Jean Loup M Faulon

List of Publications by Year
in descending order

98 papers	4,737 citations	76326 40 h-index	110387 64 g-index
114 all docs	114 docs citations	114 times ranked	4415 citing authors

#	Article	IF	Citations
1	Differentially Optimized Cell-Free Buffer Enables Robust Expression from Unprotected Linear DNA in Exonuclease-Deficient Extracts. ACS Synthetic Biology, 2022, 11, 732-746.	3.8	16
2	Cell-Free and AI Integration. Methods in Molecular Biology, 2022, 2433, 303-323.	0.9	2
3	A versatile active learning workflow for optimization of genetic and metabolic networks. Nature Communications, 2022, 13, .	12.8	34
4	Optimising protein synthesis in cellâ€free systems, a review. Engineering Biology, 2021, 5, 10-19.	1.8	7
5	In silico, inÂvitro, and inÂvivo machine learning in synthetic biology and metabolic engineering. Current Opinion in Chemical Biology, 2021, 65, 85-92.	6.1	21
6	Reinforcement Learning for Bioretrosynthesis. ACS Synthetic Biology, 2020, 9, 157-168.	3.8	77
7	Engineering Escherichia coli towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. Synthetic Biology, 2020, 5, ysaa012.	2.2	45
8	Large scale active-learning-guided exploration for in vitro protein production optimization. Nature Communications, 2020, 11, 1872.	12.8	70
9	Development of a Biosensor for Detection of Benzoic Acid Derivatives in Saccharomyces cerevisiae. Frontiers in Bioengineering and Biotechnology, 2020, 7, 372.	4.1	12
10	Synthetic Biology at the Hand of Cell-Free Systems. , 2020, , 275-288.		1
11	Optimizing Cell-Free Biosensors to Monitor Enzymatic Production. ACS Synthetic Biology, 2019, 8, 1952-1957.	3.8	37
12	Metabolic perceptrons for neural computing in biological systems. Nature Communications, 2019, 10, 3880.	12.8	51
13	Microbial Genes for a Circular and Sustainable Bio-PET Economy. Genes, 2019, 10, 373.	2.4	94
14	Custom-made transcriptional biosensors for metabolic engineering. Current Opinion in Biotechnology, 2019, 59, 78-84.	6.6	72
15	Plug-and-play metabolic transducers expand the chemical detection space of cell-free biosensors. Nature Communications, 2019, 10, 1697.	12.8	99
16	Efficient learning in metabolic pathway designs through optimal assembling. IFAC-PapersOnLine, 2019, 52, 7-12.	0.9	5
17	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in Escherichia coli. ACS Synthetic Biology, 2019, 8, 127-136.	3.8	88
18	RetroRules: a database of reaction rules for engineering biology. Nucleic Acids Research, 2019, 47, D1229-D1235.	14.5	74

