Ronan M T Fleming

List of Publications by Year
in descending order

67 papers	**9,654** citations	101543 **36** h-index	102487 **66** g-index
83 all docs	**83** docs citations	**83** times ranked	**11032** citing authors

#	Article	IF	Citations
1	Finding zeros of Hölder metrically subregular mappings via globally convergent Levenberg–Marquardt methods. Optimization Methods and Software, 2022, 37, 113-149.	2.4	6
2	DEMETER: efficient simultaneous curation of genome-scale reconstructions guided by experimental data and refined gene annotations. Bioinformatics, 2021, 37, 3974-3975.	4.1	13
3	Passive controlled flow for Parkinson's disease neuronal cell culture in 3D microfluidic devices. Organs-on-a-Chip, 2020, 2, 100005.	3.2	7
4	Phenotype-Agnostic Molecular Subtyping of Neurodegenerative Disorders: The Cincinnati Cohort Biomarker Program (CCBP). Frontiers in Aging Neuroscience, 2020, 12, 553635.	3.4	22
5	Personalized whole‐body models integrate metabolism, physiology, and the gut microbiome. Molecular Systems Biology, 2020, 16, e8982.	7.2	122
6	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
7	Structural conserved moiety splitting of a stoichiometric matrix. Journal of Theoretical Biology, 2020, 499, 110276.	1.7	4
8	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
9	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.	3.7	24
10	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.	6.4	102
11	Local convergence of the Levenberg–Marquardt method under Hölder metric subregularity. Advances in Computational Mathematics, 2019, 45, 2771-2806.	1.6	20
12	Systematic assessment of secondary bile acid metabolism in gut microbes reveals distinct metabolic capabilities in inflammatory bowel disease. Microbiome, 2019, 7, 75.	11.1	215
13	Metabolic and signalling network maps integration: application to cross-talk studies and omics data analysis in cancer. BMC Bioinformatics, 2019, 20, 140.	2.6	10
14	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
15	Automated microfluidic cell culture of stem cell derived dopaminergic neurons. Scientific Reports, 2019, 9, 1796.	3.3	81
16	The Virtual Metabolic Human database: integrating human and gut microbiome metabolism with nutrition and disease. Nucleic Acids Research, 2019, 47, D614-D624.	14.5	257
17	3D Cultures of Parkinson's Disease‐Specific Dopaminergic Neurons for High Content Phenotyping and Drug Testing. Advanced Science, 2019, 6, 1800927.	11.2	92
18	The Microbiome Modeling Toolbox: from microbial interactions to personalized microbial communities. Bioinformatics, 2019, 35, 2332-2334.	4.1	102

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19	Community-driven roadmap for integrated disease maps. Briefings in Bioinformatics, 2019, 20, 659-670.	6.5	48
20	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	17.5	520
21	Accelerating the DC algorithm for smooth functions. Mathematical Programming, 2018, 169, 95-118.	2.4	43
22	Determination of the rheological properties of Matrigel for optimum seeding conditions in microfluidic cell cultures. AIP Advances, 2018, 8, .	1.3	28
23	Reply to "Challenges in modeling the human gut microbiome". Nature Biotechnology, 2018, 36, 686-691.	17.5	12
24	ReconMap: an interactive visualization of human metabolism. Bioinformatics, 2017, 33, 605-607.	4.1	52
25	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. Scientific Reports, 2017, 7, 40863.	3.3	30
26	Derivation of Human Midbrain-Specific Organoids from Neuroepithelial StemÂCells. Stem Cell Reports, 2017, 8, 1144-1154.	4.8	321
27	DistributedFBA.jl: high-level, high-performance flux balance analysis in Julia. Bioinformatics, 2017, 33, 1421-1423.	4.1	25
28	Quantitative systems pharmacology and the personalized drug–microbiota–diet axis. Current Opinion in Systems Biology, 2017, 4, 43-52.	2.6	37
29	Embryonic development of selectively vulnerable neurons in Parkinson's disease. Npj Parkinson's Disease, 2017, 3, 21.	5.3	19
30	Comparative evaluation of atom mapping algorithms for balanced metabolic reactions: application to Recon 3D. Journal of Cheminformatics, 2017, 9, 39.	6.1	23
31	Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. Nature Biotechnology, 2017, 35, 81-89.	17.5	629
32	A systems approach reveals distinct metabolic strategies among the NCI-60 cancer cell lines. PLoS Computational Biology, 2017, 13, e1005698.	3.2	19
33	CHRR: coordinate hit-and-run with rounding for uniform sampling of constraint-based models. Bioinformatics, 2017, 33, 1741-1743.	4.1	67
34	Identification of Conserved Moieties in Metabolic Networks by Graph Theoretical Analysis of Atom Transition Networks. PLoS Computational Biology, 2016, 12, e1004999.	3.2	21
35	MetaboTools: A Comprehensive Toolbox for Analysis of Genome-Scale Metabolic Models. Frontiers in Physiology, 2016, 7, 327.	2.8	41
36	Conditions for duality between fluxes and concentrations in biochemical networks. Journal of Theoretical Biology, 2016, 409, 1-10.	1.7	15

