

Anil Wipat

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

2,971
citations

331259

21
h-index

174990

52
g-index

88
all docs

88
docs citations

88
times ranked

3045
citing authors

#	ARTICLE	IF	CITATIONS
1	Taverna: a tool for the composition and enactment of bioinformatics workflows. <i>Bioinformatics</i> , 2004, 20, 3045-3054.	1.8	1,303
2	The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology. <i>Nature Biotechnology</i> , 2014, 32, 545-550.	9.4	247
3	SynBioHub: A Standards-Enabled Design Repository for Synthetic Biology. <i>ACS Synthetic Biology</i> , 2018, 7, 682-688.	1.9	112
4	Qualitatively modelling and analysing genetic regulatory networks: a Petri net approach. <i>Bioinformatics</i> , 2007, 23, 336-343.	1.8	111
5	Sharing Structure and Function in Biological Design with SBOL 2.0. <i>ACS Synthetic Biology</i> , 2016, 5, 498-506.	1.9	88
6	SBOL Visual: A Graphical Language for Genetic Designs. <i>PLoS Biology</i> , 2015, 13, e1002310.	2.6	73
7	Quantitative Fitness Analysis Shows That NMD Proteins and Many Other Protein Complexes Suppress or Enhance Distinct Telomere Cap Defects. <i>PLoS Genetics</i> , 2011, 7, e1001362.	1.5	65
8	Harmonizing semantic annotations for computational models in biology. <i>Briefings in Bioinformatics</i> , 2019, 20, 540-550.	3.2	52
9	Structure-function studies of an engineered scaffold protein derived from Stefin A. II: Development and applications of the SQT variant. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 751-763.	1.0	43
10	The Synthetic Biology Open Language (SBOL) Version 3: Simplified Data Exchange for Bioengineering. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 1009.	2.0	40
11	An Integrated Data Driven Approach to Drug Repositioning Using Gene-Disease Associations. <i>PLoS ONE</i> , 2016, 11, e0155811.	1.1	39
12	Model annotation for synthetic biology: automating model to nucleotide sequence conversion. <i>Bioinformatics</i> , 2011, 27, 973-979.	1.8	38
13	SBOLDesigner 2: An Intuitive Tool for Structural Genetic Design. <i>ACS Synthetic Biology</i> , 2017, 6, 1150-1160.	1.9	38
14	A standard-enabled workflow for synthetic biology. <i>Biochemical Society Transactions</i> , 2017, 45, 793-803.	1.6	38
15	Communicating Structure and Function in Synthetic Biology Diagrams. <i>ACS Synthetic Biology</i> , 2019, 8, 1818-1825.	1.9	30
16	A Computational Workflow for the Automated Generation of Models of Genetic Designs. <i>ACS Synthetic Biology</i> , 2019, 8, 1548-1559.	1.9	27
17	Modelling and Analysing Genetic Networks: From Boolean Networks to Petri Nets. <i>Lecture Notes in Computer Science</i> , 2006, , 127-141.	1.0	25
18	Saint: a lightweight integration environment for model annotation. <i>Bioinformatics</i> , 2009, 25, 3026-3027.	1.8	25

