

Terence Hwa

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8060993/publications.pdf>

Version: 2024-02-01

138
papers

17,824
citations

15504

65
h-index

16650

123
g-index

151
all docs

151
docs citations

151
times ranked

11936
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbes contribute to setting the ocean carbon flux by altering the fate of sinking particulates. Nature Communications, 2022, 13, 1657.	12.8	30
2	Cellular perception of growth rate and the mechanistic origin of bacterial growth law. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2201585119.	7.1	38
3	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. Molecular Systems Biology, 2021, 17, e10064.	7.2	33
4	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. Molecular Systems Biology, 2021, 17, e9536.	7.2	82
5	Hierarchical and simultaneous utilization of carbon substrates: mechanistic insights, physiological roles, and ecological consequences. Current Opinion in Microbiology, 2021, 63, 172-178.	5.1	13
6	On the optimality of the enzyme-substrate relationship in bacteria. PLoS Biology, 2021, 19, e3001416.	5.6	29
7	A traveling-wave solution for bacterial chemotaxis with growth. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	22
8	Suboptimal resource allocation in changing environments constrains response and growth in bacteria. Molecular Systems Biology, 2021, 17, e10597.	7.2	35
9	Regulation underlying hierarchical and simultaneous utilization of carbon substrates by flux sensors in <i>Escherichia coli</i> . Nature Microbiology, 2020, 5, 206-215.	13.3	44
10	A universal trade-off between growth and lag in fluctuating environments. Nature, 2020, 584, 470-474.	27.8	139
11	General quantitative relations linking cell growth and the cell cycle in <i>Escherichia coli</i> . Nature Microbiology, 2020, 5, 995-1001.	13.3	68
12	Chemotaxis as a navigation strategy to boost range expansion. Nature, 2019, 575, 658-663.	27.8	108
13	An evolutionarily stable strategy to colonize spatially extended habitats. Nature, 2019, 575, 664-668.	27.8	48
14	Disruption of transcription-translation coordination in <i>Escherichia coli</i> leads to premature transcriptional termination. Nature Microbiology, 2019, 4, 2347-2356.	13.3	70
15	Spatiotemporal establishment of dense bacterial colonies growing on hard agar. ELife, 2019, 8, .	6.0	73
16	Slowdown of Translational Elongation in <i>Escherichia coli</i> under Hyperosmotic Stress. MBio, 2018, 9, .	4.1	53
17	Bacterial growth, flow, and mixing shape human gut microbiota density and composition. Gut Microbes, 2018, 9, 1-8.	9.8	39
18	Editorial overview: Current Opinion in Microbiology 2018 Special issue - Microbial systems biology, vol. 45. Current Opinion in Microbiology, 2018, 45, vi-viii.	5.1	0

