

Andreas Wagner

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

9,588
citations

57758

44
h-index

45317

90
g-index

192
all docs

192
docs citations

192
times ranked

9036
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Selection on growth rate and local adaptation drive genomic adaptation during experimental range expansions in the protist <i>Tetrahymena thermophila</i> . <i>Journal of Animal Ecology</i> , 2022, 91, 1088-1103. | 2.8 | 5 |
| 2 | The length scale of multivalent interactions is evolutionarily conserved in fungal and vertebrate phase-separating proteins. <i>Genetics</i> , 2022, 220, . | 2.9 | 8 |
| 3 | Multiple Novel Traits without Immediate Benefits Originate in Bacteria Evolving on Single Antibiotics. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 8.9 | 5 |
| 4 | Yeast Proteins may Reversibly Aggregate like Amphiphilic Molecules. <i>Journal of Molecular Biology</i> , 2022, 434, 167352. | 4.2 | 4 |
| 5 | Translation stalling proline motifs are enriched in slow-growing, thermophilic, and multicellular bacteria. <i>ISME Journal</i> , 2022, 16, 1065-1073. | 9.8 | 2 |
| 6 | GroEL/S Overexpression Helps to Purge Deleterious Mutations and Reduce Genetic Diversity during Adaptive Protein Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 8.9 | 5 |
| 7 | Competition for nutrients increases invasion resistance during assembly of microbial communities. <i>Molecular Ecology</i> , 2022, 31, 4188-4203. | 3.9 | 9 |
| 8 | A limit on the evolutionary rescue of an Antarctic bacterium from rising temperatures. <i>Science Advances</i> , 2022, 8, . | 10.3 | 4 |
| 9 | Low protein expression enhances phenotypic evolvability by intensifying selection on folding stability. <i>Nature Ecology and Evolution</i> , 2022, 6, 1155-1164. | 7.8 | 5 |
| 10 | Natural Selection on the Phase-Separation Properties of FUS during 160 My of Mammalian Evolution. <i>Molecular Biology and Evolution</i> , 2021, 38, 940-951. | 8.9 | 24 |
| 11 | Cryptic surface-associated multicellularity emerges through cell adhesion and its regulation. <i>PLoS Biology</i> , 2021, 19, e3001250. | 5.6 | 6 |
| 12 | Mistranslation can promote the exploration of alternative evolutionary trajectories in enzyme evolution. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1302-1315. | 1.7 | 1 |
| 13 | Adaptive evolvability through direct selection instead of indirect, second-order selection. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2021, , . | 1.3 | 3 |
| 14 | Mistranslation Reduces Mutation Load in Evolving Proteins through Negative Epistasis with DNA Mutations. <i>Molecular Biology and Evolution</i> , 2021, 38, 4792-4804. | 8.9 | 5 |
| 15 | Ecology drives the evolution of diverse social strategies in <i>Pseudomonas aeruginosa</i> . <i>Molecular Ecology</i> , 2021, 30, 5214-5228. | 3.9 | 12 |
| 16 | Diversity begets diversity during community assembly until ecological limits impose a diversity ceiling. <i>Molecular Ecology</i> , 2021, 30, 5874-5887. | 3.9 | 15 |
| 17 | Adaptive gene misregulation. <i>Genetics</i> , 2021, 217, . | 2.9 | 3 |
| 18 | Both Binding Strength and Evolutionary Accessibility Affect the Population Frequency of Transcription Factor Binding Sequences in <i>Arabidopsis thaliana</i> . <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 2 |

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|----|--|------|-----------|
| 19 | Gene swamping alters evolution during range expansions in the protist <i>Tetrahymena thermophila</i> . <i>Biology Letters</i> , 2020, 16, 20200244. | 2.3 | 14 |
| 20 | Selection enhances protein evolvability by increasing mutational robustness and foldability. <i>Science</i> , 2020, 370, . | 12.6 | 61 |
| 21 | Genotype networks of 80 quantitative <i>Arabidopsis thaliana</i> phenotypes reveal phenotypic evolvability despite pervasive epistasis. <i>PLoS Computational Biology</i> , 2020, 16, e1008082. | 3.2 | 6 |
| 22 | Signaling pathways have an inherent need for noise to acquire information. <i>BMC Bioinformatics</i> , 2020, 21, 462. | 2.6 | 8 |
| 23 | Information Theory Can Help Quantify the Potential of New Phenotypes to Originate as Exaptations. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, . | 2.2 | 1 |
| 24 | Short Residence Times of DNA-Bound Transcription Factors Can Reduce Gene Expression Noise and Increase the Transmission of Information in a Gene Regulation System. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 67. | 3.5 | 15 |
| 25 | Evolution under pH stress and high population densities leads to increased density-dependent fitness in the protist <i>Tetrahymena thermophila</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 573-586. | 2.3 | 9 |
| 26 | Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. <i>PLoS Computational Biology</i> , 2020, 16, e1007727. | 3.2 | 18 |
| 27 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . <i>PLoS Computational Biology</i> , 2020, 16, e1008433. | 3.2 | 10 |
| 28 | Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727. | | 0 |
| 29 | Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727. | | 0 |
| 30 | Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727. | | 0 |
| 31 | Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727. | | 0 |
| 32 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433. | | 0 |
| 33 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433. | | 0 |
| 34 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433. | | 0 |
| 35 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433. | | 0 |
| 36 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433. | | 0 |

