Natalio Krasnogor

List of Publications by Year
in descending order

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	Versioning biological cells for trustworthy cell engineering. Nature Communications, 2022, 13, 765.	12.8	6
2	OptDesign: Identifying Optimum Design Strategies in Strain Engineering for Biochemical Production. ACS Synthetic Biology, 2022, 11, 1531-1541.	3.8	6
3	For the sake of the Bioeconomy: define what a Synthetic Biology Chassis is!. New Biotechnology, 2021, 60, 44-51.	4.4	34
4	Toward Full-Stack *In Silico* Synthetic Biology: Integrating Model Specification, Simulation, Verification, and Biological Compilation. ACS Synthetic Biology, 2021, 10, 1931-1945.	3.8	10
5	A last-in first-out stack data structure implemented in DNA. Nature Communications, 2021, 12, 4861.	12.8	11
6	Transcriptomic Responses to Coaggregation between Streptococcus gordonii and Streptococcus oralis. Applied and Environmental Microbiology, 2021, 87, e0155821.	3.1	6
7	Targetron-Assisted Delivery of Exogenous DNA Sequences into *Pseudomonas putida* through CRISPR-Aided Counterselection. ACS Synthetic Biology, 2021, 10, 2552-2565.	3.8	8
8	Expression, Localization, and Protein Interactions of the Partitioning Proteins in the Gonococcal Type IV Secretion System. Frontiers in Microbiology, 2021, 12, 784483.	3.5	4
9	A Scalable Test Suite for Continuous Dynamic Multiobjective Optimization. IEEE Transactions on Cybernetics, 2020, 50, 2814-2826.	9.5	30
10	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.	3.2	42
11	In Situ Analysis Reveals That CFTR Is Expressed in Only a Small Minority of β-Cells in Normal Adult Human Pancreas. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1366-1374.	3.6	26
12	AREA: An adaptive reference-set based evolutionary algorithm for multiobjective optimisation. Information Sciences, 2020, 515, 365-387.	6.9	16
13	Automatic Tuning of Rule-Based Evolutionary Machine Learning via Problem Structure Identification. IEEE Computational Intelligence Magazine, 2020, 15, 28-46.	3.2	7
14	Protein interactions within and between two Fâ€type type IV secretion systems. Molecular Microbiology, 2020, 114, 823-838.	2.5	11
15	Cotranscriptional Folding of a Bio-orthogonal Fluorescent Scaffolded RNA Origami. ACS Synthetic Biology, 2020, 9, 1682-1692.	3.8	13
16	NIHBA: a network interdiction approach for metabolic engineering design. Bioinformatics, 2020, 36, 3482-3492.	4.1	7
17	Reduced Expression of the Co-regulator TLE1 in Type 2 Diabetes Is Associated with Increased Islet α-Cell Number. Endocrinology, 2020, 161, .	2.8	8
18	Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. ACS Synthetic Biology, 2020, 9, 536-545.	3.8	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. Biomaterials, 2019, 199, 63-75.	11.4	53
20	Transcriptional profiling of coaggregation interactions between Streptococcus gordonii and Veillonella parvula by Dual RNA-Seq. Scientific Reports, 2019, 9, 7664.	3.3	22
21	Immunodeficiency, autoimmune thrombocytopenia and enterocolitis caused by autosomal recessive deficiency of *PIK3CD*-encoded phosphoinositide 3-kinase δ. Haematologica, 2019, 104, e483-e486.	3.5	26
22	Easybiotics: a GUI for 3D physical modelling of multi-species bacterial populations. Bioinformatics, 2019, 35, 3859-3860.	4.1	3
23	Automatic selection of verification tools for efficient analysis of biochemical models. Bioinformatics, 2018, 34, 3187-3195.	4.1	7
24	Streptococcus gordonii Challisin protease is required for sensing cell--cell contact with Actinomyces oris. FEMS Microbiology Ecology, 2018, 94, .	2.7	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. Nature Communications, 2018, 9, 4234.	12.8	158
28	Transcriptional responses of *Streptococcus gordonii* and *Fusobacterium nucleatum* to coaggregation. Molecular Oral Microbiology, 2018, 33, 450-464.	2.7	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. Acta Biomaterialia, 2018, 74, 207-221.	8.3	34