#	ARTICLE	IF	CITATIONS
19	Effect of water flow and chemical environment on microbiota growth and composition in the human colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6438-6443.	7.1	125
20	Reduction of translating ribosomes enables <i>Escherichia coli</i> to maintain elongation rates during slow growth. <i>Nature Microbiology</i> , 2017, 2, 16231.	13.3	251
21	A global resource allocation strategy governs growth transition kinetics of <i>Escherichia coli</i> . <i>Nature</i> , 2017, 551, 119-123.	27.8	184
22	Quantifying the benefit of a proteome reserve in fluctuating environments. <i>Nature Communications</i> , 2017, 8, 1225.	12.8	108
23	Effect of flow and peristaltic mixing on bacterial growth in a gut-like channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11414-11419.	7.1	120
24	Constrained Allocation Flux Balance Analysis. <i>PLoS Computational Biology</i> , 2016, 12, e1004913.	3.2	136
25	Inflating bacterial cells by increased protein synthesis. <i>Molecular Systems Biology</i> , 2015, 11, 836.	7.2	164
26	A growth rate composition formula for the growth of <i>E. coli</i> on co-utilized carbon substrates. <i>Molecular Systems Biology</i> , 2015, 11, 801.	7.2	89
27	Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria. <i>Molecular Systems Biology</i> , 2015, 11, 784.	7.2	291
28	Overflow metabolism in <i>Escherichia coli</i> results from efficient proteome allocation. <i>Nature</i> , 2015, 528, 99-104.	27.8	566
29	Emergence of robust growth laws from optimal regulation of ribosome synthesis. <i>Molecular Systems Biology</i> , 2014, 10, 747.	7.2	374
30	Direct Coupling Analysis for Protein Contact Prediction. <i>Methods in Molecular Biology</i> , 2014, 1137, 55-70.	0.9	52
31	Predicting the spatiotemporal dynamics of hair follicle patterns in the developing mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2596-2601.	7.1	31
32	Bacterial growth: global effects on gene expression, growth feedback and proteome partition. <i>Current Opinion in Biotechnology</i> , 2014, 28, 96-102.	6.6	182
33	Coordination of bacterial proteome with metabolism by cyclic AMP signalling. <i>Nature</i> , 2013, 500, 301-306.	27.8	375
34	The Innate Growth Bistability and Fitness Landscapes of Antibiotic-Resistant Bacteria. <i>Science</i> , 2013, 342, 1237-1243.	12.6	168
35	Molecular crowding limits translation and cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16754-16759.	7.1	241
36	Coevolutionary signals across protein lineages help capture multiple protein conformations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20533-20538.	7.1	163

#	ARTICLE	IF	CITATIONS
37	Genomics-aided structure prediction. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10340-10345.	7.1	210
38	Stripe Formation in Bacterial Systems with Density-Suppressed Motility. Physical Review Letters, 2012, 108, 198102.	7.8	127
39	On the rapidity of antibiotic resistance evolution facilitated by a concentration gradient. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10775-10780.	7.1	162
40	Needle-based activation of ammonium uptake in <i>Escherichia coli</i> . Molecular Systems Biology, 2012, 8, 616.	7.2	76
41	On Ribosome Load, Codon Bias and Protein Abundance. PLoS ONE, 2012, 7, e48542.	2.5	33
42	Gene length may contribute to graded transcriptional responses in the Drosophila embryo. Developmental Biology, 2011, 360, 230-240.	2.0	17
43	Bacterial growth laws and their applications. Current Opinion in Biotechnology, 2011, 22, 559-565.	6.6	237
44	Overcoming Fluctuation and Leakage Problems in the Quantification of Intracellular 2-Oxoglutarate Levels in <i>Escherichia coli</i> . Applied and Environmental Microbiology, 2011, 77, 6763-6771.	3.1	36
45	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1293-301.	7.1	1,231
46	Quantifying the sequence-function relation in gene silencing by bacterial small RNAs. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12473-12478.	7.1	44
47	Sequential Establishment of Stripe Patterns in an Expanding Cell Population. Science, 2011, 334, 238-241.	12.6	346
48	Speed, Sensitivity, and Bistability in Auto-activating Signaling Circuits. PLoS Computational Biology, 2011, 7, e1002265.	3.2	51
49	Dissecting the Specificity of Protein-Protein Interaction in Bacterial Two-Component Signaling: Orphans and Crosstalks. PLoS ONE, 2011, 6, e19729.	2.5	91
50	Computational Modeling of Phosphotransfer Complexes in Two-Component Signaling. Methods in Enzymology, 2010, 471, 43-58.	1.0	18
51	Sources and Sinks: A Stochastic Model of Evolution in Heterogeneous Environments. Physical Review Letters, 2010, 105, 248104.	7.8	58
52	Inference of Direct Residue Contacts in Two-Component Signaling. Methods in Enzymology, 2010, 471, 17-41.	1.0	40
53	Interdependence of Cell Growth and Gene Expression: Origins and Consequences. Science, 2010, 330, 1099-1102.	12.6	1,183
54	Reversible Adenylation of Glutamine Synthetase Is Dynamically Counterbalanced during Steady-State Growth of <i>Escherichia coli</i> . Journal of Molecular Biology, 2010, 404, 522-536.	4.2	15

