

Radhakrishnan Mahadevan

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

8,054
citations

57631

44
h-index

54797

84
g-index

152
all docs

152
docs citations

152
times ranked

7576
citing authors

#	ARTICLE	IF	CITATIONS
1	On the design principles of metabolic flux sensing. <i>Biophysical Journal</i> , 2022, 121, 237-247.	0.2	1
2	REVOLVER: A low-cost automated protein purifier based on parallel preparative gravity column workflows. <i>HardwareX</i> , 2022, 11, e00291.	1.1	0
3	Genetic engineering of extremely acidophilic <i>Acidithiobacillus</i> species for biomining: Progress and perspectives. <i>Journal of Hazardous Materials</i> , 2022, 438, 129456.	6.5	17
4	Macrophage Immunomodulation Through New Polymers that Recapitulate Functional Effects of Itaconate as a Power House of Innate Immunity. <i>Advanced Functional Materials</i> , 2021, 31, 2003341.	7.8	12
5	Overcoming Challenges in Expressing Iron-Sulfur Enzymes in Yeast. <i>Trends in Biotechnology</i> , 2021, 39, 665-677.	4.9	11
6	Engineering <i>Escherichia coli</i> for the utilization of ethylene glycol. <i>Microbial Cell Factories</i> , 2021, 20, 22.	1.9	18
7	Opportunities and Challenges for Microbial Synthesis of Fatty Acid-Derived Chemicals (FACs). <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 613322.	2.0	2
8	Genomic Analysis of a Newly Isolated <i>Acidithiobacillus ferridurans</i> JAGS Strain Reveals Its Adaptation to Acid Mine Drainage. <i>Minerals (Basel, Switzerland)</i> , 2021, 11, 74.	0.8	15
9	Could open science stimulate industry partnerships in chemical engineering university research?. <i>Canadian Journal of Chemical Engineering</i> , 2021, 99, 2186-2194.	0.9	3
10	SARS-CoV-2 receptor-binding mutations and antibody contact sites. <i>Antibody Therapeutics</i> , 2021, 4, 149-158.	1.2	12
11	Advancing undergraduate synthetic biology education: insights from a Canadian iGEM student perspective. <i>Canadian Journal of Microbiology</i> , 2021, 67, 749-770.	0.8	7
12	Systematizing the different notions of growth-coupled product synthesis and a single framework for computing corresponding strain designs. <i>Biotechnology Journal</i> , 2021, 16, e2100236.	1.8	10
13	Integration of a physiologically-based pharmacokinetic model with a whole-body, organ-resolved genome-scale model for characterization of ethanol and acetaldehyde metabolism. <i>PLoS Computational Biology</i> , 2021, 17, e1009110.	1.5	9
14	Automation assisted anaerobic phenotyping for metabolic engineering. <i>Microbial Cell Factories</i> , 2021, 20, 184.	1.9	4
15	Physiologically-based pharmacokinetic model for predicting blood and tissue tetrahydrocannabinol concentrations. <i>Computers and Chemical Engineering</i> , 2021, 154, 107461.	2.0	1
16	A gap-filling algorithm for prediction of metabolic interactions in microbial communities. <i>PLoS Computational Biology</i> , 2021, 17, e1009060.	1.5	4
17	Rational engineering of 2-deoxyribose-5-phosphate aldolases for the biosynthesis of (R)-1,3-butanediol. <i>Journal of Biological Chemistry</i> , 2020, 295, 597-609.	1.6	16
18	Novel two-stage processes for optimal chemical production in microbes. <i>Metabolic Engineering</i> , 2020, 62, 186-197.	3.6	18

