

Andreas Wagner

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9240008/publications.pdf>

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	The small world inside large metabolic networks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 1803-1810.	2.6	798
2	Growthcurver: an R package for obtaining interpretable metrics from microbial growth curves. <i>BMC Bioinformatics</i> , 2016, 17, 172.	2.6	582
3	Robustness and evolvability: a paradox resolved. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2008, 275, 91-100.	2.6	495
4	Energy Constraints on the Evolution of Gene Expression. <i>Molecular Biology and Evolution</i> , 2005, 22, 1365-1374.	8.9	421
5	Robustness against mutations in genetic networks of yeast. <i>Nature Genetics</i> , 2000, 24, 355-361.	21.4	389
6	The small world of metabolism. <i>Nature Biotechnology</i> , 2000, 18, 1121-1122.	17.5	367
7	Robustness Can Evolve Gradually in Complex Regulatory Gene Networks with Varying Topology. <i>PLoS Computational Biology</i> , 2007, 3, e15.	3.2	318
8	Robustness, evolvability, and neutrality. <i>FEBS Letters</i> , 2005, 579, 1772-1778.	2.8	273
9	Distributed robustness versus redundancy as causes of mutational robustness. <i>BioEssays</i> , 2005, 27, 176-188.	2.5	258
10	Neutralism and selectionism: a network-based reconciliation. <i>Nature Reviews Genetics</i> , 2008, 9, 965-974.	16.3	244
11	How the global structure of protein interaction networks evolves. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 457-466.	2.6	224
12	Cryptic genetic variation promotes rapid evolutionary adaptation in an RNA enzyme. <i>Nature</i> , 2011, 474, 92-95.	27.8	209
13	The causes of evolvability and their evolution. <i>Nature Reviews Genetics</i> , 2019, 20, 24-38.	16.3	208
14	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
15	Influence of metabolic network structure and function on enzyme evolution. <i>Genome Biology</i> , 2006, 7, R39.	9.6	161
16	Specialization Can Drive the Evolution of Modularity. <i>PLoS Computational Biology</i> , 2010, 6, e1000719.	3.2	160
17	A latent capacity for evolutionary innovation through exaptation in metabolic systems. <i>Nature</i> , 2013, 500, 203-206.	27.8	149
18	The Robustness and Evolvability of Transcription Factor Binding Sites. <i>Science</i> , 2014, 343, 875-877.	12.6	139

#	ARTICLE	IF	CITATIONS
19	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
20	The fate of duplicated genes: loss or new function?. <i>BioEssays</i> , 1998, 20, 785-788.	2.5	133
21	Gene duplications, robustness and evolutionary innovations. <i>BioEssays</i> , 2008, 30, 367-373.	2.5	120
22	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
23	Asymmetric Functional Divergence of Duplicate Genes in Yeast. <i>Molecular Biology and Evolution</i> , 2002, 19, 1760-1768.	8.9	118
24	How to reconstruct a large genetic network from n gene perturbations in fewer than n ² easy steps. <i>Bioinformatics</i> , 2001, 17, 1183-1197.	4.1	115
25	Evolutionary Plasticity and Innovations in Complex Metabolic Reaction Networks. <i>PLoS Computational Biology</i> , 2009, 5, e1000613.	3.2	112
26	The molecular origins of evolutionary innovations. <i>Trends in Genetics</i> , 2011, 27, 397-410.	6.7	102
27	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
28	Cryptic genetic variation accelerates evolution by opening access to diverse adaptive peaks. <i>Science</i> , 2019, 365, 347-353.	12.6	96
29	Mechanisms of mutational robustness in transcriptional regulation. <i>Frontiers in Genetics</i> , 2015, 6, 322.	2.3	89
30	Selection and gene duplication: a view from the genome. <i>Genome Biology</i> , 2002, 3, reviews1012.1.	9.6	85
31	The Role of Population Size, Pleiotropy and Fitness Effects of Mutations in the Evolution of Overlapping Gene Functions. <i>Genetics</i> , 2000, 154, 1389-1401.	2.9	83
32	Estimating Coarse Gene Network Structure from Large-Scale Gene Perturbation Data. <i>Genome Research</i> , 2002, 12, 309-315.	5.5	82
33	A thousand empirical adaptive landscapes and their navigability. <i>Nature Ecology and Evolution</i> , 2017, 1, 45.	7.8	79
34	High mutation rates limit evolutionary adaptation in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2018, 14, e1007324.	3.5	72
35	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
36	Viral RNA and evolved mutational robustness. <i>The Journal of Experimental Zoology</i> , 1999, 285, 119-127.	1.4	68