#	ARTICLE	IF	CITATIONS
55	Evolutionary selection between alternative modes of gene regulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8841-8846.	7.1	44
56	High-resolution protein complexes from integrating genomic information with molecular simulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22124-22129.	7.1	174
57	Traffic patrol in the transcription of ribosomal RNA. RNA Biology, 2009, 6, 392-394.	3.1	15
58	Identification of direct residue contacts in protein-protein interaction by message passing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 67-72.	7.1	902
59	Growth Rate-Dependent Global Effects on Gene Expression in Bacteria. Cell, 2009, 139, 1366-1375.	28.9	614
60	Small RNAs establish gene expression thresholds. Current Opinion in Microbiology, 2008, 11, 574-579.	5.1	119
61	Co-Evolving Motions at Protein-Protein Interfaces of Two-Component Signaling Systems Identified by Covariance Analysis. Biochemistry, 2008, 47, 7782-7784.	2.5	22
62	Growth-rate-dependent partitioning of RNA polymerases in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20245-20250.	7.1	189
63	Stochasticity and traffic jams in the transcription of ribosomal RNA: Intriguing role of termination and antitermination. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18159-18164.	7.1	126
64	An integrated mechanobiochemical feedback mechanism describes chromosome motility from prometaphase to anaphase in mitosis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13752-13757.	7.1	18
65	Deterministic characterization of stochastic genetic circuits. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7402-7407.	7.1	71
66	Combinatorial transcriptional control of the lactose operon of Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6043-6048.	7.1	222
67	A mechanobiochemical mechanism for monooriented chromosome oscillation in mitosis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16104-16109.	7.1	14
68	Quantitative Characteristics of Gene Regulation by Small RNA. PLoS Biology, 2007, 5, e229.	5.6	346
69	Stochastic fluctuations in metabolic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9224-9229.	7.1	127
70	Features of Protein-Protein Interactions in Two-Component Signaling Deduced from Genomic Libraries. Methods in Enzymology, 2007, 422, 75-101.	1.0	44
71	Designing sequential transcription logic: a simple genetic circuit for conditional memory. Systems and Synthetic Biology, 2007, 1, 89-98.	1.0	30
72	QUANTITATIVE ASPECTS OF GENE REGULATION IN BACTERIA: AMPLIFICATION, THRESHOLD, AND COMBINATORIAL CONTROL. , 2007, , .		0

#	ARTICLE	IF	CITATIONS
73	A Novel Method Distinguishes Between Mutation Rates and Fixation Biases in Patterns of Single-Nucleotide Substitution. <i>Journal of Molecular Evolution</i> , 2006, 62, 168-175.	1.8	10
74	Substantial Regional Variation in Substitution Rates in the Human Genome: Importance of GC Content, Gene Density, and Telomere-Specific Effects. <i>Journal of Molecular Evolution</i> , 2005, 60, 748-763.	1.8	85
75	Nonlinear protein degradation and the function of genetic circuits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9559-9564.	7.1	157
76	Identification and measurement of neighbor-dependent nucleotide substitution processes. <i>Bioinformatics</i> , 2005, 21, 2322-2328.	4.1	70
77	Transcriptional regulation by the numbers: applications. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 125-135.	3.3	343
78	Transcriptional regulation by the numbers: models. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 116-124.	3.3	660
79	Regional and time-resolved mutation patterns of the human genome. <i>Bioinformatics</i> , 2004, 20, 1482-1485.	4.1	16
80	Translocation of structured polynucleotides through nanopores. <i>Physical Biology</i> , 2004, 1, 19-26.	1.8	93
81	Analytical study of the effect of recombination on evolution via DNA shuffling. <i>Physical Review E</i> , 2004, 69, 051911.	2.1	7
82	Mechanically Probing the Folding Pathway of Single RNA Molecules. <i>Biophysical Journal</i> , 2003, 84, 2831-2840.	0.5	44
83	DNA Sequence Evolution with Neighbor-Dependent Mutation. <i>Journal of Computational Biology</i> , 2003, 10, 313-322.	1.6	89
84	Localization of denaturation bubbles in random DNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4411-4416.	7.1	73
85	Distinct Changes of Genomic Biases in Nucleotide Substitution at the Time of Mammalian Radiation. <i>Molecular Biology and Evolution</i> , 2003, 20, 1887-1896.	8.9	95
86	On schemes of combinatorial transcription logic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5136-5141.	7.1	586
87	Dynamics of Competitive Evolution on a Smooth Landscape. <i>Physical Review Letters</i> , 2003, 90, 088103.	7.8	24
88	Physical constraints and functional characteristics of transcription factor-DNA interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12015-12020.	7.1	230
89	Hybrid alignment: high-performance with universal statistics. <i>Bioinformatics</i> , 2002, 18, 864-872.	4.1	24
90	DNA sequence evolution with neighbor-dependent mutation. , 2002, , .		10

