Natalio Krasnogor

List of Publications by Year
in descending order

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	Real-Coded Memetic Algorithms with Crossover Hill-Climbing. Evolutionary Computation, 2004, 12, 273-302.	2.3	285
2	EnrichNet: network-based gene set enrichment analysis. Bioinformatics, 2012, 28, i451-i457.	1.8	269
3	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
4	Transcriptional Dynamics of Two Seed Compartments with Opposing Roles in Arabidopsis Seed Germination Â. Plant Physiology, 2013, 163, 205-215.	2.3	175
5	A thermodynamic switch modulates abscisic acid receptor sensitivity. EMBO Journal, 2011, 30, 4171-4184.	3.5	161
6	Disrupted alternative splicing for genes implicated in splicing and ciliogenesis causes PRPF31 retinitis pigmentosa. Nature Communications, 2018, 9, 4234.	5.8	158
7	The imitation gameâ€"a computational chemical approach to recognizing life. Nature Biotechnology, 2006, 24, 1203-1206.	9.4	113
8	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
9	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
10	Improving the scalability of rule-based evolutionary learning. Memetic Computing, 2009, 1, 55-67.	2.7	84
11	A Study on the use of ``self-generation'' in memetic algorithms. Natural Computing, 2004, 3, 53-76.	1.8	83
12	Controlled polymer synthesisâ€"from biomimicry towards synthetic biology. Chemical Society Reviews, 2010, 39, 286-300.	18.7	75
13	Matching island topologies to problem structure in parallel evolutionary algorithms. Soft Computing, 2013, 17, 1209-1225.	2.1	71
14	Bacteria clustering by polymers induces the expression of quorum-sensing-controlled phenotypes. Nature Chemistry, 2013, 5, 1058-1065.	6.6	67
15	TopoGSA: network topological gene set analysis. Bioinformatics, 2010, 26, 1271-1272.	1.8	58
16	Automated Alphabet Reduction for Protein Datasets. BMC Bioinformatics, 2009, 10, 6.	1.2	54
17	The ten grand challenges of synthetic life. Systems and Synthetic Biology, 2011, 5, 1-9.	1.0	54
18	Adaptive Cellular Memetic Algorithms. Evolutionary Computation, 2009, 17, 231-256.	2.3	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. Biomaterials, 2019, 199, 63-75.	5.7	53
21	JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. Bioinformatics, 2014, 30, 1029-1030.	1.8	52
22	ProCKSI: a decision support system for Protein (Structure) Comparison, Knowledge, Similarity and Information. BMC Bioinformatics, 2007, 8, 416.	1.2	48
23	Performance and Efficiency of Memetic Pittsburgh Learning Classifier Systems. Evolutionary Computation, 2009, 17, 307-342.	2.3	48
24	Prediction of recursive convex hull class assignments for protein residues. Bioinformatics, 2008, 24, 916-923.	1.8	42
25	Developing a simple method to enhance the generation of cone and rod photoreceptors in pluripotent stem cell-derived retinal organoids. Stem Cells, 2020, 38, 45-51.	1.4	42
26	MODULAR ASSEMBLY OF CELL SYSTEMS BIOLOGY MODELS USINGPSYSTEMS. International Journal of Foundations of Computer Science, 2009, 20, 427-442.	0.8	41
27	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
28	Evolving cell models for systems and synthetic biology. Systems and Synthetic Biology, 2010, 4, 55-84.	1.0	40
29	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics, 2010, 11, 597.	1.2	40
30	The Infobiotics Workbench: an integrated <i>in silico</i> modelling platform for Systems and Synthetic Biology. Bioinformatics, 2011, 27, 3323-3324.	1.8	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. Bioinformatics, 2012, 28, 2441-2448.	1.8	36
33	Stochastic and deterministic multiscale models for systems biology: an auxin-transport case study. BMC Systems Biology, 2010, 4, 34.	3.0	35
34	Diolâ€"boronic acid complexes integrated by responsive polymersâ€"a route to chemical sensing and logic operations. Soft Matter, 2009, 5, 3839.	1.2	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. Acta Biomaterialia, 2018, 74, 207-221.	4.1	34
36	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. New Biotechnology, 2021, 60, 44-51.	2.4	34