30	Isothermal folding of a light-up bio-orthogonal RNA origami nanoribbon. Scientific Reports, 2018, 8, 6989.	3.3	22
31	Population Dynamics of Autocatalytic Sets in a Compartmentalized Spatial World. Life, 2018, 8, 33.	2.4	16
32	Strain Design as Multiobjective Network Interdiction Problem: A Preliminary Approach. Lecture Notes in Computer Science, 2018, , 273-282.	1.3	1
33	Predicting species emergence in simulated complex pre-biotic networks. PLoS ONE, 2018, 13, e0192871.	2.5	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. ACS Synthetic Biology, 2017, 6, 1140-1149.	3.8	21
36	CSBB: synthetic biology research at Newcastle University. Biochemical Society Transactions, 2017, 45, 781-783.	3.4	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.	0.3	2
39	Simbiotics: A Multiscale Integrative Platform for 3D Modeling of Bacterial Populations. ACS Synthetic Biology, 2017, 6, 1194-1210.	3.8	33
40	Functional networks inference from rule-based machine learning models. BioData Mining, 2016, 9, 28.	4.0	7
41	Synthesis and cell-free cloning of DNA libraries using programmable microfluidics. Nucleic Acids Research, 2016, 44, e35-e35.	14.5	23
42	In Vitro Implementation of a Stack Data Structure Based on DNA Strand Displacement. Lecture Notes in Computer Science, 2016, , 87-98.	1.3	3
43	Qualitative and Quantitative Analysis of Systems and Synthetic Biology Constructs using P Systems. ACS Synthetic Biology, 2015, 4, 83-92.	3.8	18
44	Meta-Stochastic Simulation of Biochemical Models for Systems and Synthetic Biology. ACS Synthetic Biology, 2015, 4, 39-47.	3.8	9
45	Complexity Measurement Based on Information Theory and Kolmogorov Complexity. Artificial Life, 2015, 21, 205-224.	1.3	13
46	Algorithms and models for complex natural systems. Natural Computing, 2015, 14, 339-340.	3.0	0
47	JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. Bioinformatics, 2014, 30, 1029-1030.	4.1	52
48	Blind optimisation problem instance classification via enhanced universal similarity metric. Memetic Computing, 2014, 6, 263.	4.0	5
49	Formalizing Modularization and Data Hiding in Synthetic Biology. ACM Journal on Emerging Technologies in Computing Systems, 2014, 11, 1-20.	2.3	3
50	Photochromic molecular implementations of universal computation. BioSystems, 2014, 126, 12-26.	2.0	0
51	Conventional Verification for Unconventional Computing: a Genetic XOR Gate Example. Fundamenta Informaticae, 2014, 134, 97-110.	0.4	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.	3.4	12
54	Heuristic for Maximizing DNA Reuse in Synthetic DNA Library Assembly. ACS Synthetic Biology, 2014, 3, 529-542.	3.8	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.	0.3	19
56	Chemical Production and Molecular Computing in Addressable Reaction Compartments. Lecture Notes in Computer Science, 2014, , 173-182.	1.3	2
57	Matching island topologies to problem structure in parallel evolutionary algorithms. Soft Computing, 2013, 17, 1209-1225.	3.6	71
58	A genotype-phenotype-fitness assessment protocol for evolutionary self-assembly Wang tiles design. Memetic Computing, 2013, 5, 19-33.	4.0	2
59	Bacteria clustering by polymers induces the expression of quorum-sensing-controlled phenotypes. Nature Chemistry, 2013, 5, 1058-1065.	13.6	67
60	Exploring programmable self-assembly in non-DNA based molecular computing. Natural Computing, 2013, 12, 499-515.	3.0	7
61	GAssist vs. BioHEL: critical assessment of two paradigms of genetics-based machine learning. Soft Computing, 2013, 17, 953-981.	3.6	7
62	Transcriptional Dynamics of Two Seed Compartments with Opposing Roles in Arabidopsis Seed Germination Â Â. Plant Physiology, 2013, 163, 205-215.	4.8	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.	4.1	36
64	Post-processing operators for decision lists. , 2012, , .		7
65	EnrichNet: network-based gene set enrichment analysis. Bioinformatics, 2012, 28, i451-i457.	4.1	269
66	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
