

Natalio Krasnogor

List of Publications by Year in descending order

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133
papers

3,889
citations

136885

32
h-index

143943

57
g-index

143
all docs

143
docs citations

143
times ranked

5121
citing authors

#	ARTICLE	IF	CITATIONS
1	Versioning biological cells for trustworthy cell engineering. <i>Nature Communications</i> , 2022, 13, 765.	5.8	6
2	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production. <i>ACS Synthetic Biology</i> , 2022, 11, 1531-1541.	1.9	6
3	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. <i>New Biotechnology</i> , 2021, 60, 44-51.	2.4	34
4	Toward Full-Stack <i>In Silico</i> Synthetic Biology: Integrating Model Specification, Simulation, Verification, and Biological Compilation. <i>ACS Synthetic Biology</i> , 2021, 10, 1931-1945.	1.9	10
5	A last-in first-out stack data structure implemented in DNA. <i>Nature Communications</i> , 2021, 12, 4861.	5.8	11
6	Transcriptomic Responses to Coaggregation between <i>Streptococcus gordonii</i> and <i>Streptococcus oralis</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0155821.	1.4	6
7	Targetron-Assisted Delivery of Exogenous DNA Sequences into <i>Pseudomonas putida</i> through CRISPR-Aided Counterselection. <i>ACS Synthetic Biology</i> , 2021, 10, 2552-2565.	1.9	8
8	Expression, Localization, and Protein Interactions of the Partitioning Proteins in the Gonococcal Type IV Secretion System. <i>Frontiers in Microbiology</i> , 2021, 12, 784483.	1.5	4
9	A Scalable Test Suite for Continuous Dynamic Multiobjective Optimization. <i>IEEE Transactions on Cybernetics</i> , 2020, 50, 2814-2826.	6.2	30
10	Developing a simple method to enhance the generation of cone and rod photoreceptors in pluripotent stem cell-derived retinal organoids. <i>Stem Cells</i> , 2020, 38, 45-51.	1.4	42
11	In Situ Analysis Reveals That CFTR Is Expressed in Only a Small Minority of \hat{I}^2 -Cells in Normal Adult Human Pancreas. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 1366-1374.	1.8	26
12	AREA: An adaptive reference-set based evolutionary algorithm for multiobjective optimisation. <i>Information Sciences</i> , 2020, 515, 365-387.	4.0	16
13	Automatic Tuning of Rule-Based Evolutionary Machine Learning via Problem Structure Identification. <i>IEEE Computational Intelligence Magazine</i> , 2020, 15, 28-46.	3.4	7
14	Protein interactions within and between two $\hat{F}\hat{a}C\hat{t}$ type type IV secretion systems. <i>Molecular Microbiology</i> , 2020, 114, 823-838.	1.2	11
15	Cotranscriptional Folding of a Bio-orthogonal Fluorescent Scaffolded RNA Origami. <i>ACS Synthetic Biology</i> , 2020, 9, 1682-1692.	1.9	13
16	NIHBA: a network interdiction approach for metabolic engineering design. <i>Bioinformatics</i> , 2020, 36, 3482-3492.	1.8	7
17	Reduced Expression of the Co-regulator TLE1 in Type 2 Diabetes Is Associated with Increased Islet \hat{I}^2 -Cell Number. <i>Endocrinology</i> , 2020, 161, .	1.4	8
18	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. <i>ACS Synthetic Biology</i> , 2020, 9, 536-545.	1.9	23