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|----|--|------|-----------|
| 37 | Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli.</i> , 2020, 16, e1008433. | | 0 |
| 38 | Microbial life cycles link global modularity in regulation to mosaic evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 1184-1196. | 7.8 | 18 |
| 39 | Cryptic genetic variation accelerates evolution by opening access to diverse adaptive peaks. <i>Science</i> , 2019, 365, 347-353. | 12.6 | 96 |
| 40 | Chaperonin overproduction and metabolic erosion caused by mutation accumulation in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, . | 1.8 | 2 |
| 41 | The causes of evolvability and their evolution. <i>Nature Reviews Genetics</i> , 2019, 20, 24-38. | 16.3 | 208 |
| 42 | The architecture of an empirical genotype-phenotype map. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1242-1260. | 2.3 | 27 |
| 43 | Adding levels of complexity enhances robustness and evolvability in a multilevel genotype-phenotype map. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170516. | 3.4 | 19 |
| 44 | Assessing the benefits of horizontal gene transfer by laboratory evolution and genome sequencing. <i>BMC Evolutionary Biology</i> , 2018, 18, 54. | 3.2 | 31 |
| 45 | DYNAMICS OF AN INSERTION SEQUENCE INFECTION IN A SPATIALLY STRUCTURED ENVIRONMENT. <i>Journal of Biological Systems</i> , 2018, 26, 133-166. | 1.4 | 0 |
| 46 | Population Size Affects Adaptation in Complex Ways: Simulations on Empirical Adaptive Landscapes. <i>Evolutionary Biology</i> , 2018, 45, 156-169. | 1.1 | 1 |
| 47 | Metabolic determinants of enzyme evolution in a genome-scale bacterial metabolic network. <i>Genome Biology and Evolution</i> , 2018, 10, 3076-3088. | 2.5 | 19 |
| 48 | Synthetic circuits reveal how mechanisms of gene regulatory networks constrain evolution. <i>Molecular Systems Biology</i> , 2018, 14, e8102. | 7.2 | 34 |
| 49 | An enormous potential for niche construction through bacterial cross-feeding in a homogeneous environment. <i>PLoS Computational Biology</i> , 2018, 14, e1006340. | 3.2 | 54 |
| 50 | High mutation rates limit evolutionary adaptation in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2018, 14, e1007324. | 3.5 | 72 |
| 51 | Genomic organization underlying deletional robustness in bacterial metabolic systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7075-7080. | 7.1 | 10 |
| 52 | <i>Drosophila</i> Nnf1 paralogs are partially redundant for somatic and germ line kinetochore function. <i>Chromosoma</i> , 2017, 126, 145-163. | 2.2 | 2 |
| 53 | A thousand empirical adaptive landscapes and their navigability. <i>Nature Ecology and Evolution</i> , 2017, 1, 45. | 7.8 | 79 |
| 54 | Mistranslation can enhance fitness through purging of deleterious mutations. <i>Nature Communications</i> , 2017, 8, 15410. | 12.8 | 28 |

