Costas D Maranas

List of Publications by Year
in descending order

231 papers	17,063 citations	12322 69 h-index	19726 117 g-index
265 all docs	265 docs citations	265 times ranked	11661 citing authors

#	Article	IF	Citations
1	Optknock: A bilevel programming framework for identifying gene knockout strategies for microbial strain optimization. Biotechnology and Bioengineering, 2003, 84, 647-657.	1.7	1,112
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	5.5	833
3	Managing demand uncertainty in supply chain planning. Computers and Chemical Engineering, 2003, 27, 1219-1227.	2.0	423
4	OptStrain: A computational framework for redesign of microbial production systems. Genome Research, 2004, 14, 2367-2376.	2.4	420
5	?BB: A global optimization method for general constrained nonconvex problems. Journal of Global Optimization, 1995, 7, 337-363.	1.1	383
6	In silico design and adaptive evolution ofEscherichia colifor production of lactic acid. Biotechnology and Bioengineering, 2005, 91, 643-648.	1.7	346
7	OptForce: An Optimization Procedure for Identifying All Genetic Manipulations Leading to Targeted Overproductions. PLoS Computational Biology, 2010, 6, e1000744.	1.5	346
8	OptCom: A Multi-Level Optimization Framework for the Metabolic Modeling and Analysis of Microbial Communities. PLoS Computational Biology, 2012, 8, e1002363.	1.5	322
9	Flux Coupling Analysis of Genome-Scale Metabolic Network Reconstructions. Genome Research, 2004, 14, 301-312.	2.4	320
10	Genome-scale metabolic network modeling results in minimal interventions that cooperatively force carbon flux towards malonyl-CoA. Metabolic Engineering, 2011, 13, 578-587.	3.6	300
11	An optimization framework for identifying reaction activation/inhibition or elimination candidates for overproduction in microbial systems. Metabolic Engineering, 2006, 8, 1-13.	3.6	292
12	Optimization based automated curation of metabolic reconstructions. BMC Bioinformatics, 2007, 8, 212.	1.2	285
13	Synthetic biology of cyanobacteria: unique challenges and opportunities. Frontiers in Microbiology, 2013, 4, 246.	1.5	243
14	GrowMatch: An Automated Method for Reconciling In Silico/In Vivo Growth Predictions. PLoS Computational Biology, 2009, 5, e1000308.	1.5	217
15	A genome-scale Escherichia coli kinetic metabolic model k-ecoli457 satisfying flux data for multiple mutant strains. Nature Communications, 2016, 7, 13806.	5.8	205
16	Optimization-based framework for inferring and testing hypothesized metabolic objective functions. Biotechnology and Bioengineering, 2003, 82, 670-677.	1.7	195
17	Finding all solutions of nonlinearly constrained systems of equations. Journal of Global Optimization, 1995, 7, 143-182.	1.1	190
18	Zea mays iRS1563: A Comprehensive Genome-Scale Metabolic Reconstruction of Maize Metabolism. PLoS ONE, 2011, 6, e21784.	1.1	189

