

Neil Swainston

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

5,200
citations

201575

27
h-index

161767

54
g-index

72
all docs

72
docs citations

72
times ranked

7307
citing authors

#	ARTICLE	IF	CITATIONS
1	EnzymeMLâ€”a data exchange format for biocatalysis and enzymology. FEBS Journal, 2022, 289, 5864-5874.	2.2	14
2	SynBiopython: an open-source software library for <i>Synthetic Biology</i>. Synthetic Biology, 2021, 6, .	1.2	9
3	MassGenie: A Transformer-Based Deep Learning Method for Identifying Small Molecules from Their Mass Spectra. Biomolecules, 2021, 11, 1793.	1.8	29
4	DNA Scanner: a web application for comparing DNA synthesis feasibility, price and turnaround time across vendors. Synthetic Biology, 2020, 5, .	1.2	4
5	Engineering Escherichia coli towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. Synthetic Biology, 2020, 5, ysaa012.	1.2	45
6	VAE-Sim: A Novel Molecular Similarity Measure Based on a Variational Autoencoder. Molecules, 2020, 25, 3446.	1.7	23
7	DeepGraphMolGen, a multi-objective, computational strategy for generating molecules with desirable properties: a graph convolution and reinforcement learning approach. Journal of Cheminformatics, 2020, 12, 53.	2.8	42
8	Rapid prototyping of microbial production strains for the biomanufacture of potential materials monomers. Metabolic Engineering, 2020, 60, 168-182.	3.6	48
9	Deep learning and generative methods in cheminformatics and chemical biology: navigating small molecule space intelligently. Biochemical Journal, 2020, 477, 4559-4580.	1.7	29
10	<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
11	Highly multiplexed, fast and accurate nanopore sequencing for verification of synthetic DNA constructs and sequence libraries. Synthetic Biology, 2019, 4, ysz025.	1.2	35
12	An automated pipeline for the screening of diverse monoterpene synthase libraries. Scientific Reports, 2019, 9, 11936.	1.6	21
13	GeneORator: An Effective Strategy for Navigating Protein Sequence Space More Efficiently through Boolean OR-Type DNA Libraries. ACS Synthetic Biology, 2019, 8, 1371-1378.	1.9	15
14	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in <i>Escherichia coli</i>. ACS Synthetic Biology, 2019, 8, 127-136.	1.9	88
15	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. Bioinformatics, 2018, 34, 2327-2329.	1.8	25
16	STRENDAB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	2.2	38
17	Selenzyme: enzyme selection tool for pathway design. Bioinformatics, 2018, 34, 2153-2154.	1.8	75
18	Engineering the â€œMissing Linkâ€”in Biosynthetic (âˆ—)-Menthol Production: Bacterial Isopulegone Isomerase. ACS Catalysis, 2018, 8, 2012-2020.	5.5	20

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19	Multifragment DNA Assembly of Biochemical Pathways via Automated Ligase Cycling Reaction. <i>Methods in Enzymology</i> , 2018, 608, 369-392.	0.4	11
20	Rationalizing Context-Dependent Performance of Dynamic RNA Regulatory Devices. <i>ACS Synthetic Biology</i> , 2018, 7, 1660-1668.	1.9	8
21	Fast and Flexible Synthesis of Combinatorial Libraries for Directed Evolution. <i>Methods in Enzymology</i> , 2018, 608, 59-79.	0.4	11
22	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. <i>Communications Biology</i> , 2018, 1, 66.	2.0	159
23	SpeedyGenes: Exploiting an Improved Gene Synthesis Method for the Efficient Production of Synthetic Protein Libraries for Directed Evolution. <i>Methods in Molecular Biology</i> , 2017, 1472, 63-78.	0.4	12
24	biochem4j: Integrated and extensible biochemical knowledge through graph databases. <i>PLoS ONE</i> , 2017, 12, e0179130.	1.1	31
25	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.	2.6	97
26	Bioinformatics for the synthetic biology of natural products: integrating across the Design-Build-Test cycle. <i>Natural Product Reports</i> , 2016, 33, 925-932.	5.2	58
27	SYNBIOCHEM—a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. <i>Biochemical Society Transactions</i> , 2016, 44, 675-677.	1.6	7
28	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	1.4	243
29	libChEBI: an API for accessing the ChEBI database. <i>Journal of Cheminformatics</i> , 2016, 8, 11.	2.8	19
30	ChEBI in 2016: Improved services and an expanding collection of metabolites. <i>Nucleic Acids Research</i> , 2016, 44, D1214-D1219.	6.5	752
31	RobOKoD: microbial strain design for (over)production of target compounds. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 17.	1.8	17
32	A “rule of 0.5”™ for the metabolite-likeness of approved pharmaceutical drugs. <i>Metabolomics</i> , 2015, 11, 323-339.	1.4	84
33	Synthetic biology for the directed evolution of protein biocatalysts: navigating sequence space intelligently. <i>Chemical Society Reviews</i> , 2015, 44, 1172-1239.	18.7	316
34	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. <i>Trends in Biotechnology</i> , 2015, 33, 237-246.	4.9	167
35	SBOL Visual: A Graphical Language for Genetic Designs. <i>PLoS Biology</i> , 2015, 13, e1002310.	2.6	73
36	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.	1.0	40

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37	GeneGenie: optimized oligomer design for directed evolution. <i>Nucleic Acids Research</i> , 2014, 42, W395-W400.	6.5	33
38	An analysis of a $\tilde{\text{community-driven}}$ reconstruction of the human metabolic network. <i>Metabolomics</i> , 2013, 9, 757-764.	1.4	30
39	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
40	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	1.3	113
41	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
42	SBML Level 3 Package Proposal: Annotation. <i>Nature Precedings</i> , 2011, , .	0.1	1
43	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187-203.	1.0	67
44	A QconCAT informatics pipeline for the analysis, visualization and sharing of absolute quantitative proteomics data. <i>Proteomics</i> , 2011, 11, 329-333.	1.3	9
45	Sustainable Model Building. <i>Methods in Enzymology</i> , 2011, 500, 371-395.	0.4	11
46	The SuBliMinaL Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 186.	1.0	51
47	Systematic integration of experimental data and models in systems biology. <i>BMC Bioinformatics</i> , 2010, 11, 582.	1.2	28
48	Enzyme kinetics informatics: from instrument to browser. <i>FEBS Journal</i> , 2010, 277, 3769-3779.	2.2	20
49	Waveomics: bringing experimental data to online collaboration. <i>Nature Precedings</i> , 2010, , .	0.1	0
50	The SBML Level 3 Annotation package: an initial proposal. <i>Nature Precedings</i> , 2010, , .	0.1	0
51	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
52	Integrative Information Management for Systems Biology. <i>Lecture Notes in Computer Science</i> , 2010, , 164-178.	1.0	6
53	libAnnotationSBML: a library for exploiting SBML annotations. <i>Bioinformatics</i> , 2009, 25, 2292-2293.	1.8	28
54	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	9.4	530

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55	Growth control of the eukaryote cell: a systems biology study in yeast. Journal of Biology, 2007, 6, 4.	2.7	234
56	SBML Level 3 Package Proposal: Annotation. Nature Precedings, 0, , .	0.1	1
57	CodonGenie: optimised ambiguous codon design tools. PeerJ Computer Science, 0, 3, e120.	2.7	12