

CITATION REPORT

List of articles citing

What is flux balance analysis?

DOI: 10.1038/nbt.1614

Nature Biotechnology, 2010, 28, 245-8.

Source: <https://exaly.com/paper-pdf/48503909/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2272	Engineering an NADPH/NADP+ Redox Biosensor in Yeast.		
2271	Model-Assisted Fine-Tuning of Central Carbon Metabolism in Yeast through dCas9-Based Regulation.		
2270	Modulation of Nitrous Oxide (N ₂ O) Accumulation by Primary Metabolites in Denitrifying Cultures Adapting to Changes in Environmental C and N.		
2269	Reconstruction and flux-balance analysis of the Plasmodium falciparum metabolic network. 2010 , 6, 408		101
2268	A gentle introduction to the thermodynamics of biochemical stoichiometric networks in steady state. 2010 , 187, 255-274		6
2267	A detailed genome-wide reconstruction of mouse metabolism based on human Recon 1. 2010 , 4, 140		114
2266	Systematizing the generation of missing metabolic knowledge. 2010 , 107, 403-12		114
2265	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. <i>Nature Biotechnology</i> , 2010 , 28, 1279-85	44.5	206
2264	The challenges of integrating multi-omic data sets. 2010 , 6, 787-9		123
2263	MetNetMaker: a free and open-source tool for the creation of novel metabolic networks in SBML format. 2010 , 26, 2352-3		15
2262	Understanding signalling networks as collections of signal transduction pathways. 2010 ,		5
2261	Synthetic biology: a foundation for multi-scale molecular biology. 2010 , 1, 309-12		2
2260	Environments that induce synthetic microbial ecosystems. 2010 , 6, e1001002		225
2259	Systems biology approaches to understanding mycobacterial survival mechanisms. 2010 , 7, e75-e82		16
2258	Structural and operational complexity of the Geobacter sulfurreducens genome. 2010 , 20, 1304-11		68
2257	Yeast dynamic metabolic flux measurement in nutrient-rich media by HPLC and accelerator mass spectrometry. 2010 , 82, 9812-7		13
2256	Patterns of indirect protein interactions suggest a spatial organization to metabolism. 2011 , 7, 3056-64		24

2255	Functional integration of a metabolic network model and expression data without arbitrary thresholding. 2011 , 27, 541-7	194
2254	Two-phase resolution of polyploidy in the Arabidopsis metabolic network gives rise to relative and absolute dosage constraints. 2011 , 23, 1719-28	111
2253	A Spatial Branch-and-Bound Framework for the Global Optimization of Kinetic Models of Metabolic Networks. 2011 , 50, 5225-5238	17
2252	Elimination of thermodynamically infeasible loops in steady-state metabolic models. 2011 , 100, 544-553	143
2251	Microbial laboratory evolution in the era of genome-scale science. 2011 , 7, 509	210
2250	Exploring the metabolic state of microorganisms using metabolomics. 2011 , 3, 2443-58	18
2249	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. 2011 , 6, 1290-307	1061
2248	Metabolic network destruction: Relating topology to robustness. 2011 , 2, 88-98	3
2247	Application of metabolic flux analysis in metabolic engineering. 2011 , 498, 67-93	11
2246	A practical guide to genome-scale metabolic models and their analysis. 2011 , 500, 509-32	39
2245	Whole-genome metabolic network reconstruction and constraint-based modeling. 2011 , 500, 411-33	23
2244	Microbial Growth Dynamics. 2011 , 257-283	3
2243	Reconstruction and analysis of human heart-specific metabolic network based on transcriptome and proteome data. 2011 , 415, 450-4	24
2242	Metabolic network reconstruction of Chlamydomonas offers insight into light-driven algal metabolism. 2011 , 7, 518	234
2241	Mathematical Models in Biotechnology. 2011 , 651-658	
2240	A Systems Biology Approach to the Evolution of Codon Use Pattern. 2011 ,	1
2239	. 2011 ,	22
2238	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. 2011 , 8, 187-203	55

2237	OmicsTechnologies and systems biology for engineering <i>Saccharomyces cerevisiae</i> strains for lignocellulosic bioethanol production. 2011 , 2, 659-675	2
2236	Genetic and metabolic determinants of nutritional phenotype in an insect-bacterial symbiosis. 2011 , 20, 2073-84	50
2235	Modelling the size and composition of fruit, grain and seed by process-based simulation models. 2011 , 191, 601-618	36
2234	Flux-based analysis of sulfur metabolism in desulfurizing strains of <i>Rhodococcus erythropolis</i> . 2011 , 315, 115-21	20
2233	In situ to in silico and back: elucidating the physiology and ecology of <i>Geobacter</i> spp. using genome-scale modelling. 2011 , 9, 39-50	111
2232	Post-genomics resources and tools for studying apicomplexan metabolism. 2011 , 27, 131-40	12
2231	Individualized therapy of HHT driven by network analysis of metabolomic profiles. 2011 , 5, 200	15
2230	Pathways and Networks as Functional Descriptors for Human Disease and Drug Response Endpoints. 2011 , 415-442	2
2229	Haem oxygenase is synthetically lethal with the tumour suppressor fumarate hydratase. 2011 , 477, 225-8	367
2228	Genome-enabled determination of amino acid biosynthesis in <i>Xanthomonas campestris</i> pv. <i>campestris</i> and identification of biosynthetic pathways for alanine, glycine, and isoleucine by ¹³ C-isotopologue profiling. 2011 , 286, 247-59	15
2227	Utility of gel-free, label-free shotgun proteomics approaches to investigate microorganisms. 2011 , 90, 407-16	21
2226	A systematic petri net approach for multiple-scale modeling and simulation of biochemical processes. 2011 , 164, 338-52	5
2225	Prediction of proton exchange and bacterial growth on various substrates using constraint-based modeling approach. 2011 , 16, 875-884	2
2224	Engineering strategy of yeast metabolism for higher alcohol production. 2011 , 10, 70	38
2223	Systems biology of lactic acid bacteria: a critical review. 2011 , 10 Suppl 1, S11	45
2222	A metabolic model of the mitochondrion and its use in modelling diseases of the tricarboxylic acid cycle. 2011 , 5, 102	51
2221	iAB-RBC-283: A proteomically derived knowledge-base of erythrocyte metabolism that can be used to simulate its physiological and patho-physiological states. 2011 , 5, 110	69
2220	TIGER: Toolbox for integrating genome-scale metabolic models, expression data, and transcriptional regulatory networks. 2011 , 5, 147	76

2219	Metabolic network modeling of redox balancing and biohydrogen production in purple nonsulfur bacteria. 2011 , 5, 150	57
2218	The human metabolic reconstruction Recon 1 directs hypotheses of novel human metabolic functions. 2011 , 5, 155	55
2217	A multi-tissue type genome-scale metabolic network for analysis of whole-body systems physiology. 2011 , 5, 180	134
2216	The evolution of metabolic networks of E. coli. 2011 , 5, 182	55
2215	SPABBATS: A pathway-discovery method based on Boolean satisfiability that facilitates the characterization of suppressor mutants. 2011 , 5, 5	12
2214	Networks in biology: Handling biological complexity requires novel inputs into network theory. 2011 , 16, 6-9	1
2213	Combining metabolic pathway analysis with Evolutionary Game Theory: explaining the occurrence of low-yield pathways by an analytic optimization approach. 2011 , 105, 147-53	55
2212	Special issue: integration of OMICs datasets into metabolic pathway analysis. 2011 , 105, 107-8	2
2211	Sustainable model building the role of standards and biological semantics. 2011 , 500, 371-95	11
2210	In silico evolution of early metabolism. 2011 , 17, 87-108	8
2209	Robust flux balance analysis of metabolic networks. 2011 ,	4
2208	Logic in Software, Dynamical and Biological Systems. 2011 ,	2
2207	From Pathways to Genomes and Beyond: The Metabolic Engineering Toolbox and Its Place in Biofuels Production. 2011 , 1,	3
2206	Systems glycobiology: biochemical reaction networks regulating glycan structure and function. 2011 , 21, 1541-53	38
2205	Impact of gene expression noise on organismal fitness and the efficacy of natural selection. 2011 , 108, E67-76	132
2204	Pattern Recognition in Bioinformatics. 2011 ,	1
2203	BACK MATTER. 2011 , 383-428	
2202	A comprehensive genome-scale reconstruction of Escherichia coli metabolism--2011. 2011 , 7, 535	726

2201	Selection for higher gene copy number after different types of plant gene duplications. 2011 , 3, 1369-80	22
2200	Reconciliation of genome-scale metabolic reconstructions for comparative systems analysis. 2011 , 7, e1001116	97
2199	A whole-body model for glycogen regulation reveals a critical role for substrate cycling in maintaining blood glucose homeostasis. 2011 , 7, e1002272	23
2198	Mechanistic modeling of aberrant energy metabolism in human disease. 2012 , 3, 404	16
2197	Determining host metabolic limitations on viral replication via integrated modeling and experimental perturbation. 2012 , 8, e1002746	38
2196	Integrating flux balance analysis into kinetic models to decipher the dynamic metabolism of <i>Shewanella oneidensis</i> MR-1. 2012 , 8, e1002376	50
2195	A scalable algorithm to explore the Gibbs energy landscape of genome-scale metabolic networks. 2012 , 8, e1002562	20
2194	Functional modules, structural topology, and optimal activity in metabolic networks. 2012 , 8, e1002720	23
2193	Phenomenological model for predicting the catabolic potential of an arbitrary nutrient. 2012 , 8, e1002762	2
2192	Temporal expression-based analysis of metabolism. 2012 , 8, e1002781	32
2191	Integration of expression data in genome-scale metabolic network reconstructions. 2012 , 3, 299	191
2190	The central role of the host cell in symbiotic nitrogen metabolism. 2012 , 279, 2965-73	57
2189	Frontiers in metabolic reconstruction and modeling of plant genomes. 2012 , 63, 2247-58	62
2188	Digital biology: a new era has begun. 2012 , 3, 311-2	12
2187	Truncated branch and bound achieves efficient constraint-based genetic design. 2012 , 28, 1619-23	21
2186	Plant Metabolic Pathways: Databases and Pipeline for Stoichiometric Analysis. 2012 , 345-366	1
2185	Ensemble modeling of cancer metabolism. 2012 , 3, 135	27
2184	Genome-scale metabolic reconstruction and hypothesis testing in the methanogenic archaeon <i>Methanosarcina acetivorans</i> C2A. 2012 , 194, 855-65	62

2183	Constraints-based stoichiometric analysis of hypoxic stress on steroidogenesis in fathead minnows, <i>Pimephales promelas</i> . 2012 , 215, 1753-65	13
2182	Construction and completion of flux balance models from pathway databases. 2012 , 28, 388-96	71
2181	Application of Top-Down and Bottom-up Systems Approaches in Ruminant Physiology and Metabolism. 2012 , 13, 379-94	34
2180	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. 2012 , 8, 558	114
2179	Predicting drug targets and biomarkers of cancer via genome-scale metabolic modeling. 2012 , 18, 5572-84	77
2178	Nutritional requirements of the BY series of <i>Saccharomyces cerevisiae</i> strains for optimum growth. 2012 , 12, 796-808	65
2177	Physiological tolerance and stoichiometric potential of cyanobacteria for hydrocarbon fuel production. 2012 , 162, 67-74	45
2176	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. 2012 , 196, 596-605	117
2175	Mathematical optimization applications in metabolic networks. 2012 , 14, 672-86	100
2174	Genome-wide metabolic network reconstruction of the picoalga <i>Ostreococcus</i> . 2012 , 63, 2353-62	36
2173	Engineering of microorganisms for the production of biofuels and perspectives based on systems metabolic engineering approaches. 2012 , 30, 989-1000	128
2172	GEMSiRV: a software platform for GENome-scale metabolic model simulation, reconstruction and visualization. 2012 , 28, 1752-8	33
2171	Constraining the metabolic genotype-phenotype relationship using a phylogeny of in silico methods. 2012 , 10, 291-305	571
2170	Reconstruction of the <i>Saccharopolyspora erythraea</i> genome-scale model and its use for enhancing erythromycin production. 2012 , 102, 493-502	32
2169	Metabolic shifts: a fitness perspective for microbial cell factories. 2012 , 34, 2147-60	51
2168	Synthetic approaches to understanding biological constraints. 2012 , 16, 323-8	11
2167	Reconstruction and analysis of a genome-scale metabolic model of the vitamin C producing industrial strain <i>Ketogulonicigenium vulgare</i> WSH-001. 2012 , 161, 42-8	30
2166	Rhamnolipids--next generation surfactants?. 2012 , 162, 366-80	230

2165	Systems biology of stored blood cells: can it help to extend the expiration date?. 2012 , 76 Spec No., 163-7	16
2164	Mass conserved elementary kinetics is sufficient for the existence of a non-equilibrium steady state concentration. 2012 , 314, 173-81	7
2163	Roles of sulfite oxidoreductase and sulfite reductase in improving desulfurization by <i>Rhodococcus erythropolis</i> . 2012 , 8, 2724-32	36
2162	Use of an uncertainty analysis for genome-scale models as a prediction tool for microbial growth processes in subsurface environments. 2012 , 46, 2790-8	7
2161	Optimal flux spaces of genome-scale stoichiometric models are determined by a few subnetworks. 2012 , 2, 580	52
2160	Emerging engineering principles for yield improvement in microbial cell design. 2012 , 3, e201210016	7
2159	Bioprocess systems engineering: transferring traditional process engineering principles to industrial biotechnology. 2012 , 3, e201210022	39
2158	Computational systems biology and in silico modeling of the human microbiome. 2012 , 13, 769-80	75
2157	Network context and selection in the evolution to enzyme specificity. 2012 , 337, 1101-4	204
2156	Modelling cyanobacteria: from metabolism to integrative models of phototrophic growth. 2012 , 63, 2259-74	43
2155	Detailing the optimality of photosynthesis in cyanobacteria through systems biology analysis. 2012 , 109, 2678-83	231
2154	The Integration of Biological Pathway Knowledge in Cancer Genomics: A review of existing computational approaches. 2012 , 29, 35-50	16
2153	Model-based confirmation of alternative substrates of mitochondrial electron transport chain. 2012 , 287, 11122-31	18
2152	Robust design of microbial strains. 2012 , 28, 3097-104	46
2151	Computational simulation of a gene regulatory network implementing an extendable synchronous single-input delay flip-flop. 2012 , 109, 57-71	12
2150	The dawn of virtual cell biology. 2012 , 150, 248-50	13
2149	Computational tools for the synthetic design of biochemical pathways. 2012 , 10, 191-202	181
2148	Von Neumann's growth model: Statistical mechanics and biological applications. 2012 , 212, 45-64	

2147	An in silico platform for the design of heterologous pathways in nonnative metabolite production. 2012 , 13, 93	19
2146	Production of 2,3-butanediol in <i>Saccharomyces cerevisiae</i> by in silico aided metabolic engineering. 2012 , 11, 68	109
2145	Model-based analysis of an adaptive evolution experiment with <i>Escherichia coli</i> in a pyruvate limited continuous culture with glycerol. 2012 , 2012, 14	6
2144	Comparative multi-goal tradeoffs in systems engineering of microbial metabolism. 2012 , 6, 127	11
2143	Dynamic regulatory on/off minimization for biological systems under internal temporal perturbations. 2012 , 6, 16	24
2142	Gap-filling analysis of the iJO1366 <i>Escherichia coli</i> metabolic network reconstruction for discovery of metabolic functions. 2012 , 6, 30	43
2141	Improving metabolic flux predictions using absolute gene expression data. 2012 , 6, 73	107
2140	A constraint-based model of <i>Scheffersomyces stipitis</i> for improved ethanol production. 2012 , 5, 72	20
2139	A compendium of inborn errors of metabolism mapped onto the human metabolic network. 2012 , 8, 2545-58	55
2138	Microbial Consortia Engineering for Cellular Factories: in vitro to in silico systems. 2012 , 3, e201210017	88
2137	Organization principles in genetic interaction networks. 2012 , 751, 53-78	2
2136	Development of constraint-based system-level models of microbial metabolism. 2012 , 881, 531-49	
2135	An in silico re-design of the metabolism in <i>Thermotoga maritima</i> for increased biohydrogen production. 2012 , 37, 12205-12218	23
2134	Paint4Net: COBRA Toolbox extension for visualization of stoichiometric models of metabolism. 2012 , 109, 233-9	23
2133	Systems metabolic engineering: the creation of microbial cell factories by rational metabolic design and evolution. 2013 , 131, 1-23	14
2132	Studying <i>Salmonellae</i> and <i>Yersinia</i> host-pathogen interactions using integrated 'omics and modeling. 2013 , 363, 21-41	10
2131	Microbial Systems Biology. 2012 ,	2
2130	In silico method for modelling metabolism and gene product expression at genome scale. 2012 , 3, 929	194

2129	Evolutionary Systems Biology. 2012,	24
2128	Genome-level transcription data of <i>Yersinia pestis</i> analyzed with a new metabolic constraint-based approach. 2012, 6, 150	52
2127	Integration of time-resolved transcriptomics data with flux-based methods reveals stress-induced metabolic adaptation in <i>Escherichia coli</i> . 2012, 6, 148	19
2126	VANTED v2: a framework for systems biology applications. 2012, 6, 139	123
2125	Designing optimal cell factories: integer programming couples elementary mode analysis with regulation. 2012, 6, 103	23
2124	Systems Metabolic Engineering. 2012,	10
2123	Identification of functional differences in metabolic networks using comparative genomics and constraint-based models. 2012, 7, e34670	39
2122	Understanding regulation of metabolism through feasibility analysis. 2012, 7, e39396	8
2121	Reconstruction and in silico analysis of metabolic network for an oleaginous yeast, <i>Yarrowia lipolytica</i> . 2012, 7, e51535	65
2120	Flux Analysis of the <i>Trypanosoma brucei</i> Glycolysis Based on a Multiobjective-Criteria Bioinformatic Approach. 2012, 2012, 159423	10
2119	Human metabolic network: reconstruction, simulation, and applications in systems biology. 2012, 2, 242-53	8
2118	Metabolic stasis in an ancient symbiosis: genome-scale metabolic networks from two <i>Blattabacterium cuenoti</i> strains, primary endosymbionts of cockroaches. 2012, 12 Suppl 1, S5	26
2117	Systems biology approaches to toll-like receptor signaling. 2012, 4, 497-507	15
2116	A road map for the development of community systems (CoSy) biology. 2012, 10, 366-72	115
2115	A whole-cell computational model predicts phenotype from genotype. 2012, 150, 389-401	928
2114	Genome-Scale Network Modeling. 2012, 1-23	2
2113	Systems metabolic engineering of microorganisms for natural and non-natural chemicals. 2012, 8, 536-46	551
2112	Dynamic models of metabolism: Review of the cybernetic approach. 2012, 58, 986-997	63

2111	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . 2012 , 109, 1798-807	15
2110	Using flux balance analysis to guide microbial metabolic engineering. 2012 , 834, 197-216	19
2109	Kinetic Modeling of Metabolic Networks. 2012 , 25-55	5
2108	BioNetSim: a Petri net-based modeling tool for simulations of biochemical processes. 2012 , 3, 225-9	5
2107	Using the reconstructed genome-scale human metabolic network to study physiology and pathology. 2012 , 271, 131-41	88
2106	Designing biological systems: Systems Engineering meets Synthetic Biology. 2012 , 69, 1-29	66
2105	Metabolomics methods for the synthetic biology of secondary metabolism. 2012 , 586, 2177-83	57
2104	A variational principle for computing nonequilibrium fluxes and potentials in genome-scale biochemical networks. 2012 , 292, 71-7	26
2103	Systems Engineering and Metabolic Engineering: A Side-by-Side Comparison. 2012 , 8, 226-231	2
2102	Prediction of dynamic behavior of mutant strains from limited wild-type data. 2012 , 14, 69-80	33
2101	Computational tools for metabolic engineering. 2012 , 14, 270-80	77
2100	Model-driven elucidation of the inherent capacity of <i>Geobacter sulfurreducens</i> for electricity generation. 2013 , 7, 14	16
2099	Invariance and optimality in the regulation of an enzyme. 2013 , 8, 7	3
2098	Systems Biomechanics of the Cell. 2013 ,	1
2097	Flux analysis and metabolomics for systematic metabolic engineering of microorganisms. 2013 , 31, 818-26	84
2096	Computational approaches for understanding energy metabolism. 2013 , 5, 733-50	11
2095	In Silico Systems Biology. 2013 ,	3
2094	Encyclopedia of Systems Biology. 2013 , 2034-2036	

2093	Quantitative assessment of thermodynamic constraints on the solution space of genome-scale metabolic models. 2013 , 105, 512-22	40
2092	Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. 2013 , 14, 32	33
2091	Inferring ancient metabolism using ancestral core metabolic models of enterobacteria. 2013 , 7, 46	9
2090	A metabolite-centric view on flux distributions in genome-scale metabolic models. 2013 , 7, 33	16
2089	Formal Methods for Dynamical Systems. 2013 ,	2
2088	Novel approach to engineer strains for simultaneous sugar utilization. 2013 , 20, 63-72	41
2087	Genome-scale stoichiometry analysis to elucidate the innate capability of the cyanobacterium <i>Synechocystis</i> for electricity generation. 2013 , 40, 1161-80	8
2086	Dynamic modeling of aerobic growth of <i>Shewanella oneidensis</i> . Predicting triaunic growth, flux distributions, and energy requirement for growth. 2013 , 15, 25-33	33
2085	Modelling metabolic CO ₂ evolution—a fresh perspective on respiration. 2013 , 36, 1631-40	42
2084	Dynamic metabolic flux analysis—tools for probing transient states of metabolic networks. 2013 , 24, 973-8	74
2083	Evaluation of control mechanisms for <i>Saccharomyces cerevisiae</i> central metabolic reactions using metabolome data of eight single-gene deletion mutants. 2013 , 97, 3569-77	7
2082	Genome-scale metabolic model in guiding metabolic engineering of microbial improvement. 2013 , 97, 519-39	41
2081	An analysis of a 'community-driven' reconstruction of the human metabolic network. 2013 , 9, 757-764	30
2080	Encyclopedia of Systems Biology. 2013 , 2054-2054	
2079	Connecting the dots: applications of network medicine in pharmacology and disease. 2013 , 94, 659-69	23
2078	Modelling Metabolic Networks—The Theories of Metabolism. 2013 , 67, 593-621	
2077	. 2013 , 4, 17	27
2076	Encyclopedia of Systems Biology. 2013 , 468-473	

2075	Towards a predictive systems-level model of the human microbiome: progress, challenges, and opportunities. 2013 , 24, 810-20	52
2074	Computational Models of Algae Metabolism for Industrial Applications. 2013 , 9, 185-195	7
2073	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. 2013 , 29, 2900-8	90
2072	Establishment, in silico analysis, and experimental verification of a large-scale metabolic network of the xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100. 2013 , 167, 123-34	37
2071	Omix DA Visualization Tool for Metabolic Networks with Highest Usability and Customizability in Focus. 2013 , 85, 849-862	21
2070	Microbial engineering strategies to improve cell viability for biochemical production. 2013 , 31, 903-14	48
2069	Potential of proton-pumping rhodopsins: engineering photosystems into microorganisms. 2013 , 31, 633-42	23
2068	Reconstruction and analysis of the industrial strain <i>Bacillus megaterium</i> WSH002 genome-scale in silico metabolic model. 2013 , 164, 503-9	19
2067	Modeling metabolic systems: the need for dynamics. 2013 , 2, 373-382	33
2066	Characterization and modelling of interspecies electron transfer mechanisms and microbial community dynamics of a syntrophic association. 2013 , 4, 2809	82
2065	Accelerated discovery via a whole-cell model. 2013 , 10, 1192-5	49
2064	Antibacterial mechanisms identified through structural systems pharmacology. 2013 , 7, 102	20
2063	Inferring chemical reaction patterns using rule composition in graph grammars. 2013 , 4, 4	19
2062	COBRApy: CONstraints-Based Reconstruction and Analysis for Python. 2013 , 7, 74	502
2061	Robust flux balance analysis of multiscale biochemical reaction networks. 2013 , 14, 240	17
2060	Rapid construction of metabolic models for a family of Cyanobacteria using a multiple source annotation workflow. 2013 , 7, 142	26
2059	A multi-level multi-scale approach to study essential genes in <i>Mycobacterium tuberculosis</i> . 2013 , 7, 132	14
2058	A systematic comparison of the MetaCyc and KEGG pathway databases. 2013 , 14, 112	92

2057	Sybil--efficient constraint-based modelling in R. 2013 , 7, 125	78
2056	Investigating xylose metabolism in recombinant <i>Saccharomyces cerevisiae</i> via 13C metabolic flux analysis. 2013 , 12, 114	41
2055	Solving gap metabolites and blocked reactions in genome-scale models: application to the metabolic network of <i>Blattabacterium cuenoti</i> . 2013 , 7, 114	13
2054	Development of <i>Synechocystis</i> sp. PCC 6803 as a phototrophic cell factory. 2013 , 11, 2894-916	83
2053	ArtPathDesign: rational heterologous pathway design system for the production of nonnative metabolites. 2013 , 116, 524-7	5
2052	A design automation framework for computational bioenergetics in biological networks. 2013 , 9, 2554-64	8
2051	Pareto optimality in organelle energy metabolism analysis. 2013 , 10, 1032-44	11
2050	Basic and applied uses of genome-scale metabolic network reconstructions of <i>Escherichia coli</i> . 2013 , 9, 661	244
2049	Analysis of synthetic metabolic pathways solution space. 2013 ,	
2048	Metabolic reconstruction and flux analysis of industrial <i>Pichia</i> yeasts. 2013 , 97, 1865-73	13
2047	Development of thermodynamic optimum searching (TOS) to improve the prediction accuracy of flux balance analysis. 2013 , 110, 914-23	10
2046	A reliable simulator for dynamic flux balance analysis. 2013 , 110, 792-802	82
2045	Nitrogen assimilation in <i>Escherichia coli</i> : putting molecular data into a systems perspective. 2013 , 77, 628-95	147
2044	A systems biology approach to studying the role of microbes in human health. 2013 , 24, 4-12	70
2043	Moving H5N1 studies into the era of systems biology. 2013 , 178, 151-67	12
2042	Profiling metabolic networks to study cancer metabolism. 2013 , 24, 60-8	79
2041	Design and analysis of metabolic pathways supporting formatotrophic growth for electricity-dependent cultivation of microbes. 2013 , 1827, 1039-47	103
2040	Fluxomics - connecting 'omics analysis and phenotypes. 2013 , 15, 1901-16	84

2039	Fast thermodynamically constrained flux variability analysis. 2013 , 29, 903-9	33
2038	Somewhat in control--the role of transcription in regulating microbial metabolic fluxes. 2013 , 24, 987-93	46
2037	Development of microbial cell factories for bio-refinery through synthetic bioengineering. 2013 , 163, 204-16	46
2036	Genome-scale model management and comparison. 2013 , 985, 3-16	1
2035	Resolving cell composition through simple measurements, genome-scale modeling, and a genetic algorithm. 2013 , 985, 85-101	2
2034	Reconstruction and analysis of the genome-scale metabolic network of <i>Candida glabrata</i> . 2013 , 9, 205-16	36
2033	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013 , 31, 419-25	44.5 746
2032	Yeast Systems Biology. 2013 , 343-365	6
2031	<i>Salmonella</i> modulates metabolism during growth under conditions that induce expression of virulence genes. 2013 , 9, 1522-34	38
2030	Constraint-based strain design using continuous modifications (CosMos) of flux bounds finds new strategies for metabolic engineering. 2013 , 8, 595-604	30
2029	From physiology to systems metabolic engineering for the production of biochemicals by lactic acid bacteria. 2013 , 31, 764-88	111
2028	Systems Biomechanics of the Cell. 2013 , 1-55	
2027	Genome-scale modeling of human metabolism - a systems biology approach. 2013 , 8, 985-96	86
2026	Synthetic biology and the technicity of biofuels. 2013 , 44, 190-8	15
2025	Translating next generation sequencing to practice: opportunities and necessary steps. 2013 , 7, 743-55	28
2024	Systems biology for molecular life sciences and its impact in biomedicine. 2013 , 70, 1035-53	20
2023	Modeling <i>Mycobacterium tuberculosis</i> H37Rv In Silico. 2013 , 1-19	
2022	Thermodynamics of biochemical networks and duality theorems. 2013 , 87, 052108	10

2021	Bioinformatics Approach for Finding Target Protein in Infectious Disease. 2013 , 235-255	
2020	Plant genome-scale metabolic reconstruction and modelling. 2013 , 24, 271-7	58
2019	The Neal Amundson era. Rapid evolution of chemical engineering science. 2013 , 59, 3147-3157	3
2018	In silico screening of triple reaction knockout Escherichia coli strains for overproduction of useful metabolites. 2013 , 115, 221-8	20
2017	Metabolic network modeling approaches for investigating the "hungry cancer". 2013 , 23, 227-34	11
2016	Structural systems biology evaluation of metabolic thermotolerance in Escherichia coli. 2013 , 340, 1220-3	96
2015	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of Clostridium ljungdahlii. 2013 , 12, 118	106
2014	Efficient behavior of photosynthetic organelles via Pareto optimality, identifiability, and sensitivity analysis. 2013 , 2, 274-88	10
2013	Multiscale metabolic modeling: dynamic flux balance analysis on a whole-plant scale. 2013 , 163, 637-47	98
2012	Optimization-driven identification of genetic perturbations accelerates the convergence of model parameters in ensemble modeling of metabolic networks. 2013 , 8, 1090-104	22
2011	Decomposition of flux distributions into metabolic pathways. 2013 , 10, 984-93	3
2010	Elucidating xylose metabolism of scheffersomyces stipitis by integrating principal component analysis with flux balance analysis. 2013 ,	1
2009	Applications of genome-scale metabolic network models in the biopharmaceutical industry. 2013 , 1, 337-339	2
2008	Pareto epsilon-dominance and identifiable solutions for BioCAD modeling. 2013 ,	3
2007	Elucidating rice cell metabolism under flooding and drought stresses using flux-based modeling and analysis. 2013 , 162, 2140-50	52
2006	Functional genomics of Plasmodium falciparum using metabolic modelling and analysis. 2013 , 12, 316-27	13
2005	Modeling integrated cellular machinery using hybrid Petri-Boolean networks. 2013 , 9, e1003306	12
2004	Flux imbalance analysis and the sensitivity of cellular growth to changes in metabolite pools. 2013 , 9, e1003195	45

2003	The Application of Runge-Kutta Algorithms on Dynamic Model of Simulating Glycolytic Metabolism of Escherichia coli. 2013 , 647, 554-559	
2002	Metabolic reconstruction databases and their application to metabolomics research. 2013 , 68-79	
2001	Characterizing the relationship between steady state and response using analytical expressions for the steady states of mass action models. 2013 , 9, e1002901	9
2000	Parallel exploitation of diverse host nutrients enhances Salmonella virulence. 2013 , 9, e1003301	111
1999	Recent progress in the development of metabolome databases for plant systems biology. 2013 , 4, 73	55
1998	Structural control of metabolic flux. 2013 , 9, e1003368	9
1997	Metabolic constraint-based refinement of transcriptional regulatory networks. 2013 , 9, e1003370	26
1996	Novel insights into obesity and diabetes through genome-scale metabolic modeling. 2013 , 4, 92	31
1995	Reconstruction and validation of a genome-scale metabolic model for the filamentous fungus Neurospora crassa using FARM. 2013 , 9, e1003126	44
1994	Flux balance analysis of cyanobacterial metabolism: the metabolic network of Synechocystis sp. PCC 6803. 2013 , 9, e1003081	178
1993	Building the repertoire of dispensable chromosome regions in Bacillus subtilis entails major refinement of cognate large-scale metabolic model. 2013 , 41, 687-99	62
1992	Synthetic gene circuits for metabolic control: design trade-offs and constraints. 2013 , 10, 20120671	56
1991	Heterogeneity in protein expression induces metabolic variability in a modeled Escherichia coli population. 2013 , 110, 14006-11	76
1990	Predicting the impact of diet and enzymopathies on human small intestinal epithelial cells. 2013 , 22, 2705-22	51
1989	Computational evaluation of cellular metabolic costs successfully predicts genes whose expression is deleterious. 2013 , 110, 19166-71	18
1988	Computational evaluation of Synechococcus sp. PCC 7002 metabolism for chemical production. 2013 , 8, 619-30	51
1987	Metabolic reconstruction identifies strain-specific regulation of virulence in Toxoplasma gondii. 2013 , 9, 708	35
1986	Towards a whole-cell modeling approach for synthetic biology. 2013 , 23, 025112	48

