

Eugene V Koonin

List of Publications by Year in Descending Order

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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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|--------------------|--------------------------|-----------------|-----------------|
| 582 papers | 74,841 citations | 137 h-index | 262 g-index |
| 693 ext. papers | 91,806 ext. citations | 11.5 avg, IF | 8.55 L-index |

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 582 | Evolutionary plasticity and functional versatility of CRISPR systems.. <i>PLoS Biology</i> , 2022 , 20, e3001481 | 9.7 | 8 |
| 581 | Toward a theory of evolution as multilevel learning.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, | 11.5 | 6 |
| 580 | Thermodynamics of evolution and the origin of life.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, | 11.5 | 9 |
| 579 | Is Protein Folding a Thermodynamically Unfavorable, Active, Energy-Dependent Process?. <i>International Journal of Molecular Sciences</i> , 2022 , 23, | 6.3 | 2 |
| 578 | A three-organelle complex made by wrapper contacts with peroxisomes and mitochondria responds to liver lipid flux changes. <i>Journal of Cell Science</i> , 2022 , 135, | 5.3 | 2 |
| 577 | Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape.. <i>MBio</i> , 2022 , e0013522 | 7.8 | 3 |
| 576 | Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis.. <i>Biology Direct</i> , 2022 , 17, 7 | 7.2 | 0 |
| 575 | A novel group of negative-sense RNA viruses associated with epizootics in managed and free-ranging freshwater turtles in Florida, USA.. <i>PLoS Pathogens</i> , 2022 , 18, e1010258 | 7.6 | |
| 574 | Alternating lysis and lysogeny is a winning strategy in bacteriophages due to Parrondo's paradox.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2115145119 ^{11.5} | 11.5 | 3 |
| 573 | Erratum for Benler et al., "Cargo Genes of Tn-Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes".. <i>MBio</i> , 2022 , e0025722 | 7.8 | |
| 572 | Recruitment of Mobile Genetic Elements for Diverse Cellular Functions in Prokaryotes.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 821197 | 5.6 | 1 |
| 571 | Cargo Genes of Tn-Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. <i>MBio</i> , 2021 , e0293821 | 7.8 | 1 |
| 570 | Template switching and duplications in SARS-CoV-2 genomes give rise to insertion variants that merit monitoring. <i>Communications Biology</i> , 2021 , 4, 1343 | 6.7 | 7 |
| 569 | ViroidDB: a database of viroids and viroid-like circular RNAs. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 1 |
| 568 | A phylogenomic framework for charting the diversity and evolution of giant viruses. <i>PLoS Biology</i> , 2021 , 19, e3001430 | 9.7 | 8 |
| 567 | Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. <i>Nature Communications</i> , 2021 , 12, 1044 | 17.4 | 20 |
| 566 | Ongoing Global and Regional Adaptive Evolution of SARS-CoV-2 2021 , | | 15 |