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19	Metabolically engineered recombinant <i>Saccharomyces cerevisiae</i> for the production of 2-Deoxy-scyllo-inosose (2-DOI). <i>Metabolic Engineering Communications</i> , 2020, 11, e00134.	1.9	3
20	Speeding up the core algorithm for the dual calculation of minimal cut sets in large metabolic networks. <i>BMC Bioinformatics</i> , 2020, 21, 510.	1.2	8
21	Pan-Genome Scale Network Reconstruction: Harnessing Phylogenomics Increases the Quantity and Quality of Metabolic Models. <i>Biotechnology Journal</i> , 2020, 15, e1900519.	1.8	9
22	A microplate screen to estimate metal-binding affinities of metalloproteins. <i>Analytical Biochemistry</i> , 2020, 609, 113836.	1.1	8
23	A Personalized Multiscale Modeling Framework for Dose Selection in Precision Medicine. <i>Industrial & Engineering Chemistry Research</i> , 2020, 59, 9819-9829.	1.8	0
24	Dynamic Cell Programming with Quorum Sensing-Controlled CRISPRi Circuit. <i>ACS Synthetic Biology</i> , 2020, 9, 1284-1291.	1.9	12
25	A novel C-terminal degron identified in bacterial aldehyde decarbonylases using directed evolution. <i>Biotechnology for Biofuels</i> , 2020, 13, 114.	6.2	8
26	Toward a systematic design of smart probiotics. <i>Current Opinion in Biotechnology</i> , 2020, 64, 199-209.	3.3	9
27	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
28	Complete Genome Sequence of <i>Acidithiobacillus ferridurans</i> JAGS, Isolated from Acidic Mine Drainage. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
29	Engineering Photosynthetic Bioprocesses for Sustainable Chemical Production: A Review. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 610723.	2.0	19
30	A multi-scale model for low-density lipoprotein cholesterol (LDL-C) regulation in the human body: Application to quantitative systems pharmacology. <i>Computers and Chemical Engineering</i> , 2019, 130, 106507.	2.0	8
31	A scalable method for parameter identification in kinetic models of metabolism using steady-state data. <i>Bioinformatics</i> , 2019, 35, 5216-5225.	1.8	4
32	AYbRAH: a curated ortholog database for yeasts and fungi spanning 600 million years of evolution. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	9
33	Impact framework: A python package for writing data analysis workflows to interpret microbial physiology. <i>Metabolic Engineering Communications</i> , 2019, 9, e00089.	1.9	5
34	Systems biology based metabolic engineering for non-natural chemicals. <i>Biotechnology Advances</i> , 2019, 37, 107379.	6.0	38
35	Evaluating the performance of a post-translational dynamic metabolic control system. <i>IFAC-PapersOnLine</i> , 2019, 52, 225-230.	0.5	0
36	An interspecies malate-pyruvate shuttle reconciles redox imbalance in an anaerobic microbial community. <i>ISME Journal</i> , 2019, 13, 1042-1055.	4.4	15

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37	Biocatalytic production of adipic acid from glucose using engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2018, 6, 28-32.	1.9	70
38	Model-based design of bistable cell factories for metabolic engineering. <i>Bioinformatics</i> , 2018, 34, 1363-1371.	1.8	5
39	Biosynthesis and Activity of Prenylated FMN Cofactors. <i>Cell Chemical Biology</i> , 2018, 25, 560-570.e6.	2.5	45
40	When Do Two-Stage Processes Outperform One-Stage Processes?. <i>Biotechnology Journal</i> , 2018, 13, 1700539.	1.8	52
41	MoVE identifies metabolic valves to switch between phenotypic states. <i>Nature Communications</i> , 2018, 9, 5332.	5.8	37
42	Efficient Biochemical Pathway Prediction Using Simulated Annealing. <i>IFAC-PapersOnLine</i> , 2018, 51, 56-57.	0.5	1
43	Heavy Metal Removal by Bioaccumulation Using Genetically Engineered Microorganisms. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 157.	2.0	203
44	An Optimized Bistable Metabolic Switch To Decouple Phenotypic States during Anaerobic Fermentation. <i>ACS Synthetic Biology</i> , 2018, 7, 2854-2866.	1.9	28
45	Engineering a short, aldolase-based pathway for (R)-1,3-butanediol production in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2018, 48, 13-24.	3.6	49
46	Inactivation of the transcription factor <i>mig1</i> (<i>YGL035C</i>) in <i>Saccharomyces cerevisiae</i> improves tolerance towards monocarboxylic weak acids: acetic, formic and levulinic acid. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018, 45, 735-751.	1.4	23
47	Novel Aldo-Keto Reductases for the Biocatalytic Conversion of 3-Hydroxybutanal to 1,3-Butanediol: Structural and Biochemical Studies. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	24
48	Refined experimental annotation reveals conserved corrinoid autotrophy in chloroform-respiring <i>Dehalobacter</i> isolates. <i>ISME Journal</i> , 2017, 11, 626-640.	4.4	21
49	Redesigning metabolism based on orthogonality principles. <i>Nature Communications</i> , 2017, 8, 15188.	5.8	47
50	Exploring Bacterial Carboxylate Reductases for the Reduction of Bifunctional Carboxylic Acids. <i>Biotechnology Journal</i> , 2017, 12, 1600751.	1.8	74
51	Synthetic rescue couples NADPH generation to metabolite overproduction in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2017, 43, 64-70.	3.6	14
52	Leaching characteristics of nickeliferous pyrrhotite tailings from the Sudbury, Ontario area. <i>Canadian Metallurgical Quarterly</i> , 2017, 56, 372-381.	0.4	11
53	Alkene hydrogenation activity of enoate reductases for an environmentally benign biosynthesis of adipic acid. <i>Chemical Science</i> , 2017, 8, 1406-1413.	3.7	77
54	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. <i>PLoS Computational Biology</i> , 2017, 13, e1005409.	1.5	60