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19	Decellularised extracellular matrix-derived peptides from neural retina and retinal pigment epithelium enhance the expression of synaptic markers and light responsiveness of human pluripotent stem cell derived retinal organoids. <i>Biomaterials</i> , 2019, 199, 63-75.	5.7	53
20	Transcriptional profiling of coaggregation interactions between <i>Streptococcus gordonii</i> and <i>Veillonella parvula</i> by Dual RNA-Seq. <i>Scientific Reports</i> , 2019, 9, 7664.	1.6	22
21	Immunodeficiency, autoimmune thrombocytopenia and enterocolitis caused by autosomal recessive deficiency of <i>PIK3CD</i> -encoded phosphoinositide 3-kinase β . <i>Haematologica</i> , 2019, 104, e483-e486.	1.7	26
22	Easybiotics: a GUI for 3D physical modelling of multi-species bacterial populations. <i>Bioinformatics</i> , 2019, 35, 3859-3860.	1.8	3
23	Automatic selection of verification tools for efficient analysis of biochemical models. <i>Bioinformatics</i> , 2018, 34, 3187-3195.	1.8	7
24	<i>Streptococcus gordonii</i> Challisin protease is required for sensing cell-cell contact with <i>Actinomyces oris</i> . <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	11
25	Less detectable environmental changes in dynamic multiobjective optimisation. , 2018, , .		9
26	An Empirical Study of Dynamic Triobjective Optimisation Problems. , 2018, , .		3
27	Disrupted alternative splicing for genes implicated in splicing and ciliogenesis causes PRPF31 retinitis pigmentosa. <i>Nature Communications</i> , 2018, 9, 4234.	5.8	158
28	Transcriptional responses of <i>Streptococcus gordonii</i> and <i>Fusobacterium nucleatum</i> to coaggregation. <i>Molecular Oral Microbiology</i> , 2018, 33, 450-464.	1.3	24
29	Extracellular matrix component expression in human pluripotent stem cell-derived retinal organoids recapitulates retinogenesis in vivo and reveals an important role for IMPG1 and CD44 in the development of photoreceptors and interphotoreceptor matrix. <i>Acta Biomaterialia</i> , 2018, 74, 207-221.	4.1	34
30	Isothermal folding of a light-up bio-orthogonal RNA origami nanoribbon. <i>Scientific Reports</i> , 2018, 8, 6989.	1.6	22
31	Population Dynamics of Autocatalytic Sets in a Compartmentalized Spatial World. <i>Life</i> , 2018, 8, 33.	1.1	16
32	Strain Design as Multiobjective Network Interdiction Problem: A Preliminary Approach. <i>Lecture Notes in Computer Science</i> , 2018, , 273-282.	1.0	1
33	Predicting species emergence in simulated complex pre-biotic networks. <i>PLoS ONE</i> , 2018, 13, e0192871.	1.1	11
34	The fittest, the common, and the dullest: Selection dynamics of exact autocatalytic replicators. , 2018, , .		0
35	Designing Uniquely Addressable Bio-orthogonal Synthetic Scaffolds for DNA and RNA Origami. <i>ACS Synthetic Biology</i> , 2017, 6, 1140-1149.	1.9	21
36	CSBB: synthetic biology research at Newcastle University. <i>Biochemical Society Transactions</i> , 2017, 45, 781-783.	1.6	1

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37	Optimizing nucleic acid sequences for a molecular data recorder. , 2017, , .		1
38	An Integrated In Silico Simulation and Biomatter Compilation Approach to Cellular Computation. Emergence, Complexity and Computation, 2017, , 655-676.	0.2	2
39	Simiotics: A Multiscale Integrative Platform for 3D Modeling of Bacterial Populations. ACS Synthetic Biology, 2017, 6, 1194-1210.	1.9	33
40	Functional networks inference from rule-based machine learning models. BioData Mining, 2016, 9, 28.	2.2	7
41	Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. Nucleic Acids Research, 2016, 44, e35-e35.	6.5	23
42	In Vitro Implementation of a Stack Data Structure Based on DNA Strand Displacement. Lecture Notes in Computer Science, 2016, , 87-98.	1.0	3
43	Qualitative and Quantitative Analysis of Systems and Synthetic Biology Constructs using P Systems. ACS Synthetic Biology, 2015, 4, 83-92.	1.9	18
44	Meta-Stochastic Simulation of Biochemical Models for Systems and Synthetic Biology. ACS Synthetic Biology, 2015, 4, 39-47.	1.9	9
45	Complexity Measurement Based on Information Theory and Kolmogorov Complexity. Artificial Life, 2015, 21, 205-224.	1.0	13
46	Algorithms and models for complex natural systems. Natural Computing, 2015, 14, 339-340.	1.8	0
47	JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. Bioinformatics, 2014, 30, 1029-1030.	1.8	52
48	Blind optimisation problem instance classification via enhanced universal similarity metric. Memetic Computing, 2014, 6, 263.	2.7	5
49	Formalizing Modularization and Data Hiding in Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-20.	1.8	3
50	Photochromic molecular implementations of universal computation. BioSystems, 2014, 126, 12-26.	0.9	0
51	Conventional Verification for Unconventional Computing: a Genetic XOR Gate Example. Fundamenta Informaticae, 2014, 134, 97-110.	0.3	14
52	Modelling and Stochastic Simulation of Synthetic Biological Boolean Gates. , 2014, , .		14
53	Hard Data Analytics Problems Make for Better Data Analysis Algorithms: Bioinformatics as an Example. Big Data, 2014, 2, 164-176.	2.1	12
54	Heuristic for Maximizing DNA Reuse in Synthetic DNA Library Assembly. ACS Synthetic Biology, 2014, 3, 529-542.	1.9	16

