

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	A novel method for transforming <i>Geobacillus kaustophilus</i> with a chromosomal segment of <i>Bacillus subtilis</i> transferred via pLS20-dependent conjugation. <i>Microbial Cell Factories</i> , 2022, 21, 34.	1.9	1
2	Modelling the fitness landscapes of a SCRaMbLEd yeast genome. <i>BioSystems</i> , 2022, 219, 104730.	0.9	1
3	Synthetic biology open language visual (SBOL Visual) version 2.3. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.0	6
4	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
5	Assessment of <i>Bacillus subtilis</i> Plasmid pLS20 Conjugation in the Absence of Quorum Sensing Repression. <i>Microorganisms</i> , 2021, 9, 1931.	1.6	4
6	Modelling The Fitness Landscapes of a SCRaMbLEd Yeast Genome. , 2021, , .		1
7	Virtual Parts Repository 2: Model-Driven Design of Genetic Regulatory Circuits. <i>ACS Synthetic Biology</i> , 2021, 10, 3304-3315.	1.9	6
8	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. <i>Journal of Immunological Methods</i> , 2020, 476, 112683.	0.6	1
9	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
10	Capturing Multicellular System Designs Using Synthetic Biology Open Language (SBOL). <i>ACS Synthetic Biology</i> , 2020, 9, 2410-2417.	1.9	1
11	SBOL Visual 2 Ontology. <i>ACS Synthetic Biology</i> , 2020, 9, 972-977.	1.9	3
12	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
13	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. <i>PLoS Biology</i> , 2020, 18, e3000885.	2.6	23
14	Synthetic biology open language (SBOL) version 3.0.0. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	13
15	Title is missing!. , 2020, 18, e3000885.		0
16	Title is missing!. , 2020, 18, e3000885.		0
17	Title is missing!. , 2020, 18, e3000885.		0
18	Title is missing!. , 2020, 18, e3000885.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 18, e3000885.		0
20	Title is missing!. , 2020, 18, e3000885.		0
21	Title is missing!. , 2020, 18, e3000885.		0
22	A Computational Workflow for the Automated Generation of Models of Genetic Designs. ACS Synthetic Biology, 2019, 8, 1548-1559.	1.9	27
23	Communicating Structure and Function in Synthetic Biology Diagrams. ACS Synthetic Biology, 2019, 8, 1818-1825.	1.9	30
24	Future-proofing synthetic biology: educating the next generation. Engineering Biology, 2019, 3, 25-31.	0.8	7
25	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.1. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	8
26	Synthetic Biology Open Language (SBOL) Version 2.3. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	16
27	SBOL-OWL: An Ontological Approach for Formal and Semantic Representation of Synthetic Biology Information. ACS Synthetic Biology, 2019, 8, 1498-1514.	1.9	12
28	Harmonizing semantic annotations for computational models in biology. Briefings in Bioinformatics, 2019, 20, 540-550.	3.2	52
29	sboljs: Bringing the Synthetic Biology Open Language to the Web Browser. ACS Synthetic Biology, 2019, 8, 191-193.	1.9	3
30	Design and modelling of an engineered bacteria-based, pressure-sensitive soil. Bioinspiration and Biomimetics, 2018, 13, 046004.	1.5	6
31	SynBioHub: A Standards-Enabled Design Repository for Synthetic Biology. ACS Synthetic Biology, 2018, 7, 682-688.	1.9	112
32	A Genetic Circuit Compiler: Generating Combinatorial Genetic Circuits with Web Semantics and Inference. ACS Synthetic Biology, 2018, 7, 2812-2823.	1.9	2
33	Synthetic Biology Open Language (SBOL) Version 2.2.0. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	20
34	Species-Specific Detection of <i>C. difficile</i> Using Targeted Antibody Design. Analytical Chemistry, 2018, 90, 13475-13482.	3.2	6
35	Synthetic Biology Open Language Visual (SBOL Visual) Version 2.0. Journal of Integrative Bioinformatics, 2018, 15, .	1.0	21
36	A Visual Language for Protein Design. ACS Synthetic Biology, 2017, 6, 1120-1123.	1.9	2