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55	Multiscale Metabolic Modeling Approach for Predicting Blood Alcohol Concentration. IEEE Life Sciences Letters, 2016, 2, 59-62.	1.2	9
56	Protein-Level Control of Metabolism: Design Principles and Prospects from a Representative System. IFAC-PapersOnLine, 2016, 49, 165-170.	0.5	0
57	Experimental validation of in silico modelâ€predicted isocitrate dehydrogenase and phosphomannose isomerase from <i>D. ehalococcoides mccartyi</i> . Microbial Biotechnology, 2016, 9, 47-60.	2.0	1
58	A Multi-Scale Model of the Whole Human Body based on Dynamic Parsimonious Flux Balance Analysis. IFAC-PapersOnLine, 2016, 49, 937-942.	0.5	16
59	A three-dimensional engineered tumour for spatial snapshot analysis of cell metabolism and phenotype in hypoxic gradients. Nature Materials, 2016, 15, 227-234.	13.3	113
60	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
61	Metabolic engineering of a tyrosine-overproducing yeast platform using targeted metabolomics. Microbial Cell Factories, 2015, 14, 73.	1.9	98
62	Constructing kinetic models of metabolism at genomeâ€scales: A review. Biotechnology Journal, 2015, 10, 1345-1359.	1.8	72
63	Characterizing metabolic pathway diversification in the context of perturbation size. Metabolic Engineering, 2015, 28, 114-122.	3.6	20
64	Engineering metabolism through dynamic control. Current Opinion in Biotechnology, 2015, 34, 142-152.	3.3	176
65	On the feasibility of growth-coupled product synthesis in microbial strains. Metabolic Engineering, 2015, 30, 166-178.	3.6	83
66	Sub-optimal phenotypes of double-knockout mutants of <i>Escherichia coli</i> depend on the order of gene deletions. Integrative Biology (United Kingdom), 2015, 7, 930-939.	0.6	4
67	Investigating <i>Moorella thermoacetica</i> metabolism with a genome-scale constraint-based metabolic model. Integrative Biology (United Kingdom), 2015, 7, 869-882.	0.6	33
68	Genome-scale strain designs based on regulatory minimal cut sets. Bioinformatics, 2015, 31, 2844-2851.	1.8	26
69	New Insights into <i>Dehalococcoides mccartyi</i> Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of <i>D. mccartyi</i> Transcriptomes. PLoS ONE, 2014, 9, e94808.	1.1	14
70	Engineering <i>Escherichia coli</i> for D-Ribose Production from Glucose-Xylose Mixtures. Industrial Biotechnology, 2014, 10, 106-114.	0.5	4
71	Metabolic modeling of spatial heterogeneity of biofilms in microbial fuel cells reveals substrate limitations in electrical current generation. Biotechnology Journal, 2014, 9, 1350-1361.	1.8	44
72	A defined co-culture of <i>Geobacter sulfurreducens</i> and <i>Escherichia coli</i> in a membraneâ€less microbial fuel cell. Biotechnology and Bioengineering, 2014, 111, 709-718.	1.7	45

