Jean Peccoud

List of Publications by Year
in descending order

70 papers	2,971 citations	331670 21 h-index	182427 51 g-index
79 all docs	79 docs citations	79 times ranked	2626 citing authors

#	Article	IF	Citations
1	Markovian Modeling of Gene-Product Synthesis. Theoretical Population Biology, 1995, 48, 222-234.	1.1	568
2	Superantigens interact with MHC class II molecules outside of the antigen groove. Cell, 1990, 62, 1115-1121.	28.9	452
3	Quantitative modeling of stochastic systems in molecular biology by using stochastic Petri nets. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6750-6755.	7.1	304
4	The Synthetic Biology Open Language (SBOL) provides a community standard for communicating designs in synthetic biology. Nature Biotechnology, 2014, 32, 545-550.	17.5	247
5	Writing DNA with GenoCADTM. Nucleic Acids Research, 2009, 37, W40-W47.	14.5	134
6	Gene synthesis demystified. Trends in Biotechnology, 2009, 27, 63-72.	9.3	129
7	Cyberbiosecurity: From Naive Trust to Risk Awareness. Trends in Biotechnology, 2018, 36, 4-7.	9.3	79
8	A syntactic model to design and verify synthetic genetic constructs derived from standard biological parts. Bioinformatics, 2007, 23, 2760-2767.	4.1	78
9	Cyberbiosecurity: An Emerging New Discipline to Help Safeguard the Bioeconomy. Frontiers in Bioengineering and Biotechnology, 2018, 6, 39.	4.1	75
10	GenoCAD for iGEM: a grammatical approach to the design of standard-compliant constructs. Nucleic Acids Research, 2010, 38, 2637-2644.	14.5	65
11	Targeted Development of Registries of Biological Parts. PLoS ONE, 2008, 3, e2671.	2.5	63
12	Dynamic partitioning for hybrid simulation of the bistable HIV-1 transactivation network. Bioinformatics, 2006, 22, 2782-2789.	4.1	48
13	Genetic design automation: engineering fantasy or scientific renewal?. Trends in Biotechnology, 2012, 30, 120-126.	9.3	47
14	The Selective Values of Alleles in a Molecular Network Model Are Context Dependent. Genetics, 2004, 166, 1715-1725.	2.9	43
15	A Stochastic Model of the Yeast Cell Cycle Reveals Roles for Feedback Regulation in Limiting Cellular Variability. PLoS Computational Biology, 2016, 12, e1005230.	3.2	42
16	Essential information for synthetic DNA sequences. Nature Biotechnology, 2011, 29, 22-22.	17.5	40
17	Genetic design: rising above the sequence. Trends in Biotechnology, 2008, 26, 538-544.	9.3	29
18	Yeast genetic interaction screens in the age of CRISPR/Cas. Current Genetics, 2019, 65, 307-327.	1.7	29

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19	Modeling Structure-Function Relationships in Synthetic DNA Sequences using Attribute Grammars. PLoS Computational Biology, 2009, 5, e1000529.	3.2	28
20	Stochastic exit from mitosis in budding yeast. Cell Cycle, 2011, 10, 999-1009.	2.6	26
21	Rule-Based Design of Synthetic Transcription Factors in Eukaryotes. ACS Synthetic Biology, 2014, 3, 737-744.	3.8	26
22	Experimental testing of a new integrated model of the budding yeast S<scp>tart</scp>transition. Molecular Biology of the Cell, 2015, 26, 3966-3984.	2.1	25
23	Oscillatory Dynamics of Cell Cycle Proteins in Single Yeast Cells Analyzed by Imaging Cytometry. PLoS ONE, 2011, 6, e26272.	2.5	23
24	GraphSpace: stimulating interdisciplinary collaborations in network biology. Bioinformatics, 2017, 33, 3134-3136.	4.1	23
25	Synthetic Biology: fostering the cyber-biological revolution. Synthetic Biology, 2016, 1, ysw001.	2.2	22
26	Estimation of the parameters of a branching process from migrating binomial observations. Advances in Applied Probability, 1998, 30, 948-967.	0.7	21
27	GenoLIB: a database of biological parts derived from a library of common plasmid features. Nucleic Acids Research, 2015, 43, 4823-4832.	14.5	20
28	The Open Insulin Project: A Case Study for â€˜Biohackedâ€™ Medicines. Trends in Biotechnology, 2018, 36, 1211-1218.	9.3	19
29	Measurement and modeling of transcriptional noise in the cell cycle regulatory network. Cell Cycle, 2013, 12, 3392-3407.	2.6	18
30	Strengths and limitations of the federal guidance on synthetic DNA. Nature Biotechnology, 2011, 29, 208-210.	17.5	15
31	Statistical Estimations of PCR Amplification Rates. , 1998, , 111-128.		15
32	The synthetic futures of vesicular stomatitis virus. Trends in Biotechnology, 2012, 30, 497-498.	9.3	13
33	Sequence verification of synthetic DNA by assembly of sequencing reads. Nucleic Acids Research, 2013, 41, e25-e25.	14.5	13
34	Mobius: an integrated discrete-event modeling environment. Bioinformatics, 2007, 23, 3412-3414.	4.1	12
35	Adaptive Imaging Cytometry to Estimate Parameters of Gene Networks Models in Systems and Synthetic Biology. PLoS ONE, 2014, 9, e107087.	2.5	12
36	Rapid, robust plasmid verification by de novo assembly of short sequencing reads. Nucleic Acids Research, 2020, 48, e106-e106.	14.5	12