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37	Simbiotics: A Multiscale Integrative Platform for 3D Modeling of Bacterial Populations. ACS Synthetic Biology, 2017, 6, 1194-1210.	1.9	33
38	Quorum sensing P systems. Theoretical Computer Science, 2007, 371, 20-33.	0.5	31
39	Automated probe microscopy via evolutionary optimization at the atomic scale. Applied Physics Letters, 2011, 98, .	1.5	30
40	A Scalable Test Suite for Continuous Dynamic Multiobjective Optimization. IEEE Transactions on Cybernetics, 2020, 50, 2814-2826.	6.2	30
41	Prediction of topological contacts in proteins using learning classifier systems. Soft Computing, 2009, 13, 245-258.	2.1	27
42	Immunodeficiency, autoimmune thrombocytopenia and enterocolitis caused by autosomal recessive deficiency of <i>PIK3CD</i>-encoded phosphoinositide 3-kinase δ. Haematologica, 2019, 104, e483-e486.	1.7	26
43	In Situ Analysis Reveals That CFTR Is Expressed in Only a Small Minority of β²-Cells in Normal Adult Human Pancreas. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1366-1374.	1.8	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.	2.7	24
46	Transcriptional responses of <i>Streptococcus gordonii</i> and <i>Fusobacterium nucleatum</i> to coaggregation. Molecular Oral Microbiology, 2018, 33, 450-464.	1.3	24
47	Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. Nucleic Acids Research, 2016, 44, e35-e35.	6.5	23
48	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. ACS Synthetic Biology, 2020, 9, 536-545.	1.9	23
49	A Genetic Algorithm Approach to Probing the Evolution of Self-Organized Nanostructured Systems. Nano Letters, 2007, 7, 1985-1990.	4.5	22
50	Isothermal folding of a light-up bio-orthogonal RNA origami nanoribbon. Scientific Reports, 2018, 8, 6989.	1.6	22
51	Transcriptional profiling of coaggregation interactions between Streptococcus gordonii and Veillonella parvula by Dual RNA-Seq. Scientific Reports, 2019, 9, 7664.	1.6	22
52	Designing Uniquely Addressable Bio-orthogonal Synthetic Scaffolds for DNA and RNA Origami. ACS Synthetic Biology, 2017, 6, 1140-1149.	1.9	21
53	Empirical Evaluation of Ensemble Techniques for a Pittsburgh Learning Classifier System. Lecture Notes in Computer Science, 2008, , 255-268.	1.0	20
54	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

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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.	0.2	19
57	Qualitative and Quantitative Analysis of Systems and Synthetic Biology Constructs using P Systems. ACS Synthetic Biology, 2015, 4, 83-92.	1.9	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.	1.9	16
61	Population Dynamics of Autocatalytic Sets in a Compartmentalized Spatial World. Life, 2018, 8, 33.	1.1	16
62	AREA: An adaptive reference-set based evolutionary algorithm for multiobjective optimisation. Information Sciences, 2020, 515, 365-387.	4.0	16
63	GP challenge: evolving energy function for protein structure prediction. Genetic Programming and Evolvable Machines, 2010, 11, 61-88.	1.5	15
64	Conventional Verification for Unconventional Computing: a Genetic XOR Gate Example. Fundamenta Informaticae, 2014, 134, 97-110.	0.3	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.	0.7	13
67	Nature-inspired cooperative strategies for optimization. International Journal of Intelligent Systems, 2009, 24, 723-725.	3.3	13
68	Complexity Measurement Based on Information Theory and Kolmogorov Complexity. Artificial Life, 2015, 21, 205-224.	1.0	13
69	Cotranscriptional Folding of a Bio-orthogonal Fluorescent Scaffolded RNA Origami. ACS Synthetic Biology, 2020, 9, 1682-1692.	1.9	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.	2.1	12
72	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. Current Bioinformatics, 2008, 3, 10-31.	0.7	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, .	1.3	11
74	Protein interactions within and between two Fâ€type type IV secretion systems. Molecular Microbiology, 2020, 114, 823-838.	1.2	11
75	A last-in first-out stack data structure implemented in DNA. Nature Communications, 2021, 12, 4861.	5.8	11
76	A Multiscale Modeling Framework Based on P Systems. Lecture Notes in Computer Science, 2009, , 63-77.	1.0	11
77	Predicting species emergence in simulated complex pre-biotic networks. PLoS ONE, 2018, 13, e0192871.	1.1	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.	1.9	10
79	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
80	Meta-Stochastic Simulation of Biochemical Models for Systems and Synthetic Biology. ACS Synthetic Biology, 2015, 4, 39-47.	1.9	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.	2.3	8
83	Toward High-Throughput, Multicriteria Protein-Structure Comparison and Analysis. IEEE Transactions on Nanobioscience, 2010, 9, 144-155.	2.2	8
84	Implementing conventional logic unconventionally: Photochromic molecular populations as registers and logic gates. BioSystems, 2012, 109, 35-51.	0.9	8
85	Reduced Expression of the Co-regulator TLE1 in Type 2 Diabetes Is Associated with Increased Islet Î±-Cell Number. Endocrinology, 2020, 161, .	1.4	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.	1.9	8
87	Post-processing operators for decision lists. , 2012, , .		7
88	Analysing BioHEL using challenging boolean functions. Evolutionary Intelligence, 2012, 5, 87-102.	2.3	7
89	Exploring programmable self-assembly in non-DNA based molecular computing. Natural Computing, 2013, 12, 499-515.	1.8	7
90	GAssist vs. BioHEL: critical assessment of two paradigms of genetics-based machine learning. Soft Computing, 2013, 17, 953-981.	2.1	7

