Jean Loup M Faulon

List of Publications by Year in Descending Order

99 papers	3,569 citations	37 h-index	57 g-index
114 ext. papers	4,230 ext. citations	6 avg, IF	5.6 L-index

#	Paper	IF	Citations
99	Cell-Free Biosensors and AI Integration.. *Methods in Molecular Biology*, **2022**, 2433, 303-323	1.4	0
98	Optimising protein synthesis in cell-free systems, a review. *Engineering Biology*, **2021**, 5, 10-19	1.1	3
97	In silico, in vitro, and in vivo machine learning in synthetic biology and metabolic engineering. *Current Opinion in Chemical Biology*, **2021**, 65, 85-92	9.7	3
96	Large scale active-learning-guided exploration for in vitro protein production optimization. *Nature Communications*, **2020**, 11, 1872	17.4	35
95	Synthetic Biology at the Hand of Cell-Free Systems **2020**, 275-288		1
94	Reinforcement Learning for Bioretrosynthesis. *ACS Synthetic Biology*, **2020**, 9, 157-168	5.7	30
93	Engineering towards production of gatekeeper (2)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. *Synthetic Biology*, **2020**, 5, ysaa012	3.3	17
92	Metabolic perceptrons for neural computing in biological systems. *Nature Communications*, **2019**, 10, 3880	17.4	30
91	Microbial Genes for a Circular and Sustainable Bio-PET Economy. *Genes*, **2019**, 10,	4.2	64
90	Custom-made transcriptional biosensors for metabolic engineering. *Current Opinion in Biotechnology*, **2019**, 59, 78-84	11.4	38
89	Plug-and-play metabolic transducers expand the chemical detection space of cell-free biosensors. *Nature Communications*, **2019**, 10, 1697	17.4	47
88	Development of a Biosensor for Detection of Benzoic Acid Derivatives in. *Frontiers in Bioengineering and Biotechnology*, **2019**, 7, 372	5.8	5
87	Optimizing Cell-Free Biosensors to Monitor Enzymatic Production. *ACS Synthetic Biology*, **2019**, 8, 1952-1957	5.7	19
86	Efficient learning in metabolic pathway designs through optimal assembling. *IFAC-PapersOnLine*, **2019**, 52, 7-12	0.7	3
85	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in Escherichia coli. *ACS Synthetic Biology*, **2019**, 8, 127-136	5.7	53
84	RetroRules: a database of reaction rules for engineering biology. *Nucleic Acids Research*, **2019**, 47, D1229-D1235	20.1	40
83	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. *Bioinformatics*, **2018**, 34, 2327-2329	7.2	16

82	Selenzyme: enzyme selection tool for pathway design. *Bioinformatics*, **2018**, 34, 2153-2154	7.2	41
81	A dataset of small molecules triggering transcriptional and translational cellular responses. *Data in Brief*, **2018**, 17, 1374-1378	1.2	18
80	Building a minimal and generalizable model of transcription factor-based biosensors: Showcasing flavonoids. *Biotechnology and Bioengineering*, **2018**, 115, 2292-2304	4.9	19
79	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. *Communications Biology*, **2018**, 1, 66	6.7	97
78	Extended Metabolic Space Modeling. *Methods in Molecular Biology*, **2018**, 1671, 83-96	1.4	1
77	RetroPath2.0: A retrosynthesis workflow for metabolic engineers. *Metabolic Engineering*, **2018**, 45, 158-170	9.7	108
76	Models for Cell-Free Synthetic Biology: Make Prototyping Easier, Better, and Faster. *Frontiers in Bioengineering and Biotechnology*, **2018**, 6, 182	5.8	19
75	Enzyme Discovery: Enzyme Selection and Pathway Design. *Methods in Enzymology*, **2018**, 608, 3-27	1.7	1
74	biochem4j: Integrated and extensible biochemical knowledge through graph databases. *PLoS ONE*, **2017**, 12, e0179130	3.7	18
73	Molecular structures enumeration and virtual screening in the chemical space with RetroPath2.0. *Journal of Cheminformatics*, **2017**, 9, 64	8.6	10
72	Mapping the patent landscape of synthetic biology for fine chemical production pathways. *Microbial Biotechnology*, **2016**, 9, 687-95	6.3	8
71	SYNBIOCHEM Synthetic Biology Research Centre, Manchester - A UK foundry for fine and speciality chemicals production. *Synthetic and Systems Biotechnology*, **2016**, 1, 271-275	4.2	5
70	Sensing new chemicals with bacterial transcription factors. *Current Opinion in Microbiology*, **2016**, 33, 105-112	7.9	49
69	SensiPath: computer-aided design of sensing-enabling metabolic pathways. *Nucleic Acids Research*, **2016**, 44, W226-31	20.1	47
68	Semisupervised Gaussian Process for Automated Enzyme Search. *ACS Synthetic Biology*, **2016**, 5, 518-28	5.7	37
67	Expanding Biosensing Abilities through Computer-Aided Design of Metabolic Pathways. *ACS Synthetic Biology*, **2016**, 5, 1076-1085	5.7	42
66	SYNBIOCHEM-a SynBio foundry for the biosynthesis and sustainable production of fine and speciality chemicals. *Biochemical Society Transactions*, **2016**, 44, 675-7	5.1	5
65	A Sense of Balance: Experimental Investigation and Modeling of a Malonyl-CoA Sensor in Escherichia coli. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 46	5.8	10

