Ronan M T Fleming

List of Publications by Year
in descending order

67 papers	**9,654** citations	101384 **36** h-index	102304 **66** g-index
83 all docs	**83** docs citations	**83** times ranked	**11032** citing authors

#	Article	IF	Citations
1	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	5.5	1,408
2	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	9.4	920
3	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	5.5	833
4	Advantages and challenges of microfluidic cell culture in polydimethylsiloxane devices. Biosensors and Bioelectronics, 2015, 63, 218-231.	5.3	786
5	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. Nature Biotechnology, 2017, 35, 81-89.	9.4	629
6	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	9.4	520
7	Derivation of Human Midbrain-Specific Organoids from Neuroepithelial StemÂCells. Stem Cell Reports, 2017, 8, 1144-1154.	2.3	321
8	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
9	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. Nucleic Acids Research, 2019, 47, D614-D624.	6.5	257
10	Consistent Estimation of Gibbs Energy Using Component Contributions. PLoS Computational Biology, 2013, 9, e1003098.	1.5	231
11	Systematic assessment of secondary bile acid metabolism in gut microbes reveals distinct metabolic capabilities in inflammatory bowel disease. Microbiome, 2019, 7, 75.	4.9	215
12	Systems-level characterization of a host-microbe metabolic symbiosis in the mammalian gut. Gut Microbes, 2013, 4, 28-40.	4.3	210
13	Reconstruction and Use of Microbial Metabolic Networks: the Core <i>Escherichia coli</i> Metabolic Model as an Educational Guide. EcoSal Plus, 2010, 4, .	2.1	195
14	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
15	Genome-Scale Reconstruction of Escherichia coli's Transcriptional and Translational Machinery: A Knowledge Base, Its Mathematical Formulation, and Its Functional Characterization. PLoS Computational Biology, 2009, 5, e1000312.	1.5	161
16	Differentiation of neuroepithelial stem cells into functional dopaminergic neurons in 3D microfluidic cell culture. Lab on A Chip, 2015, 15, 2419-2428.	3.1	130
17	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128
18	Personalized wholeâ€body models integrate metabolism, physiology, and the gut microbiome. Molecular Systems Biology, 2020, 16, e8982.	3.2	122

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19	fastGapFill: efficient gap filling in metabolic networks. Bioinformatics, 2014, 30, 2529-2531.	1.8	105
20	Integrated Analyses of Microbiome and Longitudinal Metabolome Data Reveal Microbial-Host Interactions on Sulfur Metabolism in Parkinson's Disease. Cell Reports, 2019, 29, 1767-1777.e8.	2.9	102
21	The Microbiome Modeling Toolbox: from microbial interactions to personalized microbial communities. Bioinformatics, 2019, 35, 2332-2334.	1.8	102
22	Multiscale Modeling of Metabolism and Macromolecular Synthesis in E. coli and Its Application to the Evolution of Codon Usage. PLoS ONE, 2012, 7, e45635.	1.1	100
23	A systems biology approach to studying the role of microbes in human health. Current Opinion in Biotechnology, 2013, 24, 4-12.	3.3	100
24	3D Cultures of Parkinson's Disease-Specific Dopaminergic Neurons for High Content Phenotyping and Drug Testing. Advanced Science, 2019, 6, 1800927.	5.6	92
25	Automated microfluidic cell culture of stem cell derived dopaminergic neurons. Scientific Reports, 2019, 9, 1796.	1.6	81
26	Quantitative assignment of reaction directionality in constraint-based models of metabolism: Application to Escherichia coli. Biophysical Chemistry, 2009, 145, 47-56.	1.5	75
27	Monitoring metabolites consumption and secretion in cultured cells using ultra-performance liquid chromatography quadrupole–time of flight mass spectrometry (UPLC–Q–ToF-MS). Analytical and Bioanalytical Chemistry, 2012, 402, 1183-1198.	1.9	74
28	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
29	CHRR: coordinate hit-and-run with rounding for uniform sampling of constraint-based models. Bioinformatics, 2017, 33, 1741-1743.	1.8	67
30	Prediction of intracellular metabolic states from extracellular metabolomic data. Metabolomics, 2015, 11, 603-619.	1.4	66
31	von Bertalanffy 1.0: a COBRA toolbox extension to thermodynamically constrain metabolic models. Bioinformatics, 2011, 27, 142-143.	1.8	59
32	Functional Characterization of Alternate Optimal Solutions of Escherichia coli's Transcriptional and Translational Machinery. Biophysical Journal, 2010, 98, 2072-2081.	0.2	58
33	Integrated stoichiometric, thermodynamic and kinetic modelling of steady state metabolism. Journal of Theoretical Biology, 2010, 264, 683-692.	0.8	55
34	ReconMap: an interactive visualization of human metabolism. Bioinformatics, 2017, 33, 605-607.	1.8	52
35	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	3.2	48
36	Quantitative Assignment of Reaction Directionality in a Multicompartmental Human Metabolic Reconstruction. Biophysical Journal, 2012, 102, 1703-1711.	0.2	44