1985	The dynamics of hybrid metabolic-genetic oscillators. 2013 , 23, 013132	12
1984	Alternate wetting and drying irrigation for rice in Bangladesh: Is it sustainable and has plant breeding something to offer?. 2013 , 2, 120-129	54
1983	Segregated flux balance analysis constrained by population structure/function data: the case of PHA production by mixed microbial cultures. 2013 , 110, 2267-76	8
1982	Exploration and comparison of inborn capacity of aerobic and anaerobic metabolisms of <i>Saccharomyces cerevisiae</i> for microbial electrical current production. 2013 , 4, 420-30	7
1981	Dynamical analysis of evolution equations in generalized models. 2013 , 78, 1051-1077	14
1980	A genome-scale modeling approach to study inborn errors of liver metabolism: toward an in silico patient. 2013 , 20, 383-97	9
1979	Cofactor modification analysis: a computational framework to identify cofactor specificity engineering targets for strain improvement. 2013 , 11, 1343006	14
1978	Systems biology methods and developments for <i>Saccharomyces cerevisiae</i> and other industrial yeasts in relation to the production of fermented food and food ingredients. 2013 , 42-80	
1977	Availability based Stabilization of Tubular Chemical Reactors. 2013 , 46, 96-101	2
1976	A new framework for metabolic modeling under non-balanced growth. Application to carbon metabolism of unicellular microalgae. 2013 , 46, 107-112	0
1975	Model-driven design of a <i>Saccharomyces cerevisiae</i> platform strain with improved tyrosine production capabilities. 2013 , 46, 221-226	6
1974	Parkinson's disease: dopaminergic nerve cell model is consistent with experimental finding of increased extracellular transport of α -synuclein. 2013 , 14, 136	13
1973	Systems biology of cancer: moving toward the integrative study of the metabolic alterations in cancer cells. 2012 , 3, 481	15
1972	Characterization of the metabolic requirements in yeast meiosis. 2013 , 8, e63707	10
1971	Analysis of enhanced current-generating mechanism of <i>Geobacter sulfurreducens</i> strain via model-driven metabolism simulation. 2013 , 8, e73907	9
1970	Dead end metabolites--defining the known unknowns of the <i>E. coli</i> metabolic network. 2013 , 8, e75210	19
1969	Steady-state metabolite concentrations reflect a balance between maximizing enzyme efficiency and minimizing total metabolite load. 2013 , 8, e75370	46
1968	Systematic construction of kinetic models from genome-scale metabolic networks. 2013 , 8, e79195	86

1967	The evolution of genome-scale models of cancer metabolism. 2013 , 4, 237	63
1966	Metabolic analyses elucidate non-trivial gene targets for amplifying dihydroartemisinic acid production in yeast. 2013 , 4, 200	11
1965	A novel methodology to estimate metabolic flux distributions in constraint-based models. 2013 , 3, 838-52	10
1964	Counting and correcting thermodynamically infeasible flux cycles in genome-scale metabolic networks. 2013 , 3, 946-66	30
1963	Complex Nonlinear Behavior in Metabolic Processes: Global Bifurcation Analysis of Escherichia coli Growth on Multiple Substrates. 2013 , 1, 263-278	20
1962	Synthetic biology of cyanobacteria: unique challenges and opportunities. 2013 , 4, 246	205
1961	Synergistic Synthetic Biology: Units in Concert. 2013 , 1, 11	6
1960	Studying the relationship between robustness against mutations in metabolic networks and lifestyle of organisms. 2013 , 2013, 615697	3
1959	Flux Balance Analysis Based Model for the Identification of Potent Drug Target: A Novel Strategy. 2013 , 2, 50	0
1958	Free Energies of Staging a Scenario and Perpetual Motion Machines of the Third Kind. 2014 , 43-56	
1957	Multi-tissue computational modeling analyzes pathophysiology of type 2 diabetes in MKR mice. 2014 , 9, e102319	10
1956	Monte-Carlo modeling of the central carbon metabolism of Lactococcus lactis: insights into metabolic regulation. 2014 , 9, e106453	18
1955	Diagnostics for stochastic genome-scale modeling via model slicing and debugging. 2014 , 9, e110380	
1954	Genome-scale reconstruction of metabolic networks of Lactobacillus casei ATCC 334 and 12A. 2014 , 9, e110785	24
1953	Predicting growth conditions from internal metabolic fluxes in an in-silico model of E. coli. 2014 , 9, e114608	10
1952	Modeling the differences in biochemical capabilities of pseudomonas species by flux balance analysis: how good are genome-scale metabolic networks at predicting the differences?. 2014 , 2014, 416289	9
1951	Membrane transporters in a human genome-scale metabolic knowledgebase and their implications for disease. 2014 , 5, 91	56
1950	Improving collaboration by standardization efforts in systems biology. 2014 , 2, 61	43

1949	Synthetic biology outside the cell: linking computational tools to cell-free systems. 2014 , 2, 66	9
1948	Microalgal Metabolic Network Model Refinement through High-Throughput Functional Metabolic Profiling. 2014 , 2, 68	22
1947	Computational strategies for a system-level understanding of metabolism. 2014 , 4, 1034-87	45
1946	Metabolic capabilities of <i>Actinobacillus succinogenes</i> for succinic acid production. 2014 , 31, 859-865	3
1945	Computational Methods in Systems Biology. 2014 ,	
1944	Genome engineering for improved recombinant protein expression in <i>Escherichia coli</i> . 2014 , 13, 177	67
1943	Development of bio-based fine chemical production through synthetic bioengineering. 2014 , 13, 173	33
1942	Design of Microbial Consortia for Industrial Biotechnology. 2014 , 65-74	22
1941	DFBAlab: a fast and reliable MATLAB code for dynamic flux balance analysis. 2014 , 15, 409	86
1940	Capturing the response of <i>Clostridium acetobutylicum</i> to chemical stressors using a regulated genome-scale metabolic model. 2014 , 7, 144	42
1939	Reaction Pathway Analysis. 2014 , 53-60	
1938	Analysis of Kinetic Reaction Mechanisms. 2014 ,	91
1937	Inferring metabolic phenotypes from the exometabolome through a thermodynamic variational principle. 2014 , 16, 115018	3
1936	Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. 2014 , 10, e1003465	59
1935	Bioremediation in marine ecosystems: a computational study combining ecological modeling and flux balance analysis. 2014 , 5, 319	10
1934	Limiting and excreting metabolites of succinate production in <i>S.cerevisiae</i> using flux balance analysis. 2014 ,	1
1933	Integrated network analysis and effective tools in plant systems biology. 2014 , 5, 598	38
1932	Metabolic erosion primarily through mutation accumulation, and not tradeoffs, drives limited evolution of substrate specificity in <i>Escherichia coli</i> . 2014 , 12, e1001789	89

1931	The origins of specialization: insights from bacteria held 25 years in captivity. 2014 , 12, e1001790	13
1930	Essential plasticity and redundancy of metabolism unveiled by synthetic lethality analysis. 2014 , 10, e1003637	28
1929	Emergent biosynthetic capacity in simple microbial communities. 2014 , 10, e1003695	71
1928	A systems approach to predict oncometabolites via context-specific genome-scale metabolic networks. 2014 , 10, e1003837	44
1927	Sequence divergence and diversity suggests ongoing functional diversification of vertebrate NAD metabolism. 2014 , 23, 39-48	11
1926	Enumeration of smallest intervention strategies in genome-scale metabolic networks. 2014 , 10, e1003378	77
1925	Variability of metabolite levels is linked to differential metabolic pathways in Arabidopsis's responses to abiotic stresses. 2014 , 10, e1003656	15
1924	Genome-scale models of plant metabolism. 2014 , 1083, 213-30	9
1923	Likelihood-based gene annotations for gap filling and quality assessment in genome-scale metabolic models. 2014 , 10, e1003882	53
1922	Generalized framework for context-specific metabolic model extraction methods. 2014 , 5, 491	50
1921	MEMOSys 2.0: an update of the bioinformatics database for genome-scale models and genomic data. 2014 , 2014, bau004	12
1920	Biofuel production: an odyssey from metabolic engineering to fermentation scale-up. 2014 , 5, 344	43
1919	Metabolic modeling of common Escherichia coli strains in human gut microbiome. 2014 , 2014, 694967	13
1918	A comparative study between flux balance analysis and kinetic model for C. acetobutylicum. 2014 ,	1
1917	Comparisons of Shewanella strains based on genome annotations, modeling, and experiments. 2014 , 8, 31	26
1916	Morphisms of reaction networks that couple structure to function. 2014 , 8, 84	47
1915	Derivative processes for modelling metabolic fluxes. 2014 , 30, 1892-8	4
1914	In silico analysis of bioethanol production from glucose/xylose mixtures during fed-batch fermentation of co-culture and mono-culture systems. 2014 , 19, 879-891	4

1913	Metabolic Flux Analysis. 2014 ,	3
1912	A Method to Calibrate Metabolic Network Models with Experimental Datasets. 2014 , 183-190	4
1911	Methods for integration of transcriptomic data in genome-scale metabolic models. 2014 , 11, 59-65	48
1910	A Practical Protocol for Genome-Scale Metabolic Reconstructions. 2014 , 197-221	8
1909	ENVIRONMENTAL DEPENDENCE OF THE ACTIVITY AND ESSENTIALITY OF REACTIONS IN THE METABOLISM OF ESCHERICHIA COLI. 2014 , 39-56	4
1908	Evaluating Pathway Enumeration Algorithms in Metabolic Engineering Case Studies. 2014 , 215-223	
1907	In Silico Analysis for Biomass Synthesis under Different CO ₂ Levels for <i>Chlamydomonas reinhardtii</i> Utilizing a Flux Balance Analysis Approach. 2014 , 279-285	3
1906	Metabolic states with maximal specific rate carry flux through an elementary flux mode. 2014 , 281, 1547-55	46
1905	Expanding Metabolic Engineering Algorithms Using Feasible Space and Shadow Price Constraint Modules. 2014 , 1, 1-11	7
1904	Genome-scale metabolic network reconstruction of <i>Saccharopolyspora spinosa</i> for spinosad production improvement. 2014 , 13, 41	14
1903	Generation and Evaluation of a Genome-Scale Metabolic Network Model of <i>Synechococcus elongatus</i> PCC7942. 2014 , 4, 680-98	22
1902	OP-Synthetic: identification of optimal genetic manipulations for the overproduction of native and non-native metabolites. 2014 , 2, 100-109	2
1901	A genome-scale metabolic flux model of <i>Escherichia coli</i> K-12 derived from the EcoCyc database. 2014 , 8, 79	34
1900	A curated <i>C. difficile</i> strain 630 metabolic network: prediction of essential targets and inhibitors. 2014 , 8, 117	34
1899	MetaNET--a web-accessible interactive platform for biological metabolic network analysis. 2014 , 8, 130	9
1898	Validation of an FBA model for <i>Pichia pastoris</i> in chemostat cultures. 2014 , 8, 142	4
1897	Systems level mapping of metabolic complexity in <i>Mycobacterium tuberculosis</i> to identify high-value drug targets. 2014 , 12, 263	23
1896	Cancer cell metabolism as new targets for novel designed therapies. 2014 , 6, 1791-810	18

1895	Metabolic changes in <i>Klebsiella oxytoca</i> in response to low oxidoreduction potential, as revealed by comparative proteomic profiling integrated with flux balance analysis. 2014 , 80, 2833-41	12
1894	Mathematical Modeling of Microbial Community Dynamics: A Methodological Review. 2014 , 2, 711-752	101
1893	Autocatalysis in reaction networks. 2014 , 76, 2570-95	4
1892	The Problem of Futile Cycles in Metabolic Flux Modeling: Flux Space Characterization and Practical Approaches to Its Solution. 2014 , 233-256	1
1891	FastPros: screening of reaction knockout strategies for metabolic engineering. 2014 , 30, 981-7	32
1890	Broad metabolic sensitivity profiling of a prototrophic yeast deletion collection. 2014 , 15, R64	39
1889	Reconciliation of metabolites and biochemical reactions for metabolic networks. 2014 , 15, 123-35	49
1888	Metabolic flux is a determinant of the evolutionary rates of enzyme-encoding genes. 2014 , 68, 605-13	10
1887	Overcoming drug resistance through in silico prediction. 2014 , 11, 101-7	6
1886	Elucidating the adaptation and temporal coordination of metabolic pathways using in-silico evolution. 2014 , 117, 68-76	9
1885	Genome-scale reconstruction of a metabolic network for <i>Gluconobacter oxydans</i> 621H. 2014 , 117, 10-4	12
1884	Metabolic model reconstruction and analysis of an artificial microbial ecosystem for vitamin C production. 2014 , 182-183, 61-7	25
1883	Global dynamic optimization approach to predict activation in metabolic pathways. 2014 , 8, 1	110
1882	Systems biology and biotechnology of <i>Streptomyces</i> species for the production of secondary metabolites. 2014 , 32, 255-68	141
1881	Improvement of constraint-based flux estimation during L-phenylalanine production with <i>Escherichia coli</i> using targeted knock-out mutants. 2014 , 111, 1406-16	16
1880	3 Systems Biology Approaches to Understanding and Predicting Fungal Virulence. 2014 , 45-74	
1879	mtDNA mutations in human aging and longevity: controversies and new perspectives opened by high-throughput technologies. 2014 , 56, 234-44	26
1878	Single-cell model of prokaryotic cell cycle. 2014 , 341, 78-87	15

1877	A conceptual review on systems biology in health and diseases: from biological networks to modern therapeutics. 2014 , 8, 99-116	37
1876	Exploring metabolism flexibility in complex organisms through quantitative study of precursor sets for system outputs. 2014 , 8, 8	3
1875	Flux modules in metabolic networks. 2014 , 69, 1151-79	14
1874	Dynamic flux balance analysis of batch fermentation: effect of genetic manipulations on ethanol production. 2014 , 37, 617-27	17
1873	Advances in metabolic engineering of yeast <i>Saccharomyces cerevisiae</i> for production of chemicals. 2014 , 9, 609-20	171
1872	Software platforms to facilitate reconstructing genome-scale metabolic networks. 2014 , 16, 49-59	58
1871	Low-Oxygen Stress in Plants. 2014 ,	9
1870	Mass spectrometry in plant metabolomics strategies: from analytical platforms to data acquisition and processing. 2014 , 31, 784-806	124
1869	Reconstruction of a high-quality metabolic model enables the identification of gene overexpression targets for enhanced antibiotic production in <i>Streptomyces coelicolor</i> A3(2). 2014 , 9, 1185-94	48
1868	Review on statistical methods for gene network reconstruction using expression data. 2014 , 362, 53-61	118
1867	Constraint-based modeling of heterologous pathways: application and experimental demonstration for overproduction of fatty acids in <i>Escherichia coli</i> . 2014 , 111, 2056-66	12
1866	In silico assessment of the metabolic capabilities of an engineered functional reversal of the Tbxidation cycle for the synthesis of longer-chain (C ₈) products. 2014 , 23, 100-15	29
1865	Modelling and Simulation of Diffusive Processes. 2014 ,	5
1864	Knowledge representation in metabolic pathway databases. 2014 , 15, 455-70	16
1863	Study of metabolic network of <i>Cupriavidus necator</i> DSM 545 growing on glycerol by applying elementary flux modes and yield space analysis. 2014 , 41, 913-30	15
1862	Plant Metabolism. 2014 ,	1
1861	Systems Biology of Metabolic and Signaling Networks. 2014 ,	4
1860	Comparative metabolic systems analysis of pathogenic <i>Burkholderia</i> . 2014 , 196, 210-26	34

1859	Prediction of therapeutic microRNA based on the human metabolic network. 2014 , 30, 1163-1171	6
1858	Applications of Membrane Computing in Systems and Synthetic Biology. 2014 ,	43
1857	Software applications for flux balance analysis. 2014 , 15, 108-22	75
1856	Predicting network functions with nested patterns. 2014 , 5, 3006	10
1855	Constraint-based models predict metabolic and associated cellular functions. 2014 , 15, 107-20	552
1854	A Systems Biology Approach to Study Metabolic Syndrome. 2014 ,	1
1853	Ischaemic accumulation of succinate controls reperfusion injury through mitochondrial ROS. 2014 , 515, 431-435	1360
1852	Green genes: bioinformatics and systems-biology innovations drive algal biotechnology. 2014 , 32, 617-26	48
1851	Preface. Immunoinformatics. 2014 , 1184, vii-xi	4
1850	Masquerading microbial pathogens: capsular polysaccharides mimic host-tissue molecules. 2014 , 38, 660-97	143
1849	Modeling metabolism and stage-specific growth of Plasmodium falciparum HB3 during the intraerythrocytic developmental cycle. 2014 , 10, 2526-37	15
1848	Reconstruction of a generic metabolic network model of cancer cells. 2014 , 10, 3014-21	16
1847	Epistatic interactions among metabolic genes depend upon environmental conditions. 2014 , 10, 2578-89	6
1846	Metabolic impact of an NADH-producing glucose-6-phosphate dehydrogenase in Escherichia coli. 2014 , 160, 2780-2793	12
1845	The role of flexibility and optimality in the prediction of intracellular fluxes of microbial central carbon metabolism. 2014 , 10, 2459-65	7
1844	Rapid editing and evolution of bacterial genomes using libraries of synthetic DNA. 2014 , 9, 2301-16	64
1843	Systems biology perspectives on minimal and simpler cells. 2014 , 78, 487-509	42
1842	Construction of robust dynamic genome-scale metabolic model structures of Saccharomyces cerevisiae through iterative re-parameterization. 2014 , 25, 159-73	22

1841	Generation of an atlas for commodity chemical production in <i>Escherichia coli</i> and a novel pathway prediction algorithm, GEM-Path. 2014 , 25, 140-58	132
1840	Efficiently gap-filling reaction networks. 2014 , 15, 225	26
1839	The avian cell line AGE1.CR.pIX characterized by metabolic flux analysis. 2014 , 14, 72	10
1838	Source and regulation of flux variability in <i>Escherichia coli</i> . 2014 , 8, 67	10
1837	Proteomics-based metabolic modeling and characterization of the cellulolytic bacterium <i>Thermobifida fusca</i> . 2014 , 8, 86	14
1836	Elucidating Xylose Metabolism of <i>Scheffersomyces stipitis</i> for Lignocellulosic Ethanol Production. 2014 , 2, 38-48	18
1835	Probing the bioethanol production potential of <i>Scheffersomyces (Pichia) stipitis</i> using validated genome-scale model. 2014 , 36, 2443-51	5
1834	An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes. 2014 , 13, 321-331	15
1833	Metabolite profiling and integrative modeling reveal metabolic constraints for carbon partitioning under nitrogen starvation in the green algae <i>Haematococcus pluvialis</i> . 2014 , 289, 30387-30403	79
1832	Functional metabolic map of <i>Faecalibacterium prausnitzii</i> , a beneficial human gut microbe. 2014 , 196, 3289-302	109
1831	8th International Conference on Practical Applications of Computational Biology & Bioinformatics (PACBB 2014). 2014 ,	1
1830	A data integration and visualization resource for the metabolic network of <i>Synechocystis</i> sp. PCC 6803. 2014 , 164, 1111-21	23
1829	Nitrogen-use efficiency in maize (<i>Zea mays</i> L.): from 'omics' studies to metabolic modelling. 2014 , 65, 5657-71	61
1828	The future of genome-scale modeling of yeast through integration of a transcriptional regulatory network. 2014 , 2, 30-46	7
1827	Genome-scale metabolic network reconstruction and in silico flux analysis of the thermophilic bacterium <i>Thermus thermophilus</i> HB27. 2014 , 13, 61	14
1826	A framework for application of metabolic modeling in yeast to predict the effects of nsSNV in human orthologs. 2014 , 9, 9	1
1825	The common ground of genomics and systems biology. 2014 , 8 Suppl 2, S1	21
1824	The genome-scale metabolic network of <i>Ectocarpus siliculosus</i> (EctoGEM): a resource to study brown algal physiology and beyond. 2014 , 80, 367-81	30

1823	Mapping the inner workings of the microbiome: genomic- and metagenomic-based study of metabolism and metabolic interactions in the human microbiome. 2014 , 20, 742-752	60
1822	Metabolic resource allocation in individual microbes determines ecosystem interactions and spatial dynamics. 2014 , 7, 1104-15	339
1821	Enzyme allocation problems in kinetic metabolic networks: optimal solutions are elementary flux modes. 2014 , 347, 182-90	37
1820	Towards predictive models of the human gut microbiome. 2014 , 426, 3907-16	70
1819	Clarifying the regulation of NO/N ₂ O production in <i>Nitrosomonas europaea</i> during anoxic-oxic transition via flux balance analysis of a metabolic network model. 2014 , 60, 267-277	43
1818	Reverse engineering and identification in systems biology: strategies, perspectives and challenges. 2014 , 11, 20130505	152
1817	Complete enumeration of elementary flux modes through scalable demand-based subnetwork definition. 2014 , 30, 1569-78	51
1816	Increased 3-hydroxypropionic acid production from glycerol, by modification of central metabolism in <i>Escherichia coli</i> . 2014 , 13, 64	53
1815	Modeling acclimatization by hybrid systems: condition changes alter biological system behavior models. 2014 , 121, 43-53	1
1814	Computational comparison of mediated current generation capacity of <i>Chlamydomonas reinhardtii</i> in photosynthetic and respiratory growth modes. 2014 , 118, 565-74	9
1813	Metabolic network discovery by top-down and bottom-up approaches and paths for reconciliation. 2014 , 2, 62	12
1812	The EcoCyc Database. 2014 , 6,	47
1811	Lazy Updating of hubs can enable more realistic models by speeding up stochastic simulations. 2014 , 141, 204109	4
1810	Systems biology-based identification of <i>Mycobacterium tuberculosis</i> persistence genes in mouse lungs. 2014 , 5,	17
1809	Modeling the metabolism of <i>Escherichia coli</i> under oxygen gradients with dynamically changing flux bounds. 2015 ,	
1808	Constraints based analysis of extended cybernetic models. 2015 , 137, 45-54	1
1807	Optimization of lipid production with a genome-scale model of <i>Yarrowia lipolytica</i> . 2015 , 9, 72	77
1806	Systems biology of host-microbe metabolomics. 2015 , 7, 195-219	64

1805	Phenotypic constraints promote latent versatility and carbon efficiency in metabolic networks. 2015 , 92, 012809	
1804	Hierarchical decomposition of metabolic networks using k-modules. 2015 , 43, 1146-50	2
1803	Resource allocation in metabolic networks: kinetic optimization and approximations by FBA. 2015 , 43, 1195-200	5
1802	Modeling cancer metabolism on a genome scale. 2015 , 11, 817	122
1801	Computational Approaches to Dissect and Understand Mechanisms of Adaptation. 2015 , 193-215	
1800	Quantitative analysis of drug effects at the whole-body level: a case study for glucose metabolism in malaria patients. 2015 , 43, 1157-63	1
1799	Selection of Organisms for Systems Biology Study of Microbial Electricity Generation: A Review. 2015 , 13-54	
1798	Do genome-scale models need exact solvers or clearer standards?. 2015 , 11, 831	41
1797	Cyanobacterial Alkanes Modulate Photosynthetic Cyclic Electron Flow to Assist Growth under Cold Stress. 2015 , 5, 14894	32
1796	Computational paradigms for analyzing genetic interaction networks. 12-35	
1795	References. 481-509	
1794	Elucidating temporal resource allocation and diurnal dynamics in phototrophic metabolism using conditional FBA. 2015 , 5, 15247	34
1793	Dynamic epistasis under varying environmental perturbations. 2015 , 10, e0114911	3
1792	Marine Microalgae: Exploring the Systems through an Omics Approach for Biofuel Production. 2015 , 168-181	1
1791	Computational inference of the structure and regulation of the lignin pathway in <i>Panicum virgatum</i> . 2015 , 8, 151	17
1790	Phenotypic differentiation of gastrointestinal microbes is reflected in their encoded metabolic repertoires. 2015 , 3, 55	27
1789	Analyse intrazellulärer Stoffflüsse in Säugetierzellen. 2015 , 21, 564-566	
1788	Metabolic modeling predicts metabolite changes in <i>Mycobacterium tuberculosis</i> . 2015 , 9, 57	14

1787	In silico Support for Eschenmoser's Glyoxylate Scenario. 2015 , 55, 919-933	8
1786	FlexFlux: combining metabolic flux and regulatory network analyses. 2015 , 9, 93	32
1785	Genome-scale metabolic reconstructions and theoretical investigation of methane conversion in <i>Methylobacterium buryatense</i> strain 5G(B1). 2015 , 14, 188	85
1784	Simulating cyanobacterial phenotypes by integrating flux balance analysis, kinetics, and a light distribution function. 2015 , 14, 206	6
1783	Designing minimal microbial strains of desired functionality using a genetic algorithm. 2015 , 10, 29	5
1782	Intracellular metabolic flux analysis of CHO cells supplemented with wheat hydrolysates for improved mAb production and cell-growth. 2015 , 90, 291-302	10
1781	Dynamic exometabolome analysis reveals active metabolic pathways in non-replicating mycobacteria. 2015 , 17, 4802-15	27
1780	Constructing kinetic models of metabolism at genome-scales: A review. 2015 , 10, 1345-59	55
1779	Designer Microorganisms for Optimized Redox Cascade Reactions [Challenges and Future Perspectives]. 2015 , 357, 1587-1618	45
1778	Optimizing eukaryotic cell hosts for protein production through systems biotechnology and genome-scale modeling. 2015 , 10, 939-49	37
1777	The Systems Biology Markup Language (SBML) Level 3 Package: Flux Balance Constraints. 2015 , 12, 660-690	15
1776	Integrative analysis of metabolic models - from structure to dynamics. 2014 , 2, 91	8
1775	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. 2015 , 3, 13	20
1774	Modeling the Contribution of Allosteric Regulation for Flux Control in the Central Carbon Metabolism of <i>E. coli</i> . 2015 , 3, 154	21
1773	RobOKoD: microbial strain design for (over)production of target compounds. 2015 , 3, 17	15
1772	Computational Studies of the Intestinal Host-Microbiota Interactome. 2015 , 3, 2-28	5
1771	Mathematical modelling of metabolic regulation in aging. 2015 , 5, 232-51	19
1770	Modeling and Simulation of Optimal Resource Management during the Diurnal Cycle in <i>Emiliana huxleyi</i> by Genome-Scale Reconstruction and an Extended Flux Balance Analysis Approach. 2015 , 5, 659-76	9

1769	Systems Biology of the Fluxome. 2015 , 3, 607-618	9
1768	Species interactions differ in their genetic robustness. 2015 , 6, 271	16
1767	Cell scale host-pathogen modeling: another branch in the evolution of constraint-based methods. 2015 , 6, 1032	9
1766	Effects of varying nitrogen sources on amino acid synthesis costs in <i>Arabidopsis thaliana</i> under different light and carbon-source conditions. 2015 , 10, e0116536	18
1765	Perception and regulatory principles of microbial growth control. 2015 , 10, e0126244	2
1764	Metabolic energy-based modelling explains product yielding in anaerobic mixed culture fermentations. 2015 , 10, e0126739	48
1763	Thermodynamics and H ₂ Transfer in a Methanogenic, Syntrophic Community. 2015 , 11, e1004364	20
1762	Multi-Target Analysis and Design of Mitochondrial Metabolism. 2015 , 10, e0133825	7
1761	Metabolic Plasticity and Inter-Compartmental Interactions in Rice Metabolism: An Analysis from Reaction Deletion Study. 2015 , 10, e0133899	2
1760	Dissecting <i>Leishmania infantum</i> Energy Metabolism - A Systems Perspective. 2015 , 10, e0137976	18
1759	Physiologically Shrinking the Solution Space of a <i>Saccharomyces cerevisiae</i> Genome-Scale Model Suggests the Role of the Metabolic Network in Shaping Gene Expression Noise. 2015 , 10, e0139590	1
1758	Pool size measurements facilitate the determination of fluxes at branching points in non-stationary metabolic flux analysis: the case of <i>Arabidopsis thaliana</i> . 2015 , 6, 386	15
1757	Flux balance analysis reveals acetate metabolism modulates cyclic electron flow and alternative glycolytic pathways in <i>Chlamydomonas reinhardtii</i> . 2015 , 6, 474	44
1756	Thermodynamical journey in plant biology. 2015 , 6, 481	8
1755	In silico analysis of bioethanol overproduction by genetically modified microorganisms in coculture fermentation. 2015 , 2015, 238082	7
1754	. 2015 ,	2
1753	Synthetic Biology: Computational Modeling Bridging the Gap between In Vitro and In Vivo Reactions. 2015 , 03,	2
1752	Perturbation Experiments: Approaches for Metabolic Pathway Analysis in Bioreactors. 2016 , 152, 91-136	3

1751	Using Genome-scale Models to Predict Biological Capabilities. 2015 , 161, 971-987	433
1750	In Silico analysis of perturbed steroidogenesis and gonad growth in fathead minnows (<i>P. promelas</i>) exposed to 17 β -ethynylestradiol. 2015 , 61, 122-38	2
1749	Flux balance analysis predicts essential genes in clear cell renal cell carcinoma metabolism. 2015 , 5, 10738	59
1748	Amino Acid Flux from Metabolic Network Benefits Protein Translation: the Role of Resource Availability. 2015 , 5, 11113	5
1747	CycleFreeFlux: efficient removal of thermodynamically infeasible loops from flux distributions. 2015 , 31, 2159-65	24
1746	Getting pumped: membrane efflux transporters for enhanced biomolecule production. 2015 , 28, 15-9	32
1745	Rapid and high-throughput construction of microbial cell-factories with regulatory noncoding RNAs. 2015 , 33, 914-30	15
1744	Using bioconductor package BiGGR for metabolic flux estimation based on gene expression changes in brain. 2015 , 10, e0119016	13
1743	Toward Applications of Genomics and Metabolic Modeling to Improve Algal Biomass Productivity. 2015 , 173-189	4
1742	Integration of metabolomics data into metabolic networks. 2015 , 6, 49	55
1741	A review on computational systems biology of pathogen-host interactions. 2015 , 6, 235	61
1740	Genome scale models of yeast: towards standardized evaluation and consistent omic integration. 2015 , 7, 846-58	57
1739	Differential flux balance analysis of quantitative proteomic data on protein interaction networks. 2015 ,	
1738	Transcriptional program for nitrogen starvation-induced lipid accumulation in <i>Chlamydomonas reinhardtii</i> . 2015 , 8, 207	43
1737	Flux balance analysis of genome-scale metabolic model of rice (<i>Oryza sativa</i>): aiming to increase biomass. 2015 , 40, 819-28	5
1736	Co-evolution of strain design methods based on flux balance and elementary mode analysis. 2015 , 2, 85-92	56
1735	Cyclohexanone-induced stress metabolism of <i>Escherichia coli</i> and <i>Corynebacterium glutamicum</i> . 2015 , 20, 1088-1098	5
1734	Towards rule-based metabolic databases: a requirement analysis based on KEGG. 2015 , 13, 289-319	1

1733	Analyzing redox balance in a synthetic yeast platform to improve utilization of brown macroalgae as feedstock. 2015 , 2, 76-84	11
1732	Resource constrained flux balance analysis predicts selective pressure on the global structure of metabolic networks. 2015 , 9, 88	4
1731	The Warburg effect: a balance of flux analysis. 2015 , 11, 787-796	41
1730	Remodeling of intermediate metabolism in the diatom <i>Phaeodactylum tricornutum</i> under nitrogen stress. 2015 , 112, 412-7	153
1729	Preface. Bacterial pangenomics. 2015 , 1231, v-vi	5
1728	Cascade catalysis--strategies and challenges en route to preparative synthetic biology. 2015 , 51, 5798-811	240
1727	<i>Synechocystis</i> sp. PCC6803 metabolic models for the enhanced production of hydrogen. 2015 , 35, 184-98	7
1726	Pantograph: A template-based method for genome-scale metabolic model reconstruction. 2015 , 13, 1550006	21
1725	Methods and advances in metabolic flux analysis: a mini-review. 2015 , 42, 317-25	139
1724	Design of homo-organic acid producing strains using multi-objective optimization. 2015 , 28, 63-73	22
1723	Integration of transcriptomics and metabolomics data specifies the metabolic response of <i>Chlamydomonas</i> to rapamycin treatment. 2015 , 81, 822-35	62
1722	MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. 2015 , 11, 137-45	25
1721	Computational methods in metabolic engineering for strain design. 2015 , 34, 135-41	97
1720	A dynamic flux balance model and bottleneck identification of glucose, xylose, xylulose co-fermentation in <i>Saccharomyces cerevisiae</i> . 2015 , 188, 153-60	17
1719	Transparency in metabolic network reconstruction enables scalable biological discovery. 2015 , 34, 105-9	18
1718	Insights from 20 years of bacterial genome sequencing. 2015 , 15, 141-61	391
1717	The Crc/CrcZ-CrcY global regulatory system helps the integration of gluconeogenic and glycolytic metabolism in <i>Pseudomonas putida</i> . 2015 , 17, 3362-78	34
1716	Double and multiple knockout simulations for genome-scale metabolic network reconstructions. 2015 , 10, 1	19

