

Neil Swainston

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

5,200
citations

201674

27
h-index

161849

54
g-index

72
all docs

72
docs citations

72
times ranked

7307
citing authors

#	ARTICLE	IF	CITATIONS
1	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	17.5	920
2	ChEBI in 2016: Improved services and an expanding collection of metabolites. <i>Nucleic Acids Research</i> , 2016, 44, D1214-D1219.	14.5	752
3	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	17.5	530
4	Synthetic biology for the directed evolution of protein biocatalysts: navigating sequence space intelligently. <i>Chemical Society Reviews</i> , 2015, 44, 1172-1239.	38.1	316
5	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	3.0	243
6	Growth control of the eukaryote cell: a systems biology study in yeast. <i>Journal of Biology</i> , 2007, 6, 4.	2.7	234
7	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
8	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. <i>Trends in Biotechnology</i> , 2015, 33, 237-246.	9.3	167
9	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. <i>Communications Biology</i> , 2018, 1, 66.	4.4	159
10	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
11	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	2.8	113
12	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. <i>PLoS Biology</i> , 2017, 15, e2001414.	5.6	97
13	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
14	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2019, 8, 127-136.	3.8	88
15	A \hat{r} rule of 0.5 \hat{r} ™ for the metabolite-likeness of approved pharmaceutical drugs. <i>Metabolomics</i> , 2015, 11, 323-339.	3.0	84
16	Selenzyme: enzyme selection tool for pathway design. <i>Bioinformatics</i> , 2018, 34, 2153-2154.	4.1	75
17	SBOL Visual: A Graphical Language for Genetic Designs. <i>PLoS Biology</i> , 2015, 13, e1002310.	5.6	73
18	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187-203.	1.5	67

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19	Bioinformatics for the synthetic biology of natural products: integrating across the Design–Build–Test cycle. <i>Natural Product Reports</i> , 2016, 33, 925-932.	10.3	58
20	The SuBLiMinaL Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 186.	1.5	51
21	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. <i>Metabolic Engineering</i> , 2020, 60, 168-182.	7.0	48
22	Engineering <i>Escherichia coli</i> towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. <i>Synthetic Biology</i> , 2020, 5, ysaa012.	2.2	45
23	DeepGraphMolGen, a multi-objective, computational strategy for generating molecules with desirable properties: a graph convolution and reinforcement learning approach. <i>Journal of Cheminformatics</i> , 2020, 12, 53.	6.1	42
24	SpeedyGenes: an improved gene synthesis method for the efficient production of error-corrected, synthetic protein libraries for directed evolution. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 273-280.	2.1	40
25	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. <i>FEBS Journal</i> , 2018, 285, 2193-2204.	4.7	38
26	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. <i>Synthetic Biology</i> , 2019, 4, ysz025.	2.2	35
27	GeneGenie: optimized oligomer design for directed evolution. <i>Nucleic Acids Research</i> , 2014, 42, W395-W400.	14.5	33
28	biochem4j: Integrated and extensible biochemical knowledge through graph databases. <i>PLoS ONE</i> , 2017, 12, e0179130.	2.5	31
29	An analysis of a “community-driven” reconstruction of the human metabolic network. <i>Metabolomics</i> , 2013, 9, 757-764.	3.0	30
30	Deep learning and generative methods in cheminformatics and chemical biology: navigating small molecule space intelligently. <i>Biochemical Journal</i> , 2020, 477, 4559-4580.	3.7	29
31	MassGenie: A Transformer-Based Deep Learning Method for Identifying Small Molecules from Their Mass Spectra. <i>Biomolecules</i> , 2021, 11, 1793.	4.0	29
32	libAnnotationSBML: a library for exploiting SBML annotations. <i>Bioinformatics</i> , 2009, 25, 2292-2293.	4.1	28
33	Systematic integration of experimental data and models in systems biology. <i>BMC Bioinformatics</i> , 2010, 11, 582.	2.6	28
34	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. <i>Bioinformatics</i> , 2018, 34, 2327-2329.	4.1	25
35	VAE-Sim: A Novel Molecular Similarity Measure Based on a Variational Autoencoder. <i>Molecules</i> , 2020, 25, 3446.	3.8	23
36	An automated pipeline for the screening of diverse monoterpene synthase libraries. <i>Scientific Reports</i> , 2019, 9, 11936.	3.3	21

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37	Enzyme kinetics informatics: from instrument to browser. FEBS Journal, 2010, 277, 3769-3779.	4.7	20
38	Engineering the "Missing Link" in Biosynthetic (âˆ“) -Menthol Production: Bacterial Isopulegone Isomerase. ACS Catalysis, 2018, 8, 2012-2020.	11.2	20
39	libChEBI: an API for accessing the ChEBI database. Journal of Cheminformatics, 2016, 8, 11.	6.1	19
40	RobOKoD: microbial strain design for (over)production of target compounds. Frontiers in Cell and Developmental Biology, 2015, 3, 17.	3.7	17
41	GeneORator: An Effective Strategy for Navigating Protein Sequence Space More Efficiently through Boolean OR-Type DNA Libraries. ACS Synthetic Biology, 2019, 8, 1371-1378.	3.8	15
42	EnzymeML" a data exchange format for biocatalysis and enzymology. FEBS Journal, 2022, 289, 5864-5874.	4.7	14
43	SpeedyGenes: Exploiting an Improved Gene Synthesis Method for the Efficient Production of Synthetic Protein Libraries for Directed Evolution. Methods in Molecular Biology, 2017, 1472, 63-78.	0.9	12
44	CodonGenie: optimised ambiguous codon design tools. PeerJ Computer Science, 0, 3, e120.	4.5	12
45	Sustainable Model Building. Methods in Enzymology, 2011, 500, 371-395.	1.0	11
46	Multifragment DNA Assembly of Biochemical Pathways via Automated Ligase Cycling Reaction. Methods in Enzymology, 2018, 608, 369-392.	1.0	11
47	Fast and Flexible Synthesis of Combinatorial Libraries for Directed Evolution. Methods in Enzymology, 2018, 608, 59-79.	1.0	11
48	A QconCAT informatics pipeline for the analysis, visualization and sharing of absolute quantitative proteomics data. Proteomics, 2011, 11, 329-333.	2.2	9
49	SynBiopython: an open-source software library for <i>Synthetic Biology</i>. Synthetic Biology, 2021, 6, .	2.2	9
50	Rationalizing Context-Dependent Performance of Dynamic RNA Regulatory Devices. ACS Synthetic Biology, 2018, 7, 1660-1668.	3.8	8
51	SYNBIOCHEM" a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. Biochemical Society Transactions, 2016, 44, 675-677.	3.4	7
52	Integrative Information Management for Systems Biology. Lecture Notes in Computer Science, 2010, , 164-178.	1.3	6
53	DNA Scanner: a web application for comparing DNA synthesis feasibility, price and turnaround time across vendors. Synthetic Biology, 2020, 5, .	2.2	4
54	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 2011, , .	0.1	1

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55	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 0, , .	0.1	1
56	Waveomics: bringing experimental data to online collaboration. Nature Precedings, 2010, , .	0.1	0
57	The SBML Level 3 Annotation package: an initial proposal. Nature Precedings, 2010, , .	0.1	0