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37	Accelerating the DC algorithm for smooth functions. Mathematical Programming, 2018, 169, 95-118.	1.6	43
38	MetaboTools: A Comprehensive Toolbox for Analysis of Genome-Scale Metabolic Models. Frontiers in Physiology, 2016, 7, 327.	1.3	41
39	A Systems Biology Approach to Drug Targets in Pseudomonas aeruginosa Biofilm. PLoS ONE, 2012, 7, e34337.	1.1	41
40	Quantitative systems pharmacology and the personalized drug–microbiota–diet axis. Current Opinion in Systems Biology, 2017, 4, 43-52.	1.3	37
41	Real-time optical pH measurement in a standard microfluidic cell culture system. Biomedical Optics Express, 2013, 4, 1749.	1.5	36
42	A variational principle for computing nonequilibrium fluxes and potentials in genome-scale biochemical networks. Journal of Theoretical Biology, 2012, 292, 71-77.	0.8	31
43	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. Scientific Reports, 2017, 7, 40863.	1.6	30
44	Modeling the effects of commonly used drugs on human metabolism. FEBS Journal, 2015, 282, 297-317.	2.2	29
45	Determination of the rheological properties of Matrigel for optimum seeding conditions in microfluidic cell cultures. AIP Advances, 2018, 8, .	0.6	28
46	DistributedFBA.jl: high-level, high-performance flux balance analysis in Julia. Bioinformatics, 2017, 33, 1421-1423.	1.8	25
47	LC–MS/MS analysis of the central energy and carbon metabolites in biological samples following derivatization by dimethylaminophenacyl bromide. Journal of Chromatography A, 2019, 1608, 460413.	1.8	24
48	Comparative evaluation of open source software for mapping between metabolite identifiers in metabolic network reconstructions: application to Recon 2. Journal of Cheminformatics, 2014, 6, 2.	2.8	23
49	Comparative evaluation of atom mapping algorithms for balanced metabolic reactions: application to Recon 3D. Journal of Cheminformatics, 2017, 9, 39.	2.8	23
50	Phenotype-Agnostic Molecular Subtyping of Neurodegenerative Disorders: The Cincinnati Cohort Biomarker Program (CCBP). Frontiers in Aging Neuroscience, 2020, 12, 553635.	1.7	22
51	Robust flux balance analysis of multiscale biochemical reaction networks. BMC Bioinformatics, 2013, 14, 240.	1.2	21
52	Identification of Conserved Moieties in Metabolic Networks by Graph Theoretical Analysis of Atom Transition Networks. PLoS Computational Biology, 2016, 12, e1004999.	1.5	21
53	Local convergence of the Levenberg–Marquardt method under Hölder metric subregularity. Advances in Computational Mathematics, 2019, 45, 2771-2806.	0.8	20
54	Embryonic development of selectively vulnerable neurons in Parkinson's disease. Npj Parkinson's Disease, 2017, 3, 21.	2.5	19

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55	A systems approach reveals distinct metabolic strategies among the NCI-60 cancer cell lines. PLoS Computational Biology, 2017, 13, e1005698.	1.5	19
56	Conditions for duality between fluxes and concentrations in biochemical networks. Journal of Theoretical Biology, 2016, 409, 1-10.	0.8	15
57	DEMETER: efficient simultaneous curation of genome-scale reconstructions guided by experimental data and refined gene annotations. Bioinformatics, 2021, 37, 3974-3975.	1.8	13
58	Reply to "Challenges in modeling the human gut microbiome". Nature Biotechnology, 2018, 36, 686-691.	9.4	12
59	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. BMC Bioinformatics, 2019, 20, 140.	1.2	10
60	Mass conserved elementary kinetics is sufficient for the existence of a non-equilibrium steady state concentration. Journal of Theoretical Biology, 2012, 314, 173-181.	0.8	7
61	Passive controlled flow for Parkinson's disease neuronal cell culture in 3D microfluidic devices. Organs-on-a-Chip, 2020, 2, 100005.	1.8	7
62	Finding zeros of Hölder metrically subregular mappings via globally convergent Levenberg–Marquardt methods. Optimization Methods and Software, 2022, 37, 113-149.	1.6	6
63	A constraint-based modelling approach to metabolic dysfunction in Parkinson's disease. Computational and Structural Biotechnology Journal, 2015, 13, 484-491.	1.9	5
64	Globally convergent algorithms for finding zeros of duplomonotone mappings. Optimization Letters, 2015, 9, 569-584.	0.9	4
65	Structural conserved moiety splitting of a stoichiometric matrix. Journal of Theoretical Biology, 2020, 499, 110276.	0.8	4
66	Integrated Analyses of Microbiome and Longitudinal Metabolome Data Reveal Microbial-Host Interactions on Sulfur Metabolism in Parkinson's Disease. SSRN Electronic Journal, 0, , .	0.4	2
67	Non-rigid estimation of cell motion in calcium time-lapse images. Proceedings of SPIE, 2016, , .	0.8	0