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37	Rule-Based Design of Plant Expression Vectors Using GenoCAD. PLoS ONE, 2015, 10, e0132502.	2.5	12
38	The PLOS ONE Synthetic Biology Collection: Six Years and Counting. PLoS ONE, 2012, 7, e43231.	2.5	10
39	ANALYSIS OF THE STABILIZING EFFECT OF ROM ON THE GENETIC NETWORK CONTROLLING COLE1 PLASMID REPLICATION. , 1998, , 65-76.		10
40	Building Block Synthesis Using the Polymerase Chain Assembly Method. Methods in Molecular Biology, 2012, 852, 3-10.	0.9	8
41	A Step-by-Step Introduction to Rule-Based Design of Synthetic Genetic Constructs Using GenoCAD. Methods in Enzymology, 2011, 498, 173-188.	1.0	7
42	If You Can't Measure It, You Can't Manage It. PLoS Computational Biology, 2014, 10, e1003462.	3.2	7
43	Development of a domain-specific genetic language to design Chlamydomonas reinhardtii expression vectors. Bioinformatics, 2014, 30, 251-257.	4.1	7
44	Securing the Exchange of Synthetic Genetic Constructs Using Digital Signatures. ACS Synthetic Biology, 2020, 9, 2656-2664.	3.8	7
45	Automating Molecular Biology: A Question of Communication. Bio/technology, 1995, 13, 741-745.	1.5	6
46	Gene Synthesis. Methods in Molecular Biology, 2012, , .	0.9	6
47	Making Security Viral: Shifting Engineering Biology Culture and Publishing. ACS Synthetic Biology, 2022, 11, 522-527.	3.8	6
48	Probability distribution of the chemical states of a closed system and thermodynamic law of mass action from kinetics: The RNA example. Journal of Chemical Physics, 1997, 107, 2913-2919.	3.0	5
49	GenoCAD Plant Grammar to Design Plant Expression Vectors for Promoter Analysis. Methods in Molecular Biology, 2016, 1482, 219-232.	0.9	5
50	Digital Signatures to Ensure the Authenticity and Integrity of Synthetic DNA Molecules. , 2018, , .		5
51	Challenges and opportunities for strain verification by whole-genome sequencing. Scientific Reports, 2020, 10, 5873.	3.3	5
52	A hybrid stochastic model of the budding yeast cell cycle. Npj Systems Biology and Applications, 2020, 6, 7.	3.0	5
53	Synthesizing DNA molecules withÂidentity-based digital signatures toÂpreventÂmalicious tampering and enabling source attribution. Journal of Computer Security, 2020, 28, 437-467.	0.8	4
54	CrossPlan: systematic planning of genetic crosses to validate mathematical models. Bioinformatics, 2018, 34, 2237-2244.	4.1	3

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55	Hands-On Introduction to Synthetic Biology for Security Professionals. Trends in Biotechnology, 2019, 37, 1143-1146.	9.3	3
56	Genetic interactions derived from high-throughput phenotyping of 6589 yeast cell cycle mutants. Npj Systems Biology and Applications, 2020, 6, 11.	3.0	3
57	Co-design in synthetic biology: a system-level analysis of the development of an environmental sensing device. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2010, , 385-96.	0.7	3
58	Data sharing policies: share well and you shall be rewarded. Synthetic Biology, 2021, 6, ysab028.	2.2	2
59	CO-DESIGN IN SYNTHETIC BIOLOGY:. , 2009, , 385-396.		2
60	La PCR quantitative : un nouvel outil pour l'analyse mÃ©dicale.. Medecine/Sciences, 1993, 9, 1378.	0.2	2
61	Opportunities to apply manufacturing systems analysis techniques in genetic manufacturing systems. Manufacturing Letters, 2017, 13, 34-38.	2.2	1
62	Structure of the TCR-Ag-MHC Complex. , 1992, , 17-23.		1
63	Aspects alÃ©atoires de la dynamique de la diffÃ©renciation cellulaire. Medecine/Sciences, 1994, 10, 877.	0.2	1
64	CrossPlan. , 2018, , .		1
65	Intricate loops: A pragmatic approach. BioEssays, 1995, 17, 183-183.	2.5	0
66	Cytoâ€¢IQ: an adaptive cytometer for extracting the noisy dynamics of molecular interactions in live cells. Proceedings of SPIE, 2010, , .	0.8	0
67	A stochastic model for error correction of kinetochore-microtubule attachments in budding yeast. PLoS ONE, 2020, 15, e0236293.	2.5	0
68	PARAMETERIZATION OF A NONLINEAR GENOTYPE TO PHENOTYPE MAP USING MOLECULAR NETWORKS. , 2004, , .		0
69	Des rÃ©seaux de PÃ©tri stochastiques pour les rÃ©seaux gÃ©nÃ©tiques.. Medecine/Sciences, 1998, 14, 991.	0.2	0
70	Cloning forever. The Winnower, 2015, , .	0.0	0