1715	Decoding the jargon of bottom-up metabolic systems biology. 2015 , 37, 588-91	9
1714	A multi-tissue genome-scale metabolic modeling framework for the analysis of whole plant systems. 2015 , 6, 4	70
1713	Network reconstruction of platelet metabolism identifies metabolic signature for aspirin resistance. 2014 , 4, 3925	27
1712	Recent advances in elementary flux modes and yield space analysis as useful tools in metabolic network studies. 2015 , 31, 1315-28	2
1711	Using Petri nets for experimental design in a multi-organ elimination pathway. 2015 , 63, 19-27	1
1710	Numerical Analysis and Optimization. 2015 ,	2
1709	Experimental approaches to phenotypic diversity in infection. 2015 , 27, 25-36	28
1708	The principles of whole-cell modeling. 2015 , 27, 18-24	48
1707	Scaling and optimal synergy: Two principles determining microbial growth in complex media. 2015 , 91, 062703	1
1706	Sub-optimal phenotypes of double-knockout mutants of Escherichia coli depend on the order of gene deletions. 2015 , 7, 930-9	3
1705	Interplay between constraints, objectives, and optimality for genome-scale stoichiometric models. 2015 , 11, e1004166	18
1704	Systems modeling approaches for microbial community studies: from metagenomics to inference of the community structure. 2015 , 6, 213	44
1703	A comparison between functional frequency and metabolic flows framed by biogeochemical cycles in metagenomes: The case of El Coquito hot spring located at Colombia's national Nevados park. 2015 , 313, 259-265	3
1702	Influence of HEK293 metabolism on the production of viral vectors and vaccine. 2015 , 33, 5974-81	17
1701	Dynamic metabolic models in context: biomass backtracking. 2015 , 7, 940-51	4
1700	Investigating Moorella thermoacetica metabolism with a genome-scale constraint-based metabolic model. 2015 , 7, 869-82	27
1699	Metabolic Design And Engineering Through Ant Colony Optimization. 2015 ,	
1698	Identification of a critical determinant that enables efficient fatty acid synthesis in oleaginous fungi. 2015 , 5, 11247	69

1697	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. 2015 , 6, 7101	32
1696	NETWORK APPROACHES FOR ANALYSIS AND MODELING OF THE HUMAN METABOLISM. 2015 , 15, 1540026	
1695	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. 2015 , 11, e1004096	31
1694	Metabolic Needs and Capabilities of <i>Toxoplasma gondii</i> through Combined Computational and Experimental Analysis. 2015 , 11, e1004261	71
1693	Predicting genetic engineering targets with Elementary Flux Mode Analysis: a review of four current methods. 2015 , 32, 534-46	7
1692	Reconstruction of genome-scale human metabolic models using omics data. 2015 , 7, 859-68	38
1691	Systems Biology Approaches Applied to Regenerative Medicine. 2015 , 3, 37-45	6
1690	Mixed Quantum Mechanical/Molecular Mechanical Molecular Dynamics Simulations of Biological Systems in Ground and Electronically Excited States. 2015 , 115, 6217-63	277
1689	PathwayBooster: a tool to support the curation of metabolic pathways. 2015 , 16, 86	5
1688	Predicting internal cell fluxes at sub-optimal growth. 2015 , 9, 18	6
1687	Metabolic dependencies drive species co-occurrence in diverse microbial communities. 2015 , 112, 6449-54	366
1686	Metabolic Fluxes in Lactic Acid Bacteria: A Review. 2015 , 29, 185-217	10
1685	Identifying a gene knockout strategy using a hybrid of the bat algorithm and flux balance analysis to enhance the production of succinate and lactate in <i>Escherichia coli</i> . 2015 , 20, 349-357	10
1684	Logical transformation of genome-scale metabolic models for gene level applications and analysis. 2015 , 31, 2324-31	28
1683	Research in Computational Molecular Biology. 2015 ,	3
1682	Parallelized small-scale production of uniformly (¹³ C)-labeled cell extract for quantitative metabolome analysis. 2015 , 478, 134-40	13
1681	SSDesign: Computational metabolic pathway design based on flux variability using elementary flux modes. 2015 , 112, 759-68	9
1680	Optimal design of growth-coupled production strains using nested hybrid differential evolution. 2015 , 54, 57-63	12

1679	Mathematical modeling of unicellular microalgae and cyanobacteria metabolism for biofuel production. 2015 , 33, 198-205	36
1678	Critical assessment of genome-scale metabolic networks: the need for a unified standard. 2015 , 16, 1057-68	47
1677	Functional Alignment of Metabolic Networks. 2015 , 243-255	
1676	Anoxic Conditions Promote Species-Specific Mutualism between Gut Microbes In Silico. 2015 , 81, 4049-61	71
1675	A Critical Evaluation of Methods for the Reconstruction of Tissue-Specific Models. 2015 , 340-352	5
1674	Inferring Transition Rates of Networks from Populations in Continuous-Time Markov Processes. 2015 , 11, 5464-72	51
1673	Systematic prediction of health-relevant human-microbial co-metabolism through a computational framework. 2015 , 6, 120-30	76
1672	Reconstruction and analysis of the genome-scale metabolic model of schizochytrium limacinum SR21 for docosahexaenoic acid production. 2015 , 16, 799	35
1671	Observability of anammox activity in single-stage nitrification/anammox reactors using mass balances. 2015 , 1, 523-534	4
1670	In silico model-driven cofactor engineering strategies for improving the overall NADP(H) turnover in microbial cell factories. 2015 , 42, 1401-14	8
1669	Genome-scale reconstruction of the metabolic network in Pseudomonas stutzeri A1501. 2015 , 11, 3022-32	10
1668	Sequence-based Network Completion Reveals the Integrality of Missing Reactions in Metabolic Networks. 2015 , 290, 19197-207	13
1667	Metabolic Pathway Databases: A Word of Caution. 2015 , 27-63	1
1666	Pareto Optimal Design for Synthetic Biology. 2015 , 9, 555-71	15
1665	Reconstruction and validation of a constraint-based metabolic network model for bone marrow-derived mesenchymal stem cells. 2015 , 48, 475-85	12
1664	Human genes with a greater number of transcript variants tend to show biological features of housekeeping and essential genes. 2015 , 11, 2798-807	8
1663	Genome-scale reconstruction of Salinispora tropica CNB-440 metabolism to study strain-specific adaptation. 2015 , 108, 1075-90	11
1662	Mapping high-growth phenotypes in the flux space of microbial metabolism. 2015 , 12, 0543	3

1661	A combined systems and structural modeling approach repositions antibiotics for <i>Mycoplasma genitalium</i> . 2015 , 59 Pt B, 91-7	8
1660	Engineering of oleaginous organisms for lipid production. 2015 , 36, 32-9	36
1659	A Practical Protocol for Integration of Transcriptomics Data into Genome-Scale Metabolic Reconstructions. 2015 , 135-152	6
1658	Screening of potential targets in <i>Plasmodium falciparum</i> using stage-specific metabolic network analysis. 2015 , 19, 991-1002	5
1657	Unraveling the Light-Specific Metabolic and Regulatory Signatures of Rice through Combined in Silico Modeling and Multiomics Analysis. 2015 , 169, 3002-20	44
1656	Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics. 2015 , 1, 283-92	71
1655	Computational Methods for Modification of Metabolic Networks. 2015 , 13, 376-81	27
1654	Re-membering the body: applications of computational neuroscience to the top-down control of regeneration of limbs and other complex organs. 2015 , 7, 1487-517	81
1653	An algorithm for the reduction of genome-scale metabolic network models to meaningful core models. 2015 , 9, 48	45
1652	Using a genome-scale metabolic model of <i>Enterococcus faecalis</i> V583 to assess amino acid uptake and its impact on central metabolism. 2015 , 81, 1622-33	20
1651	Systems and Synthetic Biology. 2015 ,	2
1650	Development and application of efficient pathway enumeration algorithms for metabolic engineering applications. 2015 , 118, 134-46	7
1649	M-path: a compass for navigating potential metabolic pathways. 2015 , 31, 905-11	25
1648	A new algorithm to find all alternate optimal flux distributions of a metabolic network. 2015 , 73, 64-69	2
1647	Dynamic optimization of metabolic networks coupled with gene expression. 2015 , 365, 469-85	53
1646	Systems biology and metabolic engineering of lactic acid bacteria for improved fermented foods. 2015 , 177-196	
1645	Principles and practice of lipidomics. 2015 , 38, 41-52	29
1644	Enhanced hexose fermentation by <i>Saccharomyces cerevisiae</i> through integration of stoichiometric modeling and genetic screening. 2015 , 194, 48-57	6

1643	Modeling metabolism: a window toward a comprehensive interpretation of networks in cancer. 2015 , 30, 79-87	20
1642	Efficient searching and annotation of metabolic networks using chemical similarity. 2015 , 31, 1016-24	41
1641	Long-term phenotypic evolution of bacteria. 2015 , 517, 369-72	54
1640	Modeling the effects of commonly used drugs on human metabolism. 2015 , 282, 297-317	25
1639	Reconstruction and analysis of the genome-scale metabolic model of Lactobacillus casei LC2W. 2015 , 554, 140-7	18
1638	MOST: a software environment for constraint-based metabolic modeling and strain design. 2015 , 31, 610-1	9
1637	An introduction to systems toxicology. 2015 , 4, 9-22	15
1636	Global optimization of hybrid kinetic/FBA models via outer-approximation. 2015 , 72, 325-333	14
1635	Bilevel optimization techniques in computational strain design. 2015 , 72, 363-372	30
1634	Visual workflows for 13C-metabolic flux analysis. 2015 , 31, 346-54	23
1633	Designing RNA-based genetic control systems for efficient production from engineered metabolic pathways. 2015 , 4, 107-15	41
1632	Global biodiversity, stoichiometry and ecosystem function responses to human-induced C-N-P imbalances. 2015 , 172, 82-91	45
1631	Combining flux balance analysis and model checking for metabolic network validation and analysis. 2015 , 14, 341-354	1
1630	IN SILICO GENE DELETION OF ESCHERICHIA COLI FOR OPTIMAL ETHANOL PRODUCTION USING A HYBRID ALGORITHM OF PARTICLE SWARM OPTIMIZATION AND FLUX BALANCE ANALYSIS. 2016 , 78,	
1629	. 2016 ,	2
1628	Strategies for Extending Metabolomics Studies with Stable Isotope Labelling and Fluxomics. 2016 , 6,	18
1627	Identifying Antimalarial Drug Targets by Cellular Network Analysis. 2016 ,	
1626	Iterative Multi Level Calibration of Metabolic Networks. 2016 , 11, 93-105	4

1625	Mathematical Modeling of a Raceway Pond System for Biofuels Production. 2016 , 2355-2360	1
1624	Genome sequencing and systems biology analysis of a lipase-producing bacterial strain. 2016 , 15,	
1623	Genomic Analysis of the Human Gut Microbiome Suggests Novel Enzymes Involved in Quinone Biosynthesis. 2016 , 7, 128	35
1622	Metabolic Network Modeling of Microbial Interactions in Natural and Engineered Environmental Systems. 2016 , 7, 673	80
1621	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. 2016 , 7, 907	28
1620	Mathematical Modeling and Dynamic Simulation of Metabolic Reaction Systems Using Metabolome Time Series Data. 2016 , 3, 15	14
1619	Reconstructed Metabolic Network Models Predict Flux-Level Metabolic Reprogramming in Glioblastoma. 2016 , 10, 156	18
1618	solveME: fast and reliable solution of nonlinear ME models. 2016 , 17, 391	35
1617	Metabolic modelling in a dynamic evolutionary framework predicts adaptive diversification of bacteria in a long-term evolution experiment. 2016 , 16, 163	44
1616	Qualitative dynamics semantics for SBGN process description. 2016 , 10, 42	4
1615	Functional centrality as a predictor of shifts in metabolic flux states. 2016 , 9, 317	
1614	A Multi-scale Computational Platform to Mechanistically Assess the Effect of Genetic Variation on Drug Responses in Human Erythrocyte Metabolism. 2016 , 12, e1005039	11
1613	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. 2016 , 10, e0004403	170
1612	Genome-Scale Model Reveals Metabolic Basis of Biomass Partitioning in a Model Diatom. 2016 , 11, e0155038	73
1611	OM-FBA: Integrate Transcriptomics Data with Flux Balance Analysis to Decipher the Cell Metabolism. 2016 , 11, e0154188	13
1610	E-Flux2 and SPOT: Validated Methods for Inferring Intracellular Metabolic Flux Distributions from Transcriptomic Data. 2016 , 11, e0157101	22
1609	Reconstruction of Tissue-Specific Metabolic Networks Using CORDA. 2016 , 12, e1004808	71
1608	Visualization of Metabolic Interaction Networks in Microbial Communities Using VisANT 5.0. 2016 , 12, e1004875	16

1607	HepatoDyn: A Dynamic Model of Hepatocyte Metabolism That Integrates 13C Isotopomer Data. 2016 , 12, e1004899	12
1606	Multiscale Metabolic Modeling of C4 Plants: Connecting Nonlinear Genome-Scale Models to Leaf-Scale Metabolism in Developing Maize Leaves. 2016 , 11, e0151722	28
1605	Integrated In Silico Analysis of Pathway Designs for Synthetic Photo-Electro-Autotrophy. 2016 , 11, e0157851	7
1604	Transition of an Anaerobic Escherichia coli Culture to Aerobiosis: Balancing mRNA and Protein Levels in a Demand-Directed Dynamic Flux Balance Analysis. 2016 , 11, e0158711	11
1603	Applications of Genome-Scale Metabolic Models in Biotechnology and Systems Medicine. 2015 , 6, 413	83
1602	MetaboTools: A Comprehensive Toolbox for Analysis of Genome-Scale Metabolic Models. 2016 , 7, 327	31
1601	Personalized Prediction of Proliferation Rates and Metabolic Liabilities in Cancer Biopsies. 2016 , 7, 644	12
1600	Analysis of Sensitive CO2 Pathways and Genes Related to Carbon Uptake and Accumulation in Chlamydomonas reinhardtii through Genomic Scale Modeling and Experimental Validation. 2016 , 7, 43	15
1599	Flux Balance Analysis of Plant Metabolism: The Effect of Biomass Composition and Model Structure on Model Predictions. 2016 , 7, 537	21
1598	Modeling Rice Metabolism: From Elucidating Environmental Effects on Cellular Phenotype to Guiding Crop Improvement. 2016 , 7, 1795	16
1597	Applications of Constraint-Based Models for Biochemical Production. 2016 , 201-226	1
1596	Adding biotic complexity alters the metabolic benefits of mutualism. 2016 , 70, 1871-81	22
1595	Advances in the integration of transcriptional regulatory information into genome-scale metabolic models. 2016 , 147, 1-10	36
1594	AB-QSSPN: Integration of Agent-Based Simulation of Cellular Populations with Quasi-Steady State Simulation of Genome Scale Intracellular Networks. 2016 , 113-122	
1593	Reconstruction of Metabolic Models for Liver Cancer Cells. 2016 , 213-221	1
1592	Transcriptomics-based strain optimization tool for designing secondary metabolite overproducing strains of Streptomyces coelicolor. 2016 , 113, 651-60	33
1591	Microalgal bioengineering for sustainable energy development: Recent transgenesis and metabolic engineering strategies. 2016 , 11, 303-14	38
1590	Genome-Scale Metabolic Model for the Green Alga Chlorella vulgaris UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. 2016 , 172, 589-602	62

1589	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. 2016 , 12, 2394-407	7
1588	Reconstruction and applications of consensus yeast metabolic network based on RNA sequencing. 2016 , 6, 264-75	3
1587	Transient dynamics of competitive exclusion in microbial communities. 2016 , 18, 1863-74	22
1586	Identified metabolic signature for assessing red blood cell unit quality is associated with endothelial damage markers and clinical outcomes. 2016 , 56, 852-62	71
1585	The space of enzyme regulation in HeLa cells can be inferred from its intracellular metabolome. 2016 , 6, 28415	10
1584	In Silico Analysis of <i>Mucor Circinelloides</i> Genome-Scale Model for Enhancing Lipid Production. 2016 ,	
1583	Toward Scalable Whole-Cell Modeling of Human Cells. 2016 ,	8
1582	A multiscale, model-based analysis of the multi-tissue interplay underlying blood glucose regulation in type I diabetes. 2016 , 2016, 1417-1421	6
1581	Improving Bioprocess Productivity Using Constraint-Based Models in a Dynamic Optimization Scheme. 2016 , 49, 245-251	6
1580	State estimation in constraint based models of metabolic-genetic networks. 2016 ,	1
1579	Computational intelligence for metabolic pathway design: Application to the pentose phosphate pathway. 2016 ,	
1578	Comparison of 432 <i>Pseudomonas</i> strains through integration of genomic, functional, metabolic and expression data. 2016 , 6, 38699	38
1577	Predicting changes of reaction networks with partial kinetic information. 2016 , 149, 113-124	7
1576	Genome wide analysis of protein production load in <i>Trichoderma reesei</i> . 2016 , 9, 132	16
1575	The application of microfluidic-based technologies in the cycle of metabolic engineering. 2016 , 1, 137-142	6
1574	Constraint-based stoichiometric modelling from single organisms to microbial communities. 2016 , 13,	55
1573	iReMet-flux: constraint-based approach for integrating relative metabolite levels into a stoichiometric metabolic models. 2016 , 32, i755-i762	26
1572	Generation of 2,000 breast cancer metabolic landscapes reveals a poor prognosis group with active serotonin production. 2016 , 6, 19771	24

1571	Predicting microbial interactions through computational approaches. 2016 , 102, 12-9	31
1570	Challenges in microbial ecology: building predictive understanding of community function and dynamics. 2016 , 10, 2557-2568	380
1569	A genome-scale metabolic network reconstruction of tomato (<i>Solanum lycopersicum</i> L.) and its application to photorespiratory metabolism. 2016 , 85, 289-304	47
1568	Modeling the Overproduction of Ribosomes when Antibacterial Drugs Act on Cells. 2016 , 110, 743-748	8
1567	Sustainability assessment of succinic acid production technologies from biomass using metabolic engineering. 2016 , 9, 2794-2805	67
1566	Bioinformatics for the synthetic biology of natural products: integrating across the Design-Build-Test cycle. 2016 , 33, 925-32	48
1565	A systems biology approach to reconcile metabolic network models with application to <i>Synechocystis</i> sp. PCC 6803 for biofuel production. 2016 , 12, 2552-61	17
1564	Understanding the cancer cell phenotype beyond the limitations of current omics analyses. 2016 , 283, 54-73	31
1563	Genome scale metabolic reconstruction of <i>Chlorella variabilis</i> for exploring its metabolic potential for biofuels. 2016 , 213, 103-110	27
1562	IdealKnock: A framework for efficiently identifying knockout strategies leading to targeted overproduction. 2016 , 61, 229-37	7
1561	Assessing Cardiac Metabolism: A Scientific Statement From the American Heart Association. 2016 , 118, 1659-701	142
1560	Synthetic biology and regulatory networks: where metabolic systems biology meets control engineering. 2016 , 13,	36
1559	comprehensive model driven analysis of the electron transfer metabolism and synthetic strain design for biomining applications. 2016 , 3, 84-96	18
1558	Metabolic constraints for a novel symbiosis. 2016 , 3, 150708	4
1557	In silico identification of gene amplification targets based on analysis of production and growth coupling. 2016 , 145, 1-8	6
1556	Metabolic engineering of enhanced glycerol-3-phosphate synthesis to increase lipid production in <i>Synechocystis</i> sp. PCC 6803. 2016 , 100, 6091-101	23
1555	High-yield anaerobic succinate production by strategically regulating multiple metabolic pathways based on stoichiometric maximum in <i>Escherichia coli</i> . 2016 , 15, 141	35
1554	Mitochondrial health, the epigenome and healthspan. 2016 , 130, 1285-305	37

1553	FROM MFA TO FBA: LEGITIMATING OBJECTIVE FUNCTION AND LINEAR CONSTRAINTS. 2016 , 49, 460-465	1
1552	Characterizing Strain Variation in Engineered E. coli Using a Multi-Omics-Based Workflow. 2016 , 2, 335-46	59
1551	Constraint-Based Reasoning for Search and Explanation: Strategies for Understanding Variation and Patterns in Biology. 2016 , 70, 343-374	13
1550	Phenotypic innovation through recombination in genome-scale metabolic networks. 2016 , 283,	7
1549	Hybrid Systems Biology. 2016 ,	
1548	Metabolite and Microbiome Interplay in Cancer Immunotherapy. 2016 , 76, 6146-6152	61
1547	Synchronous Balanced Analysis. 2016 , 85-94	
1546	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. 2016 , 3, 238-251.e12	67
1545	Big Data Analytics. 2016 ,	6
1544	Metabolic flexibility of mitochondrial respiratory chain disorders predicted by computer modelling. 2016 , 31, 45-55	30
1543	Synergizing Proteomic and Metabolomic Data to Study Cardiovascular Systems. 2016 , 365-388	
1542	Harnessing the power of microbial autotrophy. 2016 , 14, 692-706	122
1541	Computationally efficient dynamic simulation of cellular kinetics via explicit solution of flux balance analysis: xDFBA modelling and its biochemical process applications. 2016 , 113, 85-95	2
1540	Nature lessons: The whitefly bacterial endosymbiont is a minimal amino acid factory with unusual energetics. 2016 , 407, 303-317	7
1539	A methodology for building a macroscopic FBA-based dynamical simulator of cell cultures through flux variability analysis. 2016 , 114, 50-64	12
1538	Systems biology of bacteria-host interactions. 2016 , 113-137	1
1537	Understanding Protozoan Parasite Metabolism and Identifying Drug Targets through Constraint-Based Modeling. 2016 , 487-512	
1536	Attacking Blood-Borne Parasites with Mathematics. 2016 , 513-541	

1535	Law of Localization in Chemical Reaction Networks. 2016 , 117, 048101	8
1534	MapMaker and PathTracer for tracking carbon in genome-scale metabolic models. 2016 , 11, 648-61	19
1533	Effect of amino acid supplementation on titer and glycosylation distribution in hybridoma cell cultures-Systems biology-based interpretation using genome-scale metabolic flux balance model and multivariate data analysis. 2016 , 32, 1163-1173	10
1532	Construction of polyketide overproducing Escherichia coli strains via synthetic antisense RNAs based on in silico fluxome analysis and comparative transcriptome analysis. 2016 , 11, 530-41	12
1531	Multi-scale modeling of Arabidopsis thaliana response to different CO2 conditions: From gene expression to metabolic flux. 2016 , 58, 2-11	11
1530	Quantitative Analysis of Cancer Metabolism: From pSIRM to MFA. 2016 , 207, 207-20	3
1529	Metabolism in Cancer. 2016 ,	4
1528	Recombinant Escherichia coli with sulfide:quinone oxidoreductase and persulfide dioxygenase rapidly oxidises sulfide to sulfite and thiosulfate via a new pathway. 2016 , 18, 5123-5136	51
1527	Metabolic requirements for cancer cell proliferation. 2016 , 4, 16	75
1526	Mutual information upper bound of molecular communication based on cell metabolism. 2016 ,	8
1525	Stoichiometric modelling of assimilatory and dissimilatory biomass utilisation in a microbial community. 2016 , 18, 4946-4960	7
1524	The Need for Integrated Approaches in Metabolic Engineering. 2016 , 8,	34
1523	Systems Metabolic Engineering of Escherichia coli. 2016 , 7,	23
1522	Systematic identification and analysis of frequent gene fusion events in metabolic pathways. 2016 , 17, 473	10
1521	Manual of Cardiovascular Proteomics. 2016 ,	2
1520	Metabolic flux analyses of Pseudomonas aeruginosa cystic fibrosis isolates. 2016 , 38, 251-263	6
1519	Tracing insights into human metabolism using chemical engineering approaches. 2016 , 14, 72-81	9
1518	Fast-SNP: a fast matrix pre-processing algorithm for efficient loopless flux optimization of metabolic models. 2016 , 32, 3807-3814	10

1517	Guidelines for Reproducibly Building and Simulating Systems Biology Models. 2016 , 63, 2015-20	23
1516	In Silico Modeling of Liver Metabolism in a Human Disease Reveals a Key Enzyme for Histidine and Histamine Homeostasis. 2016 , 15, 2292-2300	18
1515	Systematic development and optimization of chemically defined medium supporting high cell density growth of <i>Bacillus coagulans</i> . 2016 , 100, 8121-34	5
1514	Decoding molecular interactions in microbial communities. 2016 , 40, 648-63	46
1513	Multi-objective shadow prices point at principles of metabolic regulation. 2016 , 146, 91-101	4
1512	dynamic Flux Balance Analysis of the Metabolism of Microalgae under a Diurnal Light Cycle. 2016 , 49, 791-796	4
1511	The steady-state assumption in oscillating and growing systems. 2016 , 406, 176-86	8
1510	Microbiome Data Mining for Microbial Interactions and Relationships. 2016 , 221-235	
1509	Can microbes compete with cows for sustainable protein production - A feasibility study on high quality protein. 2016 , 6, 36421	5
1508	Systematic investigation of metabolic reprogramming in different cancers based on tissue-specific metabolic models. 2016 , 14, 1644001	3
1507	Cyanobacterial Biofuels: Strategies and Developments on Network and Modeling. 2017 , 160, 75-102	2
1506	Advanced Computational Methods, NGS Tools, and Software for Mammalian Systems Biology. 2016 , 117-151	0
1505	A Combinatorial Algorithm for Microbial Consortia Synthetic Design. 2016 , 6, 29182	20
1504	Systems Biology in Animal Production and Health, Vol. 1. 2016 ,	
1503	Multi-omic data integration enables discovery of hidden biological regularities. 2016 , 7, 13091	110
1502	Flux control through protein phosphorylation in yeast. 2016 , 16,	16
1501	Model-based transcriptome engineering promotes a fermentative transcriptional state in yeast. 2016 , 113, E7428-E7437	23
1500	Farnesoid X Receptor Signaling Shapes the Gut Microbiota and Controls Hepatic Lipid Metabolism. 2016 , 1,	67

1499	Mapping the landscape of metabolic goals of a cell. 2016 , 17, 109	21
1498	Human gut microbiota and healthy aging: Recent developments and future prospective. 2016 , 4, 3-16	97
1497	Maps for when the living gets tough: Maneuvering through a hostile energy landscape. 2016 , 49, 364-370	3
1496	MUFINS: multi-formalism interaction network simulator. 2016 , 2, 16032	14
1495	A biocomputational application for the automated construction of large-scale metabolic models from transcriptomic data. 2016 ,	
1494	Effective Dynamic Models of Metabolic Networks. 2016 , 2, 51-54	4
1493	The potential for non-adaptive origins of evolutionary innovations in central carbon metabolism. 2016 , 10, 97	8
1492	In silico profiling of cell growth and succinate production in NZN111. 2016 , 3, 48	8
1491	Computational modeling of Quiescent Platelet Energy Metabolism in the Context of Whole-body Glucose Turnover. 2016 , 11, 91-101	5
1490	Assessment of nitric oxide (NO) redox reactions contribution to nitrous oxide (N ₂ O) formation during nitrification using a multispecies metabolic network model. 2016 , 113, 1124-36	9
1489	Analytic derivation of bacterial growth laws from a simple model of intracellular chemical dynamics. 2016 , 135, 121-30	14
1488	Systems biology of the structural proteome. 2016 , 10, 26	39
1487	Bridging the gap between non-targeted stable isotope labeling and metabolic flux analysis. 2016 , 4, 10	20
1486	Constructing and Analyzing Metabolic Flux Models of Microbial Communities. 2016 , 247-273	2
1485	Hydrocarbon and Lipid Microbiology Protocols. 2016 ,	
1484	Necessary and sufficient conditions for protocell growth. 2016 , 73, 1627-1664	2
1483	Reaction-centric modeling of microbial ecosystems. 2016 , 335, 74-86	8
1482	Improving the flux distributions simulated with genome-scale metabolic models of. 2016 , 3, 153-163	32

1481	A <i>Caenorhabditis elegans</i> Genome-Scale Metabolic Network Model. 2016 , 2, 297-311	55
1480	Growth against entropy in bacterial metabolism: the phenotypic trade-off behind empirical growth rate distributions in <i>E. coli</i> . 2016 , 13, 036005	21
1479	Designing intracellular metabolism for production of target compounds by introducing a heterologous metabolic reaction based on a <i>Synechocystis</i> sp. 6803 genome-scale model. 2016 , 15, 13	16
1478	Diversity of flux distribution in central carbon metabolism of <i>S. cerevisiae</i> strains from diverse environments. 2016 , 15, 58	18
1477	Deregulation of S-adenosylmethionine biosynthesis and regeneration improves methylation in the <i>E. coli</i> de novo vanillin biosynthesis pathway. 2016 , 15, 61	39
1476	Predicting compositions of microbial communities from stoichiometric models with applications for the biogas process. 2016 , 9, 17	17
1475	Comparative genome-scale modelling of <i>Staphylococcus aureus</i> strains identifies strain-specific metabolic capabilities linked to pathogenicity. 2016 , 113, E3801-9	145
1474	Current advances in molecular, biochemical, and computational modeling analysis of microalgal triacylglycerol biosynthesis. 2016 , 34, 1046-1063	61
1473	Toward efficient microaerobic processes using engineered <i>Escherichia coli</i> W3110 strains. 2016 , 16, 588-597	9
1472	Extending the biosynthetic repertoires of cyanobacteria and chloroplasts. 2016 , 87, 87-102	44
1471	Sugar Synthesis from CO ₂ in <i>Escherichia coli</i> . 2016 , 166, 115-25	190
1470	Functional Alignment of Metabolic Networks. 2016 , 23, 390-9	1
1469	Construction and analysis of a genome-scale metabolic network for <i>Bacillus licheniformis</i> WX-02. 2016 , 167, 282-289	6
1468	The elementary flux modes of a manufacturing system: a novel approach to explore the relationship of network structure and function. 2016 , 54, 4145-4160	5
1467	Systems Medicine. 2016 ,	5
1466	Genome-wide metabolic model to improve understanding of CD4(+) T cell metabolism, immunometabolism and application in drug design. 2016 , 12, 431-43	12
1465	Multiscale Model of <i>Mycobacterium tuberculosis</i> Infection Maps Metabolite and Gene Perturbations to Granuloma Sterilization Predictions. 2016 , 84, 1650-1669	28
1464	Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models. 2016 , 62, 60-9	30

1463	Algae Genome-Scale Reconstruction, Modelling and Applications. 2016 , 591-598	1
1462	Multiplexed Engineering in Biology. 2016 , 34, 198-206	34
1461	Metabolic modeling of clostridia: current developments and applications. 2016 , 363,	39
1460	Metabolic engineering with multi-objective optimization of kinetic models. 2016 , 222, 1-8	23
1459	Foundations and Emerging Paradigms for Computing in Living Cells. 2016 , 428, 893-915	16
1458	Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems. 2016 , 2, 77-88	47
1457	A kidney-specific genome-scale metabolic network model for analyzing focal segmental glomerulosclerosis. 2016 , 27, 158-67	9
1456	In silico analysis of Clostridium acetobutylicum ATCC 824 metabolic response to an external electron supply. 2016 , 39, 295-305	4
1455	Metabolic model of Synechococcus sp. PCC 7002: Prediction of flux distribution and network modification for enhanced biofuel production. 2016 , 213, 190-197	59
1454	Global characterization of in vivo enzyme catalytic rates and their correspondence to in vitro kcat measurements. 2016 , 113, 3401-6	129
1453	Assessing methanotrophy and carbon fixation for biofuel production by Methanosarcina acetivorans. 2016 , 15, 10	26
1452	Computational Modeling of Human Metabolism and Its Application to Systems Biomedicine. 2016 , 1386, 253-81	24
1451	Modeling and Simulation Tools: From Systems Biology to Systems Medicine. 2016 , 1386, 441-63	14
1450	In silico multiple-targets identification for heme detoxification in the human malaria parasite Plasmodium falciparum. 2016 , 37, 237-44	5
1449	Adaptive Genetic Robustness of Escherichia coli Metabolic Fluxes. 2016 , 33, 1164-76	13
1448	Solving Puzzles With Missing Pieces: The Power of Systems Biology. 2016 , 104, 2-7	13
1447	Low carbon fuels and commodity chemicals from waste gases: Systematic approach to understand energy metabolism in a model acetogen. 2016 , 18, 3020-3028	97
1446	Synthetic Ecology of Microbes: Mathematical Models and Applications. 2016 , 428, 837-61	132

