Giovanni Stracquadanio

List of Publications by Year
in descending order

61 papers	2,490 citations	516710 16 h-index	254184 43 g-index
75 all docs	75 docs citations	75 times ranked	2466 citing authors

#	Article	IF	Citations
1	Dissecting the heritable risk of breast cancer: From statistical methods to susceptibility genes. Seminars in Cancer Biology, 2021, 72, 175-184.	9.6	10
2	Heritable genetic variants in key cancer genes link cancer risk with anthropometric traits. Journal of Medical Genetics, 2021, 58, 392-399.	3.2	9
3	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. Cancer Research, 2021, 81, 1667-1680.	0.9	32
4	The Landscape of the Heritable Cancer Genome. Cancer Research, 2021, 81, 2588-2599.	0.9	13
5	Mutation landscape of multiple myeloma measurable residual disease: identification of targets for precision medicine. Blood Advances, 2021, , .	5.2	3
6	Design and assembly of DNA molecules using multi-objective optimization. Synthetic Biology, 2021, 6, ysab026.	2.2	2
7	Computer Aided Assembly and Verification of Synthetic Chromosomes. Methods in Molecular Biology, 2021, 2189, 169-181.	0.9	0
8	PyGNA: a unified framework for geneset network analysis. BMC Bioinformatics, 2020, 21, 476.	2.6	0
9	Systematic analysis of the <scp>IL</scp> â€17 receptor signalosome reveals a robust regulatory feedback loop. EMBO Journal, 2020, 39, e104202.	7.8	16
10	Identification of Molecular Mechanisms Responsible for the Development of Extramedullary Disease in Myeloma and Potential Novel Therapeutic Targets Using Transcriptomic and Exome Profiling. Blood, 2020, 136, 16-17.	1.4	0
11	Stochastic Methods for Global Optimization and Problem Solving. , 2019, , 321-327.		1
12	Technological challenges and milestones for writing genomes. Science, 2019, 366, 310-312.	12.6	50
13	Whole Exome Sequencing of Residual Disease in Multiple Myeloma: Searching for Novel Therapeutic Targets. Blood, 2018, 132, 3175-3175.	1.4	0
14	Design of a synthetic yeast genome. Science, 2017, 355, 1040-1044.	12.6	464
15	â€œPerfectâ€•designer chromosome V and behavior of a ring derivative. Science, 2017, 355, .	12.6	185
16	Bug mapping and fitness testing of chemically synthesized chromosome X. Science, 2017, 355, .	12.6	173
17	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. Science, 2017, 355, .	12.6	163
18	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. Science, 2017, 355, .	12.6	184

#	ARTICLE	IF	CITATIONS
19	Low escape-rate genome safeguards with minimal molecular perturbation of *Saccharomyces cerevisiae*. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1470-E1479.	7.1	26
20	BioPartsBuilder: a synthetic biology tool for combinatorial assembly of biological parts. Bioinformatics, 2016, 32, 937-939.	4.1	15
21	Pro-survival p53 target genes have evolved clusters of interacting polymorphic response elements that can affect cancer risk. European Journal of Cancer, 2016, 61, S110.	2.8	0
22	Polymorphisms in the p53 pathway are enriched in cancer susceptibility loci and share characteristics with somatic pathway mutations. European Journal of Cancer, 2016, 61, S179.	2.8	0
23	BioPartsDB: a synthetic biology workflow web-application for education and research. Bioinformatics, 2016, 32, 3519-3521.	4.1	5
24	CD44 SNPrs187115: A Novel Biomarker Signature that Predicts Survival in Resectable Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2016, 22, 6069-6077.	7.0	8
25	SCRaMbLE generates designed combinatorial stochastic diversity in synthetic chromosomes. Genome Research, 2016, 26, 36-49.	5.5	124
26	The importance of p53 pathway genetics in inherited and somatic cancer genomes. Nature Reviews Cancer, 2016, 16, 251-265.	28.4	131
27	Packing equal disks in a unit square: an immunological optimization approach. , 2015, , .		4
28	Automatic Tuning of Algorithms Through Sensitivity Minimization. Lecture Notes in Computer Science, 2015, , 14-25.	1.3	3
29	RADOM, an Efficient *In Vivo* Method for Assembling Designed DNA Fragments up to 10 kb Long in *Saccharomyces cerevisiae*. ACS Synthetic Biology, 2015, 4, 213-220.	3.8	36
30	Intrinsic biocontainment: Multiplex genome safeguards combine transcriptional and recombinational control of essential yeast genes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1803-1808.	7.1	61
31	Yeast Golden Gate (yGG) for the Efficient Assembly of *S. cerevisiae* Transcription Units. ACS Synthetic Biology, 2015, 4, 853-859.	3.8	75
32	Optimization Methods and Applications to Microelectronics CAD. Mathematics in Industry, 2015, , 435-451.	0.3	1
33	Total Synthesis of a Functional Designer Eukaryotic Chromosome. Science, 2014, 344, 55-58.	12.6	486
34	Designing Groundwater Supply Systems Using the Mesh Adaptive Basin Hopping Algorithm. , 2014, , 407-421.		0
35	Semiconductor device design using the BiMADS algorithm. Journal of Computational Physics, 2013, 242, 304-320.	3.8	14
36	Bose–Einstein condensation in satisfiability problems. European Journal of Operational Research, 2013, 227, 44-54.	5.7	1