#	Article	IF	Citations
19	Global optimization in generalized geometric programming. Computers and Chemical Engineering, 1997, 21, 351-369.	2.0	185
20	d-OptCom: Dynamic Multi-level and Multi-objective Metabolic Modeling of Microbial Communities. ACS Synthetic Biology, 2014, 3, 247-257.	1.9	180
21	Global minimum potential energy conformations of small molecules. Journal of Global Optimization, 1994, 4, 135-170.	1.1	167
22	Multiple spillovers from humans and onward transmission of SARS-CoV-2 in white-tailed deer. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	164
23	A kinetic model of Escherichia coli core metabolism satisfying multiple sets of mutant flux data. Metabolic Engineering, 2014, 25, 50-62.	3.6	160
24	Multiperiod Planning and Scheduling of Multiproduct Batch Plants under Demand Uncertainty. Industrial & Engineering Chemistry Research, 1997, 36, 4864-4881.	1.8	157
25	SteadyCom: Predicting microbial abundances while ensuring community stability. PLoS Computational Biology, 2017, 13, e1005539.	1.5	154
26	Creating multiple-crossover DNA libraries independent of sequence identity. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11248-11253.	3.3	148
27	Genomeâ€scale gene/reaction essentiality and synthetic lethality analysis. Molecular Systems Biology, 2009, 5, 301.	3.2	143
28	Rational design of a synthetic Entnerâ€“Doudoroff pathway for improved and controllable NADPH regeneration. Metabolic Engineering, 2015, 29, 86-96.	3.6	142
29	Mid-term supply chain planning under demand uncertainty: customer demand satisfaction and inventory management. Computers and Chemical Engineering, 2000, 24, 2613-2621.	2.0	140
30	A Two-Stage Modeling and Solution Framework for Multisite Midterm Planning under Demand Uncertainty. Industrial & Engineering Chemistry Research, 2000, 39, 3799-3813.	1.8	136
31	Minimal Reaction Sets for Escherichia coli Metabolism under Different Growth Requirements and Uptake Environments. Biotechnology Progress, 2001, 17, 791-797.	1.3	136
32	A global optimization approach for Lennardâ€Jones microclusters. Journal of Chemical Physics, 1992, 97, 7667-7678.	1.2	128
33	Mathematical optimization applications in metabolic networks. Metabolic Engineering, 2012, 14, 672-686.	3.6	123
34	Exploring the overproduction of amino acids using the bilevel optimization framework OptKnock. Biotechnology and Bioengineering, 2003, 84, 887-899.	1.7	121
35	MetRxn: a knowledgebase of metabolites and reactions spanning metabolic models and databases. BMC Bioinformatics, 2012, 13, 6.	1.2	120
36	A Genome-Scale Metabolic Reconstruction of Mycoplasma genitalium, iPS189. PLoS Computational Biology, 2009, 5, e1000285.	1.5	119

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37	k-OptForce: Integrating Kinetics with Flux Balance Analysis for Strain Design. PLoS Computational Biology, 2014, 10, e1003487.	1.5	117
38	Reversing methanogenesis to capture methane for liquid biofuel precursors. Microbial Cell Factories, 2016, 15, 11.	1.9	116
39	Recent advances in the reconstruction of metabolic models and integration of omics data. Current Opinion in Biotechnology, 2014, 29, 39-45.	3.3	115
40	Artificial water channels enable fast and selective water permeation through water-wire networks. Nature Nanotechnology, 2020, 15, 73-79.	15.6	111
41	Optimal Computer-Aided Molecular Design:Â A Polymer Design Case Study. Industrial & Engineering Chemistry Research, 1996, 35, 3403-3414.	1.8	109
42	A global optimization method, Î±BB, for process design. Computers and Chemical Engineering, 1996, 20, S419-S424.	2.0	108
43	Metabolic flux elucidation for large-scale models using 13C labeled isotopes. Metabolic Engineering, 2007, 9, 387-405.	3.6	104
44	An integrated computational and experimental study for overproducing fatty acids in Escherichia coli. Metabolic Engineering, 2012, 14, 687-704.	3.6	102
45	Comparative genomics reveals the molecular determinants of rapid growth of the cyanobacterium Synechococcus elongatus UTEX 2973. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11761-E11770.	3.3	102
46	Probing the performance limits of theEscherichia coli metabolic network subject to gene additions or deletions. Biotechnology and Bioengineering, 2001, 74, 364-375.	1.7	101
47	Solving long-term financial planning problems via global optimization. Journal of Economic Dynamics and Control, 1997, 21, 1405-1425.	0.9	100
48	A review of computational tools for design and reconstruction of metabolic pathways. Synthetic and Systems Biotechnology, 2017, 2, 243-252.	1.8	98
49	A deterministic global optimization approach for molecular structure determination. Journal of Chemical Physics, 1994, 100, 1247-1261.	1.2	95
50	Farnesoid X Receptor Signaling Shapes the Gut Microbiota and Controls Hepatic Lipid Metabolism. MSystems, 2016, 1, .	1.7	95
51	Computational tools for metabolic engineering. Metabolic Engineering, 2012, 14, 270-280.	3.6	93
52	Toward low-cost biological and hybrid biological/catalytic conversion of cellulosic biomass to fuels. Energy and Environmental Science, 2022, 15, 938-990.	15.6	93
53	Optimization in Polymer Design Using Connectivity Indices. Industrial & Engineering Chemistry Research, 1999, 38, 1884-1892.	1.8	92
54	Deciphering cyanobacterial phenotypes for fast photoautotrophic growth via isotopically nonstationary metabolic flux analysis. Biotechnology for Biofuels, 2017, 10, 273.	6.2	92

