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	Predicting protein-protein interactions using signature products. Bioinformatics, 2005, 21, 218-226.	4.1	353
2	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
3	RetroPath2.0: A retrosynthesis workflow for metabolic engineers. Metabolic Engineering, 2018, 45, 158-170.	7.0	174
4	An automated Design-Build-Test-Learn pipeline for enhanced microbial production of fine chemicals. Communications Biology, 2018, 1, 66.	4.4	159
5	Boolean dynamics of genetic regulatory networks inferred from microarray time series data. Bioinformatics, 2007, 23, 866-874.	4.1	144
6	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
7	Genome scale enzymeâ€“metabolite and drugâ€“target interaction predictions using the signature molecular descriptor. Bioinformatics, 2008, 24, 225-233.	4.1	139
8	Systems chemical biology. Nature Chemical Biology, 2007, 3, 447-450.	8.0	129
9	A retrosynthetic biology approach to metabolic pathway design for therapeutic production. BMC Systems Biology, 2011, 5, 122.	3.0	100
10	Plug-and-play metabolic transducers expand the chemical detection space of cell-free biosensors. Nature Communications, 2019, 10, 1697.	12.8	99
11	XTMS: pathway design in an eXTended metabolic space. Nucleic Acids Research, 2014, 42, W389-W394.	14.5	96
12	Microbial Genes for a Circular and Sustainable Bio-PET Economy. Genes, 2019, 10, 373.	2.4	94
13	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
14	The signature molecular descriptor. Journal of Molecular Graphics and Modelling, 2004, 22, 263-273.	2.4	91
15	Machine Learning of Designed Translational Control Allows Predictive Pathway Optimization in Escherichia coli. ACS Synthetic Biology, 2019, 8, 127-136.	3.8	88
16	Reinforcement Learning for Bioretrosynthesis. ACS Synthetic Biology, 2020, 9, 157-168.	3.8	77
17	Retropath: Automated Pipeline for Embedded Metabolic Circuits. ACS Synthetic Biology, 2014, 3, 565-577.	3.8	76
18	Is There Any Order in the Structure of Lignin?. Energy & Fuels, 1994, 8, 402-407.	5.1	75

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19	Selenzyme: enzyme selection tool for pathway design. Bioinformatics, 2018, 34, 2153-2154.	4.1	75
20	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
21	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
22	RetroRules: a database of reaction rules for engineering biology. Nucleic Acids Research, 2019, 47, D1229-D1235.	14.5	74
23	A three-dimensional model for lignocellulose from gymnospermous wood. Organic Geochemistry, 1994, 21, 1169-1179.	1.8	73
24	Molecular signatures-based prediction of enzyme promiscuity. Bioinformatics, 2010, 26, 2012-2019.	4.1	72
25	Custom-made transcriptional biosensors for metabolic engineering. Current Opinion in Biotechnology, 2019, 59, 78-84.	6.6	72
26	Sensing new chemicals with bacterial transcription factors. Current Opinion in Microbiology, 2016, 33, 105-112.	5.1	70
27	Large scale active-learning-guided exploration for in vitro protein production optimization. Nature Communications, 2020, 11, 1872.	12.8	70
28	Origins of Specificity and Promiscuity in Metabolic Networks. Journal of Biological Chemistry, 2011, 286, 43994-44004.	3.4	68
29	OMG: Open Molecule Generator. Journal of Cheminformatics, 2012, 4, 21.	6.1	62
30	SensiPath: computer-aided design of sensing-enabling metabolic pathways. Nucleic Acids Research, 2016, 44, W226-W231.	14.5	60
31	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
32	Enumerating metabolic pathways for the production of heterologous target chemicals in chassis organisms. BMC Systems Biology, 2012, 6, 10.	3.0	57
33	Semisupervised Gaussian Process for Automated Enzyme Search. ACS Synthetic Biology, 2016, 5, 518-528.	3.8	57
34	Expanding Biosensing Abilities through Computer-Aided Design of Metabolic Pathways. ACS Synthetic Biology, 2016, 5, 1076-1085.	3.8	54
35	Validation of RetroPath, a computerâ€aided design tool for metabolic pathway engineering. Biotechnology Journal, 2014, 9, 1446-1457.	3.5	53
36	Stereo Signature Molecular Descriptor. Journal of Chemical Information and Modeling, 2013, 53, 887-897.	5.4	51