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55	Infobiotics Workbench: A P Systems Based Tool for Systems and Synthetic Biology. Emergence, Complexity and Computation, 2014, , 1-41.	0.2	19
56	Chemical Production and Molecular Computing in Addressable Reaction Compartments. Lecture Notes in Computer Science, 2014, , 173-182.	1.0	2
57	Matching island topologies to problem structure in parallel evolutionary algorithms. Soft Computing, 2013, 17, 1209-1225.	2.1	71
58	A genotype-phenotype-fitness assessment protocol for evolutionary self-assembly Wang tiles design. Memetic Computing, 2013, 5, 19-33.	2.7	2
59	Bacteria clustering by polymers induces the expression of quorum-sensing-controlled phenotypes. Nature Chemistry, 2013, 5, 1058-1065.	6.6	67
60	Exploring programmable self-assembly in non-DNA based molecular computing. Natural Computing, 2013, 12, 499-515.	1.8	7
61	GAssist vs. BioHEL: critical assessment of two paradigms of genetics-based machine learning. Soft Computing, 2013, 17, 953-981.	2.1	7
62	Transcriptional Dynamics of Two Seed Compartments with Opposing Roles in Arabidopsis Seed Germination Á Á. Plant Physiology, 2013, 163, 205-215.	2.3	175
63	Contact map prediction using a large-scale ensemble of rule sets and the fusion of multiple predicted structural features. Bioinformatics, 2012, 28, 2441-2448.	1.8	36
64	Post-processing operators for decision lists. , 2012, , .		7
65	EnrichNet: network-based gene set enrichment analysis. Bioinformatics, 2012, 28, i451-i457.	1.8	269
66	Is There an Optimal Level of Open-Endedness in Prebiotic Evolution?. Origins of Life and Evolution of Biospheres, 2012, 42, 469-474.	0.8	9
67	Using Rule-Based Machine Learning for Candidate Disease Gene Prioritization and Sample Classification of Cancer Gene Expression Data. PLoS ONE, 2012, 7, e39932.	1.1	95
68	Implementing conventional logic unconventionally: Photochromic molecular populations as registers and logic gates. BioSystems, 2012, 109, 35-51.	0.9	8
69	Analysing BioHEL using challenging boolean functions. Evolutionary Intelligence, 2012, 5, 87-102.	2.3	7
70	Genome-wide network model capturing seed germination reveals coordinated regulation of plant cellular phase transitions. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9709-9714.	3.3	210
71	ArrayMining.net: a web-server for integrative microarray and gene set analysis. Nature Precedings, 2011, , .	0.1	0
72	Integrative analysis of large-scale biological data sets. Nature Precedings, 2011, , .	0.1	1