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55	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. Nature Methods, 2019, 16, 567-571.	9.0	90
56	Predicting biological system objectives de novo from internal state measurements. BMC Bioinformatics, 2008, 9, 43.	1.2	89
57	Improving the iMM904 S. cerevisiae metabolic model using essentiality and synthetic lethality data. BMC Systems Biology, 2010, 4, 178.	3.0	88
58	Optimal molecular design under property prediction uncertainty. AICHE Journal, 1997, 43, 1250-1264.	1.8	87
59	Real Options Based Analysis of Optimal Pharmaceutical Research and Development Portfolios. Industrial & Engineering Chemistry Research, 2002, 41, 6607-6620.	1.8	87
60	Standardizing biomass reactions and ensuring complete mass balance in genome-scale metabolic models. Bioinformatics, 2017, 33, 3603-3609.	1.8	86
61	Genome Scale Reconstruction of a Salmonella Metabolic Model. Journal of Biological Chemistry, 2009, 284, 29480-29488.	1.6	85
62	Computational design of Candida boidinii xylose reductase for altered cofactor specificity. Protein Science, 2009, 18, 2125-2138.	3.1	84
63	Diurnal Regulation of Cellular Processes in the Cyanobacterium Synechocystis sp. Strain PCC 6803: Insights from Transcriptomic, Fluxomic, and Physiological Analyses. MBio, 2016, 7, .	1.8	84
64	13C metabolic flux analysis at a genome-scale. Metabolic Engineering, 2015, 32, 12-22.	3.6	82
65	Assessing the Metabolic Impact of Nitrogen Availability Using a Compartmentalized Maize Leaf Genome-Scale Model Â Â Â. Plant Physiology, 2014, 166, 1659-1674.	2.3	80
66	Nitrogen-use efficiency in maize (Zea mays L.): from 'omics' studies to metabolic modelling. Journal of Experimental Botany, 2014, 65, 5657-5671.	2.4	80
67	Reconstruction and Comparison of the Metabolic Potential of Cyanobacteria Cyanothece sp. ATCC 51142 and Synechocystis sp. PCC 6803. PLoS ONE, 2012, 7, e48285.	1.1	79
68	Multilevel engineering of the upstream module of aromatic amino acid biosynthesis in Saccharomyces cerevisiae for high production of polymer and drug precursors. Metabolic Engineering, 2017, 42, 134-144.	3.6	79
69	Recent advances in computational protein design. Current Opinion in Structural Biology, 2011, 21, 467-472.	2.6	78
70	Analysis of NADPH supply during xylitol production by engineered Escherichia coli. Biotechnology and Bioengineering, 2009, 102, 209-220.	1.7	77
71	Computational Redesign of Acyl-ACP Thioesterase with Improved Selectivity toward Medium-Chain-Length Fatty Acids. ACS Catalysis, 2017, 7, 3837-3849.	5.5	77
72	Pathway design using de novo steps through uncharted biochemical spaces. Nature Communications, 2018, 9, 184.	5.8	77

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73	OptCircuit: An optimization based method for computational design of genetic circuits. BMC Systems Biology, 2008, 2, 24.	3.0	74
74	A Hierarchical Lagrangean Relaxation Procedure for Solving Midterm Planning Problems. Industrial & Engineering Chemistry Research, 1999, 38, 1937-1947.	1.8	73
75	OptCDR: a general computational method for the design of antibody complementarity determining regions for targeted epitope binding. Protein Engineering, Design and Selection, 2010, 23, 849-858.	1.0	72
76	Optimal synthesis of refrigeration cycles and selection of refrigerants. AICHE Journal, 1999, 45, 997-1017.	1.8	70
77	FamClash: A method for ranking the activity of engineered enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4142-4147.	3.3	70
78	Bacterial colonization reprograms the neonatal gut metabolome. Nature Microbiology, 2020, 5, 838-847.	5.9	70
79	New results in the packing of equal circles in a square. Discrete Mathematics, 1995, 142, 287-293.	0.4	69
80	Predicting crossover generation in DNA shuffling. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 3226-3231.	3.3	69
81	Systems metabolic engineering design: Fatty acid production as an emerging case study. Biotechnology and Bioengineering, 2014, 111, 849-857.	1.7	69
82	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
83	From directed evolution to computational enzyme engineeringâ€”A review. AICHE Journal, 2020, 66, e16847.	1.8	67
84	Synthesis of Mixed Refrigerant Cascade Cycles. Chemical Engineering Communications, 2002, 189, 1057-1078.	1.5	66
85	Prediction of Oligopeptide Conformations via Deterministic Global Optimization. Journal of Global Optimization, 1997, 11, 1-34.	1.1	64
86	Modeling DNA Mutation and Recombination for Directed Evolution Experiments. Journal of Theoretical Biology, 2000, 205, 483-503.	0.8	64
87	Locating All Homogeneous Azeotropes in Multicomponent Mixtures. Industrial & Engineering Chemistry Research, 1997, 36, 160-178.	1.8	63
88	Computational prediction of the effect of amino acid changes on the binding affinity between SARS-CoV-2 spike RBD and human ACE2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	61
89	Highly Active C₈-Acyl-ACP Thioesterase Variant Isolated by a Synthetic Selection Strategy. ACS Synthetic Biology, 2018, 7, 2205-2215.	1.9	60
90	OptMAVEn â€“ A New Framework for the de novo Design of Antibody Variable Region Models Targeting Specific Antigen Epitopes. PLoS ONE, 2014, 9, e105954.	1.1	59

