

# Adam M Feist

## List of Publications by Year in descending order

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101  
papers

13,190  
citations

50276

46  
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30922

102  
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122  
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122  
docs citations

122  
times ranked

9899  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , 2011, 6, 1290-1307.	12.0	1,408
2	A genome-scale metabolic reconstruction for <i>Escherichia coli</i> K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121.	7.2	1,234
3	A comprehensive genome-scale reconstruction of <i>Escherichia coli</i> metabolism. <i>Molecular Systems Biology</i> , 2011, 7, 535.	7.2	917
4	Reconstruction of biochemical networks in microorganisms. <i>Nature Reviews Microbiology</i> , 2009, 7, 129-143.	28.6	797
5	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. <i>Nature Protocols</i> , 2007, 2, 727-738.	12.0	757
6	The biomass objective function. <i>Current Opinion in Microbiology</i> , 2010, 13, 344-349.	5.1	540
7	The growing scope of applications of genome-scale metabolic reconstructions using <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2008, 26, 659-667.	17.5	491
8	Tracing Compartmentalized NADPH Metabolism in the Cytosol and Mitochondria of Mammalian Cells. <i>Molecular Cell</i> , 2014, 55, 253-263.	9.7	477
9	iML1515, a knowledgebase that computes <i>Escherichia coli</i> traits. <i>Nature Biotechnology</i> , 2017, 35, 904-908.	17.5	425
10	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
11	The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. <i>Metabolic Engineering</i> , 2019, 56, 1-16.	7.0	307
12	Basic and applied uses of genome-scale metabolic network reconstructions of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2013, 9, 661.	7.2	290
13	Genome-scale metabolic reconstructions of multiple <i>Escherichia coli</i> strains highlight strain-specific adaptations to nutritional environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20338-20343.	7.1	270
14	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of <i>Escherichia coli</i> K-12 MG1655 on Glucose Minimal Medium. <i>Applied and Environmental Microbiology</i> , 2015, 81, 17-30.	3.1	235
15	Model-driven evaluation of the production potential for growth-coupled products of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2010, 12, 173-186.	7.0	221
16	Modeling methanogenesis with a genome-scale metabolic reconstruction of <i>Methanosarcina barkeri</i> . <i>Molecular Systems Biology</i> , 2006, 2, 2006.0004.	7.2	189
17	Genome-scale reconstruction and in silico analysis of the <i>Clostridium acetobutylicum</i> ATCC 824 metabolic network. <i>Applied Microbiology and Biotechnology</i> , 2008, 80, 849-862.	3.6	161
18	Generation of an atlas for commodity chemical production in <i>Escherichia coli</i> and a novel pathway prediction algorithm, GEM-Path. <i>Metabolic Engineering</i> , 2014, 25, 140-158.	7.0	152

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19	Evolution of <i>Escherichia coli</i> to 42 °C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. <i>Molecular Biology and Evolution</i> , 2014, 31, 2647-2662.	8.9	145
20	Next-generation genome-scale models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2015, 35, 23-29.	6.6	144
21	Multi-omic data integration enables discovery of hidden biological regularities. <i>Nature Communications</i> , 2016, 7, 13091.	12.8	141
22	Maximizing biomass productivity and cell density of <i>Chlorella vulgaris</i> by using light-emitting diode-based photobioreactor. <i>Journal of Biotechnology</i> , 2012, 161, 242-249.	3.8	129
23	High-quality genome-scale metabolic modelling of <i>Pseudomonas putida</i> highlights its broad metabolic capabilities. <i>Environmental Microbiology</i> , 2020, 22, 255-269.	3.8	127
24	Multi-omics Quantification of Species Variation of <i>Escherichia coli</i> Links Molecular Features with Strain Phenotypes. <i>Cell Systems</i> , 2016, 3, 238-251.e12.	6.2	124
25	Increased production of L-serine in <i>Escherichia coli</i> through Adaptive Laboratory Evolution. <i>Metabolic Engineering</i> , 2017, 39, 141-150.	7.0	116
26	Global Rebalancing of Cellular Resources by Pleiotropic Point Mutations Illustrates a Multi-scale Mechanism of Adaptive Evolution. <i>Cell Systems</i> , 2016, 2, 260-271.	6.2	107
27	Sulfide-Driven Microbial Electrosynthesis. <i>Environmental Science &amp; Technology</i> , 2013, 47, 568-573.	10.0	101
28	ALEdb 1.0: a database of mutations from adaptive laboratory evolution experimentation. <i>Nucleic Acids Research</i> , 2019, 47, D1164-D1171.	14.5	93
29	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
30	Model-driven discovery of underground metabolic functions in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 929-934.	7.1	82
31	Reconstruction and modeling protein translocation and compartmentalization in <i>Escherichia coli</i> at the genome-scale. <i>BMC Systems Biology</i> , 2014, 8, 110.	3.0	81
32	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14368-14373.	7.1	79
33	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	76
34	Characterizing Strain Variation in Engineered <i>E. coli</i> Using a Multi-Omics-Based Workflow. <i>Cell Systems</i> , 2016, 2, 335-346.	6.2	73
35	Adaptive laboratory evolution of <i>Pseudomonas putida</i> KT2440 improves p-coumaric and ferulic acid catabolism and tolerance. <i>Metabolic Engineering Communications</i> , 2020, 11, e00143.	3.6	73
36	A Model for Designing Adaptive Laboratory Evolution Experiments. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	71