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|-----|---|------|----|
| 565 | Thousands of previously unknown phages discovered in whole-community human gut metagenomes. <i>Microbiome</i> , 2021 , 9, 78 | 16.6 | 19 |
| 564 | Mitochondria-rough-ER contacts in the liver regulate systemic lipid homeostasis. <i>Cell Reports</i> , 2021 , 34, 108873 | 10.6 | 21 |
| 563 | Incorporating Machine Learning into Established Bioinformatics Frameworks. <i>International Journal of Molecular Sciences</i> , 2021 , 22, | 6.3 | 9 |
| 562 | Toxin-antitoxin RNA pairs safeguard CRISPR-Cas systems. <i>Science</i> , 2021 , 372, | 33.3 | 16 |
| 561 | Insertions in SARS-CoV-2 genome caused by template switch and duplications give rise to new variants of potential concern 2021 , | | 2 |
| 560 | Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , 2021 , 593, 553-557 | 50.4 | 41 |
| 559 | Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021 , 10, 315 | 3.6 | 7 |
| 558 | Identification of combinations of somatic mutations that predict cancer survival and immunotherapy benefit. <i>NAR Cancer</i> , 2021 , 3, zcab017 | 5.2 | 1 |
| 557 | The healthy human virome: from virus-host symbiosis to disease. <i>Current Opinion in Virology</i> , 2021 , 47, 86-94 | 7.5 | 9 |
| 556 | Non-essential ribosomal proteins in bacteria and archaea identified using COGs. <i>Journal of Bacteriology</i> , 2021 , | 3.5 | 2 |
| 555 | Structural Basis for a Dual Function ATP Grasp Ligase That Installs Single and Bicyclic Ester Macrocycles in a New Multicore RiPP Natural Product. <i>Journal of the American Chemical Society</i> , 2021 , 143, 8056-8068 | 16.4 | 5 |
| 554 | Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021 , 10, 447 | 3.6 | 2 |
| 553 | Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. <i>MBio</i> , 2021 , 12, e0142321 | 7.8 | 5 |
| 552 | Structure-based insights into evolution of rhodopsins. <i>Communications Biology</i> , 2021 , 4, 821 | 6.7 | 5 |
| 551 | : a New Realm for Archaeal Filamentous Viruses with Linear A-Form Double-Stranded DNA Genomes. <i>Journal of Virology</i> , 2021 , 95, e0067321 | 6.6 | 9 |
| 550 | Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021 , 10, 447 | 3.6 | 2 |
| 549 | The Greater Virus World and Its Evolution 2021 , 38-46 | | |
| 548 | COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021 , 49, D274-D281 | 20.1 | 84 |

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|-----|---|------|----|
| 547 | Mutation-selection balance and compensatory mechanisms in tumour evolution. <i>Nature Reviews Genetics</i> , 2021 , 22, 251-262 | 30.1 | 16 |
| 546 | Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2021 , 589, 306-309 | 50.4 | 17 |
| 545 | CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021 , 49, e20 | 20.1 | 11 |
| 544 | Evolution of DNA packaging in gene transfer agents. <i>Virus Evolution</i> , 2021 , 7, veab015 | 3.7 | 11 |
| 543 | Evolution in the weak-mutation limit: Stasis periods punctuated by fast transitions between saddle points on the fitness landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118, | 11.5 | 2 |
| 542 | Defense Against Viruses and Other Genetic Parasites in Prokaryotes 2021 , 606-616 | | |
| 541 | Assessment of assumptions underlying models of prokaryotic pangenome evolution. <i>BMC Biology</i> , 2021 , 19, 27 | 7.3 | 1 |
| 540 | Ongoing global and regional adaptive evolution of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118, | 11.5 | 74 |
| 539 | Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021 , 29, 582-592 | 12.4 | 12 |
| 538 | An alternating active-dormitive strategy enables disadvantaged prey to outcompete the perennially active prey through Parrondo's paradox. <i>BMC Biology</i> , 2021 , 19, 168 | 7.3 | 4 |
| 537 | Epistasis at the SARS-CoV-2 RBD Interface and the Propitiously Boring Implications for Vaccine Escape 2021 , | | 4 |
| 536 | A Unique Gene Module in Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. <i>Frontiers in Microbiology</i> , 2021 , 12, 721392 | 5.7 | 0 |
| 535 | Mammalian retrovirus-like protein PEG10 packages its own mRNA and can be pseudotyped for mRNA delivery. <i>Science</i> , 2021 , 373, 882-889 | 33.3 | 45 |
| 534 | Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021 , 10, 315 | 3.6 | 6 |
| 533 | Fishing for phages in metagenomes: what do we catch, what do we miss?. <i>Current Opinion in Virology</i> , 2021 , 49, 142-150 | 7.5 | 2 |
| 532 | The Baltimore Classification of Viruses 50 Years Later: How Does It Stand in the Light of Virus Evolution?. <i>Microbiology and Molecular Biology Reviews</i> , 2021 , 85, e0005321 | 13.2 | 7 |
| 531 | CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021 , 4, 558-574 | 2.5 | 1 |
| 530 | 2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566 | 2.6 | 10 |