1445	Bioreactor Engineering Research and Industrial Applications II. 2016 ,	
1444	Some assembly required: evolutionary and systems perspectives on the mammalian reproductive system. 2016 , 363, 267-278	4
1443	Approaches to Lipid Analysis. 2016 , 41-72	1
1442	Efficient solution of ordinary differential equations with a parametric lexicographic linear program embedded. 2016 , 133, 623-653	22
1441	From sugars to biodiesel using microalgae and yeast. 2016 , 18, 461-475	34
1440	Systems biology study of mucopolysaccharidosis using a human metabolic reconstruction network. 2016 , 117, 129-39	20
1439	Advances and perspectives in computational prediction of microbial gene essentiality. 2017 , 16, 70-79	19
1438	Reframed Genome-Scale Metabolic Model to Facilitate Genetic Design and Integration with Expression Data. 2017 , 14, 1410-1418	1
1437	Addressing the Need for a Model Selection Framework in Systems Biology Using Information Theory. 2017 , 105, 330-339	5
1436	Volume of the steady-state space of financial flows in a monetary stock-flow-consistent model. 2017 , 473, 589-602	4
1435	The importance of accurately correcting for the natural abundance of stable isotopes. 2017 , 520, 27-43	30
1434	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. 2017 , 7, 41241	53
1433	Lessons from the genomes and transcriptomes of filarial nematodes. 2017 , 215, 23-29	7
1432	Integrated Regulatory and Metabolic Networks of the Marine Diatom Predict the Response to Rising CO Levels. 2017 , 2,	28
1431	Mathematical modelling of clostridial acetone-butanol-ethanol fermentation. 2017 , 101, 2251-2271	20
1430	Biomedical applications of cell- and tissue-specific metabolic network models. 2017 , 68, 35-49	24
1429	Making life difficult for <i>Clostridium difficile</i> : augmenting the pathogen's metabolic model with transcriptomic and codon usage data for better therapeutic target characterization. 2017 , 11, 25	18
1428	Identification of Dynamic Metabolic Flux Balance Models Based on Parametric Sensitivity Analysis. 2017 , 56, 1911-1919	6

1427	Integration of metabolic, regulatory and signaling networks towards analysis of perturbation and dynamic responses. 2017 , 2, 59-66	11
1426	Lessons on enzyme kinetics from quantitative proteomics. 2017 , 46, 81-89	38
1425	Identifying the Metabolic Differences of a Fast-Growth Phenotype in <i>Synechococcus</i> UTEX 2973. 2017 , 7, 41569	40
1424	Construction and simulation of the <i>Bradyrhizobium diazoefficiens</i> USDA110 metabolic network: a comparison between free-living and symbiotic states. 2017 , 13, 607-620	13
1423	What can mathematical modelling say about CHO metabolism and protein glycosylation?. 2017 , 15, 212-221	32
1422	Mini-review: Metabolic Engineering for Biomanufacturing of High-value Products. 2017 , 15, 161-167	35
1421	Current Trends in Multidrug Optimization. 2016 , 2211068216682338	6
1420	The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. 2017 , 7, 1239-1249	14
1419	Analysing Algorithms and Data Sources for the Tissue-Specific Reconstruction of Liver Healthy and Cancer Cells. 2017 , 9, 36-45	6
1418	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. 2017 , 7, 40863	24
1417	Detecting the Significant Flux Backbone of <i>Escherichia coli</i> metabolism. 2017 , 591, 1437-1451	2
1416	Exploiting the Genetic Diversity of Maize Using a Combined Metabolomic, Enzyme Activity Profiling, and Metabolic Modeling Approach to Link Leaf Physiology to Kernel Yield. 2017 , 29, 919-943	39
1415	Screening Synthesis Pathways for Biomass-Derived Sustainable Polymer Production. 2017 , 5, 4388-4398	21
1414	Systematic inference of functional phosphorylation events in yeast metabolism. 2017 , 33, 1995-2001	5
1413	A geographically-diverse collection of 418 human gut microbiome pathway genome databases. 2017 , 4, 170035	6
1412	First principle-based models in plant suspension cell cultures: a review. 2017 , 37, 1077-1089	3
1411	Development of a Framework for Metabolic Pathway Analysis-Driven Strain Optimization Methods. 2017 , 9, 46-55	1
1410	Arginine deiminase pathway provides ATP and boosts growth of the gas-fermenting acetogen <i>Clostridium autoethanogenum</i> . 2017 , 41, 202-211	55

1409	Exploring biochemical pathways for mono-ethylene glycol (MEG) synthesis from synthesis gas. 2017 , 41, 173-181	18
1408	630Band - quantitative growth and extensive polysaccharide secretion. 2017 , 7, 602-615	26
1407	MOST-visualization: software for producing automated textbook-style maps of genome-scale metabolic networks. 2017 , 33, 2596-2597	2
1406	FOCuS: a metaheuristic algorithm for computing knockouts from genome-scale models for strain optimization. 2017 , 13, 1355-1363	9
1405	Growth Trade-Offs Accompany the Emergence of Glycolytic Metabolism in <i>Shewanella oneidensis</i> MR-1. 2017 , 199,	10
1404	Model-based biotechnological potential analysis of <i>Kluyveromyces marxianus</i> central metabolism. 2017 , 44, 1177-1190	23
1403	Network Biology. 2017 ,	2
1402	Sequential computation of elementary modes and minimal cut sets in genome-scale metabolic networks using alternate integer linear programming. 2017 , 33, 2345-2353	17
1401	Model-enabled gene search (MEGS) allows fast and direct discovery of enzymatic and transport gene functions in the marine bacterium. 2017 , 292, 10250-10261	6
1400	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. 2017 , 83,	54
1399	IDENTIFYING CANCER SPECIFIC METABOLIC SIGNATURES USING CONSTRAINT-BASED MODELS. 2017 , 22, 485-496	2
1398	Anticancer drug discovery through genome-scale metabolic modeling. 2017 , 4, 1-8	9
1397	Metabolic Adaptation Establishes Disease Tolerance to Sepsis. 2017 , 169, 1263-1275.e14	138
1396	Constraint-based modeling identifies new putative targets to fight colistin-resistant <i>A. baumannii</i> infections. 2017 , 7, 3706	25
1395	Large-scale computational models of liver metabolism: How far from the clinics?. 2017 , 66, 1323-1334	17
1394	Maintenance of ATP Homeostasis Triggers Metabolic Shifts in Gas-Fermenting Acetogens. 2017 , 4, 505-515.e5	76
1393	The best models of metabolism. 2017 , 9, e1391	27
1392	Constraint-based metabolic modelling of marine microbes and communities. 2017 , 34, 1-10	5

1391	Mini Photobioreactors for in Vivo Real-Time Characterization and Evolutionary Tuning of Bacterial Optogenetic Circuit. 2017 , 6, 1793-1796	8
1390	Metabolic modeling of energy balances in <i>Mycoplasma hyopneumoniae</i> shows that pyruvate addition increases growth rate. 2017 , 114, 2339-2347	7
1389	Rerouting of carbon flux in a glycogen mutant of cyanobacteria assessed via isotopically non-stationary C metabolic flux analysis. 2017 , 114, 2298-2308	51
1388	Using Structural Kinetic Modeling To Identify Key Determinants of Stability in Reaction Networks. 2017 , 121, 4982-4992	3
1387	<i>Clostridium butyricum</i> maximizes growth while minimizing enzyme usage and ATP production: metabolic flux distribution of a strain cultured in glycerol. 2017 , 11, 58	12
1386	Seeing the wood for the trees: a forest of methods for optimization and omic-network integration in metabolic modelling. 2018 , 19, 1218-1235	23
1385	Derivation and Use of Mathematical Models in Systems Biology. 2017 , 339-367	
1384	An integrative machine learning strategy for improved prediction of essential genes in <i>Escherichia coli</i> metabolism using flux-coupled features. 2017 , 13, 1584-1596	19
1383	Remodeling adipose tissue through in silico modulation of fat storage for the prevention of type 2 diabetes. 2017 , 11, 60	4
1382	Current Trends in Multidrug Optimization: An Alley of Future Successful Treatment of Complex Disorders. 2017 , 22, 254-275	29
1381	Optimal resource allocation enables mathematical exploration of microbial metabolic configurations. 2017 , 75, 1349-1380	14
1380	A Genome Scale Model of <i>Geobacillus thermoglucosidarius</i> (C56-YS93) reveals its biotechnological potential on rice straw hydrolysate. 2017 , 251, 30-37	15
1379	Identifying the shared metabolic objectives of glycerol bioconversion in <i>Klebsiella pneumoniae</i> under different culture conditions. 2017 , 248, 59-68	4
1378	Accelerating the Drug Development Pipeline with Genome-Scale Metabolic Network Reconstructions. 2017 , 139-162	3
1377	Metabolic Modeling for Design of Cell Factories. 2017 , 71-107	1
1376	Genome-Scale Metabolic Modeling and In silico Strain Design of <i>Escherichia coli</i> . 2017 , 109-137	2
1375	A Genome-Scale Model of Simulates Mechanisms of Metabolic Diversity and Energy Conservation. 2017 , 2,	7
1374	Cooperative Metabolism in a Three-Partner Insect-Bacterial Symbiosis Revealed by Metabolic Modeling. 2017 , 199,	41

1373	IMGMD: A platform for the integration and standardisation of In silico Microbial Genome-scale Metabolic Models. 2017 , 7, 727	7
1372	A systematic reconstruction and constraint-based analysis of Leishmania donovani metabolic network: identification of potential antileishmanial drug targets. 2017 , 13, 955-969	25
1371	Absolute Quantification of Protein and mRNA Abundances Demonstrate Variability in Gene-Specific Translation Efficiency in Yeast. 2017 , 4, 495-504.e5	106
1370	Evaluating the capabilities of microbial chemical production using genome-scale metabolic models. 2017 , 2, 91-97	3
1369	In silico analysis of human metabolism: Reconstruction, contextualization and application of genome-scale models. 2017 , 2, 29-38	15
1368	Prediction of metabolic fluxes from gene expression data with Huber penalty convex optimization function. 2017 , 13, 901-909	6
1367	Computational Modeling of Microbial Communities. 2017 , 163-189	4
1366	Flux balance analysis of photoautotrophic metabolism: Uncovering new biological details of subsystems involved in cyanobacterial photosynthesis. 2017 , 1858, 276-287	28
1365	New views on the selection acting on genetic polymorphism in central metabolic genes. 2017 , 1389, 108-123	3
1364	Application of theoretical methods to increase succinate production in engineered strains. 2017 , 40, 479-497	9
1363	Hydrocarbon and Lipid Microbiology Protocols. 2017 ,	
1362	Reconstruction of a genome-scale metabolic model and in silico analysis of the polymalic acid producer Aureobasidium pullulans CCTCC M2012223. 2017 , 607, 1-8	15
1361	A Genome-Scale Modeling Approach to Quantify Biofilm Component Growth of Salmonella Typhimurium. 2017 , 82, 154-166	6
1360	Advances and challenges in logical modeling of cell cycle regulation: perspective for multi-scale, integrative yeast cell models. 2017 , 17,	10
1359	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. 2017 , 39, 220-227	23
1358	Granzyme B Disrupts Central Metabolism and Protein Synthesis in Bacteria to Promote an Immune Cell Death Program. 2017 , 171, 1125-1137.e11	39
1357	Modelling pyruvate dehydrogenase under hypoxia and its role in cancer metabolism. 2017 , 4, 170360	13
1356	Post-genomic Studies and Systems Biology of Actinobacteria: A Brief Overview. 2017 , 377-395	

1355	Modulation of Nitrous Oxide (NO) Accumulation by Primary Metabolites in Denitrifying Cultures Adapting to Changes in Environmental C and N. 2017 , 51, 13678-13688	18
1354	Modeling and analysis of flux distribution and bioproduct formation in <i>Synechocystis</i> sp. PCC 6803 using a new genome-scale metabolic reconstruction. 2017 , 27, 295-310	13
1353	Constraining Mechanism Based Simulations to Identify Ensembles of Parametrizations to Characterize Metabolic Features. 2017 , 107-117	
1352	Estimation of the Maximum Theoretical Productivity of Fed-Batch Bioreactors. 2017 , 50, 9883-9888	
1351	Functional proteomics outlines the complexity of breast cancer molecular subtypes. 2017 , 7, 10100	27
1350	EcoSynther: A Customized Platform To Explore the Biosynthetic Potential in <i>E. coli</i> . 2017 , 12, 2823-2829	8
1349	COSYS: A Computational Infrastructure for Systems Biology. 2017 , 82-92	1
1348	Resolving the central metabolism of <i>Arabidopsis</i> guard cells. 2017 , 7, 8307	32
1347	Systems Biology and the Seagrass Paradox: Adaptation, Acclimation, and Survival of Marine Angiosperms in a Changing Ocean Climate. 2017 , 167-188	2
1346	Healthcare and Big Data Management. 2017 ,	2
1345	Data Analysis for Gut Microbiota and Health. 2017 , 1028, 79-87	
1344	Photorespiration. 2017 ,	1
1343	Genome-Scale Modeling of Photorespiratory Pathway Manipulation. 2017 , 1653, 195-202	
1342	Cellular Metabolism at the Systems Level. 2017 , 1-24	
1341	Methods and Data. 2017 , 25-52	
1340	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage <i>acI</i> . 2017 , 2,	14
1339	Model-guided identification of novel gene amplification targets for improving succinate production in <i>Escherichia coli</i> NZN111. 2017 , 9, 830-835	3
1338	Learning from quantitative data to understand central carbon metabolism. 2017 , 35, 971-980	18

1337	Revealing the mystery of metabolic adaptations using a genome scale model of <i>Leishmania infantum</i> . 2017 , 7, 10262	12
1336	Integration and virtual reality exploration of biomedical data with CmPI and VANTED. 2017 , 59, 181-190	3
1335	UP Finder: A COBRA toolbox extension for identifying gene overexpression strategies for targeted overproduction. 2017 , 5, 54-59	3
1334	Predicting the murine enterocyte metabolic response to diets that differ in lipid and carbohydrate composition. 2017 , 7, 8784	5
1333	Acceleration Strategies to Enhance Metabolic Ensemble Modeling Performance. 2017 , 113, 1150-1162	17
1332	Metabolic Reconstruction and Modeling Microbial Electrosynthesis. 2017 , 7, 8391	67
1331	Standardizing biomass reactions and ensuring complete mass balance in genome-scale metabolic models. 2017 , 33, 3603-3609	55
1330	More than just a gut feeling: constraint-based genome-scale metabolic models for predicting functions of human intestinal microbes. 2017 , 5, 78	41
1329	A Logic for Checking the Probabilistic Steady-State Properties of Reaction Networks. 2017 , 24, 734-745	1
1328	Quantifying the entropic cost of cellular growth control. 2017 , 96, 010401	11
1327	Quantitative intracellular flux modeling and applications in biotherapeutic development and production using CHO cell cultures. 2017 , 114, 2717-2728	27
1326	A multiscale agent-based framework integrated with a constraint-based metabolic network model of cancer for simulating avascular tumor growth. 2017 , 13, 1888-1897	11
1325	Analyses of extracellular protein production in <i>Bacillus subtilis</i> II: Genome-scale metabolic model reconstruction based on updated gene-enzyme-reaction data. 2017 , 127, 229-241	13
1324	Selection of complementary foods based on optimal nutritional values. 2017 , 7, 5413	9
1323	Stepwise inference of likely dynamic flux distributions from metabolic time series data. 2017 , 33, 2165-2172	6
1322	Engineering <i>Escherichia coli</i> for poly-(3-hydroxybutyrate) production guided by genome-scale metabolic network analysis. 2017 , 106, 60-66	17
1321	A comprehensive evaluation of constraining amino acid biosynthesis in compartmented models for metabolic flux analysis. 2017 , 5, 34-44	8
1320	From MFA to FBA: Defining linear constraints accounting for overflow metabolism in a macroscopic FBA-based dynamical model of cell cultures in bioreactor. 2017 , 60, 34-47	12

1319	Glycosylation flux analysis reveals dynamic changes of intracellular glycosylation flux distribution in Chinese hamster ovary fed-batch cultures. 2017 , 43, 9-20	30
1318	Deciphering the regulation of metabolism with dynamic optimization: an overview of recent advances. 2017 , 45, 1035-1043	10
1317	Overflow metabolism and growth cessation in <i>Clostridium thermocellum</i> DSM1313 during high cellulose loading fermentations. 2017 , 114, 2592-2604	13
1316	Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints. 2017 , 13, 935	193
1315	Integration of Genome Scale Metabolic Networks and Gene Regulation of Metabolic Enzymes With Physiologically Based Pharmacokinetics. 2017 , 6, 732-746	10
1314	Reconstruction and analysis of a genome-scale metabolic model of <i>Nannochloropsis gaditana</i> . 2017 , 26, 354-364	22
1313	Thermodynamic Constraints Improve Metabolic Networks. 2017 , 113, 679-689	5
1312	Constraint and Contingency Pervade the Emergence of Novel Phenotypes in Complex Metabolic Systems. 2017 , 113, 690-701	1
1311	Comprehensive Mapping of Pluripotent Stem Cell Metabolism Using Dynamic Genome-Scale Network Modeling. 2017 , 21, 2965-2977	41
1310	Mathematical modelling of microbes: metabolism, gene expression and growth. 2017 , 14,	26
1309	An integrated computational and experimental study uncovers FUT9 as a metabolic driver of colorectal cancer. 2017 , 13, 956	28
1308	Genome-driven evolutionary game theory helps understand the rise of metabolic interdependencies in microbial communities. 2017 , 8, 1563	72
1307	<i>Escherichia coli</i> as a model organism for systems metabolic engineering. 2017 , 6, 80-88	7
1306	Genome-scale metabolic models applied to human health and disease. 2017 , 9, e1393	26
1305	Resource allocation in living organisms. 2017 , 45, 945-952	29
1304	Genome-Scale Model and Omics Analysis of Metabolic Capacities of Reveal a Preferential Mucin-Degrading Lifestyle. 2017 , 83,	99
1303	Flux Balance Analysis Indicates that Methane Is the Lowest Cost Feedstock for Microbial Cell Factories. 2017 , 5, 26-33	21
1302	Genome-scale modeling of yeast: chronology, applications and critical perspectives. 2017 , 17,	33

1301	Structural properties of genotype-phenotype maps. 2017 , 14,	44
1300	Computational modelling of genome-scale metabolic networks and its application to CHO cell cultures. 2017 , 88, 150-160	17
1299	Optimal management of nutrient reserves in microorganisms under time-varying environmental conditions. 2017 , 429, 124-141	2
1298	Scales and multimodal flux distributions in stationary metabolic network models via thermodynamics. 2017 , 95, 062419	2
1297	Natural selection drove metabolic specialization of the chromatophore in <i>Paulinella chromatophora</i> . 2017 , 17, 99	1
1296	The use of genome-scale metabolic network reconstruction to predict fluxes and equilibrium composition of N-fixing versus C-fixing cells in a diazotrophic cyanobacterium, <i>Trichodesmium erythraeum</i> . 2017 , 11, 4	7
1295	A scalable metabolite supplementation strategy against antibiotic resistant pathogen <i>Chromobacterium violaceum</i> induced by NAD/NADH imbalance. 2017 , 11, 51	14
1294	Emergence of microbial diversity due to cross-feeding interactions in a spatial model of gut microbial metabolism. 2017 , 11, 56	56
1293	Development of a core kinetic metabolic model consistent with multiple genetic perturbations. 2017 , 10, 108	26
1292	Large-scale detection of drug off-targets: hypotheses for drug repurposing and understanding side-effects. 2017 , 18, 18	34
1291	Comprehensive reconstruction and evaluation of genome-scale metabolic model that accounts for 1243 ORFs. 2017 , 4, 22	15
1290	Inverse statistical problems: from the inverse Ising problem to data science. 2017 , 66, 197-261	125
1289	Thermodynamics-based Metabolite Sensitivity Analysis in metabolic networks. 2017 , 39, 117-127	17
1288	Identification of active constraints in dynamic flux balance analysis. 2017 , 33, 26-36	5
1287	Systems biology for understanding and engineering of heterotrophic oleaginous microorganisms. 2017 , 12, 1600104	15
1286	In silico and in vivo stability analysis of a heterologous biosynthetic pathway for 1,4-butanediol production in metabolically engineered <i>E. coli</i> . 2017 , 35, 1874-1889	4
1285	Can a systems approach produce a better understanding of mood disorders?. 2017 , 1861, 3335-3344	
1284	Advances in the genomics and metabolomics of dairy lactobacilli: A review. 2017 , 61, 33-49	81

1283	BeReTa: a systematic method for identifying target transcriptional regulators to enhance microbial production of chemicals. 2017 , 33, 87-94	9
1282	Comprehensive reconstruction and in silico analysis of <i>Aspergillus niger</i> genome-scale metabolic network model that accounts for 1210 ORFs. 2017 , 114, 685-695	25
1281	Hydrocarbon and Lipid Microbiology Protocols. 2017 ,	
1280	The genome of <i>Onchocerca volvulus</i> , agent of river blindness. 2016 , 2, 16216	69
1279	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. <i>Nature Biotechnology</i> , 2017 , 35, 81-89	44.5 368
1278	Advances on plant-pathogen interactions from molecular toward systems biology perspectives. 2017 , 90, 720-737	56
1277	A whole-cell simulator in GNU Octave. 2017 ,	
1276	Integrating Extracellular Flux Measurements and Genome-Scale Modeling Reveals Differences between Brown and White Adipocytes. 2017 , 21, 3040-3048	13
1275	Linking physiologically-based pharmacokinetic and genome-scale metabolic networks to understand estradiol biology. 2017 , 11, 141	10
1274	Sensitivity and network topology in chemical reaction systems. 2017 , 96, 022322	3
1273	Virtualisation of gene knockout experiments based on kinetic modelling: <i>Escherichia coli</i> as an algorithmic case. 2017 , 10, 157	
1272	Computational Modeling in Liver Surgery. 2017 , 8, 906	16
1271	The Role of Soil Microorganisms in Plant Mineral Nutrition-Current Knowledge and Future Directions. 2017 , 8, 1617	478
1270	Reconstruction of Genome Scale Metabolic Model and Its Responses to Varying RuBisCO Activity, Light Intensity, and Enzymatic Cost Conditions. 2017 , 8, 2060	11
1269	Stoichiometric Correlation Analysis: Principles of Metabolic Functionality from Metabolomics Data. 2017 , 8, 2152	8
1268	A Protocol for Generating and Exchanging (Genome-Scale) Metabolic Resource Allocation Models. 2017 , 7,	15
1267	Computational Approaches for Integrative Analysis of the Metabolome and Microbiome. 2017 , 7,	55
1266	Systems Biology Approach to Bioremediation of Nitroaromatics: Constraint-Based Analysis of 2,4,6-Trinitrotoluene Biotransformation by <i>Escherichia coli</i> . 2017 , 22,	7

1265	Modeling Biofilms: From Genes to Communities. 2017 , 5, 5	2
1264	Stoichiometric Network Analysis of Cyanobacterial Acclimation to Photosynthesis-Associated Stresses Identifies Heterotrophic Niches. 2017 , 5, 32	8
1263	Mathematical and Computational Modeling in Complex Biological Systems. 2017 , 2017, 5958321	44
1262	Development of Synthetic Microbial Platforms to Convert Lignocellulosic Biomass to Biofuels. 2017 , 2, 233-278	5
1261	Perspectives and Challenges in Microbial Communities Metabolic Modeling. 2017 , 8, 88	27
1260	Comparative Genomic Analysis of the Human Gut Microbiome Reveals a Broad Distribution of Metabolic Pathways for the Degradation of Host-Synthesized Mucin Glycans and Utilization of Mucin-Derived Monosaccharides. 2017 , 8, 111	45
1259	Genome-Scale Reconstruction of the Metabolic Network in to Assess Wine Malolactic Fermentation. 2017 , 8, 534	25
1258	Time-Resolved Transcriptomics and Constraint-Based Modeling Identify System-Level Metabolic Features and Overexpression Targets to Increase Spiramycin Production in. 2017 , 8, 835	10
1257	Synthetic Microbial Ecology: Engineering Habitats for Modular Consortia. 2017 , 8, 1125	52
1256	Determinism and Contingency Shape Metabolic Complementation in an Endosymbiotic Consortium. 2017 , 8, 2290	4
1255	A Comprehensive Overview of Online Resources to Identify and Predict Bacterial Essential Genes. 2017 , 8, 2331	28
1254	Genome-Scale Reconstruction of the Human Astrocyte Metabolic Network. 2017 , 9, 23	15
1253	Genome-Scale Metabolic Modeling of Archaea Lends Insight into Diversity of Metabolic Function. 2017 , 2017, 9763848	14
1252	Model-based optimization of the recombinant protein production in <i>Pichia pastoris</i> based on dynamic flux balance analysis and elementary process functions. 2017 , 2815-2820	0
1251	Computational Studies and Biosynthesis of Natural Products with Promising Anticancer Properties. 2017 ,	4
1250	Mathematical Models in Biotechnology. 2017 , 657-667	
1249	Combining Targeted Metabolomic Data with a Model of Glucose Metabolism: Toward Progress in Chondrocyte Mechanotransduction. 2017 , 12, e0168326	13
1248	Upon Accounting for the Impact of Isoenzyme Loss, Gene Deletion Costs Anticorrelate with Their Evolutionary Rates. 2017 , 12, e0170164	6

1247	biochem4j: Integrated and extensible biochemical knowledge through graph databases. 2017 , 12, e0179130	18
1246	Compartmentalized metabolic network reconstruction of microbial communities to determine the effect of agricultural intervention on soils. 2017 , 12, e0181826	4
1245	popFBA: tackling intratumour heterogeneity with Flux Balance Analysis. 2017 , 33, i311-i318	19
1244	A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect. 2017 , 13, e1005758	38
1243	How important is thermodynamics for identifying elementary flux modes?. 2017 , 12, e0171440	16
1242	Dynamic metabolic modeling of heterotrophic and mixotrophic microalgal growth on fermentative wastes. 2017 , 13, e1005590	18
1241	Optimality principles reveal a complex interplay of intermediate toxicity and kinetic efficiency in the regulation of prokaryotic metabolism. 2017 , 13, e1005371	13
1240	Bioenergetics-based modeling of Plasmodium falciparum metabolism reveals its essential genes, nutritional requirements, and thermodynamic bottlenecks. 2017 , 13, e1005397	36
1239	Detecting similar binding pockets to enable systems polypharmacology. 2017 , 13, e1005522	24
1238	BacArena: Individual-based metabolic modeling of heterogeneous microbes in complex communities. 2017 , 13, e1005544	116
1237	A systems approach reveals distinct metabolic strategies among the NCI-60 cancer cell lines. 2017 , 13, e1005698	17
1236	Heterogeneous oxygen availability affects the titer and topology but not the fidelity of plasmid DNA produced by Escherichia coli. 2017 , 17, 60	10
1235	Integrating transcriptional activity in genome-scale models of metabolism. 2017 , 11, 134	12
1234	OptPipe - a pipeline for optimizing metabolic engineering targets. 2017 , 11, 143	10
1233	Metabolic engineering of Synechococcus elongatus PCC 7942 for improvement of 1,3-propanediol and glycerol production based on in silico simulation of metabolic flux distribution. 2017 , 16, 212	26
1232	An accurate description of organic acid batch fermentation through dynamic metabolic modelling. 2017 , 10, 258	22
1231	Reconstruction of genome-scale metabolic model of Yarrowia lipolytica and its application in overproduction of triacylglycerol. 2017 , 4,	25
1230	MitoCore: a curated constraint-based model for simulating human central metabolism. 2017 , 11, 114	19

1229	CHRR: coordinate hit-and-run with rounding for uniform sampling of constraint-based models. 2017 , 33, 1741-1743	32
1228	Improving Bioenergy Crops through Dynamic Metabolic Modeling. 2017 , 5, 61	6
1227	On the Power of Uncertainties in Microbial System Modeling: No Need To Hide Them Anymore. 2017 , 2,	4
1226	Novel Plasmodium falciparum metabolic network reconstruction identifies shifts associated with clinical antimalarial resistance. 2017 , 18, 543	29
1225	Building Metabolic Models From First Principles. 2017 , 201-221	
1224	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018 , 36, 272-281	44.5 283
1223	Grohar: Automated Visualization of Genome-Scale Metabolic Models and Their Pathways. 2018 , 25, 505-508	2
1222	Application of adaptive laboratory evolution to overcome a flux limitation in an Escherichia coli production strain. 2018 , 115, 1542-1551	17
1221	Linking Adverse Outcome Pathways to Dynamic Energy Budgets: A Conceptual Model. 2018 , 281-302	6
1220	Integration of genome-scale metabolic networks into whole-body PBPK models shows phenotype-specific cases of drug-induced metabolic perturbation. 2018 , 4, 10	17
1219	Model-based metabolism design: constraints for kinetic and stoichiometric models. 2018 , 46, 261-267	20
1218	Metabolite secretion in microorganisms: the theory of metabolic overflow put to the test. 2018 , 14, 43	29
1217	An introduction to the maximum entropy approach and its application to inference problems in biology. 2018 , 4, e00596	31
1216	Optimization of bioprocess productivity based on metabolic-genetic network models with bilevel dynamic programming. 2018 , 115, 1829-1841	11
1215	Comparison of closely related, uncultivated Coxiella tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. 2018 , 20, 1751-1764	23
1214	From reconstruction to C metabolic engineering: A case study for overproduction of polyhydroxybutyrate in bioenergy grasses. 2018 , 273, 50-60	4
1213	NADH Shuttling Couples Cytosolic Reductive Carboxylation of Glutamine with Glycolysis in Cells with Mitochondrial Dysfunction. 2018 , 69, 581-593.e7	97
1212	Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. 2018 , 46, 2901-2917	42

1211	A systematic approach for finding the objective function and active constraints for dynamic flux balance analysis. 2018 , 41, 641-655	6
1210	Metabolic modelling and flux analysis of microorganisms from the Atacama Desert used in biotechnological processes. 2018 , 111, 1479-1491	2
1209	Squeezing Flux Out of Fat. 2018 , 29, 201-202	
1208	Generation of Molecular Models and Pathways. 2018 , 274-285	
1207	Modern views of ancient metabolic networks. 2018 , 8, 117-124	32
1206	Exploiting transcriptomic data for metabolic engineering: toward a systematic strain design. 2018 , 54, 26-32	3
1205	Methane utilization in <i>Methylobacterium alcaliphilum</i> 20Z: a systems approach. 2018 , 8, 2512	57
1204	Simulating biological processes: stochastic physics from whole cells to colonies. 2018 , 81, 052601	24
1203	The spatial and metabolic basis of colony size variation. 2018 , 12, 669-680	23
1202	Model-driven design of a minimal medium for <i>Akkermansia muciniphila</i> confirms mucus adaptation. 2018 , 11, 476-485	30
1201	Control of primary metabolism by a virulence regulatory network promotes robustness in a plant pathogen. 2018 , 9, 418	21
1200	Software Applications for Phenotype Analysis and Strain Design of Cellular Systems. 2018 , 771-791	3
1199	Biosynthetic Technology and Environmental Challenges. 2018 ,	7
1198	A graph-based approach to analyze flux-balanced pathways in metabolic networks. 2018 , 165, 40-51	6
1197	Principal metabolic flux mode analysis. 2018 , 34, 2409-2417	9
1196	An enhanced genome-scale metabolic reconstruction of <i>Streptomyces clavuligerus</i> identifies novel strain improvement strategies. 2018 , 41, 657-669	15
1195	A mathematical framework for yield (vs. rate) optimization in constraint-based modeling and applications in metabolic engineering. 2018 , 47, 153-169	20
1194	Evolutionary adaptations to new environments generally reverse plastic phenotypic changes. 2018 , 9, 350	46

1193	A blueprint for human whole-cell modeling. 2018 , 7, 8-15	41
1192	Mathematical Modeling in Bioremediation. 2018 , 7-27	
1191	Metabolism-Combined Growth Model Construction and Its Application to Optimal Bioreactor Operation. 2018 , 761-769	
1190	Overview on Bioprocess Simulation. 2018 , 715-722	
1189	Linking soil biology and chemistry in biological soil crust using isolate exometabolomics. 2018 , 9, 19	83
1188	Metabolic systems analysis of LPS induced endothelial dysfunction applied to sepsis patient stratification. 2018 , 8, 6811	18
1187	Assessing the benefits of horizontal gene transfer by laboratory evolution and genome sequencing. 2018 , 18, 54	19
1186	Mathematical models of lignin biosynthesis. 2018 , 11, 34	20
1185	Leveraging knowledge engineering and machine learning for microbial bio-manufacturing. 2018 , 36, 1308-1315	37
1184	GROOLS: reactive graph reasoning for genome annotation through biological processes. 2018 , 19, 132	1
1183	Metabolome- and genome-scale model analyses for engineering of to enhance polymalic acid and malic acid production from sugarcane molasses. 2018 , 11, 94	24
1182	Review and perspective on mathematical modeling of microbial ecosystems. 2018 , 46, 403-412	28
1181	MetExplore: collaborative edition and exploration of metabolic networks. 2018 , 46, W495-W502	63
1180	Gut metabolome meets microbiome: A methodological perspective to understand the relationship between host and microbe. 2018 , 149, 3-12	71
1179	Synthesis of multi-omic data and community metabolic models reveals insights into the role of hydrogen sulfide in colon cancer. 2018 , 149, 59-68	35
1178	Constraint-based modeling in microbial food biotechnology. 2018 , 46, 249-260	18
1177	A pathway for every product? Tools to discover and design plant metabolism. 2018 , 273, 61-70	14
1176	Constrained stoichiometric network analysis. 2018 , 20, 9910-9921	3