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37	Metabolic perceptrons for neural computing in biological systems. Nature Communications, 2019, 10, 3880.	12.8	51
38	Compound toxicity screening and structureâ€“activity relationship modeling in Escherichia coli. Biotechnology and Bioengineering, 2012, 109, 846-850.	3.3	50
39	Correlation between Microporosity and Fractal Dimension of Bituminous Coal Based on Computer-Generated Models. Energy & Fuels, 1994, 8, 408-414.	5.1	49
40	Handbook of Chemoinformatics Algorithms. , 0, , .		47
41	Engineering Escherichia coli towards de novo production of gatekeeper (2S)-flavanones: naringenin, pinocembrin, eriodictyol and homoeriodictyol. Synthetic Biology, 2020, 5, ysaa012.	2.2	45
42	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
43	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
44	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
45	Optimizing Cell-Free Biosensors to Monitor Enzymatic Production. ACS Synthetic Biology, 2019, 8, 1952-1957.	3.8	37
46	Optimal bundling of transmembrane helices using sparse distance constraints. Protein Science, 2009, 13, 2613-2627.	7.6	36
47	Molecular dynamics computer simulations of silica aerogels. Journal of Non-Crystalline Solids, 1995, 186, 349-355.	3.1	34
48	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
49	A versatile active learning workflow for optimization of genetic and metabolic networks. Nature Communications, 2022, 13, .	12.8	34
50	Pore Structure of Imogolite Computer Models. Langmuir, 1996, 12, 4463-4468.	3.5	33
51	Models for Cell-Free Synthetic Biology: Make Prototyping Easier, Better, and Faster. Frontiers in Bioengineering and Biotechnology, 2018, 6, 182.	4.1	33
52	A computer-aided molecular model for high volatile bituminous coal. Fuel Processing Technology, 1993, 34, 277-293.	7.2	32
53	Designing Novel Polymers with Targeted Properties Using the Signature Molecular Descriptor. Journal of Chemical Information and Modeling, 2006, 46, 826-835.	5.4	31
54	biochem4j: Integrated and extensible biochemical knowledge through graph databases. PLoS ONE, 2017, 12, e0179130.	2.5	31

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55	Engineering antibiotic production and overcoming bacterial resistance. Biotechnology Journal, 2011, 6, 812-825.	3.5	30
56	Stochastic Generator of Chemical Structure. 3. Reaction Network Generation. Journal of Chemical Information and Computer Sciences, 2001, 41, 894-908.	2.8	29
57	Building a minimal and generalizable model of transcription factorâ€“based biosensors: Showcasing flavonoids. Biotechnology and Bioengineering, 2018, 115, 2292-2304.	3.3	29
58	Computer-aided design for metabolic engineering. Journal of Biotechnology, 2014, 192, 302-313.	3.8	26
59	A dataset of small molecules triggering transcriptional and translational cellular responses. Data in Brief, 2018, 17, 1374-1378.	1.0	26
60	PartsGenie: an integrated tool for optimizing and sharing synthetic biology parts. Bioinformatics, 2018, 34, 2327-2329.	4.1	25
61	Reverse engineering chemical structures from molecular descriptors: how many solutions?. Journal of Computer-Aided Molecular Design, 2005, 19, 637-650.	2.9	23
62	Sensitivity Analysis of a Computational Model of the IKKâ€“NFâ€ºBâ€“IÎºBÎ±â€“A20 Signal Transduction Network. Annals of the New York Academy of Sciences, 2007, 1115, 221-239.	3.8	22
63	Exploring the conformational space of membrane protein folds matching distance constraints. Protein Science, 2003, 12, 1750-1761.	7.6	21
64	Cheminformatics. Communications of the ACM, 2012, 55, 65-75.	4.5	21
65	A retrosynthetic biology approach to therapeutics: from conception to delivery. Current Opinion in Biotechnology, 2012, 23, 948-956.	6.6	21
66	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
67	Retrosynthetic Design of Heterologous Pathways. Methods in Molecular Biology, 2013, 985, 149-173.	0.9	17
68	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
69	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
70	Molecular structures enumeration and virtual screening in the chemical space with RetroPath2.0. Journal of Cheminformatics, 2017, 9, 64.	6.1	13
71	Development of a Biosensor for Detection of Benzoic Acid Derivatives in Saccharomyces cerevisiae. Frontiers in Bioengineering and Biotechnology, 2020, 7, 372.	4.1	12
72	Stochastic generator of chemical structure. 4. Building polymeric systems with specified properties. Journal of Computational Chemistry, 2001, 22, 580-590.	3.3	11

