

Natalio Krasnogor

List of Publications by Year in descending order

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133
papers

3,889
citations

136950

32
h-index

144013

57
g-index

143
all docs

143
docs citations

143
times ranked

5121
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-Coded Memetic Algorithms with Crossover Hill-Climbing. <i>Evolutionary Computation</i> , 2004, 12, 273-302.	3.0	285
2	EnrichNet: network-based gene set enrichment analysis. <i>Bioinformatics</i> , 2012, 28, i451-i457.	4.1	269
3	Genome-wide network model capturing seed germination reveals coordinated regulation of plant cellular phase transitions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9709-9714.	7.1	210
4	Transcriptional Dynamics of Two Seed Compartments with Opposing Roles in Arabidopsis Seed Germination. <i>Plant Physiology</i> , 2013, 163, 205-215.	4.8	175
5	A thermodynamic switch modulates abscisic acid receptor sensitivity. <i>EMBO Journal</i> , 2011, 30, 4171-4184.	7.8	161
6	Disrupted alternative splicing for genes implicated in splicing and ciliogenesis causes PRPF31 retinitis pigmentosa. <i>Nature Communications</i> , 2018, 9, 4234.	12.8	158
7	The imitation game—a computational chemical approach to recognizing life. <i>Nature Biotechnology</i> , 2006, 24, 1203-1206.	17.5	113
8	Using Rule-Based Machine Learning for Candidate Disease Gene Prioritization and Sample Classification of Cancer Gene Expression Data. <i>PLoS ONE</i> , 2012, 7, e39932.	2.5	95
9	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. <i>BMC Bioinformatics</i> , 2009, 10, 358.	2.6	85
10	Improving the scalability of rule-based evolutionary learning. <i>Memetic Computing</i> , 2009, 1, 55-67.	4.0	84
11	A Study on the use of "self-generation" in memetic algorithms. <i>Natural Computing</i> , 2004, 3, 53-76.	3.0	83
12	Controlled polymer synthesis—from biomimicry towards synthetic biology. <i>Chemical Society Reviews</i> , 2010, 39, 286-300.	38.1	75
13	Matching island topologies to problem structure in parallel evolutionary algorithms. <i>Soft Computing</i> , 2013, 17, 1209-1225.	3.6	71
14	Bacteria clustering by polymers induces the expression of quorum-sensing-controlled phenotypes. <i>Nature Chemistry</i> , 2013, 5, 1058-1065.	13.6	67
15	TopoGSA: network topological gene set analysis. <i>Bioinformatics</i> , 2010, 26, 1271-1272.	4.1	58
16	Automated Alphabet Reduction for Protein Datasets. <i>BMC Bioinformatics</i> , 2009, 10, 6.	2.6	54
17	The ten grand challenges of synthetic life. <i>Systems and Synthetic Biology</i> , 2011, 5, 1-9.	1.0	54
18	Adaptive Cellular Memetic Algorithms. <i>Evolutionary Computation</i> , 2009, 17, 231-256.	3.0	53