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37	Non-rigid estimation of cell motion in calcium time-lapse images. Proceedings of SPIE, 2016, , .	0.8	0
38	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
39	A constraint-based modelling approach to metabolic dysfunction in Parkinson's disease. Computational and Structural Biotechnology Journal, 2015, 13, 484-491.	4.1	5
40	Globally convergent algorithms for finding zeros of duplomonotone mappings. Optimization Letters, 2015, 9, 569-584.	1.6	4
41	Differentiation of neuroepithelial stem cells into functional dopaminergic neurons in 3D microfluidic cell culture. Lab on A Chip, 2015, 15, 2419-2428.	6.0	130
42	Modeling the effects of commonly used drugs on human metabolism. FEBS Journal, 2015, 282, 297-317.	4.7	29
43	Prediction of intracellular metabolic states from extracellular metabolomic data. Metabolomics, 2015, 11, 603-619.	3.0	66
44	Advantages and challenges of microfluidic cell culture in polydimethylsiloxane devices. Biosensors and Bioelectronics, 2015, 63, 218-231.	10.1	786
45	<scp>fast</scp>G<scp>ap</scp>F<scp>ill</scp>: efficient gap filling in metabolic networks. Bioinformatics, 2014, 30, 2529-2531.	4.1	105
46	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.	6.1	23
47	Robust flux balance analysis of multiscale biochemical reaction networks. BMC Bioinformatics, 2013, 14, 240.	2.6	21
48	A systems biology approach to studying the role of microbes in human health. Current Opinion in Biotechnology, 2013, 24, 4-12.	6.6	100
49	Systems-level characterization of a host-microbe metabolic symbiosis in the mammalian gut. Gut Microbes, 2013, 4, 28-40.	9.8	210
50	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
51	Real-time optical pH measurement in a standard microfluidic cell culture system. Biomedical Optics Express, 2013, 4, 1749.	2.9	36
52	Consistent Estimation of Gibbs Energy Using Component Contributions. PLoS Computational Biology, 2013, 9, e1003098.	3.2	231
53	Mass conserved elementary kinetics is sufficient for the existence of a non-equilibrium steady state concentration. Journal of Theoretical Biology, 2012, 314, 173-181.	1.7	7
54	Quantitative Assignment of Reaction Directionality in a Multicompartmental Human Metabolic Reconstruction. Biophysical Journal, 2012, 102, 1703-1711.	0.5	44

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55	Multiscale Modeling of Metabolism and Macromolecular Synthesis in E. coli and Its Application to the Evolution of Codon Usage. PLoS ONE, 2012, 7, e45635.	2.5	100
56	A variational principle for computing nonequilibrium fluxes and potentials in genome-scale biochemical networks. Journal of Theoretical Biology, 2012, 292, 71-77.	1.7	31
57	Monitoring metabolites consumption and secretion in cultured cells using ultra-performance liquid chromatography quadrupoleâ€"time of flight mass spectrometry (UPLCâ€"Qâ€"ToF-MS). Analytical and Bioanalytical Chemistry, 2012, 402, 1183-1198.	3.7	74
58	A Systems Biology Approach to Drug Targets in Pseudomonas aeruginosa Biofilm. PLoS ONE, 2012, 7, e34337.	2.5	41
59	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	12.0	1,408
60	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
61	von Bertalanffy 1.0: a COBRA toolbox extension to thermodynamically constrain metabolic models. Bioinformatics, 2011, 27, 142-143.	4.1	59
62	Reconstruction and Use of Microbial Metabolic Networks: the Core <i>Escherichia coli</i> Metabolic Model as an Educational Guide. EcoSal Plus, 2010, 4, .	5.4	195
63	Integrated stoichiometric, thermodynamic and kinetic modelling of steady state metabolism. Journal of Theoretical Biology, 2010, 264, 683-692.	1.7	55
64	Functional Characterization of Alternate Optimal Solutions of Escherichia coli's Transcriptional and Translational Machinery. Biophysical Journal, 2010, 98, 2072-2081.	0.5	58
65	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.	3.2	161
66	Quantitative assignment of reaction directionality in constraint-based models of metabolism: Application to Escherichia coli. Biophysical Chemistry, 2009, 145, 47-56.	2.8	75
67	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