#	ARTICLE	IF	CITATIONS
37	Neutral network sizes of biological RNA molecules can be computed and are not atypically small. BMC Bioinformatics, 2008, 9, 464.	2.6	65
38	Causality in Complex Systems. Biology and Philosophy, 1999, 14, 83-101.	1.4	64
39	Protein robustness promotes evolutionary innovations on large evolutionary time-scales. Proceedings of the Royal Society B: Biological Sciences, 2008, 275, 1595-1602.	2.6	63
40	Selection enhances protein evolvability by increasing mutational robustness and foldability. Science, 2020, 370, .	12.6	61
41	Genotype networks shed light on evolutionary constraints. Trends in Ecology and Evolution, 2011, 26, 577-584.	8.7	57
42	The Molecular Chaperone DnaK Is a Source of Mutational Robustness. Genome Biology and Evolution, 2016, 8, 2979-2991.	2.5	57
43	A survey of bacterial insertion sequences using IScan. Nucleic Acids Research, 2007, 35, 5284-5293.	14.5	55
44	Energy costs constrain the evolution of gene expression. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 322-324.	1.3	54
45	An enormous potential for niche construction through bacterial cross-feeding in a homogeneous environment. PLoS Computational Biology, 2018, 14, e1006340.	3.2	54
46	Spaces of the possible: universal Darwinism and the wall between technological and biological innovation. Journal of the Royal Society Interface, 2014, 11, 20131190.	3.4	51
47	Rapid Detection of Positive Selection in Genes and Genomes Through Variation Clusters. Genetics, 2007, 176, 2451-2463.	2.9	49
48	Genotype networks in metabolic reaction spaces. BMC Systems Biology, 2010, 4, 30.	3.0	49
49	Alternative routes and mutational robustness in complex regulatory networks. BioSystems, 2007, 88, 163-172.	2.0	48
50	Superessential reactions in metabolic networks. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1121-30.	7.1	47
51	Mistranslation drives the evolution of robustness in TEM-1 β -lactamase. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12758-12763.	7.1	47
52	Robustness, Evolvability, and the Logic of Genetic Regulation. Artificial Life, 2014, 20, 111-126.	1.3	43
53	Fitness Trade-Offs Determine the Role of the Molecular Chaperonin GroEL in Buffering Mutations. Molecular Biology and Evolution, 2015, 32, 2681-2693.	8.9	43
54	Function does not follow form in gene regulatory circuits. Scientific Reports, 2015, 5, 13015.	3.3	40

#	ARTICLE	IF	CITATIONS
55	Efficient Purging of Deleterious Mutations in Plants with Haploid Selfing. <i>Genome Biology and Evolution</i> , 2014, 6, 1238-1252.	2.5	38
56	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
57	The Genomic Basis of Evolutionary Innovation in <i>Pseudomonas aeruginosa</i> . <i>PLoS Genetics</i> , 2016, 12, e1006005.	3.5	35
58	Evolutionary constraints permeate large metabolic networks. <i>BMC Evolutionary Biology</i> , 2009, 9, 231.	3.2	34
59	Synthetic circuits reveal how mechanisms of gene regulatory networks constrain evolution. <i>Molecular Systems Biology</i> , 2018, 14, e8102.	7.2	34
60	Cooperation is Fleeting in the World of Transposable Elements. <i>PLoS Computational Biology</i> , 2006, 2, e162.	3.2	32
61	Metabolic Networks and Their Evolution. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 29-52.	1.6	31
62	Assessing the benefits of horizontal gene transfer by laboratory evolution and genome sequencing. <i>BMC Evolutionary Biology</i> , 2018, 18, 54.	3.2	31
63	Does Selection Mold Molecular Networks?. <i>Science Signaling</i> , 2003, 2003, pe41-pe41.	3.6	28
64	Mistranslation can enhance fitness through purging of deleterious mutations. <i>Nature Communications</i> , 2017, 8, 15410.	12.8	28
65	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
66	Genotype networks, innovation, and robustness in sulfur metabolism. <i>BMC Systems Biology</i> , 2011, 5, 39.	3.0	27
67	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
68	The architecture of an empirical genotype-phenotype map. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1242-1260.	2.3	27
69	Risk management in biological evolution. <i>Journal of Theoretical Biology</i> , 2003, 225, 45-57.	1.7	25
70	The genotype-phenotype map of an evolving digital organism. <i>PLoS Computational Biology</i> , 2017, 13, e1005414.	3.2	24
71	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
72	Reconstructing Pathways in Large Genetic Networks from Genetic Perturbations. <i>Journal of Computational Biology</i> , 2004, 11, 53-60.	1.6	23