#	ARTICLE	IF	CITATIONS
91	On the Selection and Evolution of Regulatory DNA Motifs. <i>Journal of Molecular Evolution</i> , 2002, 55, 386-400.	1.8	102
92	Statistical significance and extremal ensemble of gapped local hybrid alignment. , 2002, , 3-21.		3
93	Force-Induced Denaturation of RNA. <i>Biophysical Journal</i> , 2001, 81, 1324-1332.	0.5	77
94	The estimation of statistical parameters for local alignment score distributions. <i>Nucleic Acids Research</i> , 2001, 29, 351-361.	14.5	150
95	Statistical Significance of Probabilistic Sequence Alignment and Related Local Hidden Markov Models. <i>Journal of Computational Biology</i> , 2001, 8, 249-282.	1.6	55
96	Expression Patterns of Cell-type-specific Genes in <i>Dictyostelium</i> . <i>Molecular Biology of the Cell</i> , 2001, 12, 2590-2600.	2.1	52
97	An analytic study of the phase transition line in local sequence alignment with gaps. <i>Discrete Applied Mathematics</i> , 2000, 104, 113-142.	0.9	26
98	Universal susceptibility variations in 1+1 dimensional vortex glass. <i>Physica C: Superconductivity and Its Applications</i> , 2000, 332, 232-236.	1.2	0
99	Scaling Laws and Similarity Detection in Sequence Alignment with Gaps. <i>Journal of Computational Biology</i> , 2000, 7, 115-141.	1.6	16
100	RNA Secondary Structure Formation: A Solvable Model of Heteropolymer Folding. <i>Physical Review Letters</i> , 1999, 83, 1479-1482.	7.8	68
101	Thermodynamics of Mesoscopic Vortex Systems in 1+1 Dimensions. <i>Physical Review Letters</i> , 1999, 83, 4860-4863.	7.8	23
102	Hydrodynamics of the Kuramoto-Sivashinsky Equation in Two Dimensions. <i>Physical Review Letters</i> , 1999, 83, 5262-5265.	7.8	22
103	From vortices to genomics. <i>Nature</i> , 1999, 399, 17-18.	27.8	16
104	Optimal detection of sequence similarity by local alignment. , 1998, , .		9
105	On nonlinear diffusion with multiplicative noise. <i>Europhysics Letters</i> , 1998, 41, 147-152.	2.0	41
106	Polymer Reptation in Disordered Media. <i>Physical Review Letters</i> , 1998, 80, 3145-3148.	7.8	18
107	Static and dynamic properties of inhomogeneous elastic media on disordered substrate. <i>Physical Review B</i> , 1998, 57, 8235-8253.	3.2	33
108	OPTIMIZING SMITH-WATERMAN ALIGNMENTS. , 1998, , 302-13.		7