1175	Mathematical modelling of nonlinear dynamics generated from modular interconnections in cellular SOS response system. 2018 , 93, 643-652	
1174	Light-optimized growth of cyanobacterial cultures: Growth phases and productivity of biomass and secreted molecules in light-limited batch growth. 2018 , 47, 230-242	31
1173	Metabolic engineering to increase crop yield: From concept to execution. 2018 , 273, 23-32	10
1172	Achieving a Predictive Understanding of Antimicrobial Stress Physiology through Systems Biology. 2018 , 26, 296-312	10
1171	Computing Biomolecular System Steady-States. 2018 , 17, 36-43	3
1170	Towards predicting the environmental metabolome from metagenomics with a mechanistic model. 2018 , 3, 456-460	47
1169	Use of genetic and chemical synthetic lethality as probes of complexity in bacterial cell systems. 2018 , 42,	10
1168	Applications of a metabolic network model of mesenchymal stem cells for controlling cell proliferation and differentiation. 2018 , 70, 331-338	7
1167	Pathogenic mutations of the human mitochondrial citrate carrier SLC25A1 lead to impaired citrate export required for lipid, dolichol, ubiquinone and sterol synthesis. 2018 , 1859, 1-7	20
1166	Genome-wide characterization of Phytophthora infestans metabolism: a systems biology approach. 2018 , 19, 1403-1413	23
1165	Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote. 2018 , 176, 450-462	34
1164	Underground metabolism: network-level perspective and biotechnological potential. 2018 , 49, 108-114	28
1163	Nitrosomonas europaea adaptation to anoxic-oxic cycling: Insights from transcription analysis, proteomics and metabolic network modeling. 2018 , 615, 1566-1573	29
1162	Synthetic Metabolic Pathways. 2018 ,	2
1161	Computational Approaches on Stoichiometric and Kinetic Modeling for Efficient Strain Design. 2018 , 1671, 63-82	8
1160	Computational Prediction of Synthetic Lethals in Genome-Scale Metabolic Models Using Fast-SL. 2018 , 1716, 315-336	2
1159	Dynamic Flux Balance Analysis Using DFBAlab. 2018 , 1716, 353-370	5
1158	Designing Optimized Production Hosts by Metabolic Modeling. 2018 , 1716, 371-387	

1157	Analyzing and Designing Cell Factories with OptFlux. 2018 , 1716, 37-76	3
1156	Reconstruction and Analysis of Central Metabolism in Microbes. 2018 , 1716, 111-129	1
1155	Optimization of Multi-Omic Genome-Scale Models: Methodologies, Hands-on Tutorial, and Perspectives. 2018 , 1716, 389-408	10
1154	Using PSAMM for the Curation and Analysis of Genome-Scale Metabolic Models. 2018 , 1716, 131-150	5
1153	Biomedical applications of genome-scale metabolic network reconstructions of human pathogens. 2018 , 51, 70-79	20
1152	Metabolic Network Reconstruction and Modeling. 2018 ,	1
1151	Computational Modelling and Prediction of Microalgae Growth Focused Towards Improved Lipid Production. 2018 , 223-232	1
1150	Understanding regulation in substrate dependent modulation of growth and production of alcohols in <i>Clostridium sporogenes</i> NCIM 2918 through metabolic network reconstruction and flux balance analysis. 2018 , 249, 767-776	10
1149	Simulation of multicellular populations with Petri nets and genome scale intracellular networks. 2018 , 157, 3-16	
1148	Plant genome-scale reconstruction: from single cell to multi-tissue modelling and omics analyses. 2018 , 49, 42-48	23
1147	Flux balance modeling to predict bacterial survival during pulsed-activity events. 2018 , 15, 2219-2229	5
1146	Data Analysis for Metabolomics: Pathway Reconstruction and Functional Annotation. 2018 ,	
1145	Metabolomics. 2018 , 75-97	3
1144	Renal cell carcinoma classification: a case study of pitfalls associated with metabolic landscape analysis. 2018 ,	
1143	The Cost of Metabolic Interactions in Symbioses between Insects and Bacteria with Reduced Genomes. 2018 , 9,	22
1142	Combining multiple functional annotation tools increases coverage of metabolic annotation. 2018 , 19, 948	19
1141	. 2018 ,	7
1140	Genome-scale metabolic model analysis indicates low energy production efficiency in marine ammonia-oxidizing archaea. 2018 , 8, 106	3

1139	Efeitos de um treinamento de habilidades sociais no comportamento e desempenho acadêmico. 2018,	
1138	MODELING THE CORE METABOLISM OF <i>Komagataeibacter hansenii</i> ATCC 23769 TO EVALUATE NANOCELLULOSE BIOSYNTHESIS. 2018, 35, 869-886	5
1137	A Novel Method for the Integration of Stochastic Petri Net Simulation and Transcriptomic Data Applied to a Metabolic Pathway. 2018, 12,	
1136	. 2018,	
1135	Fundamentals of Metabolomics. 779-808	
1134	The EcoCyc Database. 2018, 8,	29
1133	Multiomic Data Integration and Analysis via Model-Driven Approaches. 2018, 82, 447-476	3
1132	Navigating methane metabolism: Enzymes, compartments, and networks. 2018, 613, 349-383	4
1131	Alleles of a gene differ in pleiotropy, often mediated through currency metabolite production, in <i>E. coli</i> and yeast metabolic simulations. 2018, 8, 17252	2
1130	Machine Learning Reveals Missing Edges and Putative Interaction Mechanisms in Microbial Ecosystem Networks. 2018, 3,	21
1129	The poly-omics of ageing through individual-based metabolic modelling. 2018, 19, 415	16
1128	Large-Scale Modeling Approach Reveals Functional Metabolic Shifts during Hepatic Differentiation. 2019, 18, 204-216	4
1127	Thermodynamically consistent coarse graining of biocatalysts beyond Michaelis-Menten. 2018, 20, 042002	23
1126	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. 2018, 9, 5252	80
1125	A quantitative model of nitrogen fixation in the presence of ammonium. 2018, 13, e0208282	30
1124	CiliateGEM: an open-project and a tool for predictions of ciliate metabolic variations and experimental condition design. 2018, 19, 442	1
1123	An Improved Genome-Scale Metabolic Model of <i>C1</i> (AK888) and Its Application in Glycogen Overproduction. 2018, 8,	10
1122	Searching for Essential Genes in the Cancer Genome. 2018, 12, 283-296	

1121	Modeling genome-wide enzyme evolution predicts strong epistasis underlying catalytic turnover rates. 2018 , 9, 5270	7
1120	Maintaining maximal metabolic flux by gene expression control. 2018 , 14, e1006412	10
1119	Assessing Escherichia coli metabolism models and simulation approaches in phenotype predictions: Validation against experimental data. 2018 , 34, 1344-1354	0
1118	Mechanistic modeling and applications for CHO cell culture development and production. 2018 , 22, 54-61	26
1117	Basics of genome-scale metabolic modeling and applications on C1-utilization. 2018 , 365,	7
1116	Analytical Reduction of Nonlinear Metabolic Networks Accounting for Dynamics in Enzymatic Reactions. 2018 , 2018, 1-22	3
1115	OptMDFpathway: Identification of metabolic pathways with maximal thermodynamic driving force and its application for analyzing the endogenous CO ₂ fixation potential of Escherichia coli. 2018 , 14, e1006492	27
1114	Multiscale analysis of autotroph-heterotroph interactions in a high-temperature microbial community. 2018 , 14, e1006431	7
1113	Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power. 2018 , 87, 37-49	18
1112	Synthetic Lethality and Cancer - Penetrance as the Major Barrier. 2018 , 4, 671-683	29
1111	Metabolic network reconstruction and phenome analysis of the industrial microbe, Escherichia coli BL21(DE3). 2018 , 13, e0204375	8
1110	Preface. xi-xiv	
1109	Introduction. 1-2	
1108	Enzymatic Adaptation. 3-12	
1107	Early Development of Cybernetic Models. 13-63	
1106	Revisiting Cybernetic Laws via Optimal Control Theory. 64-85	
1105	Toward Modeling of Metabolic Networks. 86-104	
1104	The Hybrid Cybernetic Model (HCM). 105-149	

1103	The Lumped Hybrid Cybernetic Model (L-HCM). 150-185	
1102	Predicting Dynamic Behavior of Mutant Strains with L-HCM. 186-212	
1101	Nonlinear Analysis of Cybernetic Models. 213-234	
1100	Metabolic Modeling Landscape. 235-251	
1099	Index. 266-270	
1098	Multi-omics integrative analysis with genome-scale metabolic model simulation reveals global cellular adaptation of <i>Aspergillus niger</i> under industrial enzyme production condition. 2018 , 8, 14404	20
1097	In Silico Identification of Microbial Partners to Form Consortia with Anaerobic Fungi. 2018 , 6, 7	13
1096	IN SILICO GENOME-SCALE RECONSTRUCTION AND ANALYSIS OF THE SHEWANELLA LOIHICA PV-4 METABOLIC NETWORK. 2018 , 26, 373-397	1
1095	Understanding the impact of the cofactor swapping of isocitrate dehydrogenase over the growth phenotype of <i>Escherichia coli</i> on acetate by using constraint-based modeling. 2018 , 13, e0196182	6
1094	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. 2018 , 115, 11096-11101	28
1093	The Induced Kinetic Differential Equation. 2018 , 77-114	
1092	Thermodynamic favorability and pathway yield as evolutionary tradeoffs in biosynthetic pathway choice. 2018 , 115, 11339-11344	20
1091	Feedbacks from the metabolic network to the genetic network reveal regulatory modules in <i>E. coli</i> and <i>B. subtilis</i> . 2018 , 13, e0203311	6
1090	Perspectives on <i>Leishmania</i> Species and Stage-specific Adaptive Mechanisms. 2018 , 34, 1068-1081	4
1089	A Prospective Study on the Fermentation Landscape of Gaseous Substrates to Biorenewables Using Metabolic Model. 2018 , 9, 1855	4
1088	Thermodynamic constraints on the regulation of metabolic fluxes. 2018 , 293, 19725-19739	10
1087	Distinct microbes, metabolites, and ecologies define the microbiome in deficient and proficient mismatch repair colorectal cancers. 2018 , 10, 78	69
1086	Grid-based computational methods for the design of constraint-based parsimonious chemical reaction networks to simulate metabolite production: GridProd. 2018 , 19, 325	3

1085	Escher-FBA: a web application for interactive flux balance analysis. 2018 , 12, 84	21
1084	Integrating -omics data into genome-scale metabolic network models: principles and challenges. 2018 , 62, 563-574	23
1083	Biochemical and Cellular Events in Controlling Microbial Performance. 2018 , 201-221	
1082	Integrated Systems and Chemical Biology Approach for Targeted Therapies. 2018 , 1-19	
1081	Systems Neuroscience. 2018 ,	
1080	Metabolic Determinants of Enzyme Evolution in a Genome-Scale Bacterial Metabolic Network. 2018 , 10, 3076-3088	10
1079	Metabolic adaptations underlying genome flexibility in prokaryotes. 2018 , 14, e1007763	17
1078	Genome-wide analysis of fitness data and its application to improve metabolic models. 2018 , 19, 368	1
1077	Genome-Scale Brain Metabolic Networks as Scaffolds for the Systems Biology of Neurodegenerative Diseases: Mapping Metabolic Alterations. 2018 , 21, 195-217	1
1076	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. 2018 , 9, 3771	52
1075	Advances in metabolic modeling of oleaginous microalgae. 2018 , 11, 241	33
1074	An Overview of Metabolomics Data Analysis: Current Tools and Future Perspectives. 2018 , 82, 387-413	21
1073	Systems Biology. 2018 ,	0
1072	Integrating genome-scale metabolic models into the prediction of microbial kinetics in natural environments. 2018 , 242, 102-122	4
1071	An Introduction to the Mathematical Modeling in the Study of Cancer Systems Biology. 2018 , 17, 1176935118799754	
1070	Doxorubicin induces an extensive transcriptional and metabolic rewiring in yeast cells. 2018 , 8, 13672	62
1069	Integrated human-virus metabolic stoichiometric modelling predicts host-based antiviral targets against Chikungunya, Dengue and Zika viruses. 2018 , 15,	20
1068	Modeling Spatio-Temporal Dynamics of Metabolic Networks with Cellular Automata and Constraint-Based Methods. 2018 , 16-29	5

1067	Robustness encoded across essential and accessory replicons of the ecologically versatile bacterium <i>Sinorhizobium meliloti</i> . 2018 , 14, e1007357	32
1066	Constraining Genome-Scale Models to Represent the Bow Tie Structure of Metabolism for C Metabolic Flux Analysis. 2018 , 8,	3
1065	Enhancing Metabolic Models with Genome-Scale Experimental Data. 2018 , 337-350	1
1064	Simulation and optimization of dynamic flux balance analysis models using an interior point method reformulation. 2018 , 119, 152-170	12
1063	The intertwined metabolism during symbiotic nitrogen fixation elucidated by metabolic modelling. 2018 , 8, 12504	27
1062	Dynamic flux balance analysis for microbial conversion of glycerol into 1,3-propanediol by <i>Klebsiella pneumoniae</i> . 2018 , 41, 1793-1805	5
1061	De novo design of biosynthetic pathways for bacterial production of bulk chemicals and biofuels. 2018 , 365,	4
1060	Metabolic modelling and simulation of the light and dark metabolism of <i>Chlamydomonas reinhardtii</i> . 2018 , 96, 1076-1088	9
1059	Integration of Plant Metabolomics Data with Metabolic Networks: Progresses and Challenges. 2018 , 1778, 297-310	10
1058	Species-specific transcriptomic network inference of interspecies interactions. 2018 , 12, 2011-2023	14
1057	Comprehensive analysis of a metabolic model for lipid production in <i>Rhodospiridium toruloides</i> . 2018 , 280, 11-18	28
1056	Yeast mitochondria: an overview of mitochondrial biology and the potential of mitochondrial systems biology. 2018 , 18,	47
1055	Mitochondrial Bioenergetics. 2018 ,	4
1054	Accelerating flux balance calculations in genome-scale metabolic models by localizing the application of loopless constraints. 2018 , 34, 4248-4255	6
1053	Integrated constraints based analysis of an engineered violacein pathway in <i>Escherichia coli</i> . 2018 , 171, 10-19	8
1052	Hepatotoxicity Prediction by Systems Biology Modeling of Disturbed Metabolic Pathways Using Gene Expression Data. 2018 , 1800, 505-518	2
1051	Metabolic Models: From DNA to Physiology (and Back). 2018 , 57-69	
1050	Theoretical and Applied Aspects of Systems Biology. 2018 ,	2

1049	HEPATOKIN1 is a biochemistry-based model of liver metabolism for applications in medicine and pharmacology. 2018 , 9, 2386	19
1048	System Biology to Access Target Relevance in the Research and Development of Molecular Inhibitors. 2018 , 221-242	2
1047	Computational Toxicology. 2018 ,	5
1046	Modeling the Metabolic State of Upon Infection. 2018 , 8, 264	11
1045	Systems analysis of intracellular pH vulnerabilities for cancer therapy. 2018 , 9, 2997	151
1044	Statistical mechanics for metabolic networks during steady state growth. 2018 , 9, 2988	19
1043	From metagenomic data to personalized in silico microbiotas: predicting dietary supplements for Crohn's disease. 2018 , 4, 27	39
1042	Metabolic model-based analysis of the emergence of bacterial cross-feeding via extensive gene loss. 2018 , 12, 69	20
1041	Modelling the metabolism of protein secretion through the Tat route in <i>Streptomyces lividans</i> . 2018 , 18, 59	7
1040	Conducting metagenomic studies in microbiology and clinical research. 2018 , 102, 8629-8646	17
1039	Reply to "Challenges in modeling the human gut microbiome". <i>Nature Biotechnology</i> , 2018 , 36, 686-691	44.5 8
1038	Constraint-Based Modeling Highlights Cell Energy, Redox Status and α -Ketoglutarate Availability as Metabolic Drivers for Anthocyanin Accumulation in Grape Cells Under Nitrogen Limitation. 2018 , 9, 421	18
1037	A Dynamic Multi-Tissue Flux Balance Model Captures Carbon and Nitrogen Metabolism and Optimal Resource Partitioning During Arabidopsis Growth. 2018 , 9, 884	29
1036	<i>Escherichia coli</i> B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. 2018 , 12, 66	22
1035	Traceability, reproducibility and wiki-exploration for "à-la-carte" reconstructions of genome-scale metabolic models. 2018 , 14, e1006146	41
1034	Modeling Plant Metabolism: Advancements and Future Capabilities. 2018 , 57-76	2
1033	Analysis of Fluxomic Experiments with Principal Metabolic Flux Mode Analysis. 2018 , 1807, 141-161	
1032	Using microalgae in the circular economy to valorise anaerobic digestate: challenges and opportunities. 2018 , 267, 732-742	110

1031	In silico predicted transcriptional regulatory control of steroidogenesis in spawning female fathead minnows (<i>Pimephales promelas</i>). 2018 , 455, 179-190	
1030	An enormous potential for niche construction through bacterial cross-feeding in a homogeneous environment. 2018 , 14, e1006340	29
1029	Dark fermentation metabolic models to study strategies for hydrogen consumers inhibition. 2018 , 267, 445-457	16
1028	A Genome-Scale Metabolic Reconstruction of With the Integration of Transcriptional Data Reveals the Key Metabolic Patterns Involved in the Interaction of Its Host. 2018 , 9, 244	8
1027	Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes. 2018 , 19, 251	1
1026	COMPUTATIONAL MODELING OF PASS EFFECTIVENESS IN SOCCER. 2018 , 21, 1850010	4
1025	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of AYE. 2018 , 9, 121	20
1024	RNA-Sequencing of Primary Retinoblastoma Tumors Provides New Insights and Challenges Into Tumor Development. 2018 , 9, 170	3
1023	Network Analyses in Plant Pathogens. 2018 , 9, 35	10
1022	Perspectives on Systems Modeling of Human Peripheral Blood Mononuclear Cells. 2017 , 4, 96	28
1021	In a quest for engineering acidophiles for biomining applications: challenges and opportunities. 2018 , 9,	47
1020	Machine Learning Methods for Analysis of Metabolic Data and Metabolic Pathway Modeling. 2018 , 8,	82
1019	Measuring Cellular Biomass Composition for Computational Biology Applications. 2018 , 6, 38	24
1018	Constraint-based metabolic targets for the improved production of heterologous compounds across molecular classification. 2018 , 64, 4208-4217	1
1017	Interkingdom microbial consortia mechanisms to guide biotechnological applications. 2018 , 11, 833-847	30
1016	Consistency Analysis for Massively Inconsistent Datasets in Bound-to-Bound Data Collaboration. 2018 , 6, 429-456	6
1015	Model-based optimization of biopharmaceutical manufacturing in <i>Pichia pastoris</i> based on dynamic flux balance analysis. 2018 , 118, 1-13	15
1014	Discovery and Evaluation of Biosynthetic Pathways for the Production of Five Methyl Ethyl Ketone Precursors. 2018 , 7, 1858-1873	19

1013	Data Mining for Systems Biology. 2018,	
1012	The evolutionary dynamics of metabolic protocells. 2018, 14, e1006265	3
1011	Evaluation of reaction gap-filling accuracy by randomization. 2018, 19, 53	9
1010	H drives metabolic rearrangements in gas-fermenting. 2018, 11, 55	62
1009	From Network Analysis to Functional Metabolic Modeling of the Human Gut Microbiota. 2018, 3,	60
1008	Plant Metabolomics. 2018,	6
1007	Genome-scale model-driven strain design for dicarboxylic acid production in <i>Yarrowia lipolytica</i> . 2018, 12, 12	36
1006	Alignment of microbial fitness with engineered product formation: obligatory coupling between acetate production and photoautotrophic growth. 2018, 11, 38	16
1005	A systems biology approach to antimalarial drug discovery. 2018, 13, 617-626	6
1004	Synthetic Biology to Improve the Production of Lipases and Esterases (Review). 2018, 1835, 229-242	2
1003	A linked organ-on-chip model of the human neurovascular unit reveals the metabolic coupling of endothelial and neuronal cells. <i>Nature Biotechnology</i> , 2018, 36, 865-874	44.5 207
1002	Inferring oncoenzymes in a genome-scale metabolic network for hepatocytes using bilevel optimization framework. 2018, 91, 97-104	6
1001	Flux-dependent graphs for metabolic networks. 2018, 4, 32	10
1000	Integrated analysis of the yeast NADPH-regulator <i>Stb5</i> reveals distinct differences in NADPH requirements and regulation in different states of yeast metabolism. 2018, 18,	7
999	Lipases and Phospholipases. 2018,	6
998	A Review of Dynamic Modeling Approaches and Their Application in Computational Strain Optimization for Metabolic Engineering. 2018, 9, 1690	37
997	Urea Cycle Dysregulation Generates Clinically Relevant Genomic and Biochemical Signatures. 2018, 174, 1559-1570.e22	102
996	DMPy: a Python package for automated mathematical model construction of large-scale metabolic systems. 2018, 12, 72	10

995	Reconstruction and analysis of a genome-scale metabolic model of <i>Methylovorus</i> sp. MP688, a high-level pyrroloquinolone quinone producer. 2018 , 172, 37-42	4
994	A Bird's-Eye View of Enzyme Evolution: Chemical, Physicochemical, and Physiological Considerations. 2018 , 118, 8786-8797	50
993	Computational Modeling of Mitochondrial Function from a Systems Biology Perspective. 2018 , 1782, 249-265	6
992	In silico reconstruction and experimental validation of <i>Saccharopolyspora erythraea</i> genome-scale metabolic model iZZ1342 that accounts for 1685 ORFs. 2018 , 5,	5
991	Using genome-scale metabolic models to compare serovars of the foodborne pathogen <i>Listeria monocytogenes</i> . 2018 , 13, e0198584	5
990	An Improved Multi-parametric Programming Algorithm for Flux Balance Analysis of Metabolic Networks. 2018 , 178, 502-537	10
989	Dissecting metabolic flux in C4 plants: experimental and theoretical approaches. 2018 , 17, 1253-1274	6
988	Genome-scale metabolic reconstruction and analysis for <i>Clostridium kluyveri</i> . 2018 , 61, 605-613	8
987	Systems-level computational modeling demonstrates fuel selection switching in high capacity running and low capacity running rats. 2018 , 14, e1005982	3
986	Genomic organization underlying deletional robustness in bacterial metabolic systems. 2018 , 115, 7075-7080	3
985	Metabolic Models. 2019 , 438-444	
984	Cell Modeling and Simulation. 2019 , 864-873	
983	Multi-objective optimization of genome-scale metabolic models: the case of ethanol production. 2019 , 276, 211-227	7
982	A yield-cost tradeoff governs s decision between fermentation and respiration in carbon-limited growth. 2019 , 5, 16	19
981	Systems biology approach in the formulation of chemically defined media for recombinant protein overproduction. 2019 , 103, 8315-8326	9
980	Stoichiometric gene-to-reaction associations enhance model-driven analysis performance: Metabolic response to chronic exposure to Aldrin in prostate cancer. 2019 , 20, 652	6
979	Microbial Growth Dynamics. 2019 , 231-273	
978	A Delicate Balance between Bacterial Iron and Reactive Oxygen Species Supports Optimal <i>C. elegans</i> Development. 2019 , 26, 400-411.e3	15

977	Predicting gastrointestinal drug effects using contextualized metabolic models. 2019 , 15, e1007100	11
976	Modeling metabolic networks of individual bacterial agents in heterogeneous and dynamic soil habitats (IndiMeSH). 2019 , 15, e1007127	21
975	Comparison of pathway analysis and constraint-based methods for cell factory design. 2019 , 20, 350	1
974	Genome-scale metabolic model of the rat liver predicts effects of diet restriction. 2019 , 9, 9807	3
973	Bayesian metabolic flux analysis reveals intracellular flux couplings. 2019 , 35, i548-i557	10
972	Metabolic Model of the -Tomato Interaction Reveals Metabolic Switches during Host Colonization. 2019 , 10,	14
971	Studying metabolic flux adaptations in cancer through integrated experimental-computational approaches. 2019 , 17, 51	8
970	iDS372, a Phenotypically Reconciled Model for the Metabolism of Strain R6. 2019 , 10, 1283	6
969	Machine and deep learning meet genome-scale metabolic modeling. 2019 , 15, e1007084	106
968	Integration of probabilistic regulatory networks into constraint-based models of metabolism with applications to Alzheimer's disease. 2019 , 20, 386	6
967	A mass and charge balanced metabolic model of <i>Setaria viridis</i> revealed mechanisms of proton balancing in C4 plants. 2019 , 20, 357	11
966	Physiological and transcriptional comparison of acetate catabolism between <i>Acinetobacter schindleri</i> ACE and <i>Escherichia coli</i> JM101. 2019 , 366,	4
965	Modelling approaches for studying the microbiome. 2019 , 4, 1253-1267	56
964	FindTargetsWEB: A User-Friendly Tool for Identification of Potential Therapeutic Targets in Metabolic Networks of Bacteria. 2019 , 10, 633	4
963	Syntrophy emerges spontaneously in complex metabolic systems. 2019 , 15, e1007169	13
962	An unconventional uptake rate objective function approach enhances applicability of genome-scale models for mammalian cells. 2019 , 5, 25	16
961	In silico identification of metabolic engineering strategies for improved lipid production in by genome-scale metabolic modeling. 2019 , 12, 187	21
960	Genomewide Assessment of <i>Mycobacterium tuberculosis</i> Conditionally Essential Metabolic Pathways. 2019 , 4,	19

959	Biological Pathway Specificity in the Cell-Does Molecular Diversity Matter?. 2019 , 41, e1800244	5
958	Biological molecular layer classification of muscle-invasive bladder cancer opens new treatment opportunities. 2019 , 19, 636	9
957	Predicting the Longitudinally and Radially Varying Gut Microbiota Composition Using Multi-Scale Microbial Metabolic Modeling. 2019 , 7, 394	12
956	Genome-driven cell engineering review: and metabolic and genome engineering. 2019 , 63, 267-284	7
955	Metabolite Profiling of Mammalian Cells. 2019 , 251-277	
954	Enhancing Product and Bioprocess Attributes Using Genome-Scale Models of CHO Metabolism. 2019 , 73-95	1
953	Adaption of Generic Metabolic Models to Specific Cell Lines for Improved Modeling of Biopharmaceutical Production and Prediction of Processes. 2019 , 127-162	
952	Big data in yeast systems biology. 2019 , 19,	7
951	Contextualized genome-scale model unveils high-order metabolic effects of the specific growth rate and oxygenation level in recombinant. 2019 , 9, e00103	8
950	Detailed profiling of carbon fixation of synthetic autotrophy with reductive tricarboxylic acid cycle and Calvin-Benson-Bassham cycle in using hydrogen as an energy source. 2019 , 4, 165-172	1
949	p13CMFA: Parsimonious 13C metabolic flux analysis. 2019 , 15, e1007310	3
948	Yeast Systems Biology. 2019 ,	
947	Systems Metabolic Engineering Approach for Recombinant Protein Production in Microbial Cell Factories. 2019 , 211-240	
946	Identification of Cancer-associated metabolic vulnerabilities by modeling multi-objective optimality in metabolism. 2019 , 17, 124	9
945	Horizons in Bioprocess Engineering. 2019 ,	6
944	. 2019 ,	1
943	Anti-virulence Therapies Through Potentiating ROS in Bacteria. 2019 , 239-253	0
942	Active nitrogen fixation by Crocosphaera expands their niche despite the presence of ammonium - A case study. 2019 , 9, 15064	3

941	Environmental boundary conditions for the origin of life converge to an organo-sulfur metabolism. 2019 , 3, 1715-1724	19
940	Comprehensive Flux Modeling of Proteome and qRT-PCR Data Indicate Biphasic Metabolic Differences Between Elementary Bodies and Reticulate Bodies During Infection. 2019 , 10, 2350	9
939	Reconstruction and analysis of a <i>Kluyveromyces marxianus</i> genome-scale metabolic model. 2019 , 20, 551	21
938	Bayesian inference of metabolic kinetics from genome-scale multiomics data. 2019 , 15, e1007424	19
937	Engineering microbial chemical factories using metabolic models. 2019 , 1,	3
936	Computer-Aided Strategies for Determining the Amino Acid Composition of Medium for Chinese Hamster Ovary Cell-Based Biomanufacturing Platforms. 2019 , 20,	9
935	Genome-Scale Identification of Essential Metabolic Processes for Targeting the Plasmodium Liver Stage. 2019 , 179, 1112-1128.e26	41
934	110th Anniversary: High-Order Interactions Can Eclipse Pairwise Interactions in Shaping the Structure of Microbial Communities. 2019 , 58, 23508-23518	3
933	Modelling microbial communities using biochemical resource allocation analysis. 2019 , 16, 20190474	6
932	Influence of the Crc global regulator on substrate uptake rates and the distribution of metabolic fluxes in <i>Pseudomonas putida</i> KT2440 growing in a complete medium. 2019 , 21, 4446-4459	7
931	Microbiome-Gut-Brain Axis as a Biomolecular Communication Network for the Internet of Bio-NanoThings. 2019 , 7, 136161-136175	7
930	Computational metabolism modeling predicts risk of distant relapse-free survival in breast cancer patients. 2019 , 15, 3483-3490	2
929	Systems Biology and Pangenome of O-Antigens. 2019 , 10,	11
928	The Microbiota-Gut-Brain Axis. 2019 , 99, 1877-2013	979
927	High-resolution C metabolic flux analysis. 2019 , 14, 2856-2877	73
926	In SILICO Simulations Predict a Causative Link Between Increased Glycolysis and Metabolic Reprogramming in Autosomal Dominant Polycystic Kidney Disease. 2019 ,	
925	Flux Balance Analysis Incorporating a Coarse-grained Proteome Constraint for Predicting Overflow Metabolism in <i>Escherichia Coli</i> . 2019 , 46, 865-870	1
924	Fast uncertainty quantification for dynamic flux balance analysis using non-smooth polynomial chaos expansions. 2019 , 15, e1007308	8

923	Systematic design and in vitro validation of novel one-carbon assimilation pathways. 2019 , 56, 142-153	28
922	Flux sampling is a powerful tool to study metabolism under changing environmental conditions. 2019 , 5, 32	19
921	Flux balance analysis with or without molecular crowding fails to predict two thirds of experimentally observed epistasis in yeast. 2019 , 9, 11837	5
920	Modeling the Interplay between Photosynthesis, CO Fixation, and the Quinone Pool in a Purple Non-Sulfur Bacterium. 2019 , 9, 12638	14
919	MOOMIN - Mathematical explORation of 'Omics data on a Metabolic Network. 2020 , 36, 514-523	4
918	RetSynth: determining all optimal and sub-optimal synthetic pathways that facilitate synthesis of target compounds in chassis organisms. 2019 , 20, 461	3
917	A comprehensive genome-scale model for IFO0880 accounting for functional genomics and phenotypic data. 2019 , 9, e00101	26
916	In silico optimization of lipid production in Rhodosporidium toruloides by gene knockout strategies. 2019 , 52, 94-99	2
915	Determining a unique solution to underdetermined metabolic networks via a systematic path through the Most Accurate Fluxes. 2019 , 52, 352-357	3
914	Conceptual Model of Biofilm Antibiotic Tolerance That Integrates Phenomena of Diffusion, Metabolism, Gene Expression, and Physiology. 2019 , 201,	23
913	CF-Targeter: A Rational Biological Cell Factory Targeting Platform for Biosynthetic Target Chemicals. 2019 , 8, 2280-2286	3
912	Utilizing genome-scale models to optimize nutrient supply for sustained algal growth and lipid productivity. 2019 , 5, 33	10
911	Exploiting Day- and Night-Time Metabolism of sp. PCC 6803 for Fitness-Coupled Fumarate Production around the Clock. 2019 , 8, 2263-2269	11
910	Process intensification by model-based design of tailor-made reactors. 2019 , 26, 46-57	9
909	Model-Assisted Fine-Tuning of Central Carbon Metabolism in Yeast through dCas9-Based Regulation. 2019 , 8, 2457-2463	23
908	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. 2019 , 157, 1279-1292.e11	101
907	Common principles and best practices for engineering microbiomes. 2019 , 17, 725-741	144
906	Deciphering Metabolic Heterogeneity by Single-Cell Analysis. 2019 , 91, 13314-13323	48