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19	libSBOLj 2.0: A Java Library to Support SBOL 2.0. IEEE Life Sciences Letters, 2015, 1, 34-37.	1.2	24
20	The SBOL Stack: A Platform for Storing, Publishing, and Sharing Synthetic Biology Designs. ACS Synthetic Biology, 2016, 5, 487-497.	1.9	24
21	Data Integration and Mining for Synthetic Biology Design. ACS Synthetic Biology, 2016, 5, 1086-1097.	1.9	23
22	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. PLoS Biology, 2020, 18, e3000885.	2.6	23
23	e-Science: relieving bottlenecks in large-scale genome analyses. Nature Reviews Microbiology, 2008, 6, 948-954.	13.6	22
24	Synthetic Biology Open Language (SBOL) Version 2.0.0. Journal of Integrative Bioinformatics, 2015, 12, 902-991.	1.0	22
25	Mining integrated semantic networks for drug repositioning opportunities. PeerJ, 2016, 4, e1558.	0.9	22
26	Genome-Wide Analysis to Identify Pathways Affecting Telomere-Initiated Senescence in Budding Yeast. G3: Genes, Genomes, Genetics, 2011, 1, 197-208.	0.8	21
27	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	21
28	Synthetic Biology Open Language (SBOL) Version 2.0.0. Journal of Integrative Bioinformatics, 2015, 12, 272.	1.0	21
29	Synthetic Biology Open Language (SBOL) Version 2.2.0. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	20
30	Data mining the human gut microbiota for therapeutic targets. Briefings in Bioinformatics, 2012, 13, 751-768.	3.2	19
31	Proposed Data Model for the Next Version of the Synthetic Biology Open Language. ACS Synthetic Biology, 2015, 4, 57-71.	1.9	19
32	VisBOL: Web-Based Tools for Synthetic Biology Design Visualization. ACS Synthetic Biology, 2016, 5, 874-876.	1.9	18
33	Annotation of rule-based models with formal semantics to enable creation, analysis, reuse and visualization. Bioinformatics, 2016, 32, 908-917.	1.8	18
34	Annotation of SBML models through rule-based semantic integration. Journal of Biomedical Semantics, 2010, 1, S3.	0.9	16
35	Synthetic Biology Open Language (SBOL) Version 2.3. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	16
36	Composable Modular Models for Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-19.	1.8	15

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37	Automatic Parameterisation of Stochastic Petri Net Models of Biological Networks. <i>Electronic Notes in Theoretical Computer Science</i> , 2006, 151, 111-129.	0.9	13
38	Synthetic biology open language (SBOL) version 3.0.0. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	13
39	BacillOndex: An Integrated Data Resource for Systems and Synthetic Biology. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 103-116.	1.0	12
40	SBOL-OWL: An Ontological Approach for Formal and Semantic Representation of Synthetic Biology Information. <i>ACS Synthetic Biology</i> , 2019, 8, 1498-1514.	1.9	12
41	Bayesian integration of networks without gold standards. <i>Bioinformatics</i> , 2012, 28, 1495-1500.	1.8	11
42	Synthetic Biology Open Language (SBOL) Version 2.1.0. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, .	1.0	11
43	Toward Full-Stack <i>In Silico</i> Synthetic Biology: Integrating Model Specification, Simulation, Verification, and Biological Compilation. <i>ACS Synthetic Biology</i> , 2021, 10, 1931-1945.	1.9	10
44	Customizable views on semantically integrated networks for systems biology. <i>Bioinformatics</i> , 2011, 27, 1299-1306.	1.8	9
45	Constructing synthetic biology workflows in the cloud. <i>Engineering Biology</i> , 2017, 1, 61-65.	0.8	9
46	An integrated dataset for in silico drug discovery. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	9
47	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.1. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	8
48	Integration of Full-Coverage Probabilistic Functional Networks with Relevance to Specific Biological Processes. <i>Lecture Notes in Computer Science</i> , 2009, , 31-46.	1.0	8
49	A grid-based system for microbial genome comparison and analysis. , 2005, , .		7
50	Future-proofing synthetic biology: educating the next generation. <i>Engineering Biology</i> , 2019, 3, 25-31.	0.8	7
51	ShortBOL: A Language for Scripting Designs for Engineered Biological Systems Using Synthetic Biology Open Language (SBOL). <i>ACS Synthetic Biology</i> , 2020, 9, 962-966.	1.9	7
52	Design and modelling of an engineered bacteria-based, pressure-sensitive soil. <i>Bioinspiration and Biomimetics</i> , 2018, 13, 046004.	1.5	6
53	Species-Specific Detection of <i>C. difficile</i> Using Targeted Antibody Design. <i>Analytical Chemistry</i> , 2018, 90, 13475-13482.	3.2	6
54	Synthetic biology open language visual (SBOL Visual) version 2.3. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.0	6