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|----|---|------|-----------|
| 55 | Innovation: an emerging focus from cells to societies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160414. | 4.0 | 28 |
| 56 | Information theory, evolutionary innovations and evolvability. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160416. | 4.0 | 17 |
| 57 | Non-adaptive origins of evolutionary innovations increase network complexity in interacting digital organisms. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160431. | 4.0 | 10 |
| 58 | Constraint and Contingency Pervade the Emergence of Novel Phenotypes in Complex Metabolic Systems. <i>Biophysical Journal</i> , 2017, 113, 690-701. | 0.5 | 1 |
| 59 | The White-Knight Hypothesis, or Does the Environment Limit Innovations?. <i>Trends in Ecology and Evolution</i> , 2017, 32, 131-140. | 8.7 | 15 |
| 60 | Effect of Population Size and Mutation Rate on the Evolution of RNA Sequences on an Adaptive Landscape Determined by RNA Folding. <i>International Journal of Biological Sciences</i> , 2017, 13, 1138-1151. | 6.4 | 6 |
| 61 | The genotype-phenotype map of an evolving digital organism. <i>PLoS Computational Biology</i> , 2017, 13, e1005414. | 3.2 | 24 |
| 62 | Parallel or convergent evolution in human population genomic data revealed by genotype networks. <i>BMC Evolutionary Biology</i> , 2016, 16, 154. | 3.2 | 9 |
| 63 | The Genomic Basis of Evolutionary Innovation in <i>Pseudomonas aeruginosa</i> . <i>PLoS Genetics</i> , 2016, 12, e1006005. | 3.5 | 35 |
| 64 | Genonets server—a web server for the construction, analysis and visualization of genotype networks. <i>Nucleic Acids Research</i> , 2016, 44, W70-W76. | 14.5 | 12 |
| 65 | Growthcurver: an R package for obtaining interpretable metrics from microbial growth curves. <i>BMC Bioinformatics</i> , 2016, 17, 172. | 2.6 | 582 |
| 66 | The Molecular Chaperone DnaK Is a Source of Mutational Robustness. <i>Genome Biology and Evolution</i> , 2016, 8, 2979-2991. | 2.5 | 57 |
| 67 | Phenotypic innovation through recombination in genome-scale metabolic networks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161536. | 2.6 | 13 |
| 68 | The potential for non-adaptive origins of evolutionary innovations in central carbon metabolism. <i>BMC Systems Biology</i> , 2016, 10, 97. | 3.0 | 12 |
| 69 | How Archiving by Freezing Affects the Genome-Scale Diversity of <i>Escherichia coli</i> Populations. <i>Genome Biology and Evolution</i> , 2016, 8, 1290-1298. | 2.5 | 11 |
| 70 | From the primordial soup to self-driving cars: standards and their role in natural and technological innovation. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20151086. | 3.4 | 7 |
| 71 | Intramolecular phenotypic capacitance in a modular RNA molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12444-12449. | 7.1 | 11 |
| 72 | Function does not follow form in gene regulatory circuits. <i>Scientific Reports</i> , 2015, 5, 13015. | 3.3 | 40 |

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|----|---|------|-----------|
| 73 | A survey of tandem repeat instabilities and associated gene expression changes in 35 colorectal cancers. <i>BMC Genomics</i> , 2015, 16, 702. | 2.8 | 27 |
| 74 | Mechanisms of mutational robustness in transcriptional regulation. <i>Frontiers in Genetics</i> , 2015, 6, 322. | 2.3 | 89 |
| 75 | Causal Drift, Robust Signaling, and Complex Disease. <i>PLoS ONE</i> , 2015, 10, e0118413. | 2.5 | 7 |
| 76 | Engineering and Biology: Counsel for a Continued Relationship. <i>Biological Theory</i> , 2015, 10, 50-59. | 1.5 | 15 |
| 77 | Mistranslation drives the evolution of robustness in TEM-1 β -lactamase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12758-12763. | 7.1 | 47 |
| 78 | Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015, 25, 1591-1599. | 5.5 | 69 |
| 79 | Fitness Trade-Offs Determine the Role of the Molecular Chaperonin GroEL in Buffering Mutations. <i>Molecular Biology and Evolution</i> , 2015, 32, 2681-2693. | 8.9 | 43 |
| 80 | VCF2Networks: applying genotype networks to single-nucleotide variants data. <i>Bioinformatics</i> , 2015, 31, 438-439. | 4.1 | 5 |
| 81 | Exhaustive Analysis of a Genotype Space Comprising 1015 Central Carbon Metabolisms Reveals an Organization Conducive to Metabolic Innovation. <i>PLoS Computational Biology</i> , 2015, 11, e1004329. | 3.2 | 13 |
| 82 | Robustness, Evolvability, and the Logic of Genetic Regulation. <i>Artificial Life</i> , 2014, 20, 111-126. | 1.3 | 43 |
| 83 | Spaces of the possible: universal Darwinism and the wall between technological and biological innovation. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20131190. | 3.4 | 51 |
| 84 | The Robustness and Evolvability of Transcription Factor Binding Sites. <i>Science</i> , 2014, 343, 875-877. | 12.6 | 139 |
| 85 | A genotype network reveals homoplastic cycles of convergent evolution in influenza A (H3N2) haemagglutinin. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132763. | 2.6 | 20 |
| 86 | Efficient Purging of Deleterious Mutations in Plants with Haploid Selfing. <i>Genome Biology and Evolution</i> , 2014, 6, 1238-1252. | 2.5 | 38 |
| 87 | Mutational Robustness Accelerates the Origin of Novel RNA Phenotypes through Phenotypic Plasticity. <i>Biophysical Journal</i> , 2014, 106, 955-965. | 0.5 | 23 |
| 88 | Historical contingency and the gradual evolution of metabolic properties in central carbon and genome-scale metabolisms. <i>BMC Systems Biology</i> , 2014, 8, 48. | 3.0 | 10 |
| 89 | Human Genome Variation and the Concept of Genotype Networks. <i>PLoS ONE</i> , 2014, 9, e99424. | 2.5 | 18 |
| 90 | A latent capacity for evolutionary innovation through exaptation in metabolic systems. <i>Nature</i> , 2013, 500, 203-206. | 27.8 | 149 |