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|-----|--|------|-----|
| 529 | Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , 2021 , | 44.5 | 20 |
| 528 | Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. <i>MBio</i> , 2021 , 12, e0149521 | 7.8 | 7 |
| 527 | A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants. <i>Nucleic Acids Research</i> , 2021 , 49, 10328-10346 | 20.1 | 5 |
| 526 | Viruses Defined by the Position of the Virosphere within the Replicator Space. <i>Microbiology and Molecular Biology Reviews</i> , 2021 , e0019320 | 13.2 | 7 |
| 525 | Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of. <i>CRISPR Journal</i> , 2021 , 4, 656-672 | 2.5 | 4 |
| 524 | Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. <i>Nature</i> , 2021 , 597, 720-725 | 35.4 | 27 |
| 523 | The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021 , 374, 57-65 | 33.3 | 25 |
| 522 | Analysis of Finite Population Evolution Models Using a Moment Closure Approximation. <i>Journal of the Physical Society of Japan</i> , 2021 , 90, 014801 | 1.5 | |
| 521 | Conflict-driven evolution 2021 , 77-96 | | |
| 520 | Modified base-binding EVE and DCD domains: striking diversity of genomic contexts in prokaryotes and predicted involvement in a variety of cellular processes. <i>BMC Biology</i> , 2020 , 18, 159 | 7.3 | 1 |
| 519 | Coevolution of Eukaryote-like Vps4 and ESCRT-III Subunits in the Asgard Archaea. <i>MBio</i> , 2020 , 11, | 7.8 | 9 |
| 518 | Deep Roots and Splendid Boughs of the Global Plant Virome. <i>Annual Review of Phytopathology</i> , 2020 , 58, 23-53 | 10.8 | 27 |
| 517 | Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15193-15199 | 11.5 | 120 |
| 516 | Response to Comment on "RNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020 , 368, | 33.3 | 14 |
| 515 | Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020 , 3, 156-163 | 2.5 | 8 |
| 514 | The replication machinery of LUCA: common origin of DNA replication and transcription. <i>BMC Biology</i> , 2020 , 18, 61 | 7.3 | 22 |
| 513 | Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. <i>Nature Communications</i> , 2020 , 11, 1234 | 17.4 | 11 |
| 512 | Global Organization and Proposed Megataxonomy of the Virus World. <i>Microbiology and Molecular Biology Reviews</i> , 2020 , 84, | 13.2 | 178 |

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| 511 | Classification and Nomenclature of Metacaspases and Paracaspases: No More Confusion with Caspases. <i>Molecular Cell</i> , 2020 , 77, 927-929 | 17.6 | 35 |
| 510 | Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. <i>Communications Biology</i> , 2020 , 3, 321 | 6.7 | 17 |
| 509 | The crAss-like Phage Group: How Metagenomics Reshaped the Human Virome. <i>Trends in Microbiology</i> , 2020 , 28, 349-359 | 12.4 | 30 |
| 508 | Predator Dormancy is a Stable Adaptive Strategy due to Parrondo's Paradox. <i>Advanced Science</i> , 2020 , 7, 1901559 | 13.6 | 34 |
| 507 | Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. <i>Frontiers in Microbiology</i> , 2020 , 11, 381 | 5.7 | 4 |
| 506 | : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. <i>Journal of Virology</i> , 2020 , 94, | 6.6 | 47 |
| 505 | A New Family of DNA Viruses Causing Disease in Crustaceans from Diverse Aquatic Biomes. <i>MBio</i> , 2020 , 11, | 7.8 | 32 |
| 504 | Fixation Probability of a Mutant in the Wright-Fisher Model under Strong Selection and Fluctuating Fitness Landscape. <i>Journal of the Physical Society of Japan</i> , 2020 , 89, 104802 | 1.5 | |
| 503 | The Evolutionary Origins of Life and Death 2020 , | | 7 |
| 502 | CRISPR Arrays Away from Genes. <i>CRISPR Journal</i> , 2020 , 3, 535-549 | 2.5 | 7 |
| 501 | Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses 2020 , | | 10 |
| 500 | Evolution of Human Respiratory Virus Epidemics 2020 , | | 7 |
| 499 | Substantial Impact of Post Vaccination Contacts on Cumulative Infections during Viral Epidemics 2020 , | | 5 |
| 498 | Phages build anti-defence barriers. <i>Nature Microbiology</i> , 2020 , 5, 8-9 | 26.6 | 4 |
| 497 | Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020 , 18, 67-83 | 22.2 | 545 |
| 496 | Evolution of a major virion protein of the giant pandoraviruses from an inactivated bacterial glycoside hydrolase. <i>Virus Evolution</i> , 2020 , 6, veaa059 | 3.7 | 8 |
| 495 | Deep phylogeny of cancer drivers and compensatory mutations. <i>Communications Biology</i> , 2020 , 3, 551 | 6.7 | 7 |
| 494 | Seeker: alignment-free identification of bacteriophage genomes by deep learning. <i>Nucleic Acids Research</i> , 2020 , 48, e121 | 20.1 | 19 |