64	Computer-aided design for metabolic engineering. *Journal of Biotechnology*, **2014**, 192 Pt B, 302-13	3.7	22
63	Retropath: automated pipeline for embedded metabolic circuits. *ACS Synthetic Biology*, **2014**, 3, 565-77	5.7	62
62	Validation of RetroPath, a computer-aided design tool for metabolic pathway engineering. *Biotechnology Journal*, **2014**, 9, 1446-57	5.6	48
61	XTMS: pathway design in an eXTended metabolic space. *Nucleic Acids Research*, **2014**, 42, W389-94	20.1	81
60	PrecisePrimer: an easy-to-use web server for designing PCR primers for DNA library cloning and DNA shuffling. *Nucleic Acids Research*, **2014**, 42, W205-9	20.1	5
59	XTMS in Action: Retrosynthetic Design in the Extended Metabolic Space of Heterologous Pathways for High-Value Compounds. *Lecture Notes in Computer Science*, **2014**, 256-259	0.9	
58	Statistical ensemble analysis for simulating extrinsic noise-driven response in NF-B signaling networks. *BMC Systems Biology*, **2013**, 7, 45	3.5	7
57	PMG: Multi-core Metabolite Identification. *Electronic Notes in Theoretical Computer Science*, **2013**, 299, 53-60	0.7	7
56	Retrosynthetic design of heterologous pathways. *Methods in Molecular Biology*, **2013**, 985, 149-73	1.4	16
55	Stereo signature molecular descriptor. *Journal of Chemical Information and Modeling*, **2013**, 53, 887-97	6.1	42
54	Compound toxicity screening and structure-activity relationship modeling in Escherichia coli. *Biotechnology and Bioengineering*, **2012**, 109, 846-50	4.9	47
53	A retrosynthetic biology approach to therapeutics: from conception to delivery. *Current Opinion in Biotechnology*, **2012**, 23, 948-56	11.4	20
52	Enumerating metabolic pathways for the production of heterologous target chemicals in chassis organisms. *BMC Systems Biology*, **2012**, 6, 10	3.5	49
51	OMG: Open Molecule Generator. *Journal of Cheminformatics*, **2012**, 4, 21	8.6	58
50	Cheminformatics. *Communications of the ACM*, **2012**, 55, 65-75	2.5	13
49	Graphs: Flexible Representations of Molecular Structures and Biological Networks **2011**, 145-177		
48	Engineering antibiotic production and overcoming bacterial resistance. *Biotechnology Journal*, **2011**, 6, 812-25	5.6	24
47	A retrosynthetic biology approach to metabolic pathway design for therapeutic production. *BMC Systems Biology*, **2011**, 5, 122	3.5	85

46	Origins of specificity and promiscuity in metabolic networks. *Journal of Biological Chemistry*, **2011**, 286, 43994-44004	5.4	53
45	Toward Quantitative Structure-Property Relationships for Charge Transfer Rates of Polycyclic Aromatic Hydrocarbons. *Journal of Chemical Theory and Computation*, **2011**, 7, 2549-55	6.4	34
44	Molecular signatures-based prediction of enzyme promiscuity. *Bioinformatics*, **2010**, 26, 2012-9	7.2	61
43	Disparate data fusion for protein phosphorylation prediction. *Annals of Operations Research*, **2010**, 174, 219-235	3.2	3
42	Reaction Network Generation. *Chapman & Hall/CRC Mathematical and Computational Biology Series*, **2010**, 317-341		4
41	Understanding virulence mechanisms in M. tuberculosis infection via a circuit-based simulation framework. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2008**, 2008, 4953-5	0.9	2
40	Genome scale enzyme-metabolite and drug-target interaction predictions using the signature molecular descriptor. *Bioinformatics*, **2008**, 24, 225-33	7.2	117
39	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, 466-75	2.8	37
38	Using product kernels to predict protein interactions. *Advances in Biochemical Engineering/Biotechnology*, **2008**, 110, 215-45	1.7	1
37	Systems chemical biology. *Nature Chemical Biology*, **2007**, 3, 447-50	11.7	116
36	Sensitivity analysis of a computational model of the IKK NF-kappaB IkappaBalpha A20 signal transduction network. *Annals of the New York Academy of Sciences*, **2007**, 1115, 221-39	6.5	16
35	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, 991-5	3.5	8
34	Boolean dynamics of genetic regulatory networks inferred from microarray time series data. *Bioinformatics*, **2007**, 23, 866-74	7.2	113
33	Designing novel polymers with targeted properties using the signature molecular descriptor. *Journal of Chemical Information and Modeling*, **2006**, 46, 826-35	6.1	28
32	Prediction of beta-strand packing interactions using the signature product. *Journal of Molecular Modeling*, **2006**, 12, 355-61	2	8
31	The Signature Molecular Descriptor. 5. The Design of Hydrofluoroether Foam Blowing Agents Using Inverse-QSAR. *Industrial & Engineering Chemistry Research*, **2005**, 44, 8883-8891	3.9	37
30	A deterministic algorithm for constrained enumeration of transmembrane protein folds. *Computational Biology and Chemistry*, **2005**, 29, 143-50	3.6	4
29	Reverse engineering chemical structures from molecular descriptors: how many solutions?. *Journal of Computer-Aided Molecular Design*, **2005**, 19, 637-50	4.2	17