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37	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 222-227.	7.1	70
38	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
39	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.	7.1	65
40	Adaptive laboratory evolution of tolerance to dicarboxylic acids in <i>Saccharomyces cerevisiae</i> . Metabolic Engineering, 2019, 56, 130-141.	7.0	63
41	Lipid and carotenoid production from wheat straw hydrolysates by different oleaginous yeasts. Journal of Cleaner Production, 2020, 249, 119308.	9.3	61
42	Generation of a platform strain for ionic liquid tolerance using adaptive laboratory evolution. Microbial Cell Factories, 2017, 16, 204.	4.0	60
43	Fast growth phenotype of <i>E. coli</i> K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. Metabolic Engineering, 2017, 44, 100-107.	7.0	59
44	Evolution of gene knockout strains of <i>E. coli</i> reveal regulatory architectures governed by metabolism. Nature Communications, 2018, 9, 3796.	12.8	59
45	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.	7.1	56
46	Evolution of <i>E. coli</i> on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. PLoS ONE, 2016, 11, e0151130.	2.5	54
47	A model-driven quantitative metabolomics analysis of aerobic and anaerobic metabolism in <i>E. coli</i> K12 MG1655 that is biochemically and thermodynamically consistent. Biotechnology and Bioengineering, 2014, 111, 803-815.	3.3	53
48	Enzyme promiscuity shapes adaptation to novel growth substrates. Molecular Systems Biology, 2019, 15, e8462.	7.2	52
49	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	8.9	52
50	Cumulative Number of Cell Divisions as a Meaningful Timescale for Adaptive Laboratory Evolution of <i>Escherichia coli</i> . PLoS ONE, 2011, 6, e26172.	2.5	50
51	MID Max: LC-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.	6.5	48
52	Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in <i>Saccharomyces cerevisiae</i> . Metabolic Engineering, 2018, 47, 73-82.	7.0	47
53	Underground metabolism: network-level perspective and biotechnological potential. Current Opinion in Biotechnology, 2018, 49, 108-114.	6.6	45
54	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in <i>Escherichia coli</i> strains lacking the Phosphotransferase System. Metabolic Engineering, 2018, 48, 233-242.	7.0	43

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55	A pH and solvent optimized reverse-phase ion-pairing-LC-MS/MS method that leverages multiple scan-types for targeted absolute quantification of intracellular metabolites. <i>Metabolomics</i> , 2015, 11, 1338-1350.	3.0	42
56	Adaptive laboratory evolution of <i>Rhodospiridium toruloides</i> to inhibitors derived from lignocellulosic biomass and genetic variations behind evolution. <i>Bioresource Technology</i> , 2021, 333, 125171.	9.6	42
57	Genomically and biochemically accurate metabolic reconstruction of <i>Methanosarcina barkeri</i> Fusaro, iMG746. <i>Biotechnology Journal</i> , 2013, 8, 1070-1079.	3.5	41
58	Optimal cofactor swapping can increase the theoretical yield for chemical production in <i>Escherichia coli</i> and <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2014, 24, 117-128.	7.0	40
59	Elucidating aromatic acid tolerance at low pH in <i>Saccharomyces cerevisiae</i> using adaptive laboratory evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27954-27961.	7.1	40
60	<i>Acidithiobacillus ferrooxidans</i> 's comprehensive model driven analysis of the electron transfer metabolism and synthetic strain design for biomining applications. <i>Metabolic Engineering Communications</i> , 2016, 3, 84-96.	3.6	39
61	Coupling S-adenosylmethionine-dependent methylation to growth: Design and uses. <i>PLoS Biology</i> , 2019, 17, e2007050.	5.6	39
62	Constraint-Based Modeling of Carbon Fixation and the Energetics of Electron Transfer in <i>Geobacter metallireducens</i> . <i>PLoS Computational Biology</i> , 2014, 10, e1003575.	3.2	38
63	Adaptation to the coupling of glycolysis to toxic methylglyoxal production in <i>tpiA</i> deletion strains of <i>Escherichia coli</i> requires synchronized and counterintuitive genetic changes. <i>Metabolic Engineering</i> , 2018, 48, 82-93.	7.0	38
64	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1819-1828.	2.6	36
65	Modeling Method for Increased Precision and Scope of Directly Measurable Fluxes at a Genome-Scale. <i>Analytical Chemistry</i> , 2016, 88, 3844-3852.	6.5	34
66	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. <i>Metabolic Engineering</i> , 2017, 39, 220-227.	7.0	34
67	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1007066.	3.2	33
68	Compensatory evolution of <i>Pseudomonas aeruginosa</i> 's slow growth phenotype suggests mechanisms of adaptation in cystic fibrosis. <i>Nature Communications</i> , 2021, 12, 3186.	12.8	33
69	Generation of <i>Pseudomonas putida</i> KT2440 Strains with Efficient Utilization of Xylose and Galactose via Adaptive Laboratory Evolution. <i>ACS Sustainable Chemistry and Engineering</i> , 2021, 9, 11512-11523.	6.7	32
70	Optimizing Cofactor Specificity of Oxidoreductase Enzymes for the Generation of Microbial Production Strains via OptSwap. <i>Industrial Biotechnology</i> , 2013, 9, 236-246.	0.8	30
71	Generation of ionic liquid tolerant <i>Pseudomonas putida</i> KT2440 strains via adaptive laboratory evolution. <i>Green Chemistry</i> , 2020, 22, 5677-5690.	9.0	29
72	Fast Swinnex filtration (FSF): a fast and robust sampling and extraction method suitable for metabolomics analysis of cultures grown in complex media. <i>Metabolomics</i> , 2015, 11, 198-209.	3.0	28