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|-----|--|------|-----------|
| 91 | Growth Temperature and Genome Size in Bacteria Are Negatively Correlated, Suggesting Genomic Streamlining During Thermal Adaptation. <i>Genome Biology and Evolution</i> , 2013, 5, 966-977. | 2.5 | 179 |
| 92 | The role of robustness in phenotypic adaptation and innovation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1249-1258. | 2.6 | 119 |
| 93 | Metabolic Networks and Their Evolution. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 29-52. | 1.6 | 31 |
| 94 | Superessential reactions in metabolic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1121-30. | 7.1 | 47 |
| 95 | Genotype networks shed light on evolutionary constraints. <i>Trends in Ecology and Evolution</i> , 2011, 26, 577-584. | 8.7 | 57 |
| 96 | Cryptic genetic variation promotes rapid evolutionary adaptation in an RNA enzyme. <i>Nature</i> , 2011, 474, 92-95. | 27.8 | 209 |
| 97 | The molecular origins of evolutionary innovations. <i>Trends in Genetics</i> , 2011, 27, 397-410. | 6.7 | 102 |
| 98 | Genotype networks, innovation, and robustness in sulfur metabolism. <i>BMC Systems Biology</i> , 2011, 5, 39. | 3.0 | 27 |
| 99 | The low cost of recombination in creating novel phenotypes. <i>BioEssays</i> , 2011, 33, 636-646. | 2.5 | 9 |
| 100 | Genotype networks in metabolic reaction spaces. <i>BMC Systems Biology</i> , 2010, 4, 30. | 3.0 | 49 |
| 101 | Specialization Can Drive the Evolution of Modularity. <i>PLoS Computational Biology</i> , 2010, 6, e1000719. | 3.2 | 160 |
| 102 | Evolutionary Plasticity and Innovations in Complex Metabolic Reaction Networks. <i>PLoS Computational Biology</i> , 2009, 5, e1000613. | 3.2 | 112 |
| 103 | Evolutionary constraints permeate large metabolic networks. <i>BMC Evolutionary Biology</i> , 2009, 9, 231. | 3.2 | 34 |
| 104 | Transposable elements as genomic diseases. <i>Molecular BioSystems</i> , 2009, 5, 32-35. | 2.9 | 21 |
| 105 | Distant horizontal gene transfer is rare for multiple families of prokaryotic insertion sequences. <i>Molecular Genetics and Genomics</i> , 2008, 280, 397-408. | 2.1 | 36 |
| 106 | Gene duplications, robustness and evolutionary innovations. <i>BioEssays</i> , 2008, 30, 367-373. | 2.5 | 120 |
| 107 | Neutralism and selectionism: a network-based reconciliation. <i>Nature Reviews Genetics</i> , 2008, 9, 965-974. | 16.3 | 244 |
| 108 | Neutral network sizes of biological RNA molecules can be computed and are not atypically small. <i>BMC Bioinformatics</i> , 2008, 9, 464. | 2.6 | 65 |