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73	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
74	Mapping the patent landscape of synthetic biology for fine chemical production pathways. Microbial Biotechnology, 2016, 9, 687-695.	4.2	11
75	Constrained walks and self-avoiding walks: implications for protein structure determination. Journal of Physics A, 2002, 35, 1-19.	1.6	9
76	Prediction of Î²-strand packing interactions using the signature product. Journal of Molecular Modeling, 2006, 12, 355-361.	1.8	9
77	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
78	Statistical ensemble analysis for simulating extrinsic noise-driven response in NF-ÎºB signaling networks. BMC Systems Biology, 2013, 7, 45.	3.0	9
79	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
80	PMG: Multi-core Metabolite Identification. Electronic Notes in Theoretical Computer Science, 2013, 299, 53-60.	0.9	8
81	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
82	Optimising protein synthesis in cellâ€free systems, a review. Engineering Biology, 2021, 5, 10-19.	1.8	7
83	Reaction Network Generation. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2010, , 317-341.	0.1	7
84	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
85	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
86	A deterministic algorithm for constrained enumeration of transmembrane protein folds. Computational Biology and Chemistry, 2005, 29, 143-150.	2.3	5
87	Efficient learning in metabolic pathway designs through optimal assembling. IFAC-PapersOnLine, 2019, 52, 7-12.	0.9	5
88	The Signature Molecular Descriptor. Part 1. Using Extended Valence Sequences in QSAR and QSPR Studies.. ChemInform, 2003, 34, no.	0.0	3
89	Disparate data fusion for protein phosphorylation prediction. Annals of Operations Research, 2010, 174, 219-235.	4.1	3
90	Understanding virulence mechanisms in M. tuberculosis infection via A circuit-based simulation framework. , 2008, 2008, 4953-5.		2

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91	Enzyme Discovery: Enzyme Selection and Pathway Design. Methods in Enzymology, 2018, 608, 3-27.	1.0	2
92	Cell-Free and AI Integration. Methods in Molecular Biology, 2022, 2433, 303-323.	0.9	2
93	Massively parallel simulations of diffusion in dense polymeric structures. , 1997, , .		1
94	The Signature Molecular Descriptor. Part 2. Enumerating Molecules from Their Extended Valence Sequences.. ChemInform, 2003, 34, no.	0.0	1
95	Using Product Kernels to Predict Protein Interactions. Advances in Biochemical Engineering/Biotechnology, 2007, 110, 215-245.	1.1	1
96	Editorial: Synthetic Biology â€“ applying new paradigms at the interface of fundamental research and innovation. Biotechnology Journal, 2011, 6, 766-767.	3.5	1
97	Extended Metabolic Space Modeling. Methods in Molecular Biology, 2018, 1671, 83-96.	0.9	1
98	Synthetic Biology at the Hand of Cell-Free Systems. , 2020, , 275-288.		1