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91	Optimization in product design with properties correlated with topological indices. Computers and Chemical Engineering, 1998, 22, 747-763.	2.0	57
92	Exploiting the Genetic Diversity of Maize Using a Combined Metabolomic, Enzyme Activity Profiling, and Metabolic Modeling Approach to Link Leaf Physiology to Kernel Yield. Plant Cell, 2017, 29, 919-943.	3.1	57
93	Genome-Scale Fluxome of Synechococcus elongatus UTEX 2973 Using Transient ¹³C-Labeling Data. Plant Physiology, 2019, 179, 761-769.	2.3	57
94	Capturing the response of Clostridium acetobutylicumto chemical stressors using a regulated genome-scale metabolic model. Biotechnology for Biofuels, 2014, 7, 144.	6.2	56
95	Identifying the Metabolic Differences of a Fast-Growth Phenotype in Synechococcus UTEX 2973. Scientific Reports, 2017, 7, 41569.	1.6	56
96	A comprehensive genome-scale model for Rhodosporidium toruloides IFO0880 accounting for functional genomics and phenotypic data. Metabolic Engineering Communications, 2019, 9, e00101.	1.9	55
97	IPRO: An Iterative Computational Protein Library Redesign and Optimization Procedure. Biophysical Journal, 2006, 90, 4167-4180.	0.2	54
98	Design of single-product campaign batch plants under demand uncertainty. AICHE Journal, 1998, 44, 896-911.	1.8	53
99	Elucidation of photoautotrophic carbon flux topology in Synechocystis PCC 6803 using genome-scale carbon mapping models. Metabolic Engineering, 2018, 47, 190-199.	3.6	52
100	Identifying residue-residue clashes in protein hybrids by using a second-order mean-field approach. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5091-5096.	3.3	50
101	PoreDesigner for tuning solute selectivity in a robust and highly permeable outer membrane pore. Nature Communications, 2018, 9, 3661.	5.8	50
102	Cyanobacterial Alkanes Modulate Photosynthetic Cyclic Electron Flow to Assist Growth under Cold Stress. Scientific Reports, 2015, 5, 14894.	1.6	49
103	A Computational Framework for the Topological Analysis and Targeted Disruption of Signal Transduction Networks. Biophysical Journal, 2006, 91, 382-398.	0.2	48
104	Designing overall stoichiometric conversions and intervening metabolic reactions. Scientific Reports, 2015, 5, 16009.	1.6	47
105	Facile Affinity Maturation of Antibody Variable Domains Using Natural Diversity Mutagenesis. Frontiers in Immunology, 2017, 8, 986.	2.2	47
106	Succinate Overproduction: A Case Study of Computational Strain Design Using a Comprehensive Escherichia coli Kinetic Model. Frontiers in Bioengineering and Biotechnology, 2014, 2, 76.	2.0	46
107	Metabolic modeling of clostridia: current developments and applications. FEMS Microbiology Letters, 2016, 363, fnw004.	0.7	46
108	Elucidation and Structural Analysis of Conserved Pools for Genome-Scale Metabolic Reconstructions. Biophysical Journal, 2005, 88, 37-49.	0.2	45