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91	Functional networks inference from rule-based machine learning models. BioData Mining, 2016, 9, 28.	2.2	7
92	Automatic selection of verification tools for efficient analysis of biochemical models. Bioinformatics, 2018, 34, 3187-3195.	1.8	7
93	Automatic Tuning of Rule-Based Evolutionary Machine Learning via Problem Structure Identification. IEEE Computational Intelligence Magazine, 2020, 15, 28-46.	3.4	7
94	NIHBA: a network interdiction approach for metabolic engineering design. Bioinformatics, 2020, 36, 3482-3492.	1.8	7
95	vrmlgen: AnRPackage for 3D Data Visualization on the Web. Journal of Statistical Software, 2010, 36, .	1.8	7
96	Modelling the initialisation stage of the ALKR representation for discrete domains and GABIL encoding. , 2011, , .		6
97	Transcriptomic Responses to Coaggregation between Streptococcus gordonii and Streptococcus oralis. Applied and Environmental Microbiology, 2021, 87, e0155821.	1.4	6
98	Versioning biological cells for trustworthy cell engineering. Nature Communications, 2022, 13, 765.	5.8	6
99	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production. ACS Synthetic Biology, 2022, 11, 1531-1541.	1.9	6
100	Automated self-assembly programming paradigm: The impact of network topology. International Journal of Intelligent Systems, 2009, 24, 793-817.	3.3	5
101	Blind optimisation problem instance classification via enhanced universal similarity metric. Memetic Computing, 2014, 6, 263.	2.7	5
102	Expression, Localization, and Protein Interactions of the Partitioning Proteins in the Gonococcal Type IV Secretion System. Frontiers in Microbiology, 2021, 12, 784483.	1.5	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. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-20.	1.8	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. Bioinformatics, 2019, 35, 3859-3860.	1.8	3
108	In Vitro Implementation of a Stack Data Structure Based on DNA Strand Displacement. Lecture Notes in Computer Science, 2016, , 87-98.	1.0	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.	0.3	2
111	A genotype-phenotype-fitness assessment protocol for evolutionary self-assembly Wang tiles design. Memetic Computing, 2013, 5, 19-33.	2.7	2
112	Chemical Production and Molecular Computing in Addressable Reaction Compartments. Lecture Notes in Computer Science, 2014, , 173-182.	1.0	2
113	An Integrated In Silico Simulation andÂBiomatter Compilation Approach toÂCellular Computation. Emergence, Complexity and Computation, 2017, , 655-676.	0.2	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.	1.6	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.	1.0	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.	1.8	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.	0.9	0
131	Algorithms and models for complex natural systems. Natural Computing, 2015, 14, 339-340.	1.8	0
132	Genotype-Fitness Correlation Analysis for Evolutionary Design of Self-assembly Wang Tiles. Studies in Computational Intelligence, 2011, , 73-84.	0.7	0
133	The fittest, the common, and the dullest: Selection dynamics of exact autocatalytic replicators. , 2018, , .		0