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19	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. Bioinformatics, 2018, 34, 2327-2329.	4.1	25
20	Selenzyme: enzyme selection tool for pathway design. Bioinformatics, 2018, 34, 2153-2154.	4.1	75
21	A dataset of small molecules triggering transcriptional and translational cellular responses. Data in Brief, 2018, 17, 1374-1378.	1.0	26
22	Extended Metabolic Space Modeling. Methods in Molecular Biology, 2018, 1671, 83-96.	0.9	1
23	RetroPath2.0: A retrosynthesis workflow for metabolic engineers. Metabolic Engineering, 2018, 45, 158-170.	7.0	174
24	Models for Cell-Free Synthetic Biology: Make Prototyping Easier, Better, and Faster. Frontiers in Bioengineering and Biotechnology, 2018, 6, 182.	4.1	33
25	Enzyme Discovery: Enzyme Selection and Pathway Design. Methods in Enzymology, 2018, 608, 3-27.	1.0	2
26	Building a minimal and generalizable model of transcription factorâ€“based biosensors: Showcasing flavonoids. Biotechnology and Bioengineering, 2018, 115, 2292-2304.	3.3	29
27	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. Communications Biology, 2018, 1, 66.	4.4	159
28	biochem4j: Integrated and extensible biochemical knowledge through graph databases. PLoS ONE, 2017, 12, e0179130.	2.5	31
29	Molecular structures enumeration and virtual screening in the chemical space with RetroPath2.0. Journal of Cheminformatics, 2017, 9, 64.	6.1	13
30	Expanding Biosensing Abilities through Computer-Aided Design of Metabolic Pathways. ACS Synthetic Biology, 2016, 5, 1076-1085.	3.8	54
31	SYNBIOCHEMâ€“a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. Biochemical Society Transactions, 2016, 44, 675-677.	3.4	7
32	Mapping the patent landscape of synthetic biology for fine chemical production pathways. Microbial Biotechnology, 2016, 9, 687-695.	4.2	11
33	SYNBIOCHEM Synthetic Biology Research Centre, Manchester â€“ A UK foundry for fine and speciality chemicals production. Synthetic and Systems Biotechnology, 2016, 1, 271-275.	3.7	6
34	Sensing new chemicals with bacterial transcription factors. Current Opinion in Microbiology, 2016, 33, 105-112.	5.1	70
35	SensiPath: computer-aided design of sensing-enabling metabolic pathways. Nucleic Acids Research, 2016, 44, W226-W231.	14.5	60
36	Semisupervised Gaussian Process for Automated Enzyme Search. ACS Synthetic Biology, 2016, 5, 518-528.	3.8	57

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37	A Sense of Balance: Experimental Investigation and Modeling of a Malonyl-CoA Sensor in Escherichia coli. Frontiers in Bioengineering and Biotechnology, 2015, 3, 46.	4.1	11
38	XTMS: pathway design in an eXTended metabolic space. Nucleic Acids Research, 2014, 42, W389-W394.	14.5	96
39	PrecisePrimer: an easy-to-use web server for designing PCR primers for DNA library cloning and DNA shuffling. Nucleic Acids Research, 2014, 42, W205-W209.	14.5	6
40	Computer-aided design for metabolic engineering. Journal of Biotechnology, 2014, 192, 302-313.	3.8	26
41	Retropath: Automated Pipeline for Embedded Metabolic Circuits. ACS Synthetic Biology, 2014, 3, 565-577.	3.8	76
42	Validation of RetroPath, a computerâ€aided design tool for metabolic pathway engineering. Biotechnology Journal, 2014, 9, 1446-1457.	3.5	53
43	Statistical ensemble analysis for simulating extrinsic noise-driven response in NF-ÎºB signaling networks. BMC Systems Biology, 2013, 7, 45.	3.0	9
44	PMG: Multi-core Metabolite Identification. Electronic Notes in Theoretical Computer Science, 2013, 299, 53-60.	0.9	8
45	Retrosynthetic Design of Heterologous Pathways. Methods in Molecular Biology, 2013, 985, 149-173.	0.9	17
46	Stereo Signature Molecular Descriptor. Journal of Chemical Information and Modeling, 2013, 53, 887-897.	5.4	51
47	Cheminformatics. Communications of the ACM, 2012, 55, 65-75.	4.5	21
48	A retrosynthetic biology approach to therapeutics: from conception to delivery. Current Opinion in Biotechnology, 2012, 23, 948-956.	6.6	21
49	Enumerating metabolic pathways for the production of heterologous target chemicals in chassis organisms. BMC Systems Biology, 2012, 6, 10.	3.0	57
50	OMG: Open Molecule Generator. Journal of Cheminformatics, 2012, 4, 21.	6.1	62
51	Compound toxicity screening and structureâ€“activity relationship modeling in Escherichia coli. Biotechnology and Bioengineering, 2012, 109, 846-850.	3.3	50
52	Origins of Specificity and Promiscuity in Metabolic Networks. Journal of Biological Chemistry, 2011, 286, 43994-44004.	3.4	68
53	Toward Quantitative Structureâ€“Property Relationships for Charge Transfer Rates of Polycyclic Aromatic Hydrocarbons. Journal of Chemical Theory and Computation, 2011, 7, 2549-2555.	5.3	37
54	Engineering antibiotic production and overcoming bacterial resistance. Biotechnology Journal, 2011, 6, 812-825.	3.5	30