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73	PathExpand: Extending biological pathways using molecular interaction networks. Nature Precedings, 2011, , .	0.1	0
74	Darwin's magic: Evolutionary computation in nanoscience, bioinformatics and systems biology. , 2011, , .		0
75	RERG (Ras-like, oestrogen-regulated, growth-inhibitor) expression in breast cancer: a marker of ER-positive luminal-like subtype. Breast Cancer Research and Treatment, 2011, 128, 315-326.	1.1	41
76	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9.	1.0	54
77	(Computational) synthetic biology. , 2011, , .		0
78	Automated probe microscopy via evolutionary optimization at the atomic scale. Applied Physics Letters, 2011, 98, .	1.5	30
79	The effect of encapsulation on molecular computing efficiency. , 2011, , .		0
80	The Infobiotics Workbench: an integrated <i>in silico</i> modelling platform for Systems and Synthetic Biology. Bioinformatics, 2011, 27, 3323-3324.	1.8	40
81	A thermodynamic switch modulates abscisic acid receptor sensitivity. EMBO Journal, 2011, 30, 4171-4184.	3.5	161
82	Modelling the initialisation stage of the ALKR representation for discrete domains and GABIL encoding. , 2011, , .		6
83	Genotype-Fitness Correlation Analysis for Evolutionary Design of Self-assembly Wang Tiles. Studies in Computational Intelligence, 2011, , 73-84.	0.7	0
84	Controlled polymer synthesis from biomimicry towards synthetic biology. Chemical Society Reviews, 2010, 39, 286-300.	18.7	75
85	A learning classifier system with mutual-information-based fitness. Evolutionary Intelligence, 2010, 3, 31-50.	2.3	8
86	Evolving cell models for systems and synthetic biology. Systems and Synthetic Biology, 2010, 4, 55-84.	1.0	40
87	A computational study of liposome logic: towards cellular computing from the bottom up. Systems and Synthetic Biology, 2010, 4, 157-179.	1.0	16
88	Synthetic biology gains momentum in Europe. Systems and Synthetic Biology, 2010, 4, 145-147.	1.0	1
89	GP challenge: evolving energy function for protein structure prediction. Genetic Programming and Evolvable Machines, 2010, 11, 61-88.	1.5	15
90	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics, 2010, 11, 597.	1.2	40

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91	Stochastic and deterministic multiscale models for systems biology: an auxin-transport case study. BMC Systems Biology, 2010, 4, 34.	3.0	35
92	Grammatical rules for the automated construction of heuristics. , 2010, , .		0
93	TopoGSA: network topological gene set analysis. Bioinformatics, 2010, 26, 1271-1272.	1.8	58
94	Analysing bioHEL using challenging boolean functions. , 2010, , .		1
95	Speeding up the evaluation of evolutionary learning systems using GPGPUs. , 2010, , .		53
96	Toward High-Throughput, Multicriteria Protein-Structure Comparison and Analysis. IEEE Transactions on Nanobioscience, 2010, 9, 144-155.	2.2	8
97	vrmIgen: AnRPackage for 3D Data Visualization on the Web. Journal of Statistical Software, 2010, 36, .	1.8	7
98	Evolutionary design of the energy function for protein structure prediction. , 2009, , .		3
99	MODULAR ASSEMBLY OF CELL SYSTEMS BIOLOGY MODELS USINGPSYSTEMS. International Journal of Foundations of Computer Science, 2009, 20, 427-442.	0.8	41
100	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. BMC Bioinformatics, 2009, 10, 358.	1.2	85
101	Automated Alphabet Reduction for Protein Datasets. BMC Bioinformatics, 2009, 10, 6.	1.2	54
102	Nature-inspired cooperative strategies for optimization. International Journal of Intelligent Systems, 2009, 24, 723-725.	3.3	13
103	Automated self-assembly programming paradigm: The impact of network topology. International Journal of Intelligent Systems, 2009, 24, 793-817.	3.3	5
104	Prediction of topological contacts in proteins using learning classifier systems. Soft Computing, 2009, 13, 245-258.	2.1	27
105	P-systems and X-machines. Natural Computing, 2009, 8, 777-779.	1.8	0
106	Improving the scalability of rule-based evolutionary learning. Memetic Computing, 2009, 1, 55-67.	2.7	84
107	Editorial to the first issue. Memetic Computing, 2009, 1, 1-2.	2.7	24
108	A mixed discrete-continuous attribute list representation for large scale classification domains. , 2009, , .		19

