Adam M Feist

List of Publications by Year
in descending order

101 papers	13,190 citations	50170 46 h-index	30848 102 g-index
122 all docs	122 docs citations	122 times ranked	9899 citing authors

#	Article	IF	Citations
1	Selection for Cell Yield Does Not Reduce Overflow Metabolism in Escherichia coli. Molecular Biology and Evolution, 2022, 39, .	3.5	3
2	Engineering Pseudomonas putida for improved utilization of syringyl aromatics. Biotechnology and Bioengineering, 2022, 119, 2541-2550.	1.7	7
3	Machine-learning from Pseudomonas putida KT2440 transcriptomes reveals its transcriptional regulatory network. Metabolic Engineering, 2022, 72, 297-310.	3.6	28
4	Membrane transporter identification and modulation via adaptive laboratory evolution. Metabolic Engineering, 2022, 72, 376-390.	3.6	16
5	Laboratory evolution of synthetic electron transport system variants reveals a larger metabolic respiratory system and its plasticity. Nature Communications, 2022, 13, .	5.8	8
6	Identifying the effect of vancomycin on health careâ€“associated methicillin-resistant Staphylococcus aureus strains using bacteriological and physiological media. GigaScience, 2021, 10, .	3.3	5
7	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. Cell Reports, 2021, 35, 108961.	2.9	13
8	Compensatory evolution of Pseudomonas aeruginosaâ€™s slow growth phenotype suggests mechanisms of adaptation in cystic fibrosis. Nature Communications, 2021, 12, 3186.	5.8	33
9	Environmental conditions dictate differential evolution of vancomycin resistance in Staphylococcus aureus. Communications Biology, 2021, 4, 793.	2.0	18
10	Genomeâ€scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	3.2	15
11	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. MSphere, 2021, 6, e0044321.	1.3	12
12	Generation of Pseudomonas putida KT2440 Strains with Efficient Utilization of Xylose and Galactose via Adaptive Laboratory Evolution. ACS Sustainable Chemistry and Engineering, 2021, 9, 11512-11523.	3.2	32
13	Adaptive laboratory evolution of Rhodosporidium toruloides to inhibitors derived from lignocellulosic biomass and genetic variations behind evolution. Bioresource Technology, 2021, 333, 125171.	4.8	42
14	Escherichia coli Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. ACS Synthetic Biology, 2021, 10, 3379-3395.	1.9	5
15	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	3.5	52
16	Highâ€quality genomeâ€scale metabolic modelling of Pseudomonas putida highlights its broad metabolic capabilities. Environmental Microbiology, 2020, 22, 255-269.	1.8	127
17	Lipid and carotenoid production from wheat straw hydrolysates by different oleaginous yeasts. Journal of Cleaner Production, 2020, 249, 119308.	4.6	61
18	Adaptive laboratory evolution of Pseudomonas putida KT2440 improves p-coumaric and ferulic acid catabolism and tolerance. Metabolic Engineering Communications, 2020, 11, e00143.	1.9	73

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19	Generation of ionic liquid tolerant Pseudomonas putida KT2440 strains via adaptive laboratory evolution. Green Chemistry, 2020, 22, 5677-5690.	4.6	29
20	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. BMC Genomics, 2020, 21, 514.	1.2	23
21	Elucidating aromatic acid tolerance at low pH in Saccharomyces cerevisiae using adaptive laboratory evolution. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27954-27961.	3.3	40
22	Kinetic profiling of metabolic specialists demonstrates stability and consistency of in vivo enzyme turnover numbers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23182-23190.	3.3	65
23	Directed Metabolic Pathway Evolution Enables Functional Pterin-Dependent Aromatic-Amino-Acid Hydroxylation in Escherichia coli. ACS Synthetic Biology, 2020, 9, 494-499.	1.9	9
24	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
25	Genetic Determinants Enabling Medium-Dependent Adaptation to Nafcillin in Methicillin-Resistant Staphylococcus aureus. MSystems, 2020, 5, .	1.7	8
26	Adaptive laboratory evolution of Escherichia coli under acid stress. Microbiology (United Kingdom), 2020, 166, 141-148.	0.7	28
27	The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. Metabolic Engineering, 2019, 56, 1-16.	3.6	307
28	Generation of an E. coli platform strain for improved sucrose utilization using adaptive laboratory evolution. Microbial Cell Factories, 2019, 18, 116.	1.9	22
29	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14368-14373.	3.3	79
30	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of Staphylococcus aureus. Applied and Environmental Microbiology, 2019, 85, .	1.4	21
31	Adaptive laboratory evolution of tolerance to dicarboxylic acids in Saccharomyces cerevisiae. Metabolic Engineering, 2019, 56, 130-141.	3.6	63
32	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	5.9	21
33	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. PLoS Computational Biology, 2019, 15, e1007066.	1.5	33
34	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	1.5	83
35	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43.	2.4	14
36	The genetic basis for adaptation of model-designed syntrophic co-cultures. PLoS Computational Biology, 2019, 15, e1006213.	1.5	17

