

# Giovanni Stracquadanio

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2307848/publications.pdf>

Version: 2024-02-01

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	Total Synthesis of a Functional Designer Eukaryotic Chromosome. <i>Science</i> , 2014, 344, 55-58.	12.6	486
2	Design of a synthetic yeast genome. <i>Science</i> , 2017, 355, 1040-1044.	12.6	464
3	“Perfect” designer chromosome V and behavior of a ring derivative. <i>Science</i> , 2017, 355, .	12.6	185
4	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. <i>Science</i> , 2017, 355, .	12.6	184
5	Bug mapping and fitness testing of chemically synthesized chromosome X. <i>Science</i> , 2017, 355, .	12.6	173
6	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	12.6	163
7	The importance of p53 pathway genetics in inherited and somatic cancer genomes. <i>Nature Reviews Cancer</i> , 2016, 16, 251-265.	28.4	131
8	SCRaMBLE generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016, 26, 36-49.	5.5	124
9	Yeast Golden Gate (yGG) for the Efficient Assembly of <i>S. cerevisiae</i> Transcription Units. <i>ACS Synthetic Biology</i> , 2015, 4, 853-859.	3.8	75
10	Intrinsic biocontainment: Multiplex genome safeguards combine transcriptional and recombinational control of essential yeast genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1803-1808.	7.1	61
11	Technological challenges and milestones for writing genomes. <i>Science</i> , 2019, 366, 310-312.	12.6	50
12	RANDOM, an Efficient <i>In Vivo</i> Method for Assembling Designed DNA Fragments up to 10 kb Long in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2015, 4, 213-220.	3.8	36
13	Generalized Pattern Search Algorithm for Peptide Structure Prediction. <i>Biophysical Journal</i> , 2008, 95, 4988-4999.	0.5	33
14	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. <i>Cancer Research</i> , 2021, 81, 1667-1680.	0.9	32
15	Low escape-rate genome safeguards with minimal molecular perturbation of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1470-E1479.	7.1	26
16	An Advanced Clonal Selection Algorithm with Ad-Hoc Network-Based Hypermutation Operators for Synthesis of Topology and Sizing of Analog Electrical Circuits. <i>Lecture Notes in Computer Science</i> , 2008, , 60-70.	1.3	21
17	Systematic analysis of the <i>IL-17</i> receptor signalosome reveals a robust regulatory feedback loop. <i>EMBO Journal</i> , 2020, 39, e104202.	7.8	16
18	Computational energy-based redesign of robust proteins. <i>Computers and Chemical Engineering</i> , 2011, 35, 464-473.	3.8	15

#	ARTICLE	IF	CITATIONS
19	BioPartsBuilder: a synthetic biology tool for combinatorial assembly of biological parts. <i>Bioinformatics</i> , 2016, 32, 937-939.	4.1	15
20	Semiconductor device design using the BiMADS algorithm. <i>Journal of Computational Physics</i> , 2013, 242, 304-320.	3.8	14
21	The Landscape of the Heritable Cancer Genome. <i>Cancer Research</i> , 2021, 81, 2588-2599.	0.9	13
22	Design of robust metabolic pathways. , 2011, , .		12
23	Nominal-Yield-Area Tradeoff in Automatic Synthesis of Analog Circuits: A Genetic Programming Approach Using Immune-Inspired Operators. , 2009, , .		11
24	Analysis and Optimization of C3 Photosynthetic Carbon Metabolism. , 2010, , .		11
25	Design of Robust Space Trajectories. , 2011, , 341-354.		11
26	Efficient Behavior of Photosynthetic Organelles via Pareto Optimality, Identifiability, and Sensitivity Analysis. <i>ACS Synthetic Biology</i> , 2013, 2, 274-288.	3.8	10
27	Dissecting the heritable risk of breast cancer: From statistical methods to susceptibility genes. <i>Seminars in Cancer Biology</i> , 2021, 72, 175-184.	9.6	10
28	Heritable genetic variants in key cancer genes link cancer risk with anthropometric traits. <i>Journal of Medical Genetics</i> , 2021, 58, 392-399.	3.2	9
29	CD44 SNPrs187115: A Novel Biomarker Signature that Predicts Survival in Resectable Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2016, 22, 6069-6077.	7.0	8
30	Robust Bio-active Peptide Prediction Using Multi-objective Optimization. , 2010, , .		6
31	An Information-Theoretic Approach for Clonal Selection Algorithms. <i>Lecture Notes in Computer Science</i> , 2010, , 144-157.	1.3	6
32	New coupled EM and circuit simulation flow for integrated spiral inductor by introducing symbolic simplified expressions. , 2008, , .		5
33	Identification of Sensitive Enzymes in the Photosynthetic Carbon Metabolism. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 441-459.	1.6	5
34	BioPartsDB: a synthetic biology workflow web-application for education and research. <i>Bioinformatics</i> , 2016, 32, 3519-3521.	4.1	5
35	Optimization Approaches for Solving String Selection Problems. <i>SpringerBriefs in Optimization</i> , 2013, , .	0.3	5
36	Entropic divergence for population based optimization algorithms. , 2010, , .		4