905	A Tale of Three Species: Adaptation of <i>Sodalis glossinidius</i> to Tsetse Biology, Metabolism, and Host Diet. 2019 , 10,	14
904	A computational knowledge-base elucidates the response of <i>Staphylococcus aureus</i> to different media types. 2019 , 15, e1006644	18
903	Multi-Omics and Genome-Scale Modeling Reveal a Metabolic Shift During Aging. 2019 , 6, 2	24
902	Metabolic Modeling of Human Gut Microbiota on a Genome Scale: An Overview. 2019 , 9,	50
901	Constraint-Based Modeling of Metabolic Interactions in and Between Astrocytes and Neurons. 2019 , 393-420	
900	A diurnal flux balance model of <i>Synechocystis</i> sp. PCC 6803 metabolism. 2019 , 15, e1006692	17
899	Metabolomics for understanding stomatal movements. 2019 , 31, 91-102	9
898	SLIMEr: probing flexibility of lipid metabolism in yeast with an improved constraint-based modeling framework. 2019 , 13, 4	19
897	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. 2019 , 13, 2	30
896	A genome-scale metabolic network of the aroma bacterium <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> . 2019 , 103, 3153-3165	12
895	Extended Utilization of Constraint-Based Metabolic Model in a Long-Growing Crop. 2019 , 7, 259	
894	Towards the Integration of Metabolic Network Modelling and Machine Learning for the Routine Analysis of High-Throughput Patient Data. 2019 , 401-424	
893	Identification of critical connectors in the directed reaction-centric graphs of microbial metabolic networks. 2019 , 20, 328	4
892	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. 2019 , 9,	31
891	Predicting Metabolism from Gene Expression in an Improved Whole-Genome Metabolic Network Model of. 2019 , 16, 348-362	10
890	iMet: A graphical user interface software tool to merge metabolic networks. 2019 , 5, e01766	
889	Introduction. 2019 , xi-xviii	
888	Part I. 2019 , 1-2	

887 A Flyover Introduction to Integer Linear Programming. **2019**, 3-14

886 Biological Networks, Graphs, and High-Density Subgraphs. **2019**, 15-48

885 Maximum Character Compatibility in Phylogenetics. **2019**, 49-64

884 Near Cliques, Dense Subgraphs, and Motifs in Biological Networks. **2019**, 65-88

883 Convergent and Maximum Parsimony Problems in Phylogenetics. **2019**, 89-104

882 The RNA-Folding Problem. **2019**, 105-121

881 Protein Problems Solved By Integer Programming. **2019**, 122-141

880 Tanglegrams and Coevolution. **2019**, 142-155

879 Traveling Salesman Problems in Genomics. **2019**, 156-185

878 Integer Programming in Molecular Sequence Analysis. **2019**, 186-204

877 Metabolic Networks and Metabolic Engineering. **2019**, 205-220

876 ILP Idioms. **2019**, 221-232

875 Part II. **2019**, 233-234

874 Communities, Cuts, and High-Density Subgraphs. **2019**, 235-259

873 Character Compatibility with Corrupted Data and Generalized Phylogenetic Models. **2019**, 260-272

872 More Tanglegrams, More Trees, More ILPs. **2019**, 273-286

871 Return to Steiner Trees and Maximum Parsimony. **2019**, 287-294

870 Exploiting and Leveraging Protein Networks. **2019**, 295-312

869	More String and Sequence Problems Solved by ILP. 2019 , 313-330	
868	Maximum Likelihood Pedigree Reconstruction. 2019 , 331-342	
867	Two DNA Haplotyping Problems. 2019 , 343-356	
866	More Extended Exercises. 2019 , 357-381	
865	What's Next?. 2019 , 382-384	
864	Epilogue: Some Very Opinionated Comments for Advanced Readers. 2019 , 385-392	
863	Bibliography. 2019 , 393-404	
862	Index. 2019 , 405-412	
861	Meta-Omics- and Metabolic Modeling-Assisted Deciphering of Human Microbiota Metabolism. 2019 , 14, e1800445	6
860	Enhanced flux prediction by integrating relative expression and relative metabolite abundance into thermodynamically consistent metabolic models. 2019 , 15, e1007036	34
859	Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System. 2019 , 115-126	1
858	Graph Transformations, Semigroups, and Isotopic Labeling. 2019 , 196-207	1
857	Rational metabolic engineering for enhanced alpha-tocopherol production in <i>Helianthus annuus</i> cell culture. 2019 , 151, 107256	9
856	Human Systems Biology and Metabolic Modelling: A Review-From Disease Metabolism to Precision Medicine. 2019 , 2019, 8304260	38
855	Metabolic reprogramming dynamics in tumor spheroids: Insights from a multicellular, multiscale model. 2019 , 15, e1007053	12
854	Current status and applications of genome-scale metabolic models. 2019 , 20, 121	208
853	The Power of Metabolism for Predicting Microbial Community Dynamics. 2019 , 4,	1
852	Improving the accuracy of flux balance analysis through the implementation of carbon availability constraints for intracellular reactions. 2019 , 116, 2339-2352	16

851	Dynamic Network Modeling of Stem Cell Metabolism. 2019 , 1975, 305-320	11
850	Modeling Host-Pathogen Interaction to Elucidate the Metabolic Drug Response of Intracellular. 2019 , 9, 144	11
849	Circumventing kinetics in biogeochemical modeling. 2019 , 116, 11329-11338	6
848	Flux prediction using artificial neural network (ANN) for the upper part of glycolysis. 2019 , 14, e0216178	9
847	Control Theory Concepts for Modeling Uncertainty in Enzyme Kinetics of Biochemical Networks. 2019 , 58, 13544-13554	9
846	Advanced Gene Technology and Synthetic Biology Approaches to Custom Design Microalgae for Biodiesel Production. 2019 , 147-175	2
845	Systematic assessment of secondary bile acid metabolism in gut microbes reveals distinct metabolic capabilities in inflammatory bowel disease. 2019 , 7, 75	98
844	A genome-scale metabolic network reconstruction of extremely halophilic bacterium <i>Salinibacter ruber</i> . 2019 , 14, e0216336	2
843	System-level analysis of metabolic trade-offs during anaerobic photoheterotrophic growth in <i>Rhodospseudomonas palustris</i> . 2019 , 20, 233	10
842	Predicting the decision making chemicals used for bacterial growth. 2019 , 9, 7251	4
841	Systems Biology and Multi-Omics Integration: Viewpoints from the Metabolomics Research Community. 2019 , 9,	236
840	Two Experimental Protocols for Accurate Measurement of Gas Component Uptake and Production Rates in Bioconversion Processes. 2019 , 9, 5899	6
839	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. 2019 , 15, e1006971	39
838	Kinetic ensemble model of gas fermenting <i>Clostridium autoethanogenum</i> for improved ethanol production. 2019 , 148, 46-56	18
837	Investigating the deregulation of metabolic tasks via Minimum Network Enrichment Analysis (MiNEA) as applied to nonalcoholic fatty liver disease using mouse and human omics data. 2019 , 15, e1006760	5
836	Metabolic acclimation-a key to enhancing photosynthesis in changing environments?. 2019 , 70, 3043-3056	16
835	The Fate of Glutamine in Human Metabolism. The Interplay with Glucose in Proliferating Cells. 2019 , 9,	14
834	Integrated In Vitro and In Silico Modeling Delineates the Molecular Effects of a Synbiotic Regimen on Colorectal-Cancer-Derived Cells. 2019 , 27, 1621-1632.e9	31

833	Leveraging the effects of chloroquine on resistant malaria parasites for combination therapies. 2019 , 20, 186	3
832	Impact of iron reduction on the metabolism of <i>Clostridium acetobutylicum</i> . 2019 , 21, 3548-3563	17
831	Metabolic Pathway Analysis of Nitrogen and Phosphorus Uptake by the Consortium between and. 2019 , 20,	8
830	Saccharibacteria (TM7) in the Human Oral Microbiome. 2019 , 98, 500-509	58
829	Genome-scale network model of metabolism and histone acetylation reveals metabolic dependencies of histone deacetylase inhibitors. 2019 , 20, 49	17
828	Data-Driven Systems Level Approaches for Drug Repurposing: Combating Drug Resistance in Priority Pathogens. 2019 , 229-253	2
827	Integration of single-cell RNA-seq data into population models to characterize cancer metabolism. 2019 , 15, e1006733	36
826	Metagenome level metabolic network reconstruction analysis reveals the microbiome in the Bogotá River is functionally close to the microbiome in produced water. 2019 , 399, 1-12	5
825	Feedback-induced self-oscillations in large interacting systems subjected to phase transitions. 2019 , 52, 045002	2
824	Metabolomics in systems medicine: an overview of methods and applications. 2019 , 15, 91-99	7
823	Enhanced production of poly-3-hydroxybutyrate (PHB) by expression of response regulator DR1558 in recombinant <i>Escherichia coli</i> . 2019 , 131, 29-35	17
822	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. 2019 , 15, e1006848	31
821	Bioinformatics applied to biotechnology: A review towards bioenergy research. 2019 , 123, 195-224	14
820	Approaches to Computational Strain Design in the Multiomics Era. 2019 , 10, 597	12
819	Mechanistic identification of biofluid metabolite changes as markers of acetaminophen-induced liver toxicity in rats. 2019 , 372, 19-32	17
818	Metabolic Modeling of SCC3193 Provides Insights into Metabolic Pathways of Plant Pathogenic Bacteria. 2019 , 7,	7
817	Systems Metabolic Engineering Meets Machine Learning: A New Era for Data-Driven Metabolic Engineering. 2019 , 14, e1800416	27
816	Pervasive System Biology for Active Compound Valorization in <i>Jatropha</i> . 2019 , 199-251	

815	Microbial community design: methods, applications, and opportunities. 2019 , 58, 117-128	22
814	Metabolic Games. 2019 , 5,	6
813	Systems biology based metabolic engineering for non-natural chemicals. 2019 , 37, 107379	24
812	<i>Pseudomonas putida</i> KT2440 metabolism undergoes sequential modifications during exponential growth in a complete medium as compounds are gradually consumed. 2019 , 21, 2375-2390	22
811	Risk-Based Bioengineering Strategies for Reliable Bacterial Vaccine Production. 2019 , 37, 805-816	2
810	Computing Weakly Reversible Deficiency Zero Network Translations Using Elementary Flux Modes. 2019 , 81, 1613-1644	4
809	New Applications of Synthetic Biology Tools for Cyanobacterial Metabolic Engineering. 2019 , 7, 33	86
808	A Protocol for the Construction and Curation of Genome-Scale Integrated Metabolic and Regulatory Network Models. 2019 , 1927, 203-214	3
807	Elucidating cancer metabolic plasticity by coupling gene regulation with metabolic pathways. 2019 , 116, 3909-3918	138
806	Use of genome-scale models to get new insights into the marine actinomycete genus <i>Salinispora</i> . 2019 , 13, 11	2
805	Computational modelling of energy balance in individuals with Metabolic Syndrome. 2019 , 13, 24	5
804	Identification of bioactive metabolites using activity metabolomics. 2019 , 20, 353-367	258
803	Understanding carbon utilization routes between high and low starch-producing cultivars of cassava through Flux Balance Analysis. 2019 , 9, 2964	7
802	Microbial Metabolic Engineering. 2019 ,	1
801	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. 2019 , 14, 639-702	385
800	Determination of Microbial Maintenance in Acetogenesis and Methanogenesis by Experimental and Modeling Techniques. 2019 , 10, 166	6
799	Metabolic Responses to Polymyxin Treatment in ATCC 19606: Integrating Transcriptomics and Metabolomics with Genome-Scale Metabolic Modeling. 2019 , 4,	16
798	Metabolic pathway analysis for in silico design of efficient autotrophic production of advanced biofuels. 2019 , 6,	4

797	Quantifying Methane and Methanol Metabolism of "" 5GB1C under Substrate Limitation. 2019 , 4,	12
796	In vitro fucoxanthin production by the <i>Phaeodactylum tricornutum</i> diatom. 2019 , 63, 211-242	6
795	Rewiring of Metabolic Network in During Adaptation to Different Stresses. 2019 , 10, 2417	14
794	FBA-based simulator of <i>Saccharomyces cerevisiae</i> fed-batch cultures involving an internal unbalanced metabolite. 2019 , 52, 169-174	1
793	Towards the construction of GSMN-based community model for an oral biofilm. 2019 , 52, 193-199	1
792	DISCOPOLIS: an algorithm for uniform sampling of metabolic flux distributions via iterative sequences of linear programs. 2019 , 52, 269-274	2
791	Provitamin D modulation through prebiotics supplementation: simulation based assessment. 2019 , 9, 19267	5
790	Metabolic Modeling Elucidates the Transactions in the Rumen Microbiome and the Shifts Upon Virome Interactions. 2019 , 10, 2412	13
789	AMON: annotation of metabolite origins via networks to integrate microbiome and metabolome data. 2019 , 20, 614	16
788	Time Integrated Flux Analysis: Exploiting the Concentration Measurements Directly for Cost-Effective Metabolic Network Flux Analysis. 2019 , 7,	1
787	Integrative Computational Framework for Understanding Metabolic Modulation in <i>Leishmania</i> . 2019 , 7, 336	3
786	Developing a Microbial Consortium for Enhanced Metabolite Production from Simulated Food Waste. 2019 , 5, 98	9
785	Conversion of <i>Escherichia coli</i> to Generate All Biomass Carbon from CO. 2019 , 179, 1255-1263.e12	186
784	FlySilico: Flux balance modeling of <i>Drosophila</i> larval growth and resource allocation. 2019 , 9, 17156	5
783	In silico-guided engineering of <i>Pseudomonas putida</i> towards growth under micro-oxic conditions. 2019 , 18, 179	13
782	Microbial Controls on the Biogeochemical Dynamics in the Subsurface. 2019 , 85, 265-302	12
781	. 2019 ,	1
780	Multiscale Multiobjective Systems Analysis (MiMoSA): an advanced metabolic modeling framework for complex systems. 2019 , 9, 16948	6

779	From Escherichia coli mutant 13C labeling data to a core kinetic model: A kinetic model parameterization pipeline. 2019 , 15, e1007319	21
778	Deciphering the metabolic capabilities of Bifidobacteria using genome-scale metabolic models. 2019 , 9, 18222	26
777	9. Microbial Controls on the Biogeochemical Dynamics in the Subsurface. 2019 , 265-302	
776	Dynamical reduction of linearized metabolic networks through quasi steady state approximation. 2019 , 65, 18-31	3
775	Extension of the yeast metabolic model to include iron metabolism and its use to estimate global levels of iron-recruiting enzyme abundance from cofactor requirements. 2019 , 116, 610-621	12
774	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. 2019 , 52, 324-340	19
773	Systematic selection of chemical fingerprint features improves the Gibbs energy prediction of biochemical reactions. 2019 , 35, 2634-2643	8
772	Exhaustive Analysis of a Genotype Space Comprising 10(15)Central Carbon Metabolisms Reveals an Organization Conducive to Metabolic Innovation. 2015 , 11, e1004329	11
771	Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5'-Phosphate Production in E. coli. 2016 , 12, e1004705	17
770	Rapid Prediction of Bacterial Heterotrophic Fluxomics Using Machine Learning and Constraint Programming. 2016 , 12, e1004838	36
769	Constrained Allocation Flux Balance Analysis. 2016 , 12, e1004913	90
768	Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks. 2017 , 13, e1005276	42
767	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. 2017 , 13, e1005409	39
766	Population FBA predicts metabolic phenotypes in yeast. 2017 , 13, e1005728	11
765	Characterizing steady states of genome-scale metabolic networks in continuous cell cultures. 2017 , 13, e1005835	13
764	Metabolic plasticity in synthetic lethal mutants: Viability at higher cost. 2018 , 14, e1005949	1
763	Elementary Growth Modes provide a molecular description of cellular self-fabrication. 2020 , 16, e1007559	13
762	Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. 2020 , 16, e1007727	3

761	Transforming the study of organisms: Phenomic data models and knowledge bases. 2020 , 16, e1008376	2
760	Acetate and glycerol are not uniquely suited for the evolution of cross-feeding in <i>E. coli</i> . 2020 , 16, e1008433	3
759	Genome-scale metabolic models highlight stage-specific differences in essential metabolic pathways in <i>Trypanosoma cruzi</i> . 2020 , 14, e0008728	5
758	A systems biology approach to drug targets in <i>Pseudomonas aeruginosa</i> biofilm. 2012 , 7, e34337	28
757	Reaction networks as systems for resource allocation: a variational principle for their non-equilibrium steady states. 2012 , 7, e39849	5
756	Design constraints on a synthetic metabolism. 2012 , 7, e39903	7
755	Contextualization procedure and modeling of monocyte specific TLR signaling. 2012 , 7, e49978	4
754	MultiMetEval: comparative and multi-objective analysis of genome-scale metabolic models. 2012 , 7, e51511	28
753	Fumaric acid production in <i>Saccharomyces cerevisiae</i> by in silico aided metabolic engineering. 2012 , 7, e52086	47
752	Simulation of <i>E. coli</i> gene regulation including overlapping cell cycles, growth, division, time delays and noise. 2013 , 8, e62380	5
751	ReacKnock: identifying reaction deletion strategies for microbial strain optimization based on genome-scale metabolic network. 2013 , 8, e72150	27
750	Inactivation of metabolic genes causes short- and long-range dys-regulation in <i>Escherichia coli</i> metabolic network. 2013 , 8, e78360	10
749	Genome-scale NAD(H/(+)) availability patterns as a differentiating feature between <i>Saccharomyces cerevisiae</i> and <i>Scheffersomyces stipitis</i> in relation to fermentative metabolism. 2014 , 9, e87494	5
748	DRUM: a new framework for metabolic modeling under non-balanced growth. Application to the carbon metabolism of unicellular microalgae. 2014 , 9, e104499	45
747	Computational analysis of reciprocal association of metabolism and epigenetics in the budding yeast: a genome-scale metabolic model (GSMM) approach. 2014 , 9, e111686	9
746	Prediction of metabolic flux distribution from gene expression data based on the flux minimization principle. 2014 , 9, e112524	34
745	Context-Specific Metabolic Model Extraction Based on Regularized Least Squares Optimization. 2015 , 10, e0131875	30
744	Flux Balance Analysis with Objective Function Defined by Proteomics Data-Metabolism of <i>Mycobacterium tuberculosis</i> Exposed to Mefloquine. 2015 , 10, e0134014	11

743	Integrating Kinetic Model of <i>E. coli</i> with Genome Scale Metabolic Fluxes Overcomes Its Open System Problem and Reveals Bistability in Central Metabolism. 2015 , 10, e0139507	15
742	Estimating Metabolic Fluxes Using a Maximum Network Flexibility Paradigm. 2015 , 10, e0139665	2
741	Construction of a Genome-Scale Metabolic Model of <i>Arthrospira platensis</i> NIES-39 and Metabolic Design for Cyanobacterial Bioproduction. 2015 , 10, e0144430	20
740	Predicting Essential Metabolic Genome Content of Niche-Specific Enterobacterial Human Pathogens during Simulation of Host Environments. 2016 , 11, e0149423	12
739	Assessment of FBA Based Gene Essentiality Analysis in Cancer with a Fast Context-Specific Network Reconstruction Method. 2016 , 11, e0154583	9
738	Pathway-Consensus Approach to Metabolic Network Reconstruction for <i>Pseudomonas putida</i> KT2440 by Systematic Comparison of Published Models. 2017 , 12, e0169437	21
737	Ethanol production improvement driven by genome-scale metabolic modeling and sensitivity analysis in <i>Scheffersomyces stipitis</i> . 2017 , 12, e0180074	8
736	Parametric studies of metabolic cooperativity in <i>Escherichia coli</i> colonies: Strain and geometric confinement effects. 2017 , 12, e0182570	6
735	Prediction of reaction knockouts to maximize succinate production by <i>Actinobacillus succinogenes</i> . 2018 , 13, e0189144	8
734	Reconstruction of a regulated two-cell metabolic model to study biohydrogen production in a diazotrophic cyanobacterium <i>Anabaena variabilis</i> ATCC 29413. 2020 , 15, e0227977	8
733	Genome-scale reconstructions to assess metabolic phylogeny and organism clustering. 2020 , 15, e0240953	1
732	Enhanced in planta Fitness through Adaptive Mutations in EfpR, a Dual Regulator of Virulence and Metabolic Functions in the Plant Pathogen <i>Ralstonia solanacearum</i> . 2016 , 12, e1006044	26
731	Metabolism of non-growing bacteria. 2020 , 401, 1479-1485	11
730	Modeling tissue-relevant <i>Caenorhabditis elegans</i> metabolism at network, pathway, reaction, and metabolite levels. 2020 , 16, e9649	8
729	[Searching for essential genes in cancer genomes]. 2018 , 64, 303-314	1
728	Reconstruction and analysis of genome-scale metabolic model of weak Crabtree positive yeast <i>Lachancea kluyveri</i> .	1
727	Integrated Analyses of Microbiome and Longitudinal Metabolome Data Reveal Microbial-Host Interactions on Sulfur Metabolism in Parkinson's Disease.	1
726	Metabolic Modeling of Microbial Community Interactions for Health, Environmental and Biotechnological Applications. 2018 , 19, 712-722	13

725	Metabolic Reprogramming of Fibroblasts as Therapeutic Target in Rheumatoid Arthritis and Cancer: Deciphering Key Mechanisms Using Computational Systems Biology Approaches. 2020 , 13,	3
724	Identifying Personalized Metabolic Signatures in Breast Cancer. 2020 , 11,	3
723	Systems biology approaches for studying the pathogenesis of non-alcoholic fatty liver disease. 2014 , 20, 15070-8	17
722	ToMI-FBA: A genome-scale metabolic flux based algorithm to select optimum hosts and media formulations for expressing pathways of interest. 2015 , 2, 335-374	3
721	The three-legged stool of understanding metabolism: integrating metabolomics with biochemical genetics and computational modeling. 2018 , 4, 289-303	9
720	Calibration and analysis of genome-based models for microbial ecology. 2015 , 4, e08208	42
719	Fine-tuning citrate synthase flux potentiates and refines metabolic innovation in the Lenski evolution experiment. 2015 , 4,	48
718	Evolution of substrate specificity in a retained enzyme driven by gene loss. 2017 , 6,	19
717	Essential metabolism for a minimal cell. 2019 , 8,	54
716	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. 2018 , 7,	34
715	Effects of microcompartmentation on flux distribution and metabolic pools in chloroplasts. 2018 , 7,	17
714	Metabolic network percolation quantifies biosynthetic capabilities across the human oral microbiome. 2019 , 8,	11
713	Evolution of C4 photosynthesis predicted by constraint-based modelling. 2019 , 8,	19
712	Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets. 2020 , 9,	6
711	Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species. 2020 , 9,	10
710	Combining graph and flux-based structures to decipher phenotypic essential metabolites within metabolic networks. 2017 , 5, e3860	4
709	In silico engineering of metabolism reveals new biomarkers for increased biosurfactant production. 2018 , 6, e6046	11
708	Metabolic traits specific for lipid-overproducing strain of WJ11 identified by genome-scale modeling approach. 2019 , 7, e7015	2

707	Investigation of microbial community interactions between Lake Washington methanotrophs using -----genome-scale metabolic modeling. 2020 , 8, e9464	2
706	A novel approach in analyzing agriculture and food systems: Review of modeling and its applications. 2016 , 43, 163-175	3
705	Insights on the Advancements of In Silico Metabolic Studies of Succinic Acid Producing Microorganisms: A Review with Emphasis on Actinobacillus succinogenes. 2021 , 7, 220	0
704	Intelligent host engineering for metabolic flux optimisation in biotechnology. 2021 , 478, 3685-3721	3
703	MPA_Pathway_Tool: User-Friendly, Automatic Assignment of Microbial Community Data on Metabolic Pathways. 2021 , 22,	0
702	Improving the performance of machine learning models for biotechnology: The quest for deus ex machina. 2021 , 53, 107858	0
701	Global connectivity in genome-scale metabolic networks revealed by comprehensive FBA-based pathway analysis. 2021 , 21, 292	0
700	Nonlinear Predictive Control of a Bioreactor by Surrogate Model Approximation of Flux Balance Analysis. 2021 , 60, 14464-14475	0
699	A multi-organ metabolic model of tomato predicts plant responses to nutritional and genetic perturbations.	
698	Genome-scale modeling specifies the metabolic capabilities of Rhizophagus irregularis.	
697	Conceptualizing Biogeochemical Reactions With an Ohm’s Law Analogy. 2021 , 13, e2021MS002469	0
696	A hybrid kinetic and constraint-based model of leaf metabolism allows predictions of metabolic fluxes in different environments. 2021 ,	0
695	Predicting Microbiome Metabolism and Interactions through Integrating Multidisciplinary Principles. 2021 , 6, e0076821	
694	Metabolic engineering design to enhance (R,R)-2,3-butanediol production from glycerol in Bacillus subtilis based on flux balance analysis. 2021 , 20, 196	2
693	Set Membership Estimation with Dynamic Flux Balance Models. 2021 , 9, 1762	1
692	Uncovering the Role of Metabolism in Oomycete-Host Interactions Using Genome-Scale Metabolic Models. 2021 , 12, 748178	
691	Modelling The Fitness Landscapes of a SCRaMbLEd Yeast Genome. 2021 ,	0
690	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. 2021 , 17, e10427	2

689	Photoprotection is regulated by light-independent CO ₂ availability.	0
688	Two classes of functional connectivity in dynamical processes in networks. 2021 , 18, 20210486	0
687	Predictive regulatory and metabolic network models for systems analysis of <i>Clostridioides difficile</i> . 2021 , 29, 1709-1723.e5	4
686	MetAMDB: Metabolic Atom Mapping Database.	
685	A metabolic modeling platform for the computation of microbial ecosystems in time and space (COMETS). 2021 , 16, 5030-5082	12
684	Non-destructive quantification of anaerobic gut fungi and methanogens in co-culture reveals increased fungal growth rate and changes in metabolic flux relative to mono-culture. 2021 , 20, 199	2
683	DCcov: Repositioning of drugs and drug combinations for SARS-CoV-2 infected lung through constraint-based modeling. 2021 , 24, 103331	3
682	Constraint-based modeling of yeast mitochondria reveals the dynamics of protein import and iron-sulfur cluster biogenesis. 2021 , 24, 103294	0
681	Network Biology Approaches to Achieve Precision Medicine in Inflammatory Bowel Disease. 2021 , 12, 760501	2
680	Bacterial metabolism and pathogenesis intimate intertwining: time for metabolic modelling to come into action. 2021 ,	4
679	Recent advances in model-assisted metabolic engineering. 2021 , 28, 100392	3
678	Modeling gut microbe interactions reveals metabolic interconnectivity. 2021 , 24, 103216	
677	Engineering <i>Bacteroides thetaiotaomicron</i> to produce non-native butyrate based on a genome-scale metabolic model-guided design. 2021 , 68, 174-186	0
676	Kinetic model of <i>Clostridium beijerinckii</i> 's Acetone-Butanol-Ethanol fermentation considering metabolically diverse cell types. 2021 , 342, 1-12	
675	Constraint-based Modeling (Flux Balance Analysis). 2004 ,	
674	Rewriting in Practice. 2011 , 6-8	
673	Flux Measurement Selection in Metabolic Networks. 2011 , 214-224	
672	From Structure to Dynamics in Biological Networks. 2011 , 73-92	

671 Encyclopedia of Systems Biology. **2013**, 2054-2057

670 A Roadmap Towards a Systems Biology Description of Bacterial Nitrogen Fixation. **2013**, 27-51

669 Assessment of *Zymomonas mobilis* biotechnological potential in ethanol production by flux variability analysis. **2013**, 3, 1-5

1

668 Computational Tools and Resources for Integrative Modeling in Systems Biology. **2013**, 399-428

667 Systems Biology and Metabolic Engineering in Bacteria. **2014**, 351-367

666 An ensemble approach to the study of the emergence of metabolic and proliferative disorders via Flux Balance Analysis. **2013**, 130, 92-97

665 Optimal design of isotope labeling experiments. **2014**, 1083, 133-47

664 Extensible and Executable Stochastic Models of Fatty Acid and Lipid Metabolism. **2014**, 244-247

663 Fast Flux Module Detection Using Matroid Theory. **2014**, 192-206

662 Systems Approaches to Study Infectious Diseases. **2015**, 151-172

661 Engineering Hemicellulose-Derived Xylose Utilization in *Saccharomyces cerevisiae* for Biotechnological Applications. **2016**, 41-56

660 Design, Principles, Network Architecture and Their Analysis Strategies as Applied to Biological Systems. **2016**, 21-31

659 Modeling Lipid Metabolism in Yeast. **2016**, 1-14

658 Effective Dynamic Models of Metabolic Networks.

657 Advances in the integration of transcriptional regulatory information into genome-scale metabolic models.

656 Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion.

655 Parameter estimation in tree graph metabolic networks. **2016**, 4, e2417

654 Systems Metabolic Engineering of *Saccharomyces cerevisiae* for Production of Biochemicals from Biomass. **2017**, 31-65

653 **Big Data and Dynamics** The Mathematical Toolkit Towards Personalized Medicine. **2017**, 338-369

652 Constraint-Based Modeling and Simulation of Cell Populations. **2017**, 126-137

1

651 Constraint-based modeling identifies new putative targets to fight colistin-resistant *A. baumannii* infections.

650 GROOLS: reactive graph reasoning for genome annotation through biological processes.

649 Glycosylation flux analysis reveals dynamic changes of intracellular glycosylation flux distribution in Chinese hamster ovary fed-batch cultures.

648 Quantifying the entropic cost of cellular growth control.

647 Novel *Plasmodium falciparum* metabolic network reconstruction identifies shifts associated with clinical antimalarial resistance.

1

646 MitoCore: A curated constraint-based model for simulating human central metabolism.

645 Integrated Human-Virus Metabolic Modelling Predicts Host-Based Antiviral Targets Against Chikungunya, Dengue and Zika Viruses.

644 Combining multiple functional annotation tools increases coverage of metabolic annotation.

643 Grid-based computational methods for the design of constraint-based parsimonious chemical reaction networks to simulate metabolite production: GridProd.

642 A genome-scale study of metabolic complementation in endosymbiotic consortia: the case of the cedar aphid.

641 Metabolic Model-Based Analysis of the Emergence of Bacterial Cross-Feeding through Extensive Gene Loss.

1

640 Identification of Cancer-Associated Metabolic Vulnerabilities by Modeling Multi-objective Optimality in Metabolism.

639 Robustness encoded across essential and accessory replicons in an ecologically versatile bacterium.

5

638 Discovery and Evaluation of Biosynthetic Pathways for the Production of Five Methyl Ethyl Ketone Precursors.

637 RetSynth: Solving all optimal retrosynthesis solutions using dynamically constrained integer linear programming.

636 Estimating global enzyme abundance levels from cofactor requirements: a model-based analysis of the iron metabolism in yeast.

- 635 MaREA: Metabolic feature extraction, enrichment and visualization of RNAseq data. 1
- 634 Integrated in Vitro and in Silico Modelling Delineates the Molecular Effects of a Symbiotic Regimen on Colorectal Cancer-Derived Cells.
- 633 Metabolic modeling of *Pectobacterium parmentieri* SCC3193 provides insights into metabolic pathways of plant pathogenic bacteria. 1
- 632 Flux-dependent graphs for metabolic networks.
- 631 Different alleles of the same gene vary in pleiotropy, often mediated through currency metabolite production.
- 630 Escher-FBA: A web application for interactive flux balance analysis. 1
- 629 Machine learning reveals missing edges and putative interaction mechanisms in microbial ecosystem networks.
- 628 Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a synthetic gut community.
- 627 Network analysis reveals differential metabolic functionality in antibiotic-resistant *Pseudomonas aeruginosa*. 1
- 626 Flux Balance Analysis Identifies Distinct NADPH Production Strategies Across NCI 60 Cancer Cell Lines.
- 625 DynamicME: Dynamic simulation and refinement of integrated models of metabolism and protein expression. 0
- 624 Novel Molecular Classification of Muscle-Invasive Bladder Cancer Opens New Treatment Opportunities.
- 623 Thermodynamic constraints on the regulation of metabolic fluxes.
- 622 Cofactors revisited \square predicting the impact of flavoprotein-related diseases on a genome scale.
- 621 Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers.
- 620 Representation of Chemical Reactions. 121-154
- 619 Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. 3
- 618 Computational metabolomics hints at the relevance of glutamine metabolism in breast cancer.