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109	Metabolic reconstruction of the archaeon methanogen Methanosarcina Acetivorans. BMC Systems Biology, 2011, 5, 28.	3.0	45
110	MinGenome: An In Silico Top-Down Approach for the Synthesis of Minimized Genomes. ACS Synthetic Biology, 2018, 7, 462-473.	1.9	45
111	Thermodynamic analysis of the pathway for ethanol production from cellobiose in Clostridium thermocellum. Metabolic Engineering, 2019, 55, 161-169.	3.6	44
112	Computational biophysical characterization of the SARS-CoV-2 spike protein binding with the ACE2 receptor and implications for infectivity. Computational and Structural Biotechnology Journal, 2020, 18, 2573-2582.	1.9	43
113	Construction of an E. Coli genomeâ€scale atom mapping model for MFA calculations. Biotechnology and Bioengineering, 2011, 108, 1372-1382.	1.7	42
114	OptMAVEn-2.0: De novo Design of Variable Antibody Regions Against Targeted Antigen Epitopes. Antibodies, 2018, 7, 23.	1.2	42
115	Review of the BRENDA Database. Metabolic Engineering, 2003, 5, 71-73.	3.6	41
116	Microbial 1â€butanol production: Identification of nonâ€native production routes and in silico engineering interventions. Biotechnology Journal, 2010, 5, 716-725.	1.8	41
117	Assessing methanotrophy and carbon fixation for biofuel production by Methanosarcina acetivorans. Microbial Cell Factories, 2016, 15, 10.	1.9	40
118	Optimal protein library design using recombination or point mutations based on sequence-based scoring functions. Protein Engineering, Design and Selection, 2007, 20, 361-373.	1.0	37
119	Global optimization for molecular conformation problems. Annals of Operations Research, 1993, 42, 85-117.	2.6	35
120	Identification of optimal measurement sets for complete flux elucidation in metabolic flux analysis experiments. Biotechnology and Bioengineering, 2008, 100, 1039-1049.	1.7	35
121	Improving prediction fidelity of cellular metabolism with kinetic descriptions. Current Opinion in Biotechnology, 2015, 36, 57-64.	3.3	35
122	Bilevel optimization techniques in computational strain design. Computers and Chemical Engineering, 2015, 72, 363-372.	2.0	35
123	Development of a core Clostridium thermocellum kinetic metabolic model consistent with multiple genetic perturbations. Biotechnology for Biofuels, 2017, 10, 108.	6.2	35
124	Metabolic model guided strain design of cyanobacteria. Current Opinion in Biotechnology, 2020, 64, 17-23.	3.3	35
125	K-FIT: An accelerated kinetic parameterization algorithm using steady-state fluxomic data. Metabolic Engineering, 2020, 61, 197-205.	3.6	35
126	OptGraft: A computational procedure for transferring a binding site onto an existing protein scaffold. Protein Science, 2009, 18, 180-195.	3.1	34

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127	The Iterative Protein Redesign and Optimization (IPRO) suite of programs. Journal of Computational Chemistry, 2015, 36, 251-263.	1.5	34
128	CLCA: Maximum Common Molecular Substructure Queries within the MetRxn Database. Journal of Chemical Information and Modeling, 2014, 54, 3417-3438.	2.5	33
129	Using multiple sequence correlation analysis to characterize functionally important protein regions. Protein Engineering, Design and Selection, 2003, 16, 397-406.	1.0	32
130	Methane oxidation by anaerobic archaea for conversion to liquid fuels. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 391-401.	1.4	32
131	Computational challenges in combinatorial library design for protein engineering. AICHE Journal, 2004, 50, 262-272.	1.8	31
132	Impact of Stoichiometry Representation on Simulation of Genotype-Phenotype Relationships in Metabolic Networks. PLoS Computational Biology, 2012, 8, e1002758.	1.5	31
133	Coupled Enzyme Reactions Performed in Heterogeneous Reaction Media: Experiments and Modeling for Glucose Oxidase and Horseradish Peroxidase in a PEG/Citrate Aqueous Two-Phase System. Journal of Physical Chemistry B, 2014, 118, 2506-2517.	1.2	31
134	Using Gene Essentiality and Synthetic Lethality Information to Correct Yeast and CHO Cell Genome-Scale Models. Metabolites, 2015, 5, 536-570.	1.3	31
135	In VivoThermodynamic Analysis of Glycolysis in Clostridium thermocellum and Thermoanaerobacterium saccharolyticum Using¹³C and²H Tracers. MSystems, 2020, 5, .	1.7	31
136	A Computational Procedure for Optimal Engineering Interventions Using Kinetic Models of Metabolism. Biotechnology Progress, 2006, 22, 1507-1517.	1.3	31
137	Down-Regulation of HtrA1 Activates the Epithelial-Mesenchymal Transition and ATM DNA Damage Response Pathways. PLoS ONE, 2012, 7, e39446.	1.1	30
138	Advances in de novo strain design using integrated systems and synthetic biology tools. Current Opinion in Chemical Biology, 2015, 28, 105-114.	2.8	30
139	Building kinetic models for metabolic engineering. Current Opinion in Biotechnology, 2021, 67, 35-41.	3.3	30
140	Design of combinatorial protein libraries of optimal size. Proteins: Structure, Function and Bioinformatics, 2005, 60, 769-777.	1.5	28
141	Rapid construction of metabolic models for a family of Cyanobacteria using a multiple source annotation workflow. BMC Systems Biology, 2013, 7, 142.	3.0	28
142	From Escherichia coli mutant 13C labeling data to a core kinetic model: A kinetic model parameterization pipeline. PLoS Computational Biology, 2019, 15, e1007319.	1.5	28
143	Improved computational performance of MFA using elementary metabolite units and flux coupling. Metabolic Engineering, 2010, 12, 123-128.	3.6	27
144	De novo design of antibody complementarity determining regions binding a FLAG tetra-peptide. Scientific Reports, 2017, 7, 10295.	1.6	27