#	ARTICLE	IF	CITATIONS
37	Packing equal disks in a unit square: an immunological optimization approach. , 2015, , .		4
38	Automatic Tuning of Algorithms Through Sensitivity Minimization. Lecture Notes in Computer Science, 2015, , 14-25.	1.3	3
39	Mutation landscape of multiple myeloma measurable residual disease: identification of targets for precision medicine. Blood Advances, 2021, , .	5.2	3
40	Large Scale Agent-Based Modeling of the Humoral and Cellular Immune Response. Lecture Notes in Computer Science, 2011, , 15-29.	1.3	3
41	Generalized Pattern Search and Mesh Adaptive Direct Search Algorithms for Protein Structure Prediction. Lecture Notes in Computer Science, 2007, , 183-193.	1.3	3
42	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
43	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
44	An Immunological Algorithm for Doping Profile Optimization in Semiconductors Design. Lecture Notes in Computer Science, 2010, , 213-222.	1.3	2
45	Design and assembly of DNA molecules using multi-objective optimization. Synthetic Biology, 2021, 6, ysab026.	2.2	2
46	Effective design of semiconductor devices using evolutionary-based derivative free optimization. , 2010, , .		1
47	Multi-objective optimization of doping profile in semiconductor design. , 2010, , .		1
48	Boseâ€Einstein condensation in satisfiability problems. European Journal of Operational Research, 2013, 227, 44-54.	5.7	1
49	Stochastic Methods for Global Optimization and Problem Solving. , 2019, , 321-327.		1
50	Mathematical Optimization. SpringerBriefs in Optimization, 2013, , 13-25.	0.3	1
51	String Selection Problems. SpringerBriefs in Optimization, 2013, , 27-49.	0.3	1
52	Optimization Methods and Applications to Microelectronics CAD. Mathematics in Industry, 2015, , 435-451.	0.3	1
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	PyGNA: a unified framework for geneset network analysis. BMC Bioinformatics, 2020, 21, 476.	2.6	0
56	A CLONAL SELECTION ALGORITHM FOR THE AUTOMATIC SYNTHESIS OF LOW-PASS FILTERS. , 2009, , .		0
57	Biological Sequences. SpringerBriefs in Optimization, 2013, , 1-6.	0.3	0
58	Designing Groundwater Supply Systems Using the Mesh Adaptive Basin Hopping Algorithm. , 2014, , 407-421.		0
59	Whole Exome Sequencing of Residual Disease in Multiple Myeloma: Searching for Novel Therapeutic Targets. Blood, 2018, 132, 3175-3175.	1.4	0
60	Computer Aided Assembly and Verification of Synthetic Chromosomes. Methods in Molecular Biology, 2021, 2189, 169-181.	0.9	0
61	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