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37	Coupling S-adenosylmethionineâ€“dependent methylation to growth: Design and uses. PLoS Biology, 2019, 17, e2007050.	2.6	39
38	Enzyme promiscuity shapes adaptation to novel growth substrates. Molecular Systems Biology, 2019, 15, e8462.	3.2	52
39	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322.	2.4	8
40	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25287-25292.	3.3	56
41	ALEdb 1.0: a database of mutations from adaptive laboratory evolution experimentation. Nucleic Acids Research, 2019, 47, D1164-D1171.	6.5	93
42	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 222-227.	3.3	70
43	Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in Saccharomyces cerevisiae. Metabolic Engineering, 2018, 47, 73-82.	3.6	47
44	Underground metabolism: network-level perspective and biotechnological potential. Current Opinion in Biotechnology, 2018, 49, 108-114.	3.3	45
45	Reframing gene essentiality in terms of adaptive flexibility. BMC Systems Biology, 2018, 12, 143.	3.0	11
46	Enhanced Metabolite Productivity of Escherichia coli Adapted to Glucose M9 Minimal Medium. Frontiers in Bioengineering and Biotechnology, 2018, 6, 166.	2.0	20
47	Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. Microbiology Resource Announcements, 2018, 7, .	0.3	3
48	Identification of growth-coupled production strains considering protein costs and kinetic variability. Metabolic Engineering Communications, 2018, 7, e00080.	1.9	19
49	Evolution of gene knockout strains of E. coli reveal regulatory architectures governed by metabolism. Nature Communications, 2018, 9, 3796.	5.8	59
50	Growth Adaptation of gnd and sdhCB Escherichia coli Deletion Strains Diverges From a Similar Initial Perturbation of the Transcriptome. Frontiers in Microbiology, 2018, 9, 1793.	1.5	23
51	Adaptation to the coupling of glycolysis to toxic methylglyoxal production in tpiA deletion strains of Escherichia coli requires synchronized and counterintuitive genetic changes. Metabolic Engineering, 2018, 48, 82-93.	3.6	38
52	Multiple Optimal Phenotypes Overcome Redox and Glycolytic Intermediate Metabolite Imbalances in Escherichia coli pgi Knockout Evolutions. Applied and Environmental Microbiology, 2018, 84, .	1.4	22
53	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in Escherichia coli strains lacking the Phosphotransferase System. Metabolic Engineering, 2018, 48, 233-242.	3.6	43
54	Computational Methods to Assess the Production Potential of Bio-Based Chemicals. Methods in Molecular Biology, 2018, 1671, 97-116.	0.4	4

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55	A Model for Designing Adaptive Laboratory Evolution Experiments. Applied and Environmental Microbiology, 2017, 83, .	1.4	71
56	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. Applied and Environmental Microbiology, 2017, 83, .	1.4	76
57	Increased production of L-serine in Escherichia coli through Adaptive Laboratory Evolution. Metabolic Engineering, 2017, 39, 141-150.	3.6	116
58	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. Metabolic Engineering, 2017, 39, 220-227.	3.6	34
59	Fast growth phenotype of E. coli K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. Metabolic Engineering, 2017, 44, 100-107.	3.6	59
60	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	9.4	425
61	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. Microbial Cell Factories, 2017, 16, 204.	1.9	60
62	Evolution of E. coli on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. PLoS ONE, 2016, 11, e0151130.	1.1	54
63	What do cells actually want?. Genome Biology, 2016, 17, 110.	3.8	18
64	Acidithiobacillus ferrooxidans's comprehensive model driven analysis of the electron transfer metabolism and synthetic strain design for biomining applications. Metabolic Engineering Communications, 2016, 3, 84-96.	1.9	39
65	Characterizing Strain Variation in Engineered E.Âcoli Using a Multi-Omics-Based Workflow. Cell Systems, 2016, 2, 335-346.	2.9	73
66	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	2.9	124
67	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	5.8	141
68	Global Rebalancing of Cellular Resources by Pleiotropic Point Mutations Illustrates a Multi-scale Mechanism of Adaptive Evolution. Cell Systems, 2016, 2, 260-271.	2.9	107
69	Modeling Method for Increased Precision and Scope of Directly Measurable Fluxes at a Genome-Scale. Analytical Chemistry, 2016, 88, 3844-3852.	3.2	34
70	MID Max: LCâ€“MS/MS Method for Measuring the Precursor and Product Mass Isotopomer Distributions of Metabolic Intermediates and Cofactors for Metabolic Flux Analysis Applications. Analytical Chemistry, 2016, 88, 1362-1370.	3.2	48
71	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
72	Model-driven discovery of underground metabolic functions in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 929-934.	3.3	82