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37	Efficient Behavior of Photosynthetic Organelles via Pareto Optimality, Identifiability, and Sensitivity Analysis. ACS Synthetic Biology, 2013, 2, 274-288.	3.8	10
38	Optimization Approaches for Solving String Selection Problems. SpringerBriefs in Optimization, 2013, , .	0.3	5
39	Mathematical Optimization. SpringerBriefs in Optimization, 2013, , 13-25.	0.3	1
40	String Selection Problems. SpringerBriefs in Optimization, 2013, , 27-49.	0.3	1
41	Biological Sequences. SpringerBriefs in Optimization, 2013, , 1-6.	0.3	0
42	Identification of Sensitive Enzymes in the Photosynthetic Carbon Metabolism. Advances in Experimental Medicine and Biology, 2012, 736, 441-459.	1.6	5
43	A Mesh Adaptive Basin Hopping Method for the Design of Circular Antenna Arrays. Journal of Optimization Theory and Applications, 2012, 155, 1008-1024.	1.5	2
44	Design of Robust Space Trajectories. , 2011, , 341-354.		11
45	Computational energy-based redesign of robust proteins. Computers and Chemical Engineering, 2011, 35, 464-473.	3.8	15
46	Design of robust metabolic pathways. , 2011, , .		12
47	Large Scale Agent-Based Modeling of the Humoral and Cellular Immune Response. Lecture Notes in Computer Science, 2011, , 15-29.	1.3	3
48	Effective design of semiconductor devices using evolutionary-based derivative free optimization. , 2010, , .		1
49	Entropic divergence for population based optimization algorithms. , 2010, , .		4
50	Multi-objective optimization of doping profile in semiconductor design. , 2010, , .		1
51	Robust Bio-active Peptide Prediction Using Multi-objective Optimization. , 2010, , .		6
52	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism. , 2010, , .		11
53	An Information-Theoretic Approach for Clonal Selection Algorithms. Lecture Notes in Computer Science, 2010, , 144-157.	1.3	6
54	An Immunological Algorithm for Doping Profile Optimization in Semiconductors Design. Lecture Notes in Computer Science, 2010, , 213-222.	1.3	2

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55	Nominal-Yield-Area Tradeoff in Automatic Synthesis of Analog Circuits: A Genetic Programming Approach Using Immune-Inspired Operators. , 2009, , .		11
56	A Design-for-Yield Algorithm to Assess and Improve the Structural and Energetic Robustness of Proteins and Drugs. Lecture Notes in Computer Science, 2009, , 245-256.	1.3	2
57	A CLONAL SELECTION ALGORITHM FOR THE AUTOMATIC SYNTHESIS OF LOW-PASS FILTERS. , 2009, , .		0
58	Generalized Pattern Search Algorithm for Peptide Structure Prediction. Biophysical Journal, 2008, 95, 4988-4999.	0.5	33
59	An Advanced Clonal Selection Algorithm with Ad-Hoc Network-Based Hypermutation Operators for Synthesis of Topology and Sizing of Analog Electrical Circuits. Lecture Notes in Computer Science, 2008, , 60-70.	1.3	21
60	New coupled EM and circuit simulation flow for integrated spiral inductor by introducing symbolic simplified expressions. , 2008, , .		5
61	Generalized Pattern Search and Mesh Adaptive Direct Search Algorithms for Protein Structure Prediction. Lecture Notes in Computer Science, 2007, , 183-193.	1.3	3