#	ARTICLE	IF	CITATIONS
109	Denaturation of Heterogeneous DNA. Physical Review Letters, 1997, 79, 2375-2378.	7.8	160
110	Polymer Adsorption on Disordered Substrates. Physical Review Letters, 1997, 79, 4930-4930.	7.8	5
111	Topological order in the vortex-glass phase of high-temperature superconductors. Physical Review B, 1997, 55, 626-629.	3.2	113
112	DNA Sequence Alignment and Critical Phenomena. Materials Research Society Symposia Proceedings, 1996, 463, 75.	0.1	1
113	Mode-coupling and renormalization group results for the noisy Burgers equation. Physical Review E, 1996, 53, 4424-4438.	2.1	73
114	Similarity Detection and Localization. Physical Review Letters, 1996, 76, 2591-2594.	7.8	68
115	Interacting Arrays of Lines and Steps in Random Media. Physical Review Letters, 1996, 77, 4233-4236.	7.8	5
116	Tribology of Sliding Elastic Media. Physical Review Letters, 1996, 77, 278-281.	7.8	60
117	Defect-mediated stability: an effective hydrodynamic theory of spatiotemporal chaos. Physica D: Nonlinear Phenomena, 1995, 84, 494-512.	2.8	33
118	Disorder-induced depinning transition. Physical Review B, 1995, 51, 455-469.	3.2	34
119	Vortex glass phase and universal susceptibility variations in planar arrays of flux lines. Physical Review Letters, 1994, 72, 2466-2469.	7.8	67
120	Dynamic and Static Properties of the Randomly Pinned Planar Flux Array. Physical Review Letters, 1994, 72, 4133-4136.	7.8	47
121	Anomalous fluctuations of directed polymers in random media. Physical Review B, 1994, 49, 3136-3154.	3.2	89
122	Hwa, Kardar, and Paczuski reply. Physical Review Letters, 1994, 72, 785-785.	7.8	3
123	Flux pinning and forced vortex entanglement by splayed columnar defects. Physical Review Letters, 1993, 71, 3545-3548.	7.8	202
124	Comment on "Random disorder in a model vortex liquid". Physical Review Letters, 1993, 71, 2349-2349.	7.8	4
125	Flux-line pinning by competing disorders. Physical Review B, 1993, 48, 1167-1174.	3.2	103
126	Nonequilibrium dynamics of driven line liquids. Physical Review Letters, 1992, 69, 1552-1555.	7.8	58

#	ARTICLE	IF	CITATIONS
127	$1/\sqrt{t}$ noise in dissipative transport. Physical Review A, 1992, 45, R559-R562.	2.5	30
128	Avalanches, hydrodynamics, and discharge events in models of sandpiles. Physical Review A, 1992, 45, 7002-7023.	2.5	290
129	Crumpled and collapsed conformation in graphite oxide membranes. Nature, 1992, 355, 426-428.	27.8	160
130	Conformation of graphite oxide membranes in solution. Physical Review A, 1991, 44, R2235-R2238.	2.5	93
131	Exact scaling function of interface growth dynamics. Physical Review A, 1991, 44, R7873-R7876.	2.5	72
132	Growth-induced roughening of crystalline facets. Physical Review Letters, 1991, 66, 441-444.	7.8	70
133	Self-avoiding crumpled manifolds: Perturbative analysis and renormalizability. Physical Review Letters, 1990, 64, 2022-2025.	7.8	22
134	Generalized μ -expansion for self-avoiding tethered manifolds. Physical Review A, 1990, 41, 1751-1756.	2.5	26
135	Fractals and self-organized criticality in dissipative dynamics. Physica D: Nonlinear Phenomena, 1989, 38, 198-202.	2.8	14
136	Dissipative transport in open systems: An investigation of self-organized criticality. Physical Review Letters, 1989, 62, 1813-1816.	7.8	273
137	Burgers equation with correlated noise: Renormalization-group analysis and applications to directed polymers and interface growth. Physical Review A, 1989, 39, 3053-3075.	2.5	616
138	Evolution of Surface Patterns on Swelling Gels. Physical Review Letters, 1988, 61, 106-109.	7.8	60