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19	Speeding up the evaluation of evolutionary learning systems using GPGPUs. , 2010, , .		53
20	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.	11.4	53
21	JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. <i>Bioinformatics</i> , 2014, 30, 1029-1030.	4.1	52
22	ProCKSI: a decision support system for Protein (Structure) Comparison, Knowledge, Similarity and Information. <i>BMC Bioinformatics</i> , 2007, 8, 416.	2.6	48
23	Performance and Efficiency of Memetic Pittsburgh Learning Classifier Systems. <i>Evolutionary Computation</i> , 2009, 17, 307-342.	3.0	48
24	Prediction of recursive convex hull class assignments for protein residues. <i>Bioinformatics</i> , 2008, 24, 916-923.	4.1	42
25	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.	3.2	42
26	MODULAR ASSEMBLY OF CELL SYSTEMS BIOLOGY MODELS USINGPSYSTEMS. <i>International Journal of Foundations of Computer Science</i> , 2009, 20, 427-442.	1.1	41
27	RERG (Ras-like, oestrogen-regulated, growth-inhibitor) expression in breast cancer: a marker of ER-positive luminal-like subtype. <i>Breast Cancer Research and Treatment</i> , 2011, 128, 315-326.	2.5	41
28	Evolving cell models for systems and synthetic biology. <i>Systems and Synthetic Biology</i> , 2010, 4, 55-84.	1.0	40
29	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. <i>BMC Bioinformatics</i> , 2010, 11, 597.	2.6	40
30	The Infobiotics Workbench: an integrated <i>in silico</i> modelling platform for Systems and Synthetic Biology. <i>Bioinformatics</i> , 2011, 27, 3323-3324.	4.1	40
31	Automated alphabet reduction method with evolutionary algorithms for protein structure prediction. , 2007, , .		38
32	Contact map prediction using a large-scale ensemble of rule sets and the fusion of multiple predicted structural features. <i>Bioinformatics</i> , 2012, 28, 2441-2448.	4.1	36
33	Stochastic and deterministic multiscale models for systems biology: an auxin-transport case study. <i>BMC Systems Biology</i> , 2010, 4, 34.	3.0	35
34	Diolâ€“boronic acid complexes integrated by responsive polymersâ€“a route to chemical sensing and logic operations. <i>Soft Matter</i> , 2009, 5, 3839.	2.7	34
35	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.	8.3	34
36	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. <i>New Biotechnology</i> , 2021, 60, 44-51.	4.4	34

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37	Simbiotics: A Multiscale Integrative Platform for 3D Modeling of Bacterial Populations. ACS Synthetic Biology, 2017, 6, 1194-1210.	3.8	33
38	Quorum sensing P systems. Theoretical Computer Science, 2007, 371, 20-33.	0.9	31
39	Automated probe microscopy via evolutionary optimization at the atomic scale. Applied Physics Letters, 2011, 98, .	3.3	30
40	A Scalable Test Suite for Continuous Dynamic Multiobjective Optimization. IEEE Transactions on Cybernetics, 2020, 50, 2814-2826.	9.5	30
41	Prediction of topological contacts in proteins using learning classifier systems. Soft Computing, 2009, 13, 245-258.	3.6	27
42	Immunodeficiency, autoimmune thrombocytopenia and enterocolitis caused by autosomal recessive deficiency of <i>PIK3CD</i> -encoded phosphoinositide 3-kinase β . Haematologica, 2019, 104, e483-e486.	3.5	26
43	In Situ Analysis Reveals That CFTR Is Expressed in Only a Small Minority of β 2-Cells in Normal Adult Human Pancreas. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1366-1374.	3.6	26
44	Memetic Algorithms: The Polynomial Local Search Complexity Theory Perspective. Mathematical Modelling and Algorithms, 2008, 7, 3-24.	0.5	25
45	Editorial to the first issue. Memetic Computing, 2009, 1, 1-2.	4.0	24
46	Transcriptional responses of <i>Streptococcus gordonii</i> and <i>Fusobacterium nucleatum</i> to coaggregation. Molecular Oral Microbiology, 2018, 33, 450-464.	2.7	24
47	Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. Nucleic Acids Research, 2016, 44, e35-e35.	14.5	23
48	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. ACS Synthetic Biology, 2020, 9, 536-545.	3.8	23
49	A Genetic Algorithm Approach to Probing the Evolution of Self-Organized Nanostructured Systems. Nano Letters, 2007, 7, 1985-1990.	9.1	22
50	Isothermal folding of a light-up bio-orthogonal RNA origami nanoribbon. Scientific Reports, 2018, 8, 6989.	3.3	22
51	Transcriptional profiling of coaggregation interactions between <i>Streptococcus gordonii</i> and <i>Veillonella parvula</i> by Dual RNA-Seq. Scientific Reports, 2019, 9, 7664.	3.3	22
52	Designing Uniquely Addressable Bio-orthogonal Synthetic Scaffolds for DNA and RNA Origami. ACS Synthetic Biology, 2017, 6, 1140-1149.	3.8	21
53	Empirical Evaluation of Ensemble Techniques for a Pittsburgh Learning Classifier System. Lecture Notes in Computer Science, 2008, , 255-268.	1.3	20
54	A fuzzy sets based generalization of contact maps for the overlap of protein structures. Fuzzy Sets and Systems, 2005, 152, 103-123.	2.7	19