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|-----|---|------|----|
| 493 | Functional Long Non-coding RNAs Evolve from Junk Transcripts. <i>Cell</i> , 2020 , 183, 1151-1161 | 56.2 | 59 |
| 492 | Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. <i>Nature Microbiology</i> , 2020 , 5, 1262-1270 | 26.6 | 50 |
| 491 | The LUCA and its complex virome. <i>Nature Reviews Microbiology</i> , 2020 , 18, 661-670 | 22.2 | 27 |
| 490 | Selection for Reducing Energy Cost of Protein Production Drives the GC Content and Amino Acid Composition Bias in Gene Transfer Agents. <i>MBio</i> , 2020 , 11, | 7.8 | 5 |
| 489 | Prediction of the incubation period for COVID-19 and future virus disease outbreaks. <i>BMC Biology</i> , 2020 , 18, 186 | 7.3 | 10 |
| 488 | Phage lysis-lysogeny switches and programmed cell death: Danse macabre. <i>BioEssays</i> , 2020 , 42, e2000114 | 14.1 | 9 |
| 487 | Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020 , 11, 3784 | 17.4 | 21 |
| 486 | Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020 , 48, 8828-8847 | 20.1 | 21 |
| 485 | Evolution of regulatory signatures in primate cortical neurons at cell-type resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28422-28432 | 11.5 | 1 |
| 484 | Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020 , 369, 1077-1084 | 33.3 | 78 |
| 483 | No waves of intelligent design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 19639-19640 | 11.5 | 1 |
| 482 | Viral rhodopsins 1 are an unique family of light-gated cation channels. <i>Nature Communications</i> , 2020 , 11, 5707 | 17.4 | 14 |
| 481 | Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , 2020 , 21, 119-131 | 30.1 | 77 |
| 480 | Classify viruses - the gain is worth the pain. <i>Nature</i> , 2019 , 566, 318-320 | 50.4 | 78 |
| 479 | Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019 , 10, 4006 | 17.4 | 21 |
| 478 | Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019 , 14, 3013-3031 | 18.8 | 12 |
| 477 | Origin of programmed cell death from antiviral defense?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16167-16169 | 11.5 | 5 |
| 476 | Key role of recombination in evolutionary processes with migration between two habitats. <i>Physical Review E</i> , 2019 , 100, 030401 | 2.4 | 2 |