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55	Virtual Parts Repository 2: Model-Driven Design of Genetic Regulatory Circuits. ACS Synthetic Biology, 2021, 10, 3304-3315.	1.9	6
56	Assessment of Bacillus subtilis Plasmid pLS20 Conjugation in the Absence of Quorum Sensing Repression. Microorganisms, 2021, 9, 1931.	1.6	4
57	BacillusRegNet: a transcriptional regulation database and analysis platform for Bacillus species. Journal of Integrative Bioinformatics, 2014, 11, 244.	1.0	4
58	BacillusRegNet: A transcriptional regulation database and analysis platform for Bacillus species. Journal of Integrative Bioinformatics, 2014, 11, 106-119.	1.0	3
59	sboljs: Bringing the Synthetic Biology Open Language to the Web Browser. ACS Synthetic Biology, 2019, 8, 191-193.	1.9	3
60	SBOL Visual 2 Ontology. ACS Synthetic Biology, 2020, 9, 972-977.	1.9	3
61	Microbase2.0: A Generic Framework for Computationally Intensive Bioinformatics Workflows in the Cloud. Journal of Integrative Bioinformatics, 2012, 9, 101-112.	1.0	2
62	A distributed computational search strategy for the identification of diagnostics targets: Application to finding aptamer targets for methicillin-resistant staphylococci. Journal of Integrative Bioinformatics, 2014, 11, 80-92.	1.0	2
63	A Visual Language for Protein Design. ACS Synthetic Biology, 2017, 6, 1120-1123.	1.9	2
64	A Genetic Circuit Compiler: Generating Combinatorial Genetic Circuits with Web Semantics and Inference. ACS Synthetic Biology, 2018, 7, 2812-2823.	1.9	2
65	Probabilistic latent semantic analysis applied to whole bacterial genomes identifies common genomic features. Journal of Integrative Bioinformatics, 2014, 11, 243.	1.0	2
66	Annotation of SBML Models Through Rule-Based Semantic Integration. Nature Precedings, 2009, , .	0.1	1
67	The quantification of antibody elements and receptors subunit expression using qPCR: The design of VH, VL, CH, CL, FcR subunits primers for a more holistic view of the immune system. Journal of Immunological Methods, 2020, 476, 112683.	0.6	1
68	Capturing Multicellular System Designs Using Synthetic Biology Open Language (SBOL). ACS Synthetic Biology, 2020, 9, 2410-2417.	1.9	1
69	Microbase2.0: a generic framework for computationally intensive bioinformatics workflows in the cloud. Journal of Integrative Bioinformatics, 2012, 9, 212.	1.0	1
70	Modelling The Fitness Landscapes of a SCRaMbLEd Yeast Genome. , 2021, , .		1
71	A novel method for transforming Geobacillus kaustophilus with a chromosomal segment of Bacillus subtilis transferred via pLS20-dependent conjugation. Microbial Cell Factories, 2022, 21, 34.	1.9	1
72	Modelling the fitness landscapes of a SCRaMbLEd yeast genome. BioSystems, 2022, 219, 104730.	0.9	1

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73	Introduction to the Special Issue on Computational Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-5.	1.8	0
74	Engineering bacterial populations for pattern formation. , 2016, , .		0
75	Title is missing!. , 2020, 18, e3000885.		0
76	Title is missing!. , 2020, 18, e3000885.		0
77	Title is missing!. , 2020, 18, e3000885.		0
78	Title is missing!. , 2020, 18, e3000885.		0
79	Title is missing!. , 2020, 18, e3000885.		0
80	Title is missing!. , 2020, 18, e3000885.		0
81	Title is missing!. , 2020, 18, e3000885.		0