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55	A mixed discrete-continuous attribute list representation for large scale classification domains. , 2009, , .		19
56	Infobiotics Workbench: A P Systems Based Tool for Systems and Synthetic Biology. Emergence, Complexity and Computation, 2014, , 1-41.	0.3	19
57	Qualitative and Quantitative Analysis of Systems and Synthetic Biology Constructs using P Systems. ACS Synthetic Biology, 2015, 4, 83-92.	3.8	18
58	Coordination number prediction using learning classifier systems. , 2006, , .		16
59	A computational study of liposome logic: towards cellular computing from the bottom up. Systems and Synthetic Biology, 2010, 4, 157-179.	1.0	16
60	Heuristic for Maximizing DNA Reuse in Synthetic DNA Library Assembly. ACS Synthetic Biology, 2014, 3, 529-542.	3.8	16
61	Population Dynamics of Autocatalytic Sets in a Compartmentalized Spatial World. Life, 2018, 8, 33.	2.4	16
62	AREA: An adaptive reference-set based evolutionary algorithm for multiobjective optimisation. Information Sciences, 2020, 515, 365-387.	6.9	16
63	GP challenge: evolving energy function for protein structure prediction. Genetic Programming and Evolvable Machines, 2010, 11, 61-88.	2.2	15
64	Conventional Verification for Unconventional Computing: a Genetic XOR Gate Example. Fundamenta Informaticae, 2014, 134, 97-110.	0.4	14
65	Modelling and Stochastic Simulation of Synthetic Biological Boolean Gates. , 2014, , .		14
66	Search Strategies in Structural Bioinformatics. Current Protein and Peptide Science, 2008, 9, 260-274.	1.4	13
67	Nature-inspired cooperative strategies for optimization. International Journal of Intelligent Systems, 2009, 24, 723-725.	5.7	13
68	Complexity Measurement Based on Information Theory and Kolmogorov Complexity. Artificial Life, 2015, 21, 205-224.	1.3	13
69	Cotranscriptional Folding of a Bio-orthogonal Fluorescent Scaffolded RNA Origami. ACS Synthetic Biology, 2020, 9, 1682-1692.	3.8	13
70	Evolving tiles for automated self-assembly design. , 2007, , .		12
71	Hard Data Analytics Problems Make for Better Data Analysis Algorithms: Bioinformatics as an Example. Big Data, 2014, 2, 164-176.	3.4	12
72	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. Current Bioinformatics, 2008, 3, 10-31.	1.5	11