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145	A diurnal flux balance model of Synechocystis sp. PCC 6803 metabolism. PLoS Computational Biology, 2019, 15, e1006692.	1.5	27
146	Quantitative assessment of uncertainty in the optimization of metabolic pathways. , 1997, 56, 145-161.		26
147	Recent advances in constraint and machine learning-based metabolic modeling by leveraging stoichiometric balances, thermodynamic feasibility and kinetic law formalisms. Metabolic Engineering, 2021, 63, 13-33.	3.6	26
148	Developmental changes in lignin composition are driven by both monolignol supply and laccase specificity. Science Advances, 2022, 8, eabm8145.	4.7	26
149	Elucidation of directionality for co-expressed genes: predicting intra-operon termination sites. Bioinformatics, 2006, 22, 209-214.	1.8	25
150	Extending Iterative Protein Redesign and Optimization (IPRO) in Protein Library Design for Ligand Specificity. Biophysical Journal, 2007, 92, 2120-2130.	0.2	25
151	Computational de novo design of antibodies binding to a peptide with high affinity. Biotechnology and Bioengineering, 2017, 114, 1331-1342.	1.7	25
152	Market-Based Pollution Abatement Strategies:â€‰ Risk Management Using Emission Option Contracts. Industrial & Engineering Chemistry Research, 2003, 42, 802-810.	1.8	24
153	Designing the substrate specificity of d-hydantoinase using a rational approach. Enzyme and Microbial Technology, 2009, 44, 170-175.	1.6	24
154	MAPs: a database of modular antibody parts for predicting tertiary structures and designing affinity matured antibodies. BMC Bioinformatics, 2013, 14, 168.	1.2	24
155	Engineering of E. coli inherent fatty acid biosynthesis capacity to increase octanoic acid production. Biotechnology for Biofuels, 2018, 11, 87.	6.2	24
156	Optimizationâ€driven identification of genetic perturbations accelerates the convergence of model parameters in ensemble modeling of metabolic networks. Biotechnology Journal, 2013, 8, 1090-1104.	1.8	22
157	OptZyme: Computational Enzyme Redesign Using Transition State Analogues. PLoS ONE, 2013, 8, e75358.	1.1	22
158	Clostridium butyricum maximizes growth while minimizing enzyme usage and ATP production: metabolic flux distribution of a strain cultured in glycerol. BMC Systems Biology, 2017, 11, 58.	3.0	22
159	Accelerating flux balance calculations in genome-scale metabolic models by localizing the application of loopless constraints. Bioinformatics, 2018, 34, 4248-4255.	1.8	22
160	Using a residue clash map to functionally characterize protein recombination hybrids. Protein Engineering, Design and Selection, 2003, 16, 1025-1034.	1.0	21
161	Real-Options-Based Planning Strategies under Uncertainty. Industrial & Engineering Chemistry Research, 2004, 43, 3870-3878.	1.8	21
162	Large-scale inference and graph-theoretical analysis of gene-regulatory networks in B. Subtilis. Physica A: Statistical Mechanics and Its Applications, 2007, 373, 796-810.	1.2	21