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37	SBOLDesigner 2: An Intuitive Tool for Structural Genetic Design. ACS Synthetic Biology, 2017, 6, 1150-1160.	1.9	38
38	A standard-enabled workflow for synthetic biology. Biochemical Society Transactions, 2017, 45, 793-803.	1.6	38
39	Constructing synthetic biology workflows in the cloud. Engineering Biology, 2017, 1, 61-65.	0.8	9
40	Synthetic Biology Open Language (SBOL) Version 2.1.0. Journal of Integrative Bioinformatics, 2016, 13, .	1.0	11
41	An Integrated Data Driven Approach to Drug Repositioning Using Gene-Disease Associations. PLoS ONE, 2016, 11, e0155811.	1.1	39
42	Engineering bacterial populations for pattern formation. , 2016, , .		0
43	Sharing Structure and Function in Biological Design with SBOL 2.0. ACS Synthetic Biology, 2016, 5, 498-506.	1.9	88
44	Data Integration and Mining for Synthetic Biology Design. ACS Synthetic Biology, 2016, 5, 1086-1097.	1.9	23
45	The SBOL Stack: A Platform for Storing, Publishing, and Sharing Synthetic Biology Designs. ACS Synthetic Biology, 2016, 5, 487-497.	1.9	24
46	VisBOL: Web-Based Tools for Synthetic Biology Design Visualization. ACS Synthetic Biology, 2016, 5, 874-876.	1.9	18
47	Annotation of rule-based models with formal semantics to enable creation, analysis, reuse and visualization. Bioinformatics, 2016, 32, 908-917.	1.8	18
48	Mining integrated semantic networks for drug repositioning opportunities. PeerJ, 2016, 4, e1558.	0.9	22
49	libSBOLj 2.0: A Java Library to Support SBOL 2.0. IEEE Life Sciences Letters, 2015, 1, 34-37.	1.2	24
50	Synthetic Biology Open Language (SBOL) Version 2.0.0. Journal of Integrative Bioinformatics, 2015, 12, 902-991.	1.0	22
51	Proposed Data Model for the Next Version of the Synthetic Biology Open Language. ACS Synthetic Biology, 2015, 4, 57-71.	1.9	19
52	SBOL Visual: A Graphical Language for Genetic Designs. PLoS Biology, 2015, 13, e1002310.	2.6	73
53	Synthetic Biology Open Language (SBOL) Version 2.0.0. Journal of Integrative Bioinformatics, 2015, 12, 272.	1.0	21
54	BacillusRegNet: A transcriptional regulation database and analysis platform for Bacillus species. Journal of Integrative Bioinformatics, 2014, 11, 106-119.	1.0	3

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55	Introduction to the Special Issue on Computational Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-5.	1.8	0
56	Composable Modular Models for Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-19.	1.8	15
57	The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology. Nature Biotechnology, 2014, 32, 545-550.	9.4	247
58	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
59	BacillusRegNet: a transcriptional regulation database and analysis platform for Bacillus species. Journal of Integrative Bioinformatics, 2014, 11, 244.	1.0	4
60	Probabilistic latent semantic analysis applied to whole bacterial genomes identifies common genomic features. Journal of Integrative Bioinformatics, 2014, 11, 243.	1.0	2
61	BacillOndex: An Integrated Data Resource for Systems and Synthetic Biology. Journal of Integrative Bioinformatics, 2013, 10, 103-116.	1.0	12
62	Bayesian integration of networks without gold standards. Bioinformatics, 2012, 28, 1495-1500.	1.8	11
63	Microbase2.0: A Generic Framework for Computationally Intensive Bioinformatics Workflows in the Cloud. Journal of Integrative Bioinformatics, 2012, 9, 101-112.	1.0	2
64	Data mining the human gut microbiota for therapeutic targets. Briefings in Bioinformatics, 2012, 13, 751-768.	3.2	19
65	Microbase2.0: a generic framework for computationally intensive bioinformatics workflows in the cloud. Journal of Integrative Bioinformatics, 2012, 9, 212.	1.0	1
66	Model annotation for synthetic biology: automating model to nucleotide sequence conversion. Bioinformatics, 2011, 27, 973-979.	1.8	38
67	Customizable views on semantically integrated networks for systems biology. Bioinformatics, 2011, 27, 1299-1306.	1.8	9
68	Structure-function studies of an engineered scaffold protein derived from Stefin A. II: Development and applications of the SQT variant. Protein Engineering, Design and Selection, 2011, 24, 751-763.	1.0	43
69	Genome-Wide Analysis to Identify Pathways Affecting Telomere-Initiated Senescence in Budding Yeast. G3: Genes, Genomes, Genetics, 2011, 1, 197-208.	0.8	21
70	Quantitative Fitness Analysis Shows That NMD Proteins and Many Other Protein Complexes Suppress or Enhance Distinct Telomere Cap Defects. PLoS Genetics, 2011, 7, e1001362.	1.5	65
71	Annotation of SBML models through rule-based semantic integration. Journal of Biomedical Semantics, 2010, 1, S3.	0.9	16
72	An integrated dataset for in silico drug discovery. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	9

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73	Annotation of SBML Models Through Rule-Based Semantic Integration. Nature Precedings, 2009, , .	0.1	1
74	Saint: a lightweight integration environment for model annotation. Bioinformatics, 2009, 25, 3026-3027.	1.8	25
75	Integration of Full-Coverage Probabilistic Functional Networks with Relevance to Specific Biological Processes. Lecture Notes in Computer Science, 2009, , 31-46.	1.0	8
76	e-Science: relieving bottlenecks in large-scale genome analyses. Nature Reviews Microbiology, 2008, 6, 948-954.	13.6	22
77	Qualitatively modelling and analysing genetic regulatory networks: a Petri net approach. Bioinformatics, 2007, 23, 336-343.	1.8	111
78	Automatic Parameterisation of Stochastic Petri Net Models of Biological Networks. Electronic Notes in Theoretical Computer Science, 2006, 151, 111-129.	0.9	13
79	Modelling and Analysing Genetic Networks: From Boolean Networks to Petri Nets. Lecture Notes in Computer Science, 2006, , 127-141.	1.0	25
80	A grid-based system for microbial genome comparison and analysis. , 2005, , .		7
81	Taverna: a tool for the composition and enactment of bioinformatics workflows. Bioinformatics, 2004, 20, 3045-3054.	1.8	1,303