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55	Editorial: Synthetic Biology â€“ applying new paradigms at the interface of fundamental research and innovation. Biotechnology Journal, 2011, 6, 766-767.	3.5	1
56	A retrosynthetic biology approach to metabolic pathway design for therapeutic production. BMC Systems Biology, 2011, 5, 122.	3.0	100
57	Disparate data fusion for protein phosphorylation prediction. Annals of Operations Research, 2010, 174, 219-235.	4.1	3
58	Molecular signatures-based prediction of enzyme promiscuity. Bioinformatics, 2010, 26, 2012-2019.	4.1	72
59	Reaction Network Generation. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2010, , 317-341.	0.1	7
60	Optimal bundling of transmembrane helices using sparse distance constraints. Protein Science, 2009, 13, 2613-2627.	7.6	36
61	Data mining PubChem using a support vector machine with the Signature molecular descriptor: Classification of factor XIa inhibitors. Journal of Molecular Graphics and Modelling, 2008, 27, 466-475.	2.4	41
62	Understanding virulence mechanisms in M. tuberculosis infection via A circuit-based simulation framework. , 2008, 2008, 4953-5.		2
63	Genome scale enzymeâ€“metabolite and drugâ€“target interaction predictions using the signature molecular descriptor. Bioinformatics, 2008, 24, 225-233.	4.1	139
64	Identification of Expression Patterns of IL-2-Responsive Genes in the Murine T Cell Line CTLL-2. Journal of Interferon and Cytokine Research, 2007, 27, 991-996.	1.2	9
65	Using Product Kernels to Predict Protein Interactions. Advances in Biochemical Engineering/Biotechnology, 2007, 110, 215-245.	1.1	1
66	Boolean dynamics of genetic regulatory networks inferred from microarray time series data. Bioinformatics, 2007, 23, 866-874.	4.1	144
67	Systems chemical biology. Nature Chemical Biology, 2007, 3, 447-450.	8.0	129
68	Sensitivity Analysis of a Computational Model of the IKKâ€“NFâ€Bâ€“IÎºBÎ±â€“A20 Signal Transduction Network. Annals of the New York Academy of Sciences, 2007, 1115, 221-239.	3.8	22
69	Designing Novel Polymers with Targeted Properties Using the Signature Molecular Descriptor. Journal of Chemical Information and Modeling, 2006, 46, 826-835.	5.4	31
70	Prediction of Î²-strand packing interactions using the signature product. Journal of Molecular Modeling, 2006, 12, 355-361.	1.8	9
71	A deterministic algorithm for constrained enumeration of transmembrane protein folds. Computational Biology and Chemistry, 2005, 29, 143-150.	2.3	5
72	Reverse engineering chemical structures from molecular descriptors: how many solutions?. Journal of Computer-Aided Molecular Design, 2005, 19, 637-650.	2.9	23