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163	Engineering biology approaches for food and nutrient production by cyanobacteria. Current Opinion in Biotechnology, 2021, 67, 1-6.	3.3	21
164	Identifying Regulatory Changes to Facilitate Nitrogen Fixation in the Nondiazotroph Synechocystis sp. PCC 6803. ACS Synthetic Biology, 2016, 5, 250-258.	1.9	20
165	Development of a Genome-Scale Metabolic Model of Clostridium thermocellum and Its Applications for Integration of Multi-Omics Datasets and Computational Strain Design. Frontiers in Bioengineering and Biotechnology, 2020, 8, 772.	2.0	20
166	Genome-scale metabolic reconstruction of the non-model yeast Issatchenkia orientalis SD108 and its application to organic acids production. Metabolic Engineering Communications, 2020, 11, e00148.	1.9	20
167	Valuation and design of pharmaceutical R&D licensing deals. AICHE Journal, 2005, 51, 198-209.	1.8	19
168	Predicting the Longitudinally and Radially Varying Gut Microbiota Composition Using Multi-Scale Microbial Metabolic Modeling. Processes, 2019, 7, 394.	1.3	18
169	eCodonOpt: a systematic computational framework for optimizing codon usage in directed evolution experiments. Nucleic Acids Research, 2002, 30, 2407-2416.	6.5	17
170	Molecular Design Using Quantum Chemical Calculations for Property Estimation. Industrial & Engineering Chemistry Research, 2004, 43, 3419-3432.	1.8	17
171	Large-scale inference of the transcriptional regulation of Bacillus subtilis. Computers and Chemical Engineering, 2005, 29, 565-576.	2.0	17
172	7 Log Virus Removal in a Simple Functionalized Sand Filter. Environmental Science & Technology, 2019, 53, 12706-12714.	4.6	17
173	SNPeffect: identifying functional roles of SNPs using metabolic networks. Plant Journal, 2020, 103, 512-531.	2.8	17
174	Directed Evolution Reveals the Functional Sequence Space of an Adenylation Domain Specificity Code. ACS Chemical Biology, 2019, 14, 2044-2054.	1.6	16
175	Pareto Optimality Explanation of the Glycolytic Alternatives in Nature. Scientific Reports, 2019, 9, 2633.	1.6	16
176	Recombination and lineage-specific mutations linked to the emergence of SARS-CoV-2. Genome Medicine, 2021, 13, 124.	3.6	16
177	A Computational Procedure for Optimal Engineering Interventions Using Kinetic Models of Metabolism. Biotechnology Progress, 2006, 22, 1507-1517.	1.3	16
178	Locating all azeotropes in homogeneous azeotropic systems. Computers and Chemical Engineering, 1996, 20, S413-S418.	2.0	15
179	Predicting Out-of-Sequence Reassembly in DNA Shuffling. Journal of Theoretical Biology, 2002, 219, 9-17.	0.8	15
180	Achieving Metabolic Flux Analysis for S. cerevisiae at a Genome-Scale: Challenges, Requirements, and Considerations. Metabolites, 2015, 5, 521-535.	1.3	15

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181	Metabolic engineering of Rhodotorula toruloides IFO0880 improves C16 and C18 fatty alcohol production from synthetic media. Microbial Cell Factories, 2022, 21, 26.	1.9	15
182	Predicting Out-of-Sequence Reassembly in DNA Shuffling. Journal of Theoretical Biology, 2002, 219, 9-17.	0.8	14
183	Exploring the combinatorial space of complete pathways to chemicals. Biochemical Society Transactions, 2018, 46, 513-522.	1.6	14
184	The importance and future of biochemical engineering. Biotechnology and Bioengineering, 2020, 117, 2305-2318.	1.7	13
185	Quantifying the propagation of parametric uncertainty on flux balance analysis. Metabolic Engineering, 2022, 69, 26-39.	3.6	13
186	Review of the Enzymes and Metabolic Pathways (EMP) Database. Metabolic Engineering, 2001, 3, 193-194.	3.6	12
187	Dissecting the metabolic reprogramming of maize root under nitrogen-deficient stress conditions. Journal of Experimental Botany, 2022, 73, 275-291.	2.4	12
188	Modeling and optimization of DNA recombination. Computers and Chemical Engineering, 2000, 24, 693-699.	2.0	10
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