- 617 Genome-scale metabolic reconstruction of the stress-tolerant hybrid yeast *Zygosaccharomyces parvii*.
- 616 Investigating the deregulation of metabolic tasks via Minimum Network Enrichment Analysis (MiNEA) as applied to nonalcoholic fatty liver disease using mouse and human omics data. 1
- 615 Towards Decoding the Metabolic Plasticity in Cancer: Coupling of Gene Regulation and Metabolic Pathways.
- 614 System-level analysis of metabolic trade-offs during anaerobic photoheterotrophic growth in *Rhodospirillum rubrum*.
- 613 Metabolic adaptations underlying genome flexibility in prokaryotes.
- 612 Leveraging the effects of chloroquine on resistant malaria parasites for combination therapies.
- 611 AMON: Annotation of metabolite origins via networks to better integrate microbiome and metabolome data.
- 610 Dynamic load balancing enables large-scale flux variability analysis. 1
- 609 Bayesian inference of metabolic kinetics from genome-scale multiomics data. 1
- 608 Momo [Multi-Objective Metabolic mixed integer Optimization: application to yeast strain engineering.
- 607 Computational metabolism modeling predicts risk of distant relapse-free survival in breast cancer patients.
- 606 The Fate of Glutamine in Human Metabolism. The interplay with glucose in proliferating cells. 1
- 605 Metabolic reprogramming dynamics in tumor spheroids: Insights from a multicellular, multiscale model.
- 604 Data Management in Computational Systems Biology: Exploring Standards, Tools, Databases, and Packaging Best Practices. **2019**, 2049, 285-314 1
- 603 Computing Difference Abstractions of Metabolic Networks Under Kinetic Constraints. **2019**, 266-285 2
- 602 Systems and Synthetic Biology Approach to Understand the Importance of Host-Pathogen Interaction. **2019**, 433-446
- 601 Analysis of metabolic pathways in mycobacteria to aid drug-target identification. 2
- 600 Microbial Bio-production of Proteins and Valuable Metabolites. **2019**, 381-418 1

- 599 Medusa: software to build and analyze ensembles of genome-scale metabolic network reconstructions. 1
- 598 Modeling microbial communities using biochemical resource allocation analysis.
- 597 Efficient reaction deletion algorithms for redesign of constraint-based metabolic networks for metabolite production with weak coupling.
- 596 A comprehensive genome-scale model for *Rhodospiridium toruloides* IFO0880 accounting for functional genomics and phenotypic data.
- 595 Control Theory Concepts for Modeling Uncertainty in Enzyme Kinetics of Biochemical Networks. 0
- 594 Transcriptome-guided parsimonious flux analysis improves predictions with metabolic networks in complex environments.
- 593 SAFEPPP: a Simple And Fast method to Find and analyze Extreme Points of a metabolic Phenotypic Phase Plane.
- 592 Impact of insertion sequences on convergent evolution of *Shigella* species. 0
- 591 Multiscale MultiObjective Systems Analysis (MIMOSA): an advanced metabolic modeling framework for complex systems.
- 590 An integrated computational and experimental study to elucidate *Staphylococcus aureus* metabolism.
- 589 Modeling the Interplay between Photosynthesis, CO₂ Fixation, and the Quinone Pool in a Purple Non-Sulfur Bacterium.
- 588 Metabolic Modeling Elucidates the Transactions in the Rumen Microbiome and the Shifts upon Virome Interactions. 0
- 587 A computational framework for a Lyapunov-enabled analysis of biochemical reaction networks.
- 586 Parkinson's disease-associated alterations of the gut microbiome can invoke disease-relevant metabolic changes. 7
- 585 Wax ester production in nitrogen-rich conditions by metabolically engineered *Acinetobacter baylyi* ADP1.
- 584 Flux-based hierarchical organization of *Escherichia coli*'s metabolic network.
- 583 A Computational Framework to Study the Primary Lifecycle Metabolism of *Arabidopsis thaliana*. 1
- 582 Modeling the metabolic interplay between a parasitic worm and its bacterial endosymbiont allows the identification of novel drug targets.

- 581 A Virtual Nodule Environment (ViNE) for modelling the inter-kingdom metabolic integration during symbiotic nitrogen fixation.
- 580 Systems-level physiology of the human red blood cell is computed from metabolic and macromolecular mechanisms. 1
- 579 Simulating the evolutionary trajectories of metabolic pathways for insect symbionts in the *Sodalis* genus.
- 578 Enzyme-constrained models and omics analysis of *Streptomyces coelicolor* reveal metabolic changes that enhance heterologous production.
- 577 Disruption of Redox Balance Enhances the Effects of BRAF-inhibition in Melanoma Cells. 0
- 576 Temperature dependence of platelet metabolism.
- 575 Genetic profile and functional proteomics of anal squamous cell carcinoma: proposal for a molecular classification.
- 574 Detecting and Isolating Mass Balance Errors in Reaction Based Models in Systems Biology.
- 573 Regulatory dynamic enzyme-cost flux balance analysis: A unifying framework for constraint-based modeling.
- 572 Pan-organ model integration of metabolic and regulatory processes in type 1 diabetes.
- 571 Gene expression profiles based flux balance model to predict the carbon source for *Bacillus subtilis*. 1
- 570 Microbial metabolically cohesive consortia and ecosystem functioning. 1
- 569 Maximization of non-nitrogenous metabolite production in *E. coli* using population systems biology.
- 568 The Use of In Silico Genome-Scale Models for the Rational Design of Minimal Cells. **2020**, 141-175
- 567 Parameter Estimation for Dynamic Resource Allocation in Microorganisms: A Bi-level Optimization Problem. **2020**, 53, 16814-16819
- 566 Dynamic Flux Analysis: An Experimental Approach of Fluxomics. **2020**, 2096, 179-196 1
- 565 Providing new insights on the byphasic lifestyle of the predatory bacterium *Bdellovibrio bacteriovorus* through genome-scale metabolic modeling. 1
- 564 Gene expression noise can promote the fixation of beneficial mutations in fluctuating environments. 0

563	Personalized Genome-Scale Metabolic Models Identify Targets of Redox Metabolism in Radiation-Resistant Tumors.	0
562	Using automated reasoning to explore the metabolism of unconventional organisms: a first step to explore host-microbial interactions. 2020 , 48, 901-913	2
561	Emergence and Propagation of Epistasis in Metabolic Networks.	0
560	Using optimal control to understand complex metabolic pathways.	1
559	Modeling a co-culture of <i>Clostridium autoethanogenum</i> and <i>Clostridium kluyverito</i> increase syngas conversion to medium-chain fatty-acids.	0
558	Cancer cells depend on environmental lipids for proliferation when electron acceptors are limited.	0
557	Unlocking Elementary Conversion Modes: ecmtool unveils all capabilities of metabolic networks.	
556	Functional characterization of SARS-CoV-2 infection suggests a complex inflammatory response and metabolic alterations.	
555	Current Update on the Risk Factor Modification and Exercise Following Coronary Artery Disease. 2020 , 3, 56	
554	Integrated metabolic modeling, culturing and transcriptomics explains enhanced virulence of <i>V. cholerae</i> during co-infection with ETEC.	
553	Dynamic allocation of carbon storage and nutrient-dependent exudation in a revised genome-scale model of <i>Prochlorococcus</i> .	0
552	Dissecting the regulatory roles of ORM proteins in the sphingolipid pathway of plants.	
551	Heterologous Metabolic Pathways: Strategies for Optimal Expression in Eukaryotic Hosts. 2020 , 12, 28-39	1
550	dfba: Software for efficient simulation of dynamic flux-balance analysis models in Python. 2020 , 5, 2342	2
549	A sparse mapping of structure to function in microbial communities.	2
548	Predictive regulatory and metabolic network models for systems analysis of <i>Clostridioides difficile</i> .	
547	GEM-based metabolic profiling for Human Bone Osteosarcoma under different glucose and glutamine availability.	
546	Application of the Metabolic Modeling Pipeline in KBase to Categorize Reactions, Predict Essential Genes, and Predict Pathways in an Isolate Genome. 2022 , 2349, 291-320	1

545	A Beginner's Guide to the COBRA Toolbox. 2022 , 2349, 339-365	0
544	Parameter estimation for models of chemical reaction networks from experimental data of reaction rates. 1-23	
543	Computational Framework for Machine-Learning-Enabled C Fluxomics. 2021 ,	0
542	Curating COBRA Models of Microbial Metabolism. 2022 , 2349, 321-338	1
541	Ecological stoichiometry as a foundation for omics-enabled biogeochemical models of soil organic matter decomposition. 2022 , 157, 31	1
540	Identification of Cross-Pathway Connections via Protein-Protein Interactions Linked to Altered States of Metabolic Enzymes in Cervical Cancer. 2021 , 8, 736495	1
539	Integrating Omics Data to Prioritize Target Genes in Pathogenic Bacteria. 2020 , 217-276	1
538	Software and Methods for Computational Flux Balance Analysis. 2020 , 2096, 165-177	
537	moped - A Python package for metabolic modelling and topological analysis.	
536	Integrating thermodynamic and enzymatic constraints into genome-scale metabolic models.	1
535	Exposure of mammary cells to lipid activates gene expression changes associated with ER-negative breast cancer via chromatin remodeling.	
534	Active and machine learning-based approaches to rapidly enhance microbial chemical production.	
533	Quantifying the propagation of parametric uncertainty on flux balance analysis. 2021 , 69, 26-39	0
532	Metabolic Network. 2020 , 47-52	
531	In Silico Modeling of Metabolic State in Single Th17 Cells Reveals Novel Regulators of Inflammation and Autoimmunity.	6
530	Modeling metabolic variation with single-cell expression data.	3
529	Essentiality of local topology and regulation in kinetic metabolic modeling.	
528	A Novel Optimization-Based Tool to Automate Infeasible Cycle-Free Gapfilling of Genome-Scale Metabolic Models.	

- 527 Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata. **2020**, 207-215 ○
- 526 T-Cell Activation and Differentiation: Role of Signaling and Metabolic Cross-Talk. **2020**, 153-182
- 525 Luenberger observer design for a dynamic system with embedded linear program, applied to bioprocesses. **2020**, 53, 15884-15891
- 524 Understanding biochemical design principles with ensembles of canonical non-linear models.
- 523 Physicochemical and metabolic constraints for thermodynamics-based stoichiometric modelling under mesophilic growth conditions.
- 522 Investigation of microbial community interactions between lake Washington methanotrophs using genome-scale metabolic modeling.
- 521 Metabolic multi-stability and hysteresis in a model aerobe-anaerobe microbiome community.
- 520 Flux balance analysis-based ranking for model order reduction of biochemical networks. **2021**, 54, 556-561
- 519 Comparison of Optimization-Modelling Methods for Metabolites Production in Escherichia coli. **2020**, 17, 1 ○
- 518 CeMbio - TheC. elegansmicrobiome resource.
- 517 GPRuler: Metabolic gene-protein-reaction rules automatic reconstruction. **2021**, 17, e1009550 1
- 516 Agent Clustering Strategy Based on Metabolic Flux Distribution and Transcriptome Expression for Novel Drug Development. **2021**, 9, 1
- 515 Comparison of metabolic states using genome-scale metabolic models. **2021**, 17, e1009522
- 514 Improved production of the non-native cofactor F in Escherichia coli. **2021**, 11, 21774 ○
- 513 Dynamic Flux Balance Analysis Game.
- 512 Error propagation in constraint-based modeling of Chinese hamster ovary cells. ○
- 511 DEXOM: Diversity-based enumeration of optimal context-specific metabolic networks.
- 510 The quantitative metabolome is shaped by abiotic constraints.

- 509 Genome-scale reconstructions to assess metabolic phylogeny and organism clustering.
- 508 Constraint-based modelling revealed changes in metabolic flux modes associated with the Kok effect.
- 507 Multiomics data collection, visualization, and utilization for guiding metabolic engineering. 0
- 506 Genome-scale metabolic model of the diatom *Thalassiosira pseudonana* highlights the importance of nitrogen and sulfur metabolism in redox balance. 1
- 505 Integrated Metabolic Modeling, Culturing, and Transcriptomics Explain Enhanced Virulence of *Vibrio cholerae* during Coinfection with Enterotoxigenic *Escherichia coli*. **2020**, 5, 6
- 504 ComMet: A method for comparing metabolic states in genome-scale metabolic models.
- 503 Stoichiometric modeling of artificial string chemistries.
- 502 Structure of autotrophic models of balanced cell growth and numerical optimization of their growth rate. 1
- 501 From sequence to information. **2020**, 375, 20190448 2
- 500 Accelerated Simulation of Large Reaction Systems Using a Constraint-Based Algorithm.
- 499 Resource uptake and the evolution of moderately efficient enzymes.
- 498 A Scalable, Open-Source Implementation of a Large-Scale Mechanistic Model for Single Cell Proliferation and Death Signaling.
- 497 Automatic reconstruction of metabolic pathways from identified biosynthetic gene clusters.
- 496 An evolutionary algorithm for designing microbial communities via environmental modification.
- 495 Constraint-based metabolic control analysis for rational strain engineering.
- 494 Genome Scale-Differential Flux Analysis reveals deregulation of lung cell metabolism on SARS Cov2 infection.
- 493 Genome-Scale Metabolic Network Models of *Bacillus* Species Suggest that Model Improvement is Necessary for Biotechnological Applications. **2018**, 16, e1684 1
- 492 Metabolomics and flux balance analysis. **2022**, 337-365

491	Toward modeling metabolic state from single-cell transcriptomics. 2021 , 57, 101396	2
490	Genome-Scale Reconstruction of Microbial Dynamic Phenotype: Successes and Challenges. 2021 , 9,	2
489	COBREXAJL: constraint-based reconstruction and exascale analysis. 2021 ,	0
488	Metabolic Reprogramming and Reconstruction: Integration of Experimental and Computational Studies to Set the Path Forward in ADPKD.. 2021 , 8, 740087	0
487	Quantitative genome-scale metabolic modeling of human CD4 T cell differentiation reveals subset-specific regulation of glycosphingolipid pathways. 2021 , 37, 109973	0
486	Compartmentalization of metabolism between cell types in multicellular organisms: a computational perspective.. 2022 , 29, 100407-100407	0
485	FBA-Predicting metabolic flux alterations using genome-scale metabolic models and differential transcriptomic data. 2021 , 17, e1009589	2
484	A Standardized Brain Molecular Atlas: A Resource for Systems Modeling and Simulation. 2021 , 14, 604559	1
483	XomicsToModel: Multiomics data integration and generation of thermodynamically consistent metabolic models.	0
482	Aerobic glycolysis in cancer cells supplies ATP while preventing excess metabolic thermogenesis.	
481	Channeling Anabolic Side Products toward the Production of Nonessential Metabolites: Stable Malate Production in sp. PCC6803. 2021 ,	0
480	Exploring the associations between transcript levels and fluxes in constraint-based models of metabolism. 2021 , 22, 574	0
479	Flux balance analysis for overproduction of organic acids by <i>Synechocystis</i> sp. PCC 6803 under dark anoxic condition. 2021 , 108297	1
478	Diversifying Isoprenoid Platforms Atypical Carbon Substrates and Non-model Microorganisms.. 2021 , 12, 791089	1
477	Metagenome-Scale Metabolic Network Suggests Folate Produced by Microbes Contribute to High-Fiber-Diet-Induced Weight Loss in a Prader-Willi Syndrome Child.. 2021 , 9,	0
476	Constraint-Based Modeling to Understand ROS-Mediated Effects in Cancer. 2021 , 1-21	
475	Mathematical-based microbiome analytics for clinical translation.. 2021 , 19, 6272-6281	3
474	A Computational Framework to Identify Metabolic Engineering Strategies for the Co-Production of Metabolites.. 2021 , 9, 779405	0

- 473 Heterologous Production of Glycine Betaine Using sp. PCC 6803-Based Chassis Lacking Native Compatible Solutes.. **2021**, 9, 821075 0
- 472 Genome-Scale Metabolic Modelling of Lifestyle Changes in *Rhizobium leguminosarum*.. **2022**, e0097521 0
- 471 A Constraint-based modeling approach to reach an improved chemically defined minimal medium for recombinant antiEpEX-scFv production by *Escherichia coli*. **2022**, 179, 108339 0
- 470 Resource-allocation constraint governs structure and function of microbial communities in metabolic modeling.. **2022**, 70, 12-22 0
- 469 Heterologous phasin expression in CGA009 for bioplastic production from lignocellulosic biomass.. **2022**, 14, e00191 0
- 468 MetAMDB: Metabolic Atom Mapping Database.. **2022**, 12, 0
- 467 Computational modeling of the evolutionary transition from C3 to C4 photosynthesis. 0
- 466 Constraint-Based Modeling to Understand ROS-Mediated Effects in Cancer. **2022**, 2209-2229 0
- 465 Synthetic Control of Metabolic States in *Pseudomonas putida* by Tuning Polyhydroxyalkanoate Cycle.. **2022**, e0179421 1
- 464 Sulfate-dependant microbially induced corrosion of mild steel in the deep sea: a 10-year microbiome study.. **2022**, 10, 4 0
- 463 Advances in systems metabolic engineering of autotrophic carbon oxide-fixing biocatalysts towards a circular economy.. **2022**, 3
- 462 Modeling approaches for probing cross-feeding interactions in the human gut microbiome.. **2022**, 20, 79-89 4
- 461 It's a model and it's looking good: A multi-organ metabolic model predicts developmental responses in tomato.. **2022**, 188, 1417-1418 0
- 460 Critical assessment of genome-scale metabolic models of .. **2022**, 0
- 459 Inferring Microbial Biomass Yield and Cell Weight using Probabilistic Macrochemical Modeling.. **2022**, PP, 0
- 458 Genomic structure predicts metabolite dynamics in microbial communities.. **2022**, 6
- 457 Synthetic Biology in the *Candida* (CTG) Clade. **2022**, 337-375 0
- 456 Genome-scale modeling of yeast metabolism: retrospectives and perspectives.. **2022**, 1

- 455 Reconstructing Kinetic Models for Dynamical Studies of Metabolism using Generative Adversarial Networks.
- 454 Pool size measurements improve precision of flux estimates but increase sensitivity to unmodeled reactions outside the core network in isotopically nonstationary metabolic flux analysis (INST-MFA).. **2022**, e2000427 ○
- 453 Metabolic signatures of regulation by phosphorylation and acetylation.. **2022**, 25, 103730 ○
- 452 Multiomics approaches for the improvements of postharvest systems. **2022**, 251-276
- 451 Inspecting the Solution Space of Genome-Scale Metabolic Models.. **2022**, 12, 1
- 450 ECMpy, a Simplified Workflow for Constructing Enzymatic Constrained Metabolic Network Model.. **2022**, 12, ○
- 449 Vivarium: an interface and engine for integrative multiscale modeling in computational biology.. **2022**, ○
- 448 Experimental determination of Escherichia coli biomass composition for constraint-based metabolic modeling.. **2022**, 17, e0262450 ○
- 447 Project-based learning course on metabolic network modelling in computational systems biology.. **2022**, 18, e1009711 ○
- 446 Genome-Scale Modeling Specifies the Metabolic Capabilities of .. **2022**, e0121621 ○
- 445 Metabolic switch in the aging astrocyte evidenced via integrative approach comprising network and transcriptome analyses.
- 444 Constraint-based modeling identifies metabolic vulnerabilities during the epithelial to mesenchymal transition. ○
- 443 Flux balance analysis of the ammonia-oxidizing bacterium Nitrosomonas europaea ATCC19718 unravels specific metabolic activities while degrading toxic compounds.. **2022**, 18, e1009828 ○
- 442 An ensemble approach to the structure-function problem in microbial communities.. **2022**, 25, 103761 1
- 441 Machine learning-assisted discovery of growth decision elements by relating bacterial population dynamics to environmental diversity. ○
- 440 A mechanistic modeling framework reveals the key principles underlying tumor metabolism.. **2022**, 18, e1009841 ○
- 439 Time-Optimal Adaptation in Metabolic Network Models.
- 438 INTEGRATE: Model-based multi-omics data integration to characterize multi-level metabolic regulation.. **2022**, 18, e1009337 2

437	Quantifying cumulative phenotypic and genomic evidence for procedural generation of metabolic network reconstructions.. 2022 , 18, e1009341	0
436	Cellular limitation of enzymatic capacity explains glutamine addiction in cancers.	0
435	Systems-based approaches to study immunometabolism.. 2022 ,	3
434	Identifying the essential nutritional requirements of the probiotic bacteria <i>Bifidobacterium animalis</i> and <i>Bifidobacterium longum</i> through genome-scale modeling. 2021 , 7, 47	2
433	A compendium of predicted growths and derived symbiotic relationships between 803 gut microbes in 13 different diets. 2022 , 3, 100127	
432	Mathematical Modelling in Plant Synthetic Biology.. 2022 , 2379, 209-251	
431	NCMW: A Python Package to Analyze Metabolic Interactions in the Nasal Microbiome. 2022 , 2,	1
430	CRISPR-assisted rational flux-tuning and arrayed CRISPRi screening of an L-proline exporter for L-proline hyperproduction.. 2022 , 13, 891	2
429	Using Omics to Study Leprosy, Tuberculosis, and Other Mycobacterial Diseases.. 2022 , 12, 792617	0
428	Probing Genome-Scale Model Reveals Metabolic Capability and Essential Nutrients for Growth of Probiotic KUB-AC5.. 2022 , 11,	1
427	Genetically personalised organ-specific metabolic models in health and disease.	0
426	System-level metabolic modeling facilitates unveiling metabolic signature in exceptional longevity.. 2022 , e13595	3
425	Prescription Drugs and Mitochondrial Metabolism.. 2022 ,	0
424	Quantitative metabolic fluxes regulated by trans-omic networks.. 2022 , 479, 787-804	0
423	All Driven by Energy Demand? Integrative Comparison of Metabolism of <i>Enterococcus faecalis</i> Wildtype and a Glutamine Synthase Mutant.. 2022 , e0240021	1
422	Integrative Genome-Scale Metabolic Modeling Reveals Versatile Metabolic Strategies for Methane Utilization in <i>Methylobacterium album</i> BG8.. 2022 , e0007322	0
421	Metabolic Engineering Interventions for Sustainable 2,3-Butanediol Production in Gas-Fermenting .. 2022 , e0111121	0
420	Genome-Scale Metabolic Model's multi-objective solving algorithm based on the inflexion point of Pareto front including maximum energy utilization and its application in <i>A.niger</i> DS03043.. 2022 ,	

419	Protein cost minimization promotes the emergence of coenzyme redundancy.. 2022 , 119, e2110787119	0
418	Fluxomics - New Metabolomics Approaches to Monitor Metabolic Pathways.. 2022 , 13, 805782	1
417	Reconstruction and analysis of genome-scale metabolic model for thermophilic fungus <i>Myceliophthora thermophila</i> .. 2022 ,	1
416	Characterizing the interplay of rubisco and nitrogenase enzymes in anaerobic-photoheterotrophically grown <i>Rhodospseudomonas palustris</i> CGA009 through a genome-scale metabolic and expression model.	
415	Hybrid modelling of biological systems: current progress and future prospects.. 2022 ,	1
414	Prediction of gene essentiality using machine learning and genome-scale metabolic models.	
413	PITX1 Is a Regulator of TERT Expression in Prostate Cancer with Prognostic Power.. 2022 , 14,	0
412	Applications of Coarse-Grained Models in Metabolic Engineering.. 2022 , 9, 806213	0
411	Required Gene Set for Autotrophic Growth of .. 2022 , e0247921	0
410	Reconstruction of a generic genome-scale metabolic network for chicken: Investigating network connectivity and finding potential biomarkers.. 2022 , 17, e0254270	1
409	The choice of the objective function in flux balance analysis is crucial for predicting replicative lifespans in yeast.	0
408	Interrogation of Essentiality in the Reconstructed <i>Haemophilus influenzae</i> Metabolic Network Identifies Lipid Metabolism Antimicrobial Targets: Preclinical Evaluation of a FabH β Ketoacyl-ACP Synthase Inhibitor.. 2022 , e0145921	0
407	The hidden simplicity of metabolic networks is revealed by multireaction dependencies.. 2022 , 8, eabl6962	
406	Mathematical models to study the biology of pathogens and the infectious diseases they cause.. 2022 , 25, 104079	0
405	Human/SARS-CoV-2 Genome-Scale Metabolic Modeling to Discover Potential Antiviral Targets for COVID-19.. 2022 , 104273	0
404	Growth promotion and antibiotic induced metabolic shifts in the chicken gut microbiome.. 2022 , 5, 293	2
403	Cross-kingdom expression of synthetic genetic elements promotes discovery of metabolites in the human microbiome.. 2022 ,	2
402	A genetic toolkit and gene switches to limit <i>Mycoplasma</i> growth for biosafety applications.. 2022 , 13, 1910	1

401	Absolute Proteome Quantification in the Gas-Fermenting Acetogen .. 2022 , e0002622	0
400	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production.. 2022 ,	0
399	Perspective: a stirring role for metabolism in cells.. 2022 , 18, e10822	0
398	Contribution of genome-scale metabolic modelling to niche theory.. 2022 ,	0
397	Primary carbon sources and self-induced metabolic landscapes shape community structure in soil bacterial hotspots. 2022 , 168, 108620	1
396	Integrative metabolic flux analysis reveals an indispensable dimension of phenotypes.. 2022 , 75, 102701	1
395	Integration of omics data to generate and analyse COVID-19 specific genome-scale metabolic models.. 2022 , 145, 105428	2
394	Sustainable optimization of global aquatic omega-3 supply chain could substantially narrow the nutrient gap. 2022 , 181, 106260	1
393	Engineering of managed aquifer recharge systems to optimize biotransformation of trace organic chemicals. 2022 , 27, 100343	1
392	A multi-organ metabolic model of tomato predicts plant responses to nutritional and genetic perturbations.. 2021 ,	1
391	Enhancing Microbiome Research through Genome-Scale Metabolic Modeling.. 2021 , 6, e0059921	2
390	Genome-Scale Metabolic Modeling Enables In-Depth Understanding of Big Data.. 2021 , 12,	2
389	From fruit growth to ripening in plantain: a careful balance between carbohydrate synthesis and breakdown.	
388	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production.	
387	Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. 2021 , 7, 43	1
386	Non-random organization of flux control mechanisms in yeast central metabolic pathways.	
385	Can Systems Biology Advance Clinical Precision Oncology?. 2021 , 13,	1
384	Adaptations in metabolism and protein translation give rise to the Crabtree effect in yeast.. 2021 , 118,	3

- 383 Parkinson's Disease and the Metal-Microbiome-Gut-Brain Axis: A Systems Toxicology Approach.. **2021**, 11, 0
- 382 Underground metabolism as a rich reservoir for pathway engineering.. **2022**,
- 381 Pareto Optimal Metabolic Engineering for the Growth-coupled Overproduction of Sustainable Chemicals.. **2022**, 1
- 380 Whole-body metabolic modelling predicts isoleucine dependency of SARS-CoV-2 replication.
- 379 PyMiner: A method for metabolic pathway design based on the uniform similarity of substrate-product pairs and conditional search.. **2022**, 17, e0266783
- 378 Computational Methods for the Study of Peroxisomes in Health and Disease.
- 377 Faster Growth Enhances Low Carbon Fuel and Chemical Production Through Gas Fermentation.. **2022**, 10, 879578 0
- 376 Integrative Gene Expression and Metabolic Analysis Tool .. **2022**, 12, 0
- 375 Exploring synergies between plant metabolic modelling and machine learning.. **2022**, 20, 1885-1900 1
- 374 A metabolic axis in obesity and type 2 diabetes.. **2022**, 14, 2057778 2
- 373 A Genome-Scale Metabolic Model of Marine Heterotroph *Vibrio splendidus* sp. 1A01.
- 372 Genome-scale metabolic modelling enables deciphering ethanol metabolism via the acrylate pathway in the propionate-producer *Anaerotignum neopropionicum*. 0
- 371 Chapter 9. Current Challenges in the Computational Modelling of Molecular Recognition Processes. 221-246
- 370 Data_Sheet_1.xlsx. **2020**,
- 369 Data_Sheet_1.XLS. **2018**,
- 368 Data_Sheet_2.ZIP. **2018**,
- 367 Data_Sheet_3.ZIP. **2018**,
- 366 Image_1.PDF. **2018**,

365 Image_2.PDF. 2018,

364 Image_3.PDF. 2018,

363 Table_1.XLS. 2018,

362 Table_2.xls. 2018,

361 Table_3.XLS. 2018,

360 Table_4.XLS. 2018,

359 Table_5.xls. 2018,

358 Table_6.XLS. 2018,

357 Table_7.XLS. 2018,

356 Data_Sheet_1.XLSX. 2018,

355 Data_Sheet_2.zip. 2018,

354 Image_1.JPEG. 2018,

353 Image_2.JPEG. 2018,

352 Image_3.JPEG. 2018,

351 DataSheet_1.xlsx. 2019,

350 DataSheet_2.zip. 2019,

349 Table_1.xlsx. 2019,

348 Data_Sheet_1.ZIP. 2018,

347 Data_Sheet_2.XLSX. 2018,

346 Data_Sheet_3.DOCX. 2018,

345 Table_1.DOCX. 2018,

344 Table_2.DOCX. 2018,

343 Data_Sheet_1.PDF. 2020,

342 Table_1.XLSX. 2020,

341 Data_Sheet_1.PDF. 2019,

340 Data_Sheet_2.PDF. 2019,

339 Data_Sheet_3.PDF. 2019,

338 Image_1.pdf. 2019,

337 Image_2.tif. 2019,

336 Image_3.tif. 2019,

335 Table_1.docx. 2019,

334 Table_2.docx. 2019,

333 Table_3.docx. 2019,

332 Table_4.xlsx. 2019,

331 Table_5.xlsx. 2019,

330 Data_Sheet_1.pdf. 2019,

329 Data_Sheet_2.zip. **2019,**

328 Data_Sheet_3.xlsx. **2019,**

327 Data_Sheet_1.zip. **2019,**

326 Data_Sheet_1.PDF. **2020,**

325 Table_1.XLSX. **2020,**

324 Data_Sheet_1.pdf. **2019,**

323 Data_Sheet_2.ZIP. **2019,**

322 Table_1.XLSX. **2019,**

321 Data_Sheet_1.docx. **2018,**

320 Data_Sheet_2.pdf. **2018,**

319 Data_Sheet_1.pdf. **2019,**

318 Data_Sheet_2.zip. **2019,**

317 Table_1.xls. **2019,**

316 Data_Sheet_1.ZIP. **2019,**

315 Data_Sheet_1.ZIP. **2019,**

314 Data_Sheet_2.ZIP. **2019,**

313 Data_Sheet_3.ZIP. **2019,**

312 Data_Sheet_4.ZIP. **2019,**

311 Data_Sheet_5.ZIP. **2019**,

310 Data_Sheet_6.ZIP. **2019**,

309 Data_Sheet_7.ZIP. **2019**,

308 Data_Sheet_8.ZIP. **2019**,

307 Data_Sheet_1.PDF. **2019**,

306 Data_Sheet_2.ZIP. **2019**,

305 Table_1.xls. **2019**,

304 Table_2.XLS. **2019**,

303 Data_Sheet_1.pdf. **2020**,

302 Data_Sheet_2.pdf. **2020**,

301 Data_Sheet_3.pdf. **2020**,

300 Table_1.pdf. **2020**,

299 Table_2.xlsx. **2020**,

298 Data_Sheet_1.PDF. **2020**,

297 Presentation_1.PDF. **2018**,

296 Presentation_2.pdf. **2018**,

295 Table_1.xlsx. **2018**,

294 Data_Sheet_1.xlsx. **2020**,

293 Data_Sheet_2.docx. **2020**,

292 Data_Sheet_1.ZIP. **2018**,

291 Data_Sheet_2.XLS. **2018**,

290 Data_Sheet_3.XLS. **2018**,

289 Data_Sheet_4.XLS. **2018**,

288 Data_Sheet_5.XLS. **2018**,

287 Data_Sheet_6.XLS. **2018**,

286 Data_Sheet_7.XLS. **2018**,

285 Data_Sheet_8.ZIP. **2018**,

284 Network Reconstruction and Modelling Made Reproducible with moped.. **2022**, 12, ○

283 Constraint-Based Modeling of Diatoms Metabolism and Quantitative Biology Approaches. **2022**, 775-808

282 Metabolic flux simulation of microbial systems based on optimal planning algorithms. **2022**, ○

281 Combination of Genome-Scale Models and Bioreactor Dynamics to Optimize the Production of Commodity Chemicals.. **2022**, 9, 855735

280 Discovering Circular Process Solutions through Automated Reaction Network Optimization.

279 Systems Biology in Periodontitis. **2022**, 3,

278 Systems biology approach to functionally assess the pangenome reveals genetic diversity with discriminatory power.. **2022**, 119, e2119396119 1

277 Principles, Tools, and Applications of Synthetic Consortia Toward Microbiome Engineering. **2022**, 195-218

276 Reconstruction of a Genome-Scale Metabolic Network for *Shewanella oneidensis* MR-1 and Analysis of its Metabolic Potential for Bioelectrochemical Systems. **2022**, 10, ○

275	Phenotype-centric modeling for rational metabolic engineering.. 2022,	
274	Elucidating Human Milk Oligosaccharide biosynthetic genes through network-based multi-omics integration.. 2022, 13, 2455	1
273	From fruit growth to ripening in plantain: a careful balance between carbohydrate synthesis and breakdown.. 2022,	0
272	Lipid exposure activates gene expression changes associated with estrogen receptor negative breast cancer.. 2022, 8, 59	0
271	Metabolic pathway engineering for the non-growth-associated succinate production in Escherichia coli based on flux solution space.. 2022,	0
270	Modeling Reactive Species Metabolism in Colorectal Cancer for Identifying Metabolic Targets and Devising Therapeutics.	
269	Design, Analysis, and Implementation of a Novel Biochemical Pathway for Ethylene Glycol Production in .. 2022, 11, 1790-1800	0
268	Genome-scale metabolic modeling in antimicrobial pharmacology. 2022, 2, 100021	0
267	Flux Balance Network Expansion Predicts Stage-Specific Human Peri_Implantation Embryo Metabolism.	0
266	Predicting Metabolic Adaptation Under Dynamic Substrate Conditions Using a Resource-Dependent Kinetic Model: A Case Study Using <i>Saccharomyces cerevisiae</i> . 2022, 9,	0
265	Ecological modelling approaches for predicting emergent properties in microbial communities.. 2022,	5
264	Metabolic Modeling of Wine Fermentation at Genome Scale. 2022, 395-454	
263	Microbial metabolism of aromatic pollutants: High-throughput OMICS and metabolic engineering for efficient bioremediation. 2022, 151-199	0
262	Analysis and modeling tools of metabolic flux. 2022, 45-68	
261	A Practical Guide to Integrating Multimodal Machine Learning and Metabolic Modeling. 2022, 87-122	0
260	Metabolic engineering: tools for pathway rewiring and value creation. 2022, 3-26	
259	Crypto consumers personality traits, and the impact of brand personality on cryptocurrencies identity. 2022,	
258	Growth phase estimation for abundant bacterial populations sampled longitudinally from human stool metagenomes.	0