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73	Analysis and Design of a Genetic Circuit for Dynamic Metabolic Engineering. ACS Synthetic Biology, 2013, 2, 442-452.	1.9	59
74	Novel approach to engineer strains for simultaneous sugar utilization. Metabolic Engineering, 2013, 20, 63-72.	3.6	50
75	Prediction of Weak Acid Toxicity in <i>Saccharomyces cerevisiae</i> Using Genome-Scale Metabolic Models. Industrial Biotechnology, 2013, 9, 229-235.	0.5	3
76	Pore-scale simulation of microbial growth using a genome-scale metabolic model: Implications for Darcy-scale reactive transport. Advances in Water Resources, 2013, 59, 256-270.	1.7	26
77	Design principles for generating robust gene expression patterns in dynamic engineered tissues. Integrative Biology (United Kingdom), 2013, 5, 578-589.	0.6	12
78	Metabolic Model Refinement Using Phenotypic Microarray Data. Methods in Molecular Biology, 2013, 985, 47-59.	0.4	2
79	Dynamic strain scanning optimization: an efficient strain design strategy for balanced yield, titer, and productivity. DySScO strategy for strain design. BMC Biotechnology, 2013, 13, 8.	1.7	50
80	Characterizing metabolic interactions in a clostridial co-culture for consolidated bioprocessing. BMC Biotechnology, 2013, 13, 95.	1.7	41
81	Structure and activity of the NAD(P) ⁺ -dependent succinate semialdehyde dehydrogenase Ynel from <i>Salmonella typhimurium</i> . Proteins: Structure, Function and Bioinformatics, 2013, 81, 1031-1041.	1.5	16
82	Model-driven design of a <i>Saccharomyces cerevisiae</i> platform strain with improved tyrosine production capabilities. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2013, 46, 221-226.	0.4	6
83	Ensemble Modeling of Cancer Metabolism. Frontiers in Physiology, 2012, 3, 135.	1.3	30
84	Integrative analysis of <i>Geobacter</i> spp. and sulfate-reducing bacteria during uranium bioremediation. Biogeosciences, 2012, 9, 1033-1040.	1.3	31
85	GENOME-BASED MODELING AND DESIGN OF METABOLIC INTERACTIONS IN MICROBIAL COMMUNITIES. Computational and Structural Biotechnology Journal, 2012, 3, e201210008.	1.9	25
86	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnos</i> a and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	1.2	125
87	The design of long-term effective uranium bioremediation strategy using a community metabolic model. Biotechnology and Bioengineering, 2012, 109, 2475-2483.	1.7	65
88	Synthetic biosystems for the production of high-value plant metabolites. Trends in Biotechnology, 2012, 30, 127-131.	4.9	128
89	Omics technologies and systems biology for engineering <i>Saccharomyces cerevisiae</i> strains for lignocellulosic bioethanol production. Biofuels, 2011, 2, 659-675.	1.4	2
90	Economics of membrane occupancy and respiratory fermentation. Molecular Systems Biology, 2011, 7, 500.	3.2	162

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91	In situ to in silico and back: elucidating the physiology and ecology of <i>Geobacter</i> spp. using genome-scale modelling. <i>Nature Reviews Microbiology</i> , 2011, 9, 39-50.	13.6	128
92	Genome-scale dynamic modeling of the competition between <i>Rhodoferrax</i> and <i>Geobacter</i> in anoxic subsurface environments. <i>ISME Journal</i> , 2011, 5, 305-316.	4.4	275
93	Direct coupling of a genome-scale microbial in silico model and a groundwater reactive transport model. <i>Journal of Contaminant Hydrology</i> , 2011, 122, 96-103.	1.6	44
94	In silico characterization of microbial electrosynthesis for metabolic engineering of biochemicals. <i>Microbial Cell Factories</i> , 2011, 10, 76.	1.9	46
95	Model-based analysis of the role of biological, hydrological and geochemical factors affecting uranium bioremediation. <i>Biotechnology and Bioengineering</i> , 2011, 108, 1537-1548.	1.7	19
96	EMILIO: A fast algorithm for genome-scale strain design. <i>Metabolic Engineering</i> , 2011, 13, 272-281.	3.6	112
97	Chemical and Synthetic Genetic Array Analysis Identifies Genes that Suppress Xylose Utilization and Fermentation in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 247-258.	0.8	22
98	Model-driven design based on sensitivity analysis for a synthetic biology application. <i>Computer Aided Chemical Engineering</i> , 2011, 29, 1446-1450.	0.3	1
99	Metabolic Modeling of Spatial Heterogeneity of Biofilms in Microbial Fuel Cells. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2010, 43, 215-220.	0.4	2
100	Rapid design of system-wide metabolic network modifications using iterative linear programming. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2010, 43, 391-396.	0.4	1
101	Genome-scale metabolic modeling of a clostridial co-culture for consolidated bioprocessing. <i>Biotechnology Journal</i> , 2010, 5, 726-738.	1.8	115
102	Modeling and sensitivity analysis of electron capacitance for <i>Geobacter</i> in sedimentary environments. <i>Journal of Contaminant Hydrology</i> , 2010, 112, 30-44.	1.6	16
103	Thermodynamic analysis of regulation in metabolic networks using constraint-based modeling. <i>BMC Research Notes</i> , 2010, 3, 125.	0.6	13
104	Characterization of Proton Production and Consumption Associated with Microbial Metabolism. <i>BMC Biotechnology</i> , 2010, 10, 2.	1.7	41
105	Characterizing the Metabolism of <i>Dehalococcoides</i> with a Constraint-Based Model. <i>PLoS Computational Biology</i> , 2010, 6, e1000887.	1.5	46
106	Genome-scale comparison and constraint-based metabolic reconstruction of the facultative anaerobic Fe(III)-reducer <i>Rhodoferrax ferrireducens</i> . <i>BMC Genomics</i> , 2009, 10, 447.	1.2	76
107	Genome-scale constraint-based modeling of <i>Geobacter metallireducens</i> . <i>BMC Systems Biology</i> , 2009, 3, 15.	3.0	65
108	Coupling a genome-scale metabolic model with a reactive transport model to describe <i>in situ</i> uranium bioremediation. <i>Microbial Biotechnology</i> , 2009, 2, 274-286.	2.0	92