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109	Performance and Efficiency of Memetic Pittsburgh Learning Classifier Systems. <i>Evolutionary Computation</i> , 2009, 17, 307-342.	2.3	48
110	Adaptive Cellular Memetic Algorithms. <i>Evolutionary Computation</i> , 2009, 17, 231-256.	2.3	53
111	Diolâ€“boronic acid complexes integrated by responsive polymersâ€“a route to chemical sensing and logic operations. <i>Soft Matter</i> , 2009, 5, 3839.	1.2	34
112	A Multiscale Modeling Framework Based on P Systems. <i>Lecture Notes in Computer Science</i> , 2009, , 63-77.	1.0	11
113	Memetic Algorithms: The Polynomial Local Search Complexity Theory Perspective. <i>Mathematical Modelling and Algorithms</i> , 2008, 7, 3-24.	0.5	25
114	Prediction of recursive convex hull class assignments for protein residues. <i>Bioinformatics</i> , 2008, 24, 916-923.	1.8	42
115	Chapter 13 Automated Self-Assembling Programming. <i>Studies in Multidisciplinarity</i> , 2008, , 281-307.	0.0	1
116	Learning classifier systems for optimisation problems. , 2008, , .		3
117	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. <i>Current Bioinformatics</i> , 2008, 3, 10-31.	0.7	11
118	An unorthodox introduction to Memetic Algorithms. <i>ACM SIGEVolution</i> , 2008, 3, 6-15.	0.3	2
119	Search Strategies in Structural Bioinformatics. <i>Current Protein and Peptide Science</i> , 2008, 9, 260-274.	0.7	13
120	Empirical Evaluation of Ensemble Techniques for a Pittsburgh Learning Classifier System. <i>Lecture Notes in Computer Science</i> , 2008, , 255-268.	1.0	20
121	Automated alphabet reduction method with evolutionary algorithms for protein structure prediction. , 2007, , .		38
122	A Genetic Algorithm Approach to Probing the Evolution of Self-Organized Nanostructured Systems. <i>Nano Letters</i> , 2007, 7, 1985-1990.	4.5	22
123	Evolving tiles for automated self-assembly design. , 2007, , .		12
124	Quorum sensing P systems. <i>Theoretical Computer Science</i> , 2007, 371, 20-33.	0.5	31
125	ProCKSI: a decision support system for Protein (Structure) Comparison, Knowledge, Similarity and Information. <i>BMC Bioinformatics</i> , 2007, 8, 416.	1.2	48
126	The imitation gameâ€“a computational chemical approach to recognizing life. <i>Nature Biotechnology</i> , 2006, 24, 1203-1206.	9.4	113

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127	Coordination number prediction using learning classifier systems. , 2006, , .		16
128	PREDICTION OF RESIDUE EXPOSURE AND CONTACT NUMBER FOR SIMPLIFIED HP LATTICE MODEL PROTEINS USING LEARNING CLASSIFIER SYSTEMS. , 2006, , .		3
129	A fuzzy sets based generalization of contact maps for the overlap of protein structures. Fuzzy Sets and Systems, 2005, 152, 103-123.	1.6	19
130	A Study on the use of "self-generation" in memetic algorithms. Natural Computing, 2004, 3, 53-76.	1.8	83
131	Real-Coded Memetic Algorithms with Crossover Hill-Climbing. Evolutionary Computation, 2004, 12, 273-302.	2.3	285
132	Modelling string folding with G2L grammars (poster). ACM SIGPLAN Notices, 1997, 32, 314.	0.2	0
133	Protein folding meets functional programming (poster). ACM SIGPLAN Notices, 1997, 32, 313.	0.2	0