- 257 Method for quantifying the metabolic boundary fluxes of cell cultures in large cohorts by high resolution hydrophilic liquid chromatography mass spectrometry.
- 256 Characterizing metabolism from bulk and single-cell RNA-seq data using METAFlex.
- 255 Examining organic acid production potential and growth-coupled strategies in *Issatchenkia orientalis* using constraint-based modeling.
- 254 Construction of Multiscale Genome-Scale Metabolic Models: Frameworks and Challenges. **2022**, 12, 721 1
- 253 A genome-scale metabolic model of *Cupriavidus necator* H16 integrated with TraDIS and transcriptomic data reveals metabolic insights for biotechnological applications. **2022**, 18, e1010106 0
- 252 Metabolic Rewiring and Cultivation Optimization for Photosynthetic Biofuel Production in Cyanobacteria. **2022**, 45-80
- 251 Integrating proteomic data with metabolic modelling provides insight into key pathways of *Bordetella pertussis* biofilms.
- 250 Dynamic genome-scale modeling of *Saccharomyces cerevisiae* unravels mechanisms for higher alcohol and ester formation during alcoholic fermentation.
- 249 A study of a diauxic growth experiment using an expanded dynamic flux balance framework.
- 248 Dual transcriptome based reconstruction of *Salmonella*-human integrated metabolic network to screen potential drug targets. **2022**, 17, e0268889 0
- 247 Coordination of CcpA and CodY regulators in *Staphylococcus aureus* USA300 strains.
- 246 Exploring the metabolic landscape of pancreatic ductal adenocarcinoma cells using genome-scale metabolic modeling. **2022**, 104483 0
- 245 Multi-Omics Integrative Analysis Coupled to Control Theory and Computational Simulation of a Genome-Scale metabolic Model Reveal Controlling Biological Switches in Human Astrocytes Under Palmitic Acid-Induced Lipotoxicity. **2022**, 2,
- 244 Reconstruction of the Genome-Scale Metabolic Model of *Saccharopolyspora erythraea* and Its Application in the Overproduction of Erythromycin. **2022**, 12, 509 0
- 243 Artificial neural networks enable genome-scale simulations of intracellular signaling. **2022**, 13, 1
- 242 De novo biosynthesis of rubusoside and rebaudiosides in engineered yeasts. **2022**, 13, 1
- 241 Trimming gene deletion strategies for growth-coupled production in constraint-based metabolic networks: TrimGdel. **2022**, 1-10
- 240 Machine learning-guided evaluation of extraction and simulation methods for cancer patient-specific metabolic models. **2022**, 20, 3041-3052 0

- 239 Metabolic systems analysis identifies a novel mechanism contributing to shock in patients with Endotheliopathy of Trauma (EoT) involving thromboxane A2 and LTC4. **2022**, 100115 1
- 238 Methods for Quantifying the Metabolic Boundary Fluxes of Cell Cultures in Large Cohorts by High-Resolution Hydrophilic Liquid Chromatography Mass Spectrometry. 1
- 237 Linear programming based gene expression model (LPM-GEM) predicts the carbon source for *Bacillus subtilis*. **2022**, 23,
- 236 Characterizing the Interplay of Rubisco and Nitrogenase Enzymes in Anaerobic-Photoheterotrophically Grown *Rhodospseudomonas palustris* CGA009 through a Genome-Scale Metabolic and Expression Model.
- 235 A scalable, open-source implementation of a large-scale mechanistic model for single cell proliferation and death signaling. **2022**, 13, 0
- 234 Cancer cells depend on environmental lipids for proliferation when electron acceptors are limited. 0
- 233 Analyzing and Resolving Infeasibility in Flux Balance Analysis of Metabolic Networks. **2022**, 12, 585
- 232 A pipeline for the reconstruction and evaluation of context-specific human metabolic models at a large-scale. **2022**, 18, e1009294 0
- 231 Standardization of Human Metabolic Stoichiometric Models: Challenges and Directions. 2,
- 230 pH sensing controls tissue inflammation by modulating cellular metabolism and endo-lysosomal function of immune cells. 2
- 229 *Lactobacillus rhamnosus* colonisation antagonizes *Candida albicans* by forcing metabolic adaptations that compromise pathogenicity. **2022**, 13, 3
- 228 SALARECON connects the Atlantic salmon genome to growth and feed efficiency. **2022**, 18, e1010194 0
- 227 Genome-scale metabolic modelling enables deciphering ethanol metabolism via the acrylate pathway in the propionate-producer *Anaerostignum neopropionicum*. **2022**, 21, 1
- 226 Acetyl-CoA synthesis through a bicyclic carbon-fixing pathway in gas-fermenting bacteria. 0
- 225 Competition for nutrients increases invasion resistance during assembly of microbial communities. 0
- 224 Modelling the metabolic consequences of antimicrobial exposure.
- 223 Genome-Wide Analysis of Yeast Metabolic Cycle through Metabolic Network Models Reveals Superiority of Integrated ATAC-seq Data over RNA-seq Data.
- 222 Hyaluronic acid biosynthesis promotes an invasive, stem-like cancer cell phenotype by broadly altering metabolism.

- 221 Genome-scale modeling of the primary-specialized metabolism interface. **2022**, 68, 102244
- 220 Advances in constraint-based models: methods for improved predictive power based on resource allocation constraints. **2022**, 68, 102168 ○
- 219 Models of Cellular Metabolism from Single Cell Expression Data Reveals Cell Type Specific Metabolic Heterogeneity.
- 218 Reconstruction of Genome-Scale Metabolic Model for *Hansenula polymorpha* Using RAVEN. **2022**, 271-290
- 217 Exploring the metabolic versatility of cyanobacteria for an emerging carbon-neutral bioeconomy. **2022**, 165-187
- 216 Model-based driving mechanism analysis for butyric acid production in *Clostridium tyrobutyricum*. **2022**, 15, ○
- 215 Reconstruction of a catalogue of genome-scale metabolic models with enzymatic constraints using GECKO 2.0. **2022**, 13, ○
- 214 Genome-scale metabolic network model of *Eriocheir sinensis* icrab4665 and nutritional requirement analysis. **2022**, 23,
- 213 Enzyme activity profiling for physiological phenotyping within functional phenomics: plant growth and stress responses. 1
- 212 Multi-Objective Optimization of Microalgae Metabolism: An Evolutive Algorithm Based on FBA. **2022**, 12, 603
- 211 Teasing out Missing Reactions in Genome-scale Metabolic Networks through Deep Learning.
- 210 Understanding the adaptive laboratory evolution of multiple stress-resistant yeast strains by genome scale modeling.
- 209 A universal dynamical metabolic model representing mixotrophic growth of *Chlorella* sp.
- 208 Metabolic modeling-based drug repurposing in Glioblastoma. **2022**, 12, ○
- 207 Time-Optimal Adaptation in Metabolic Network Models. 9,
- 206 Genome-scale metabolic network models: from first-generation to next-generation. 1
- 205 Validated In Silico Population Model of *Escherichia coli*.
- 204 Whither Chemical Engineering?.

- 203 Nonlinear Multi-Objective Flux Balance Analysis of the Warburg Effect. **2022**, 111223
- 202 Constraint-Based Reconstruction and Analyses of Metabolic Models: Open-Source Python Tools and Applications to Cancer. 12,
- 201 Understanding HMF Inhibition on Yeast Growth Coupled with Ethanol Production for the Improvement of Bio-Based Industrial Processes. **2022**, 0
- 200 Interrogating the effect of enzyme kinetics on metabolism using differentiable constraint-based models.
- 199 Modelling the fitness landscapes of a SCRaMbLEd yeast genome. **2022**, 219, 104730 0
- 198 Data-driven and model-guided systematic framework for media development in CHO cell culture. **2022**, 73, 114-123 0
- 197 Digital models in biotechnology: Towards multi-scale integration and implementation. **2022**, 60, 108015 1
- 196 Iron availability enhances the cellular energetics of aerobic Escherichia coli cultures while upregulating anaerobic respiratory chains. **2022**, 71, 11-20 0
- 195 Whole-body metabolic modelling predicts isoleucine dependency of SARS-CoV-2 replication. **2022**, 0
- 194 Advances and applications of machine learning and intelligent optimization algorithms in genome-scale metabolic network models.
- 193 Engineering of Pseudomonas putida for accelerated co-utilization of glucose and cellobiose yields aerobic overproduction of pyruvate explained by an upgraded metabolic model.
- 192 Comparative genome-scale constraint-based metabolic modeling reveals key lifestyle features of plant-associated Pseudomonas spp..
- 191 Emerging metabolomic tools to study cancer metastasis. **2022**, 1
- 190 Phenotypic response of yeast metabolic network to availability of proteinogenic amino acids.
- 189 A synthetic C2 auxotroph of Pseudomonas putida for evolutionary engineering of alternative sugar catabolic routes.
- 188 Multi-omics profiling of the cold tolerant Monoraphidium minutum 26B-AM in response to abiotic stress. **2022**, 66, 102794
- 187 Characterizing control of memory CD8 T cell differentiation by BTB-ZF transcription factor Zbtb20.
- 186 Study of Metabolic Flux Distribution in Rice (Oryza sativa) Cultures for Starch Production. **2022**, 31,

- 185 Rapid-SL identifies synthetic lethal sets with an arbitrary cardinality. **2022**, 12, ○
- 184 Single-cell RNA-sequencing identifies anti-cancer immune phenotypes in the early lung metastatic niche during breast cancer. ○
- 183 Bioinformatics and Metabolic flux analysis highlight a new mechanism involved in lactate oxidation in *Clostridium tyrobutyricum*.
- 182 Nucleobase adduct-containing metabolites are MR1 ligands that stimulate self-reactive MR1T cells.
- 181 Orally administered *Odoribacter laneus* improves glucose control and inflammatory profile in obese mice by depleting circulating succinate. **2022**, 10, 4
- 180 FlowGEN. **2022**,
- 179 Phenotypic response of yeast metabolic network to availability of proteinogenic amino acids. 9,
- 178 Machine learning-assisted discovery of growth decision elements by relating bacterial population dynamics to environmental diversity. 11, ○
- 177 A genome-scale metabolic model of *Drosophila melanogaster* for integrative analysis of brain diseases.
- 176 Integrated Profiling of Gram-Positive and Gram-Negative Probiotic Genomes, Proteomes and Metabolomes Revealed Small Molecules with Differential Growth Inhibition of Antimicrobial-Resistant Pathogens. 1-23 ○
- 175 FluxomicsExplorer: Differential visual analysis of Flux Sampling based on Metabolomics. **2022**, 108, 11-21 ○
- 174 Metabolic flux analysis: a comprehensive review on sample preparation, analytical techniques, data analysis, computational modelling, and main application areas. **2022**, 12, 25528-25548 ○
- 173 Linking process and metabolic modelling for the estimation of carbon flux distribution in *Corynebacterium glutamicum* growth in spent sulfite liquor. **2022**, 55, 228-233 ○
- 172 Problems in the Development of Efficient Biotechnology for the Synthesis of Valuable Components from Microalgae Biomass. **2022**, 56, 425-439 ○
- 171 Reconstructing Kinetic Models for Dynamical Studies of Metabolism using Generative Adversarial Networks. **2022**, 4, 710-719 ○
- 170 Systematic assessment of template-based genome-scale metabolic models created with the BiGG Integration Tool. **2022**, 19, ○
- 169 Bioinformatics and Metabolic flux analysis highlight a new mechanism involved in lactate oxidation in *Clostridium tyrobutyricum*. ○
- 168 MERRIN: METabolic regulation rule INFERENCE from time series data. **2022**, 38, ii127-ii133 ○

- 167 Optimal energy and redox metabolism in the cyanobacterium *Synechocystis* sp. PCC 6803. ○
- 166 Data Processing and Analysis in Mass Spectrometry-Based Metabolomics. **2023**, 207-239 ○
- 165 A Multiscale Spatiotemporal Model Including a Switch from Aerobic to Anaerobic Metabolism Reproduces Succession in the Early Infant Gut Microbiota. ○
- 164 What makes a reaction network "chemical"? **2022**, 14, ○
- 163 Microbial containment device: A platform for comprehensive analysis of microbial metabolism without sample preparation. 13, ○
- 162 Accurate flux predictions using tissue-specific gene expression in plant metabolic modeling. ○
- 161 Mathematical reconstruction of the metabolic network in an in-vitro multiple myeloma model. ○
- 160 Research-driven education: An introductory course to systems and synthetic biology. 2, ○
- 159 Interspecies Metabolic Interactions in a Synergistic Consortium Drive Efficient Degradation of the Herbicide Bromoxynil Octanoate. **2022**, 70, 11613-11622 ○
- 158 Interaction Networks Are Driven by Community-Responsive Phenotypes in a Chitin-Degrading Consortium of Soil Microbes. ○
- 157 Optimization and Scale-Up of Fermentation Processes Driven by Models. **2022**, 9, 473 2
- 156 De novo biosynthesis of L-lysine via multi-strategy metabolic engineering in *Escherichia coli*. **2022**, 11, 1 ○
- 155 Transcriptomics data integration for context-specific modeling of Atlantic salmon metabolism: functional evaluation of methods based on metabolic tasks. ○
- 154 Evaluating proteome allocation of *Saccharomyces cerevisiae* phenotypes with resource balance analysis. ○
- 153 Dynamic Kinetic Models Capture Cell-Free Metabolism for Improved Butanol Production. ○
- 152 Insight into the Relationship between Oral Microbiota and the Inflammatory Bowel Disease. **2022**, 10, 1868 1
- 151 Metabolomics: Going Deeper, Going Broader, Going Further. **2023**, 155-178 ○
- 150 A synthetic C2 auxotroph of *Pseudomonas putida* for evolutionary engineering of alternative sugar catabolic routes. **2022**, 74, 83-97 ○

- 149 Interrogating the effect of enzyme kinetics on metabolism using differentiable constraint-based models. **2022**, 74, 72-82 ○
- 148 Recent computational drug repositioning strategies against SARS-CoV-2. **2022**, 20, 5713-5728 ○
- 147 Synthetic Biology Tools in Cyanobacterial Biotechnology: Recent Developments and Opportunities. **2022**, 181-203 ○
- 146 The functional microbiome of grapevine throughout plant evolutionary history and lifetime. **2022**, 1 ○
- 145 In silico analysis of metabolic effects of bipolar disorder on prefrontal cortex identified altered GABA, glutamate-glutamine cycle, energy metabolism and amino acid synthesis pathways. ○
- 144 NEMETEX: a Python software for the visualisation of the network of metabolic exchanges. ○
- 143 Engineered synthetic one-carbon fixation exceeds yield of the Calvin Cycle. ○
- 142 Functional Decomposition of Metabolism allows a system-level quantification of fluxes and protein allocation towards specific metabolic functions. ○
- 141 Machine Learning and Hybrid Methods for Metabolic Pathway Modeling. **2023**, 417-439 2
- 140 Combining denoising of RNA-seq data and flux balance analysis for cluster analysis of single cells. **2022**, 23, ○
- 139 Metabolic modeling of *Hermetia illucens* larvae resource allocation for high-value fatty acid production. ○
- 138 Inference of metabolic fluxes in nutrient-limited continuous cultures: A Maximum Entropy approach with minimum information. **2022**, 105450 ○
- 137 Arduino Soft Sensor for Monitoring *Schizochytrium* sp. Fermentation, a Proof of Concept for the Industrial Application of Genome-Scale Metabolic Models in the Context of Pharma 4.0. **2022**, 10, 2226 ○
- 136 Towards a hybrid user interface for the visual exploration of large biomolecular networks using virtual reality. **2022**, ○
- 135 Construction and Analysis of an Enzyme-Constrained Metabolic Model of *Corynebacterium glutamicum*. **2022**, 12, 1499 ○
- 134 The choice of the objective function in flux balance analysis is crucial for predicting replicative lifespans in yeast. **2022**, 17, e0276112 ○
- 133 Reconstructed Genome-Scale Metabolic Model Characterizes Adaptive Metabolic Flux Changes in Peripheral Blood Mononuclear Cells in Severe COVID-19 Patients. **2022**, 23, 12400 ○
- 132 Towards the human nasal microbiome: Simulating *D. pigrum* and *S. aureus*. 12, ○

- 131 An Investigation of the Effects of Nitrate vs. Ammonium on Plants Using Metabolic Modeling. 0
- 130 Whole-genome sequencing and genome-scale metabolic modeling of *Chromohalobacter canadensis* 85B to explore its salt tolerance and biotechnological use. **2022**, 11, 0
- 129 Synthetic Biology Meets Machine Learning. **2023**, 21-39 0
- 128 MAMBA: a model-driven, constraint-based multiomic integration method. 0
- 127 Clinical stratification improves the diagnostic accuracy of small omics datasets within machine learning and genome-scale metabolic modelling methods. **2022**, 106244 0
- 126 Genome-scale modeling of Chinese hamster ovary cells by hybrid semi-parametric flux balance analysis. **2022**, 45, 1889-1904 2
- 125 A systems toxicological analysis of oxybenzone effects on the metabolic physiology of embryo-larval zebrafish (*Danio rerio*). **2022**, 9, 100308 0
- 124 Coordination of CcpA and CodY Regulators in *Staphylococcus aureus* USA300 Strains. 0
- 123 Metabolic modeling of single bronchoalveolar macrophages reveals regulators of hyperinflammation in COVID-19. **2022**, 25, 105319 1
- 122 Metabolomics and modelling approaches for systems metabolic engineering. **2022**, 15, e00209 1
- 121 Protocol for CAROM: A machine learning tool to predict post-translational regulation from metabolic signatures. **2022**, 3, 101799 0
- 120 Engineering of *Pseudomonas putida* for accelerated co-utilization of glucose and cellobiose yields aerobic overproduction of pyruvate explained by an upgraded metabolic model. **2023**, 75, 29-46 0
- 119 Modulation of Nutrient Precursors for Controlling Metabolic Inhibitors by Genome-Scale Flux Balance Analysis. 0
- 118 Brain energy metabolism is optimized to minimize the cost of enzyme synthesis and transport. 0
- 117 Predicting the impact of temperature on metabolic fluxes using resource allocation modelling: application to polyphosphate accumulating organisms.. **2022**, 119365 0
- 116 gMCStool: automated network-based tool to search for metabolic vulnerabilities in cancer. 0
- 115 Turnover number predictions for kinetically uncharacterized enzymes using machine and deep learning. 0
- 114 Integrative Teaching of Metabolic Modeling and Flux Analysis with Interactive Python Modules. 0

- 113 Computational Approaches to Assess Abnormal Metabolism in Alzheimer's Disease Using Transcriptomics. **2023**, 173-189 ○
- 112 Network location and clustering of genetic mutations determine chronicity in a stylized model of genetic diseases. **2022**, 12, ○
- 111 Regulators of Genetic Risk for the Progression of Non-alcoholic Fatty Liver Disease to Hepatocellular Carcinoma: Reconstruction of Transcriptional Network and Signature-Based Metabolic Profiling. **2022**, ○
- 110 Recent advances in machine learning applications in metabolic engineering. **2023**, 62, 108069 1
- 109 Modeling the metabolic dynamics at the genome-scale by optimized yield analysis. **2023**, 75, 119-130 ○
- 108 A universal dynamical metabolic model representing mixotrophic growth of *Chlorella* sp. on wastes. **2023**, 229, 119388 ○
- 107 Detailed analysis of metabolism reveals growth-rate-promoting interactions between *Anaerostipes caccae* and *Bacteroides* spp.. **2023**, 79, 102680 ○
- 106 Machine learning in bioprocess development: from promise to practice. **2022**, 2
- 105 Advances in experimental and computational methodologies for the study of microbial-surface interactions at different omics levels. 13, ○
- 104 Genetically personalised organ-specific metabolic models in health and disease. **2022**, 13, ○
- 103 Analysis of the Propionate Metabolism in *Bacillus subtilis* during 3-Indolacetic Production. **2022**, 10, 2352 ○
- 102 Computer-Based Design of a Cell Factory for High-Yield Cytidine Production. **2022**, 11, 4123-4133 ○
- 101 Data analysis guidelines for single-cell RNA-seq in biomedical studies and clinical applications. **2022**, 9, ○
- 100 Longitudinal flux balance analyses of a patient with Crohn's disease highlight microbiome metabolic alterations. ○
- 99 Systematic evaluation of genome-wide metabolic landscapes in lactic acid bacteria reveals diet- and strain-specific probiotic idiosyncrasies. **2022**, 41, 111735 ○
- 98 Minireview: Engineering evolution to reconfigure phenotypic traits in microbes for biotechnological applications. **2022**, ○
- 97 Convergent Approaches to Delineate the Metabolic Regulation of Tumor Invasion by Hyaluronic Acid Biosynthesis. 2202224 ○
- 96 Transcriptome guided metabolic network analysis reveals rearrangements of carbon flux distribution in *Neisseria gonorrhoeae* during neutrophil co-culture. ○

- 95 The necessity of considering enzymes as compartments in constraint-based genome-scale metabolic models. ○
- 94 Metabolic reprogramming in Rheumatoid Arthritis Synovial Fibroblasts: A hybrid modeling approach. **2022**, 18, e1010408 ○
- 93 Construction of microbial consortia for microbial degradation of complex compounds. 10, ○
- 92 Nonlinear programming reformulation of dynamic flux balance analysis models. **2022**, 108101 ○
- 91 Flux balance analysis of metabolic networks for efficient engineering of microbial cell factories. 1-34 ○
- 90 A microbial community growth model for dynamic phenotype predictions. ○
- 89 MitoMouse is a model reconstruction of murine mitochondrial metabolism. ○
- 88 Antioxidant Green Factories: Toward Sustainable Production of Vitamin E in Plant In Vitro Cultures. 1
- 87 Unveiling abundance-dependent metabolic phenotypes of microbial communities. ○
- 86 Preterm birth is associated with xenobiotics and predicted by the vaginal metabolome. ○
- 85 Analysis of the genome-scale metabolic model of *Bacillus subtilis* to design novel in-silico strategies for native and recombinant L-asparaginase overproduction. ○
- 84 Comprehensive genome-scale metabolic model of the human pathogen *Cryptococcus neoformans*: A platform for understanding pathogen metabolism and identifying new drug targets. 3, ○
- 83 Insights into the metabolic specificities of pathogenic strains from the *Ralstonia solanacearum* species complex. ○
- 82 Identifying metabolic shifts in Crohn's disease using omics-driven contextualized computational metabolic network models. **2023**, 13, ○
- 81 The phenotype and genotype of fermentative microbes. ○
- 80 Context-Specific Genome-Scale Metabolic Modelling and Its Application to the Analysis of COVID-19 Metabolic Signatures. **2023**, 13, 126 ○
- 79 An Automated Scientist to Design and Optimize Microbial Strains for the Industrial Production of Small Molecules. ○
- 78 Investigation of two metabolic engineering approaches for (R,R)-2,3-butanediol production from glycerol in *Bacillus subtilis*. **2023**, 17, ○

- 77 A Novel Algorithm to Calculate Elementary Modes: Analysis of *Campylobacter jejuni* Metabolism. ○
- 76 Redox integration of signaling and metabolism in a head and neck cancer model of radiation resistance using COSMRO. 12, ○
- 75 Bioinformatics and metabolic flux analysis highlight a new mechanism involved in lactate oxidation in *Clostridium tyrobutyricum*. ○
- 74 A study of a diauxic growth experiment using an expanded dynamic flux balance framework. 2023, 18, e0280077 ○
- 73 Comparative study of two *Saccharomyces cerevisiae* strains with kinetic models at genome-scale. 2023, 76, 1-17 ○
- 72 Predicting stress response and improved protein overproduction in *Bacillus subtilis*. 2022, 8, ○
- 71 Metabolic Engineering: Methodologies and Applications. ○
- 70 On the computation of the minimum set of reactions for optimal growth in constraint-based models. 2022, ○
- 69 Genome-scale metabolic reconstruction of 7,302 human microorganisms for personalized medicine. 1
- 68 CONTRABASS: exploiting flux constraints in genome-scale models for the detection of vulnerabilities. 2023, 39, ○
- 67 Parameter Identification in Metabolic Reaction Networks by Means of Multiple Steady-State Measurements. 2023, 15, 368 ○
- 66 The Weimberg pathway: an alternative for *Myceliophthora thermophila* to utilize d-xylose. 2023, 16, ○
- 65 A nutrition algorithm to optimize feed and medium composition using genome-scale metabolic models. 2023, ○
- 64 Endothelial Cell Phenotypes Demonstrate Different Metabolic Patterns and Predict Mortality in Trauma Patients. 2023, 24, 2257 ○
- 63 Model-driven experimental design workflow expands understanding of regulatory role of Nac in *Escherichia coli*. 2023, 5, ○
- 62 Conic analysis of nonlinear metabolic networks. ○
- 61 Unlocking the magic in mycelium: Using synthetic biology to optimize filamentous fungi for biomanufacturing and sustainability. 2023, 19, 100560 ○
- 60 Automating the design-build-test-learn cycle towards next-generation bacterial cell factories. 2023, 74, 1-15 ○

- 59 Coupling Flux Balance Analysis with Reactive Transport Modeling through Machine Learning for Rapid and Stable Simulation of Microbial Metabolic Switching. ○
- 58 Integrated Constraint-Based Modeling of *E. coli* Cell-Free Protein Synthesis. ○
- 57 Computational biology predicts metabolic engineering targets for increased production of 102 valuable chemicals in yeast. ○
- 56 Simultaneous application of enzyme and thermodynamic constraints to metabolic models using an updated Python implementation of GECKO. ○
- 55 Deciphering mechanisms of production of natural compounds using inducer-producer microbial consortia. **2023**, 64, 108117 ○
- 54 ParaLINGAM: Parallel causal structure learning for linear non-Gaussian acyclic models. **2023**, 176, 114-127 ○
- 53 Moving beyond DNA: towards functional analysis of the vaginal microbiome by non-sequencing-based methods. **2023**, 73, 102292 ○
- 52 Amino acid auxotrophies in human gut bacteria are linked to higher microbiome diversity and long-term stability. ○
- 51 Systematic diet composition swap in a mouse genome-scale metabolic model reveals determinants of obesogenic diet metabolism in liver cancer. **2023**, 26, 106040 ○
- 50 Genome-scale community modeling for deciphering the inter-microbial metabolic interactions in fungus-farming termite gut microbiome. **2023**, 154, 106600 ○
- 49 A dynamic kinetic model captures cell-free metabolism for improved butanol production. **2023**, 76, 133-145 ○
- 48 FMO rewires metabolism to promote longevity through tryptophan and one carbon metabolism in *C. elegans*. **2023**, 14, ○
- 47 Networks of climate change: connecting causes and consequences. **2023**, 8, ○
- 46 Prediction of gene essentiality using machine learning and genome-scale metabolic models. **2022**, 55, 13-18 ○
- 45 A structured evaluation of genome-scale constraint-based modeling tools for microbial consortia. ○
- 44 Models and molecular mechanisms for trade-offs in the context of metabolism. ○
- 43 Light and carbon: Synthetic biology toward new cyanobacteria-based living biomaterials. **2023**, 19, 100583 ○
- 42 Qualitative Behavior of a Metabolic Pathway with Hybrid Feedback. **2023**, 22, 339-381 ○

- 41 Phenotype-specific estimation of metabolic fluxes using gene expression data. **2023**, 26, 106201
- 40 et i Bsu1209: A comprehensive multiscale metabolic model for *Bacillus subtilis*.
- 39 Controlling the human microbiome. **2023**, 14, 135-159
- 38 Systematizing Microbial Bioplastic Production for Developing Sustainable Bioeconomy: Metabolic Nexus Modeling, Economic and Environmental Technologies Assessment.
- 37 Gene Deletion Algorithms for Minimum Reaction Network Design by Mixed-Integer Linear Programming for Metabolite Production in Constraint-Based Models: gDel_minRN.
- 36 Design, evaluation and implementation of synthetic isopentyl diol pathways in *Escherichia coli*.
- 35 *Vibrio natriegens* genome-scale modeling reveals insights into halophilic adaptations and resource allocation. **2023**, 19,
- 34 A Genome-Scale Metabolic Model of Marine Heterotroph *Vibrio splendidus* Strain 1A01.
- 33 Competitive, multi-objective, and compartmented Flux Balance Analysis for addressing tissue-specific inborn errors of metabolism.
- 32 Inferring Pathological Metabolic Patterns in Breast Cancer Tissue from Genome-Scale Models. **2023**, 596-612
- 31 Mapping out the gut microbiota-dependent trimethylamine N-oxide super pathway for systems biology applications. 3,
- 30 FBA-PRCC. Partial Rank Correlation Coefficient (PRCC) Global Sensitivity Analysis (GSA) in Application to Constraint-Based Models. **2023**, 13, 500
- 29 Best Practices in Flux Sampling of Constrained-Based Models. **2023**, 234-248
- 28 Towards applications of genome-scale metabolic model-based approaches in designing synthetic microbial communities. **2023**, 11, 15
- 27 Ensemble-based genome-scale modeling predicts metabolic differences between macrophage subtypes in colorectal cancer.
- 26 2-Fucosyllactose helps butyrate producers outgrow competitors in infant gut microbiota simulations.
- 25 Highlighting the potential of *Synechococcus elongatus* PCC 7942 as platform to produce β -linolenic acid through an updated genome-scale metabolic modeling. 14,
- 24 Mathematical Modeling of Eicosanoid Metabolism in Macrophage Cells: Cybernetic Framework Combined with Novel Information-Theoretic Approaches. **2023**, 11, 874

- 23 High throughput ¹³C-metabolic flux analysis of 3-hydroxypropionic acid producing *Pichia pastoris* reveals limited availability of acetyl-CoA and ATP due to tight control of the glycolytic flux. ○
- 22 Microbial diversity and processes in groundwater. **2023**, 211-240 ○
- 21 More is Different: Metabolic Modeling of Diverse Microbial Communities. ○
- 20 A Multi-Level Systems Biology Analysis of Aldrin's Metabolic Effects on Prostate Cancer Cells. **2023**, 11, 11 ○
- 19 CompLaB v1.0: a scalable pore-scale model for flow, biogeochemistry, microbial metabolism, and biofilm dynamics. **2023**, 16, 1683-1696 ○
- 18 Engineering *Escherichia coli* for Poly- γ -Hydroxybutyrate Production from Methanol. **2023**, 10, 415 ○
- 17 Machine learning for metabolic pathway optimization: A review. **2023**, 21, 2381-2393 ○
- 16 A model industrial workhorse: *Bacillus subtilis* strain 168 and its genome after a quarter of a century. ○
- 15 High Growth Rate of Diatoms Explained by Reduced Carbon Requirement and Low Energy Cost of Silica Deposition. ○
- 14 L-lactate production in engineered *Saccharomyces cerevisiae* using a multistage multiobjective automated design framework. ○
- 13 The unraveling of balanced complexes in metabolic networks. **2023**, 13, ○
- 12 High-throughput metabolomics for the design and validation of a diauxic shift model. **2023**, 9, ○
- 11 Engineering yeast mitochondrial metabolism for 3-hydroxypropionate production. **2023**, 16, ○
- 10 A benchmark of optimization solvers for genome-scale metabolic modeling. ○
- 9 New Insights on Metabolic Features of *Bacillus subtilis* Based on Multistrain Genome-Scale Metabolic Modeling. **2023**, 24, 7091 ○
- 8 Evaluating proteome allocation of *Saccharomyces cerevisiae* phenotypes with resource balance analysis. **2023**, ○
- 7 Metabolic switch in the aging astrocyte supported via integrative approach comprising network and transcriptome analyses. ○
- 6 Metabolic role of the hepatic valine/3-hydroxyisobutyrate (3-HIB) pathway in fatty liver disease. **2023**, 91, 104569 ○

- 5 Metabolic complexity increases adaptability. ○
- 4 Flux Sampling in Genome-scale Metabolic Modeling of Microbial Communities. ○
- 3 Genome-scale metabolic modeling reveals metabolic trade-offs associated with lipid production in *Rhodotorula toruloides*. **2023**, 19, e10111009 ○
- 2 Systems Immunology Approaches to Metabolism. **2023**, 41, 317-342 ○
- 1 A Holistic Approach from Systems Biology Reveals the Direct Influence of the Quorum-Sensing Phenomenon on *Pseudomonas aeruginosa* Metabolism to Pyoverdine Biosynthesis. **2023**, 13, 659 ○