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|-----|---|------|-----|
| 475 | Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019 , 10, 212 | 17.4 | 149 |
| 474 | CRISPR: a new principle of genome engineering linked to conceptual shifts in evolutionary biology. <i>Biology and Philosophy</i> , 2019 , 34, 9 | 1.7 | 17 |
| 473 | Multiplicative fitness, rapid haplotype discovery, and fitness decay explain evolution of human MHC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14098-14104 | 11.5 | 12 |
| 472 | RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019 , 365, 48-53 | 33.3 | 232 |
| 471 | Origin of viruses: primordial replicators recruiting capsids from hosts. <i>Nature Reviews Microbiology</i> , 2019 , 17, 449-458 | 22.2 | 85 |
| 470 | CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019 , 17, 513-525 | 22.2 | 105 |
| 469 | Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonsel Self Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019 , 10, | 7.8 | 23 |
| 468 | In silico learning of tumor evolution through mutational time series. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 9501-9510 | 11.5 | 11 |
| 467 | Predicted highly derived class 1 CRISPR-Cas system in Haloarchaea containing diverged Cas5 and Cas7 homologs but no CRISPR array. <i>FEMS Microbiology Letters</i> , 2019 , 366, | 2.9 | 9 |
| 466 | Unexpected connections between type VI-B CRISPR-Cas systems, bacterial natural competence, ubiquitin signaling network and DNA modification through a distinct family of membrane proteins. <i>FEMS Microbiology Letters</i> , 2019 , 366, | 2.9 | 9 |
| 465 | Reply to Holmes and Duch e, "Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?": Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. <i>MBio</i> , 2019 , 10, | 7.8 | 9 |
| 464 | Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019 , 10, | 7.8 | 44 |
| 463 | Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180087 | 5.8 | 126 |
| 462 | Genome and Environmental Activity of a Virus and Its Virophages. <i>Frontiers in Microbiology</i> , 2019 , 10, 703 | 5.7 | 11 |
| 461 | Grammar of protein domain architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3636-3645 | 11.5 | 23 |
| 460 | Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019 , 47, 389-398 | 5.1 | 16 |
| 459 | Allele fixation probability in a Moran model with fluctuating fitness landscapes. <i>Physical Review E</i> , 2019 , 99, 022407 | 2.4 | 3 |
| 458 | Reply to 'Evolutionary placement of Methanonatronarchaeia'. <i>Nature Microbiology</i> , 2019 , 4, 560-561 | 26.6 | 2 |

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|-----|---|------|-----|
| 457 | Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019 , 16, 435-448 | 4.8 | 20 |
| 456 | Proteomic and genomic signatures of repeat instability in cancer and adjacent normal tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16987-16996 | 11.5 | 6 |
| 455 | Selection and Genome Plasticity as the Key Factors in the Evolution of Bacteria. <i>Physical Review X</i> , 2019 , 9, | 9.1 | 5 |
| 454 | Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. <i>Nature Communications</i> , 2019 , 10, 3425 | 17.4 | 55 |
| 453 | Identification of Dephospho-Coenzyme A (Dephospho-CoA) Kinase in <i>Thermococcus kodakarensis</i> and Elucidation of the Entire CoA Biosynthesis Pathway in Archaea. <i>MBio</i> , 2019 , 10, | 7.8 | 7 |
| 452 | On the feasibility of saltational evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21068-21075 | 11.5 | 7 |
| 451 | Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019 , 10, 4939 | 17.4 | 29 |
| 450 | A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000 | 3.6 | 7 |
| 449 | A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000 | 3.6 | 13 |
| 448 | Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. <i>Methods in Molecular Biology</i> , 2019 , 1910, 241-269 | 1.4 | 3 |
| 447 | Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019 , 21, 2056-2073 | 3.2 | 19 |
| 446 | Lamarckian or not, CRISPR-Cas is an elaborate engine of directed evolution. <i>Biology and Philosophy</i> , 2019 , 34, 1 | 1.7 | |
| 445 | Reply to Hedrick and Klitz: High haplotype discovery rate in the HLA locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23388-23389 | 11.5 | 1 |
| 444 | Crossing fitness valleys via double substitutions within codons. <i>BMC Biology</i> , 2019 , 17, 105 | 7.3 | 1 |
| 443 | Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. <i>Nature Communications</i> , 2019 , 10, 5376 | 17.4 | 24 |
| 442 | Virus-borne mini-CRISPR arrays are involved in interviral conflicts. <i>Nature Communications</i> , 2019 , 10, 5204 | 17.4 | 27 |
| 441 | CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019 , 431, 3-20 | 6.5 | 41 |
| 440 | Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37 | 44.5 | 180 |