#	ARTICLE	IF	CITATIONS
73	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
74	Mutational Robustness Accelerates the Origin of Novel RNA Phenotypes through Phenotypic Plasticity. <i>Biophysical Journal</i> , 2014, 106, 955-965.	0.5	23
75	Transposable elements as genomic diseases. <i>Molecular BioSystems</i> , 2009, 5, 32-35.	2.9	21
76	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
77	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
78	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
79	Microbial life cycles link global modularity in regulation to mosaic evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 1184-1196.	7.8	18
80	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. <i>PLoS Computational Biology</i> , 2020, 16, e1007727.	3.2	18
81	Human Genome Variation and the Concept of Genotype Networks. <i>PLoS ONE</i> , 2014, 9, e99424.	2.5	18
82	Information theory, evolutionary innovations and evolvability. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160416.	4.0	17
83	Engineering and Biology: Counsel for a Continued Relationship. <i>Biological Theory</i> , 2015, 10, 50-59.	1.5	15
84	The White-Knight Hypothesis, or Does the Environment Limit Innovations?. <i>Trends in Ecology and Evolution</i> , 2017, 32, 131-140.	8.7	15
85	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
86	Diversity begets diversity during community assembly until ecological limits impose a diversity ceiling. <i>Molecular Ecology</i> , 2021, 30, 5874-5887.	3.9	15
87	Gene swamping alters evolution during range expansions in the protist <i>Tetrahymena thermophila</i> . <i>Biology Letters</i> , 2020, 16, 20200244.	2.3	14
88	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
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	The potential for non-adaptive origins of evolutionary innovations in central carbon metabolism. <i>BMC Systems Biology</i> , 2016, 10, 97.	3.0	12
92	Ecology drives the evolution of diverse social strategies in <i>Pseudomonas aeruginosa</i> . <i>Molecular Ecology</i> , 2021, 30, 5214-5228.	3.9	12
93	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
94	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
95	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
96	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
97	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
98	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
99	The low cost of recombination in creating novel phenotypes. <i>BioEssays</i> , 2011, 33, 636-646.	2.5	9
100	Parallel or convergent evolution in human population genomic data revealed by genotype networks. <i>BMC Evolutionary Biology</i> , 2016, 16, 154.	3.2	9
101	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
102	Competition for nutrients increases invasion resistance during assembly of microbial communities. <i>Molecular Ecology</i> , 2022, 31, 4188-4203.	3.9	9
103	Signaling pathways have an inherent need for noise to acquire information. <i>BMC Bioinformatics</i> , 2020, 21, 462.	2.6	8
104	The length scale of multivalent interactions is evolutionarily conserved in fungal and vertebrate phase-separating proteins. <i>Genetics</i> , 2022, 220, .	2.9	8
105	Causal Drift, Robust Signaling, and Complex Disease. <i>PLoS ONE</i> , 2015, 10, e0118413.	2.5	7
106	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
107	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
108	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

#	ARTICLE	IF	CITATIONS
109	Cryptic surface-associated multicellularity emerges through cell adhesion and its regulation. <i>PLoS Biology</i> , 2021, 19, e3001250.	5.6	6
110	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
111	VCF2Networks: applying genotype networks to single-nucleotide variants data. <i>Bioinformatics</i> , 2015, 31, 438-439.	4.1	5
112	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
113	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
114	Multiple Novel Traits without Immediate Benefits Originate in Bacteria Evolving on Single Antibiotics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
115	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
116	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
117	Yeast Proteins may Reversibly Aggregate like Amphiphilic Molecules. <i>Journal of Molecular Biology</i> , 2022, 434, 167352.	4.2	4
118	A limit on the evolutionary rescue of an Antarctic bacterium from rising temperatures. <i>Science Advances</i> , 2022, 8, .	10.3	4
119	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
120	Adaptive gene misregulation. <i>Genetics</i> , 2021, 217, .	2.9	3
121	<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
122	Chaperonin overproduction and metabolic erosion caused by mutation accumulation in <i>Escherichia coli</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	2
123	Viral RNA and evolved mutational robustness. , 1999, 285, 119.		2
124	Translation stalling proline motifs are enriched in slow-growing, thermophilic, and multicellular bacteria. <i>ISME Journal</i> , 2022, 16, 1065-1073.	9.8	2
125	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
126	Constraint and Contingency Pervade the Emergence of Novel Phenotypes in Complex Metabolic Systems. <i>Biophysical Journal</i> , 2017, 113, 690-701.	0.5	1

#	ARTICLE	IF	CITATIONS
127	Population Size Affects Adaptation in Complex Ways: Simulations on Empirical Adaptive Landscapes. <i>Evolutionary Biology</i> , 2018, 45, 156-169.	1.1	1
128	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
129	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
130	The fate of duplicated genes: loss or new function?. <i>BioEssays</i> , 1998, 20, 785-788.	2.5	1
131	DYNAMICS OF AN INSERTION SEQUENCE INFECTION IN A SPATIALLY STRUCTURED ENVIRONMENT. <i>Journal of Biological Systems</i> , 2018, 26, 133-166.	1.4	0
132	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727.		0
133	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727.		0
134	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727.		0
135	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. , 2020, 16, e1007727.		0
136	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0
137	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0
138	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0
139	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0
140	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0
141	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . , 2020, 16, e1008433.		0