28	Predicting protein-protein interactions using signature products. *Bioinformatics*, **2005**, 21, 218-26	7.2	299
27	Optimal bundling of transmembrane helices using sparse distance constraints. *Protein Science*, **2004**, 13, 2613-27	6.3	35
26	The signature molecular descriptor. 4. Canonizing molecules using extended valence sequences. *Journal of Chemical Information and Computer Sciences*, **2004**, 44, 427-36		62
25	The signature molecular descriptor. 3. Inverse-quantitative structure-activity relationship of ICAM-1 inhibitory peptides. *Journal of Molecular Graphics and Modelling*, **2004**, 22, 263-73	2.8	72
24	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	1.4	15
23	Exploring the conformational space of membrane protein folds matching distance constraints. *Protein Science*, **2003**, 12, 1750-61	6.3	19
22	The signature molecular descriptor. 2. Enumerating molecules from their extended valence sequences. *Journal of Chemical Information and Computer Sciences*, **2003**, 43, 721-34		120
21	The signature molecular descriptor. 1. Using extended valence sequences in QSAR and QSPR studies. *Journal of Chemical Information and Computer Sciences*, **2003**, 43, 707-20		185
20	The Signature Molecular Descriptor. Part 1. Using Extended Valence Sequences in QSAR and QSPR Studies.. *ChemInform*, **2003**, 34, no		3
19	Developing a methodology for an inverse quantitative structure-activity relationship using the signature molecular descriptor. *Journal of Molecular Graphics and Modelling*, **2002**, 20, 429-38	2.8	80
18	Constrained walks and self-avoiding walks: implications for protein structure determination. *Journal of Physics A*, **2002**, 35, 1-19		4
17	Stochastic generator of chemical structure. 4. Building polymeric systems with specified properties. *Journal of Computational Chemistry*, **2001**, 22, 580-590	3.5	10
16	Stochastic generator of chemical structure. 3. Reaction network generation. *Journal of Chemical Information and Computer Sciences*, **2001**, 41, 894-908		24
15	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		51
14	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		28
13	Pore Structure of Imogolite Computer Models. *Langmuir*, **1996**, 12, 4463-4468	4	32
12	Molecular dynamics computer simulations of silica aerogels. *Journal of Non-Crystalline Solids*, **1995**, 186, 349-355	3.9	28
11	Correlation between Microporosity and Fractal Dimension of Bituminous Coal Based on Computer-Generated Models. *Energy & Fuels*, **1994**, 8, 408-414	4.1	40

10	Is There Any Order in the Structure of Lignin?. *Energy & Fuels*, **1994**, 8, 402-407	4.1	66
9	A three-dimensional model for lignocellulose from gymnospermous wood. *Organic Geochemistry*, **1994**, 21, 1169-1179	3.1	65
8	Calculating the Number-Averaged Molecular Weight (M0) of Aromatic and Hydroaromatic Clusters in Coal using Rubber Elasticity Theory. *Energy & Fuels*, **1994**, 8, 1020-1023	4.1	8
7	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		66
6	A computer-aided molecular model for high volatile bituminous coal. *Fuel Processing Technology*, **1993**, 34, 277-293	7.2	27
5	Handbook of Chemoinformatics Algorithms		35
4	Galaxy-SynBioCAD: Synthetic Biology Design Automation tools in Galaxy workflows		1
3	Plug-and-Play Metabolic Transducers Expand the Chemical Detection Space of Cell-Free Biosensors		3
2	Reinforcement Learning for Bio-Retrosynthesis		1
1	RetroPath2.0: a retrosynthesis workflow for metabolic engineers		1