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|-----|---|------|-----|
| 439 | New archaeal viruses discovered by metagenomic analysis of viral communities in enrichment cultures. <i>Environmental Microbiology</i> , 2019 , 21, 2002-2014 | 5.2 | 11 |
| 438 | Evolution of the Large Nucleocytoplasmic DNA Viruses of Eukaryotes and Convergent Origins of Viral Gigantism. <i>Advances in Virus Research</i> , 2019 , 103, 167-202 | 10.7 | 80 |
| 437 | Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , 2019 , 363, 88-91 | 33.3 | 169 |
| 436 | Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1063-1070 | 13.4 | 80 |
| 435 | Towards physical principles of biological evolution. <i>Physica Scripta</i> , 2018 , 93, 043001 | 2.6 | 15 |
| 434 | Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018 , 3, 461-469 | 26.6 | 87 |
| 433 | Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in <i>Haloferax volcanii</i> . <i>Molecular Biology and Evolution</i> , 2018 , 35, 1855-1868 | 8.3 | 12 |
| 432 | Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2295-2310 | 2.6 | 108 |
| 431 | Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses. <i>Journal of Virology</i> , 2018 , 92, | 6.6 | 56 |
| 430 | Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2283-2294 | 2.6 | 111 |
| 429 | Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018 , 200, | 3.5 | 29 |
| 428 | Vast diversity of prokaryotic virus genomes encoding double jelly-roll major capsid proteins uncovered by genomic and metagenomic sequence analysis. <i>Virology Journal</i> , 2018 , 15, 67 | 6.1 | 35 |
| 427 | Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. <i>Molecular Cell</i> , 2018 , 70, 327-339.e5 | 17.6 | 215 |
| 426 | Discovery of Oligonucleotide Signaling Mediated by CRISPR-Associated Polymerases Solves Two Puzzles but Leaves an Enigma. <i>ACS Chemical Biology</i> , 2018 , 13, 309-312 | 4.9 | 25 |
| 425 | The depths of virus exaptation. <i>Current Opinion in Virology</i> , 2018 , 31, 1-8 | 7.5 | 41 |
| 424 | Proteomic Analysis of <i>Methanonaeronarchaeum thermophilum</i> AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanonaeronarchaeia". <i>Genes</i> , 2018 , 9, | 4.2 | 5 |
| 423 | Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018 , 10, | 6.2 | 4 |
| 422 | How genetic parasites persist despite the purge of natural selection. <i>Europhysics Letters</i> , 2018 , 122, 58001 | 16 | 5 |

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| 421 | Physical foundations of biological complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8678-E8687 | 11.5 | 46 |
| 420 | Hunting for Treasure Chests in Microbial Defense Islands. <i>Molecular Cell</i> , 2018 , 70, 761-762 | 17.6 | 6 |
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| 16 | Towards comprehensive characterization of CRISPR-linked genes | | 1 |
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| 7 | Expanding diversity of Asgard archaea and the elusive ancestry of eukaryotes | 1 |
| 6 | CRISPRidentify: identification of CRISPR arrays using machine learning approach | 2 |
| 5 | Virus genomes from deep sea sediments expand the ocean megavirome and support independent origins of viral gigantism | 2 |
| 4 | Inevitability of the emergence and persistence of genetic parasites caused by thermodynamic instability of parasite-free states | 1 |
| 3 | Alternating lysis and lysogeny is a winning strategy in bacteriophages due to Parrondo's Paradox | 1 |
| 2 | Insertions in SARS-CoV-2 genome caused by template switch and duplications give rise to new variants of potential concern | 2 |
| 1 | A Phylogenomic Framework for Charting the Diversity and Evolution of Giant Viruses | 6 |