by selection. *Nature Communications*, **2021**, 12, 1098 | 17.4 | 16 |
| 41 | Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. *Human Molecular Genetics*, **2016**, 25, 5244-5253 | 5.6 | 15 |
| 40 | An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease gene discovery. *Npj Genomic Medicine*, **2018**, 3, 21 | 6.2 | 15 |
| 39 | Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. *PLoS Genetics*, **2019**, 15, e1007739 | 6 | 14 |

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| 38 | Identifying DNase I hypersensitive sites as driver distal regulatory elements in breast cancer. *Nature Communications*, **2017**, 8, 436 | 17.4 | 14 |
| 37 | From analysis of protein structural alignments toward a novel approach to align protein sequences. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 569-82 | 4.2 | 13 |
| 36 | Increasing Generality and Power of Rare-Variant Tests by Utilizing Extended Pedigrees. *American Journal of Human Genetics*, **2016**, 99, 846-859 | 11 | 13 |
| 35 | Evidence for secondary-variant genetic burden and non-random distribution across biological modules in a recessive ciliopathy. *Nature Genetics*, **2020**, 52, 1145-1150 | 36.3 | 12 |
| 34 | PINES: phenotype-informed tissue weighting improves prediction of pathogenic noncoding variants. *Genome Biology*, **2018**, 19, 173 | 18.3 | 12 |
| 33 | Fine-Scale Haplotype Structure Reveals Strong Signatures of Positive Selection in a Recombining Bacterial Pathogen. *Molecular Biology and Evolution*, **2020**, 37, 417-428 | 8.3 | 11 |
| 32 | Individual variation in protein-coding sequences of human genome. *Advances in Protein Chemistry*, **2000**, 54, 409-37 | | 10 |
| 31 | Applicability of the Mutation-Selection Balance Model to Population Genetics of Heterozygous Protein-Truncating Variants in Humans. *Molecular Biology and Evolution*, **2019**, 36, 1701-1710 | 8.3 | 9 |
| 30 | Inherited CHST11/MIR3922 deletion is associated with a novel recessive syndrome presenting with skeletal malformation and malignant lymphoproliferative disease. *Molecular Genetics & Genomic Medicine*, **2015**, 3, 413-23 | 2.3 | 8 |
| 29 | SNP2RFLP: a computational tool to facilitate genetic mapping using benchtop analysis of SNPs. *Mammalian Genome*, **2008**, 19, 687-90 | 3.2 | 8 |
| 28 | Population sequencing data reveal a compendium of mutational processes in the human germ line. *Science*, **2021**, 373, 1030-1035 | 33.3 | 7 |
| 27 | Maintenance of Adaptive Dynamics and No Detectable Load in a Range-Edge Outcrossing Plant Population. *Molecular Biology and Evolution*, **2021**, 38, 1820-1836 | 8.3 | 6 |
| 26 | StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants | | 5 |
| 25 | Lessons from the CAGI-4 Hopkins clinical panel challenge. *Human Mutation*, **2017**, 38, 1155-1168 | 4.7 | 4 |
| 24 | An argument for early genomic sequencing in atypical cases: a WISP3 variant leads to diagnosis of progressive pseudorheumatoid arthropathy of childhood. *Rheumatology*, **2016**, 55, 586-9 | 3.9 | 4 |
| 23 | StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants.. *American Journal of Human Genetics*, **2022**, | 11 | 4 |
| 22 | Population sequencing data reveal a compendium of mutational processes in human germline | | 4 |
| 21 | Population-specific causal disease effect sizes in functionally important regions impacted by selection | | 4 |

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| 20 | Polygenic adaptation of rosette growth in Arabidopsis thaliana. *PLoS Genetics*, **2021**, 17, e1008748 | 6 | 4 |
| 19 | Unexpected variability of allelic imbalance estimates from RNA sequencing | | 3 |
| 18 | Non-parametric polygenic risk prediction using partitioned GWAS summary statistics | | 3 |
| 17 | Maintenance of adaptive dynamics and no detectable load in a range-edge out-crossing plant population | | 2 |
| 16 | The origin of human mutation in light of genomic data. *Nature Reviews Genetics*, **2021**, 22, 672-686 | 30.1 | 2 |
| 15 | Commonalities across computational workflows for uncovering explanatory variants in undiagnosed cases. *Genetics in Medicine*, **2021**, 23, 1075-1085 | 8.1 | 2 |
| 14 | Genome-wide analysis of somatic noncoding mutation patterns in cancer.. *Science*, **2022**, 376, eabg5601 | 33.3 | 2 |
| 13 | A literature review at genome scale: improving clinical variant assessment. *Genetics in Medicine*, **2018**, 20, 936-941 | 8.1 | 1 |
| 12 | Low-frequency variant functional architectures reveal strength of negative selection across coding and non-coding annotations | | 1 |
| 11 | Excess of Deleterious Mutations around HLA Genes Reveals Evolutionary Cost of Balancing Selection | | 1 |
| 10 | Estimating the Selective Effect of Heterozygous Protein Truncating Variants from Human Exome Data | | 1 |
| 9 | Fine-scale haplotype structure reveals strong signatures of positive selection in a recombining bacterial pathogen | | 1 |
| 8 | Leveraging pleiotropy to discover and interpret GWAS results for sleep-associated traits | | 1 |
| 7 | Purifying selection on noncoding deletions of human regulatory loci detected using their cellular pleiotropy. *Genome Research*, **2021**, 31, 935-946 | 9.7 | 1 |
| 6 | The missing link between genetic association and regulatory function | | 1 |
| 5 | Reply to ‘Selective effects of heterozygous protein-truncating variants’ *Nature Genetics*, **2019**, 51, 3-4 | 36.3 | 1 |
| 4 | Maintenance of Complex Trait Variation: Classic Theory and Modern Data. *Frontiers in Genetics*, **2021**, 12, 763363 | 4.5 | 0 |
| 3 | Shared associations identify causal relationships between gene expression and immune cell phenotypes. *Communications Biology*, **2021**, 4, 279 | 6.7 | 0 |

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|---|---|---|---|
| 2 | Replicate sequencing libraries are important for quantification of allelic imbalance. *Nature Communications*, **2021**, 12, 3370 | 17.4 | 0 |
| 1 | Understanding the Functional Importance of Human Single Nucleotide Polymorphisms **2006**, 126-132 | | |