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73	Predicting protein-protein interactions using signature products. Bioinformatics, 2005, 21, 218-226.	4.1	353
74	The Signature Molecular Descriptor. 5. The Design of Hydrofluoroether Foam Blowing Agents Using Inverse-QSAR. Industrial & Engineering Chemistry Research, 2005, 44, 8883-8891.	3.7	39
75	The Signature Molecular Descriptor. 4. Canonizing Molecules Using Extended Valence Sequences. Journal of Chemical Information and Computer Sciences, 2004, 44, 427-436.	2.8	74
76	The signature molecular descriptor. Journal of Molecular Graphics and Modelling, 2004, 22, 263-273.	2.4	91
77	Thermodynamic Properties of Asphaltenes Through Computer Assisted Structure Elucidation and Atomistic Simulations. 1. Bulk Arabian Light Asphaltenes. Petroleum Science and Technology, 2004, 22, 877-899.	1.5	15
78	Exploring the conformational space of membrane protein folds matching distance constraints. Protein Science, 2003, 12, 1750-1761.	7.6	21
79	The Signature Molecular Descriptor. 2. Enumerating Molecules from Their Extended Valence Sequences. Journal of Chemical Information and Computer Sciences, 2003, 43, 721-734.	2.8	139
80	The Signature Molecular Descriptor. 1. Using Extended Valence Sequences in QSAR and QSPR Studies. Journal of Chemical Information and Computer Sciences, 2003, 43, 707-720.	2.8	209
81	The Signature Molecular Descriptor. Part 1. Using Extended Valence Sequences in QSAR and QSPR Studies.. ChemInform, 2003, 34, no.	0.0	3
82	The Signature Molecular Descriptor. Part 2. Enumerating Molecules from Their Extended Valence Sequences.. ChemInform, 2003, 34, no.	0.0	1
83	Constrained walks and self-avoiding walks: implications for protein structure determination. Journal of Physics A, 2002, 35, 1-19.	1.6	9
84	Developing a methodology for an inverse quantitative structure-activity relationship using the signature molecular descriptor. Journal of Molecular Graphics and Modelling, 2002, 20, 429-438.	2.4	93
85	Stochastic Generator of Chemical Structure. 3. Reaction Network Generation. Journal of Chemical Information and Computer Sciences, 2001, 41, 894-908.	2.8	29
86	Stochastic generator of chemical structure. 4. Building polymeric systems with specified properties. Journal of Computational Chemistry, 2001, 22, 580-590.	3.3	11
87	Isomorphism, Automorphism Partitioning, and Canonical Labeling Can Be Solved in Polynomial-Time for Molecular Graphs. Journal of Chemical Information and Computer Sciences, 1998, 38, 432-444.	2.8	57
88	Massively parallel simulations of diffusion in dense polymeric structures. , 1997, , .		1
89	Stochastic Generator of Chemical Structure. 2. Using Simulated Annealing To Search the Space of Constitutional Isomers. Journal of Chemical Information and Computer Sciences, 1996, 36, 731-740.	2.8	34
90	Pore Structure of Imogolite Computer Models. Langmuir, 1996, 12, 4463-4468.	3.5	33

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91	Molecular dynamics computer simulations of silica aerogels. Journal of Non-Crystalline Solids, 1995, 186, 349-355.	3.1	34
92	Correlation between Microporosity and Fractal Dimension of Bituminous Coal Based on Computer-Generated Models. Energy & Fuels, 1994, 8, 408-414.	5.1	49
93	Is There Any Order in the Structure of Lignin?. Energy & Fuels, 1994, 8, 402-407.	5.1	75
94	A three-dimensional model for lignocellulose from gymnospermous wood. Organic Geochemistry, 1994, 21, 1169-1179.	1.8	73
95	Calculating the Number-Averaged Molecular Weight (M0) of Aromatic and Hydroaromatic Clusters in Coal using Rubber Elasticity Theory. Energy & Fuels, 1994, 8, 1020-1023.	5.1	8
96	Stochastic Generator of Chemical Structure. 1. Application to the Structure Elucidation of Large Molecules. Journal of Chemical Information and Computer Sciences, 1994, 34, 1204-1218.	2.8	74
97	A computer-aided molecular model for high volatile bituminous coal. Fuel Processing Technology, 1993, 34, 277-293.	7.2	32
98	Handbook of Chemoinformatics Algorithms. , 0, , .		47