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73	Streptococcus gordonii Challisin protease is required for sensing cell–cell contact with Actinomyces oris. FEMS Microbiology Ecology, 2018, 94, .	2.7	11
74	Protein interactions within and between two Fâ€¢type type IV secretion systems. Molecular Microbiology, 2020, 114, 823-838.	2.5	11
75	A last-in first-out stack data structure implemented in DNA. Nature Communications, 2021, 12, 4861.	12.8	11
76	A Multiscale Modeling Framework Based on P Systems. Lecture Notes in Computer Science, 2009, , 63-77.	1.3	11
77	Predicting species emergence in simulated complex pre-biotic networks. PLoS ONE, 2018, 13, e0192871.	2.5	11
78	Toward Full-Stack <i>In Silico</i> Synthetic Biology: Integrating Model Specification, Simulation, Verification, and Biological Compilation. ACS Synthetic Biology, 2021, 10, 1931-1945.	3.8	10
79	Is There an Optimal Level of Open-Endedness in Prebiotic Evolution?. Origins of Life and Evolution of Biospheres, 2012, 42, 469-474.	1.9	9
80	Meta-Stochastic Simulation of Biochemical Models for Systems and Synthetic Biology. ACS Synthetic Biology, 2015, 4, 39-47.	3.8	9
81	Less detectable environmental changes in dynamic multiobjective optimisation. , 2018, , .		9
82	A learning classifier system with mutual-information-based fitness. Evolutionary Intelligence, 2010, 3, 31-50.	3.6	8
83	Toward High-Throughput, Multicriteria Protein-Structure Comparison and Analysis. IEEE Transactions on Nanobioscience, 2010, 9, 144-155.	3.3	8
84	Implementing conventional logic unconventionally: Photochromic molecular populations as registers and logic gates. BioSystems, 2012, 109, 35-51.	2.0	8
85	Reduced Expression of the Co-regulator TLE1 in Type 2 Diabetes Is Associated with Increased Islet Î±-Cell Number. Endocrinology, 2020, 161, .	2.8	8
86	Targetron-Assisted Delivery of Exogenous DNA Sequences into <i>Pseudomonas putida</i> through CRISPR-Aided Counterselection. ACS Synthetic Biology, 2021, 10, 2552-2565.	3.8	8
87	Post-processing operators for decision lists. , 2012, , .		7
88	Analysing BioHEL using challenging boolean functions. Evolutionary Intelligence, 2012, 5, 87-102.	3.6	7
89	Exploring programmable self-assembly in non-DNA based molecular computing. Natural Computing, 2013, 12, 499-515.	3.0	7
90	GAssist vs. BioHEL: critical assessment of two paradigms of genetics-based machine learning. Soft Computing, 2013, 17, 953-981.	3.6	7

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91	Functional networks inference from rule-based machine learning models. <i>BioData Mining</i> , 2016, 9, 28.	4.0	7
92	Automatic selection of verification tools for efficient analysis of biochemical models. <i>Bioinformatics</i> , 2018, 34, 3187-3195.	4.1	7
93	Automatic Tuning of Rule-Based Evolutionary Machine Learning via Problem Structure Identification. <i>IEEE Computational Intelligence Magazine</i> , 2020, 15, 28-46.	3.2	7
94	NIHBA: a network interdiction approach for metabolic engineering design. <i>Bioinformatics</i> , 2020, 36, 3482-3492.	4.1	7
95	vrmIgen: AnRPackage for 3D Data Visualization on the Web. <i>Journal of Statistical Software</i> , 2010, 36, .	3.7	7
96	Modelling the initialisation stage of the ALKR representation for discrete domains and GABIL encoding. , 2011, , .		6
97	Transcriptomic Responses to Coaggregation between <i>Streptococcus gordonii</i> and <i>Streptococcus oralis</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0155821.	3.1	6
98	Versioning biological cells for trustworthy cell engineering. <i>Nature Communications</i> , 2022, 13, 765.	12.8	6
99	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production. <i>ACS Synthetic Biology</i> , 2022, 11, 1531-1541.	3.8	6
100	Automated self-assembly programming paradigm: The impact of network topology. <i>International Journal of Intelligent Systems</i> , 2009, 24, 793-817.	5.7	5
101	Blind optimisation problem instance classification via enhanced universal similarity metric. <i>Memetic Computing</i> , 2014, 6, 263.	4.0	5
102	Expression, Localization, and Protein Interactions of the Partitioning Proteins in the Gonococcal Type IV Secretion System. <i>Frontiers in Microbiology</i> , 2021, 12, 784483.	3.5	4
103	Learning classifier systems for optimisation problems. , 2008, , .		3
104	Evolutionary design of the energy function for protein structure prediction. , 2009, , .		3
105	Formalizing Modularization and Data Hiding in Synthetic Biology. <i>ACM Journal on Emerging Technologies in Computing Systems</i> , 2014, 11, 1-20.	2.3	3
106	An Empirical Study of Dynamic Triobjective Optimisation Problems. , 2018, , .		3
107	Easybiotics: a GUI for 3D physical modelling of multi-species bacterial populations. <i>Bioinformatics</i> , 2019, 35, 3859-3860.	4.1	3
108	In Vitro Implementation of a Stack Data Structure Based on DNA Strand Displacement. <i>Lecture Notes in Computer Science</i> , 2016, , 87-98.	1.3	3