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|-----|---|------|-----------|
| 109 | Protein robustness promotes evolutionary innovations on large evolutionary time-scales. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 1595-1602. | 2.6 | 63 |
| 110 | Robustness and evolvability: a paradox resolved. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 91-100. | 2.6 | 495 |
| 111 | A survey of bacterial insertion sequences using IScan. <i>Nucleic Acids Research</i> , 2007, 35, 5284-5293. | 14.5 | 55 |
| 112 | Robustness Can Evolve Gradually in Complex Regulatory Gene Networks with Varying Topology. <i>PLoS Computational Biology</i> , 2007, 3, e15. | 3.2 | 318 |
| 113 | Rapid Detection of Positive Selection in Genes and Genomes Through Variation Clusters. <i>Genetics</i> , 2007, 176, 2451-2463. | 2.9 | 49 |
| 114 | Energy costs constrain the evolution of gene expression. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 322-324. | 1.3 | 54 |
| 115 | Alternative routes and mutational robustness in complex regulatory networks. <i>BioSystems</i> , 2007, 88, 163-172. | 2.0 | 48 |
| 116 | From bit to it: How a complex metabolic network transforms information into living matter. <i>BMC Systems Biology</i> , 2007, 1, 33. | 3.0 | 23 |
| 117 | Influence of metabolic network structure and function on enzyme evolution. <i>Genome Biology</i> , 2006, 7, R39. | 9.6 | 161 |
| 118 | Cooperation is Fleeting in the World of Transposable Elements. <i>PLoS Computational Biology</i> , 2006, 2, e162. | 3.2 | 32 |
| 119 | Periodic Extinctions of Transposable Elements in Bacterial Lineages: Evidence from Intragenomic Variation in Multiple Genomes. <i>Molecular Biology and Evolution</i> , 2006, 23, 723-733. | 8.9 | 99 |
| 120 | Distributed robustness versus redundancy as causes of mutational robustness. <i>BioEssays</i> , 2005, 27, 176-188. | 2.5 | 258 |
| 121 | Circuit topology and the evolution of robustness in two-gene circadian oscillators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11775-11780. | 7.1 | 135 |
| 122 | Energy Constraints on the Evolution of Gene Expression. <i>Molecular Biology and Evolution</i> , 2005, 22, 1365-1374. | 8.9 | 421 |
| 123 | Robustness, evolvability, and neutrality. <i>FEBS Letters</i> , 2005, 579, 1772-1778. | 2.8 | 273 |
| 124 | COMPACTNESS AND CYCLES IN SIGNAL TRANSDUCTION AND TRANSCRIPTIONAL REGULATION NETWORKS: A SIGNATURE OF NATURAL SELECTION?. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2004, 07, 419-432. | 1.4 | 5 |
| 125 | Reconstructing Pathways in Large Genetic Networks from Genetic Perturbations. <i>Journal of Computational Biology</i> , 2004, 11, 53-60. | 1.6 | 23 |
| 126 | Risk management in biological evolution. <i>Journal of Theoretical Biology</i> , 2003, 225, 45-57. | 1.7 | 25 |

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|-----|--|------|-----------|
| 127 | How the global structure of protein interaction networks evolves. Proceedings of the Royal Society B: Biological Sciences, 2003, 270, 457-466. | 2.6 | 224 |
| 128 | Does Selection Mold Molecular Networks?. Science Signaling, 2003, 2003, pe41-pe41. | 3.6 | 28 |
| 129 | Estimating Coarse Gene Network Structure from Large-Scale Gene Perturbation Data. Genome Research, 2002, 12, 309-315. | 5.5 | 82 |
| 130 | Asymmetric Functional Divergence of Duplicate Genes in Yeast. Molecular Biology and Evolution, 2002, 19, 1760-1768. | 8.9 | 118 |
| 131 | Selection and gene duplication: a view from the genome. Genome Biology, 2002, 3, reviews1012.1. | 9.6 | 85 |
| 132 | The small world inside large metabolic networks. Proceedings of the Royal Society B: Biological Sciences, 2001, 268, 1803-1810. | 2.6 | 798 |
| 133 | How to reconstruct a large genetic network from n gene perturbations in fewer than n ² easy steps. Bioinformatics, 2001, 17, 1183-1197. | 4.1 | 115 |
| 134 | The small world of metabolism. Nature Biotechnology, 2000, 18, 1121-1122. | 17.5 | 367 |
| 135 | Robustness against mutations in genetic networks of yeast. Nature Genetics, 2000, 24, 355-361. | 21.4 | 389 |
| 136 | The Role of Population Size, Pleiotropy and Fitness Effects of Mutations in the Evolution of Overlapping Gene Functions. Genetics, 2000, 154, 1389-1401. | 2.9 | 83 |
| 137 | Causality in Complex Systems. Biology and Philosophy, 1999, 14, 83-101. | 1.4 | 64 |
| 138 | Viral RNA and evolved mutational robustness. The Journal of Experimental Zoology, 1999, 285, 119-127. | 1.4 | 68 |
| 139 | Viral RNA and evolved mutational robustness. , 1999, 285, 119. | | 2 |
| 140 | The fate of duplicated genes: loss or new function?. BioEssays, 1998, 20, 785-788. | 2.5 | 133 |
| 141 | The fate of duplicated genes: loss or new function?. BioEssays, 1998, 20, 785-788. | 2.5 | 1 |