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109	Systems Biology: The synergistic interplay between biology and mathematics. Canadian Journal of Chemical Engineering, 2008, 86, 127-141.	0.9	18
110	A bilevel optimization algorithm to identify enzymatic capacity constraints in metabolic networks. Computers and Chemical Engineering, 2008, 32, 2072-2085.	2.0	15
111	Dynamic metabolic engineering for increasing bioprocess productivity. Metabolic Engineering, 2008, 10, 255-266.	3.6	126
112	Geobacter sulfurreducens strain engineered for increased rates of respiration. Metabolic Engineering, 2008, 10, 267-275.	3.6	102
113	The Degree of Redundancy in Metabolic Genes Is Linked to Mode of Metabolism. Biophysical Journal, 2008, 94, 1216-1220.	0.2	63
114	Characterizing Regulation of Metabolism in <i>Geobacter sulfurreducens</i> through Genome-Wide Expression Data and Sequence Analysis. OMICS A Journal of Integrative Biology, 2008, 12, 33-59.	1.0	24
115	Genome Regions Involved in Multiple Regulatory Pathways Identified Using GSEL, A Genome-Wide Database of Regulatory Sequence Elements of <i>Geobacter sulfurreducens</i> . , 2008, , .		0
116	Computational and Experimental Analysis of Redundancy in the Central Metabolism of <i>Geobacter sulfurreducens</i> . PLoS Computational Biology, 2008, 4, e36.	1.5	72
117	Genome-scale Reconstruction of Metabolic Network in <i>Bacillus subtilis</i> Based on High-throughput Phenotyping and Gene Essentiality Data. Journal of Biological Chemistry, 2007, 282, 28791-28799.	1.6	387
118	Genome-scale analysis of <i>Saccharomyces cerevisiae</i> metabolism and ethanol production in fed-batch culture. Biotechnology and Bioengineering, 2007, 97, 1190-1204.	1.7	120
119	Characterization of Metabolism in the Fe(III)-Reducing Organism <i>Geobacter sulfurreducens</i> by Constraint-Based Modeling. Applied and Environmental Microbiology, 2006, 72, 1558-1568.	1.4	290
120	Optimal genetic manipulations in batch bioreactor control. Automatica, 2006, 42, 1723-1733.	3.0	15
121	Estimating optimal profiles of genetic alterations using constraint-based models. Biotechnology and Bioengineering, 2005, 89, 243-251.	1.7	72
122	Applications of metabolic modeling to drive bioprocess development for the production of value-added chemicals. Biotechnology and Bioprocess Engineering, 2005, 10, 408-417.	1.4	33
123	k-Cone Analysis: Determining All Candidate Values for Kinetic Parameters on a Network Scale. Biophysical Journal, 2005, 88, 1616-1625.	0.2	79
124	Properties of Metabolic Networks: Structure versus Function. Biophysical Journal, 2005, 88, L07-L09.	0.2	83
125	Using metabolic flux data to further constrain the metabolic solution space and predict internal flux patterns: the <i>Escherichia coli</i> spectrum. Biotechnology and Bioengineering, 2004, 86, 317-331.	1.7	85
126	The effects of alternate optimal solutions in constraint-based genome-scale metabolic models. Metabolic Engineering, 2003, 5, 264-276.	3.6	1,083

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127	Reconstructing metabolic flux vectors from extreme pathways: defining the $\hat{\pm}$ -spectrum. Journal of Theoretical Biology, 2003, 224, 313-324.	0.8	148
128	On-Line Optimization of Recombinant Product in a Fed-Batch Bioreactor. Biotechnology Progress, 2003, 19, 639-646.	1.3	21
129	Dynamic Flux Balance Analysis of Diauxic Growth in Escherichia coli. Biophysical Journal, 2002, 83, 1331-1340.	0.2	806
130	Control-relevant scheduling of polymer grade transitions. AIChE Journal, 2002, 48, 1754-1764.	1.8	46
131	Differential flatness based nonlinear predictive control of fed-batch bioreactors. Control Engineering Practice, 2001, 9, 889-899.	3.2	56
132	Efficient Enumeration of Branched Novel Biochemical Pathways Using a Probabilistic Technique. Industrial & Engineering Chemistry Research, 0, , .	1.8	1