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109	PREDICTION OF RESIDUE EXPOSURE AND CONTACT NUMBER FOR SIMPLIFIED HP LATTICE MODEL PROTEINS USING LEARNING CLASSIFIER SYSTEMS. , 2006, , .		3
110	An unorthodox introduction to Memetic Algorithms. ACM SIGEVolution, 2008, 3, 6-15.	0.5	2
111	A genotype-phenotype-fitness assessment protocol for evolutionary self-assembly Wang tiles design. Memetic Computing, 2013, 5, 19-33.	4.0	2
112	Chemical Production and Molecular Computing in Addressable Reaction Compartments. Lecture Notes in Computer Science, 2014, , 173-182.	1.3	2
113	An Integrated In Silico Simulation andÂBiomatter Compilation Approach toÂCellular Computation. Emergence, Complexity and Computation, 2017, , 655-676.	0.3	2
114	Chapter 13 Automated Self-Assembling Programming. Studies in Multidisciplinarity, 2008, , 281-307.	0.0	1
115	Synthetic biology gains momentum in Europe. Systems and Synthetic Biology, 2010, 4, 145-147.	1.0	1
116	Analysing bioHEL using challenging boolean functions. , 2010, , .		1
117	Integrative analysis of large-scale biological data sets. Nature Precedings, 2011, , .	0.1	1
118	CSBB: synthetic biology research at Newcastle University. Biochemical Society Transactions, 2017, 45, 781-783.	3.4	1
119	Optimizing nucleic acid sequences for a molecular data recorder. , 2017, , .		1
120	Strain Design as Multiobjective Network Interdiction Problem: A Preliminary Approach. Lecture Notes in Computer Science, 2018, , 273-282.	1.3	1
121	Modelling string folding with G2L grammars (poster). ACM SIGPLAN Notices, 1997, 32, 314.	0.2	0
122	Protein folding meets functional programming (poster). ACM SIGPLAN Notices, 1997, 32, 313.	0.2	0
123	P-systems and X-machines. Natural Computing, 2009, 8, 777-779.	3.0	0
124	Grammatical rules for the automated construction of heuristics. , 2010, , .		0
125	ArrayMining.net: a web-server for integrative microarray and gene set analysis. Nature Precedings, 2011, , .	0.1	0
126	PathExpand: Extending biological pathways using molecular interaction networks. Nature Precedings, 2011, , .	0.1	0

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127	Darwin's magic: Evolutionary computation in nanoscience, bioinformatics and systems biology. , 2011, , .		0
128	(Computational) synthetic biology. , 2011, , .		0
129	The effect of encapsulation on molecular computing efficiency. , 2011, , .		0
130	Photochromic molecular implementations of universal computation. BioSystems, 2014, 126, 12-26.	2.0	0
131	Algorithms and models for complex natural systems. Natural Computing, 2015, 14, 339-340.	3.0	0
132	Genotype-Fitness Correlation Analysis for Evolutionary Design of Self-assembly Wang Tiles. Studies in Computational Intelligence, 2011, , 73-84.	0.9	0
133	The fittest, the common, and the dullest: Selection dynamics of exact autocatalytic replicators. , 2018, , .		0