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73	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	1.8	28
74	Machine-learning from <i>Pseudomonas putida</i> KT2440 transcriptomes reveals its transcriptional regulatory network. <i>Metabolic Engineering</i> , 2022, 72, 297-310.	7.0	28
75	Growth Adaptation of <i>gnd</i> and <i>sdhCB</i> <i>Escherichia coli</i> Deletion Strains Diverges From a Similar Initial Perturbation of the Transcriptome. <i>Frontiers in Microbiology</i> , 2018, 9, 1793.	3.5	23
76	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	2.8	23
77	Multiple Optimal Phenotypes Overcome Redox and Glycolytic Intermediate Metabolite Imbalances in <i>Escherichia coli</i> <i>pgi</i> Knockout Evolutions. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	22
78	Generation of an <i>E. coli</i> platform strain for improved sucrose utilization using adaptive laboratory evolution. <i>Microbial Cell Factories</i> , 2019, 18, 116.	4.0	22
79	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of <i>Staphylococcus aureus</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	21
80	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	13.3	21
81	Enhanced Metabolite Productivity of <i>Escherichia coli</i> Adapted to Glucose M9 Minimal Medium. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 166.	4.1	20
82	Identification of growth-coupled production strains considering protein costs and kinetic variability. <i>Metabolic Engineering Communications</i> , 2018, 7, e00080.	3.6	19
83	What do cells actually want?. <i>Genome Biology</i> , 2016, 17, 110.	8.8	18
84	Environmental conditions dictate differential evolution of vancomycin resistance in <i>Staphylococcus aureus</i> . <i>Communications Biology</i> , 2021, 4, 793.	4.4	18
85	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	3.2	17
86	Membrane transporter identification and modulation via adaptive laboratory evolution. <i>Metabolic Engineering</i> , 2022, 72, 376-390.	7.0	16
87	Genome-scale metabolic modeling reveals key features of a minimal gene set. <i>Molecular Systems Biology</i> , 2021, 17, e10099.	7.2	15
88	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43.	5.3	14
89	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. <i>Cell Reports</i> , 2021, 35, 108961.	6.4	13
90	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321.	2.9	12

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91	Reframing gene essentiality in terms of adaptive flexibility. <i>BMC Systems Biology</i> , 2018, 12, 143.	3.0	11
92	Directed Metabolic Pathway Evolution Enables Functional Pterin-Dependent Aromatic-Amino-Acid Hydroxylation in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2020, 9, 494-499.	3.8	9
93	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322.	5.3	8
94	Genetic Determinants Enabling Medium-Dependent Adaptation to Nafcillin in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020, 5, .	3.8	8
95	Laboratory evolution of synthetic electron transport system variants reveals a larger metabolic respiratory system and its plasticity. <i>Nature Communications</i> , 2022, 13, .	12.8	8
96	Engineering <i>Pseudomonas putida</i> for improved utilization of syringyl aromatics. <i>Biotechnology and Bioengineering</i> , 2022, 119, 2541-2550.	3.3	7
97	Identifying the effect of vancomycin on health care-associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. <i>GigaScience</i> , 2021, 10, .	6.4	5
98	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. <i>ACS Synthetic Biology</i> , 2021, 10, 3379-3395.	3.8	5
99	Computational Methods to Assess the Production Potential of Bio-Based Chemicals. <i>Methods in Molecular Biology</i> , 2018, 1671, 97-116.	0.9	4
100	Gapless, Unambiguous Genome Sequence for <i>Escherichia coli</i> C, a Workhorse of Industrial Biology. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
101	Selection for Cell Yield Does Not Reduce Overflow Metabolism in <i>Escherichia coli</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3