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73	Next-generation genome-scale models for metabolic engineering. Current Opinion in Biotechnology, 2015, 35, 23-29.	3.3	144
74	A pH and solvent optimized reverse-phase ion-paring-LCâ€“MS/MS method that leverages multiple scan-types for targeted absolute quantification of intracellular metabolites. Metabolomics, 2015, 11, 1338-1350.	1.4	42
75	Fast Swinnex filtration (FSF): a fast and robust sampling and extraction method suitable for metabolomics analysis of cultures grown in complex media. Metabolomics, 2015, 11, 198-209.	1.4	28
76	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of Escherichia coli K-12 MG1655 on Glucose Minimal Medium. Applied and Environmental Microbiology, 2015, 81, 17-30.	1.4	235
77	Constraint-Based Modeling of Carbon Fixation and the Energetics of Electron Transfer in Geobacter metallireducens. PLoS Computational Biology, 2014, 10, e1003575.	1.5	38
78	Reconstruction and modeling protein translocation and compartmentalization in Escherichia coli at the genome-scale. BMC Systems Biology, 2014, 8, 110.	3.0	81
79	A modelâ€driven quantitative metabolomics analysis of aerobic and anaerobic metabolism in E. coli Kâ€12 MG1655 that is biochemically and thermodynamically consistent. Biotechnology and Bioengineering, 2014, 111, 803-815.	1.7	53
80	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1819-1828.	1.5	36
81	Optimal cofactor swapping can increase the theoretical yield for chemical production in Escherichia coli and Saccharomyces cerevisiae. Metabolic Engineering, 2014, 24, 117-128.	3.6	40
82	Generation of an atlas for commodity chemical production in Escherichia coli and a novel pathway prediction algorithm, GEM-Path. Metabolic Engineering, 2014, 25, 140-158.	3.6	152
83	Evolution of Escherichia coli to 42 Â°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	3.5	145
84	Tracing Compartmentalized NADPH Metabolism in the Cytosol and Mitochondria of Mammalian Cells. Molecular Cell, 2014, 55, 253-263.	4.5	477
85	Optimizing Cofactor Specificity of Oxidoreductase Enzymes for the Generation of Microbial Production Strainsâ€”OptSwap. Industrial Biotechnology, 2013, 9, 236-246.	0.5	30
86	Basic and applied uses of genomeâ€scale metabolic network reconstructions of Escherichia coli. Molecular Systems Biology, 2013, 9, 661.	3.2	290
87	Genomically and biochemically accurate metabolic reconstruction of Methanosarcina barkeri Fusaro, iMG746. Biotechnology Journal, 2013, 8, 1070-1079.	1.8	41
88	Sulfide-Driven Microbial Electrosynthesis. Environmental Science & Technology, 2013, 47, 568-573.	4.6	101
89	Genome-scale metabolic reconstructions of multiple Escherichia coli strains highlight strain-specific adaptations to nutritional environments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20338-20343.	3.3	270
90	Maximizing biomass productivity and cell density of Chlorella vulgaris by using light-emitting diode-based photobioreactor. Journal of Biotechnology, 2012, 161, 242-249.	1.9	129

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91	Cumulative Number of Cell Divisions as a Meaningful Timescale for Adaptive Laboratory Evolution of Escherichia coli. PLoS ONE, 2011, 6, e26172.	1.1	50
92	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	5.5	1,408
93	A comprehensive genomeâ€scale reconstruction of Escherichia coli metabolismâ€”2011. Molecular Systems Biology, 2011, 7, 535.	3.2	917
94	Model-driven evaluation of the production potential for growth-coupled products of Escherichia coli. Metabolic Engineering, 2010, 12, 173-186.	3.6	221
95	The biomass objective function. Current Opinion in Microbiology, 2010, 13, 344-349.	2.3	540
96	Reconstruction of biochemical networks in microorganisms. Nature Reviews Microbiology, 2009, 7, 129-143.	13.6	797
97	Genome-scale reconstruction and in silico analysis of the Clostridium acetobutylicum ATCC 824 metabolic network. Applied Microbiology and Biotechnology, 2008, 80, 849-862.	1.7	161
98	The growing scope of applications of genome-scale metabolic reconstructions using Escherichia coli. Nature Biotechnology, 2008, 26, 659-667.	9.4	491
99	A genomeâ€scale metabolic reconstruction for Escherichia coli Kâ€12 MG1655 that accounts for 1260 ORFs and thermodynamic information. Molecular Systems Biology, 2007, 3, 121.	3.2	1,234
100	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. Nature Protocols, 2007, 2, 727-738.	5.5	757
101	Modeling methanogenesis with a genomeâ€scale metabolic reconstruction of Methanosarcina barkeri. Molecular Systems Biology, 2006, 2, 2006.0004.	3.2	189