67	Using Rule-Based Machine Learning for Candidate Disease Gene Prioritization and Sample Classification of Cancer Gene Expression Data. PLoS ONE, 2012, 7, e39932.	2.5	95
68	Implementing conventional logic unconventionally: Photochromic molecular populations as registers and logic gates. BioSystems, 2012, 109, 35-51.	2.0	8
69	Analysing BioHEL using challenging boolean functions. Evolutionary Intelligence, 2012, 5, 87-102.	3.6	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.	7.1	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.	2.5	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, .	3.3	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.	4.1	40
81	A thermodynamic switch modulates abscisic acid receptor sensitivity. EMBO Journal, 2011, 30, 4171-4184.	7.8	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.	0.9	0
84	Controlled polymer synthesisâ€"from biomimicry towards synthetic biology. Chemical Society Reviews, 2010, 39, 286-300.	38.1	75
85	A learning classifier system with mutual-information-based fitness. Evolutionary Intelligence, 2010, 3, 31-50.	3.6	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.	2.2	15
90	Extending pathways and processes using molecular interaction networks to analyse cancer genome data. BMC Bioinformatics, 2010, 11, 597.	2.6	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.	4.1	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.	3.3	8
97	vrmlgen: AnRPackage for 3D Data Visualization on the Web. Journal of Statistical Software, 2010, 36, .	3.7	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.	1.1	41
100	ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization. BMC Bioinformatics, 2009, 10, 358.	2.6	85
101	Automated Alphabet Reduction for Protein Datasets. BMC Bioinformatics, 2009, 10, 6.	2.6	54
102	Nature-inspired cooperative strategies for optimization. International Journal of Intelligent Systems, 2009, 24, 723-725.	5.7	13
103	Automated self-assembly programming paradigm: The impact of network topology. International Journal of Intelligent Systems, 2009, 24, 793-817.	5.7	5
104	Prediction of topological contacts in proteins using learning classifier systems. Soft Computing, 2009, 13, 245-258.	3.6	27
105	P-systems and X-machines. Natural Computing, 2009, 8, 777-779.	3.0	0
106	Improving the scalability of rule-based evolutionary learning. Memetic Computing, 2009, 1, 55-67.	4.0	84
107	Editorial to the first issue. Memetic Computing, 2009, 1, 1-2.	4.0	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. Evolutionary Computation, 2009, 17, 307-342.	3.0	48
110	Adaptive Cellular Memetic Algorithms. Evolutionary Computation, 2009, 17, 231-256.	3.0	53
111	Diolâ€"boronic acid complexes integrated by responsive polymersâ€"a route to chemical sensing and logic operations. Soft Matter, 2009, 5, 3839.	2.7	34
112	A Multiscale Modeling Framework Based on P Systems. Lecture Notes in Computer Science, 2009, , 63-77.	1.3	11
113	Memetic Algorithms: The Polynomial Local Search Complexity Theory Perspective. Mathematical Modelling and Algorithms, 2008, 7, 3-24.	0.5	25
114	Prediction of recursive convex hull class assignments for protein residues. Bioinformatics, 2008, 24, 916-923.	4.1	42
115	Chapter 13 Automated Self-Assembling Programming. Studies in Multidisciplinarity, 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. Current Bioinformatics, 2008, 3, 10-31.	1.5	11
118	An unorthodox introduction to Memetic Algorithms. ACM SIGEVOlution, 2008, 3, 6-15.	0.5	2
119	Search Strategies in Structural Bioinformatics. Current Protein and Peptide Science, 2008, 9, 260-274.	1.4	13
120	Empirical Evaluation of Ensemble Techniques for a Pittsburgh Learning Classifier System. Lecture Notes in Computer Science, 2008, , 255-268.	1.3	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. Nano Letters, 2007, 7, 1985-1990.	9.1	22
123	Evolving tiles for automated self-assembly design. , 2007, , .		12
124	Quorum sensing P systems. Theoretical Computer Science, 2007, 371, 20-33.	0.9	31
125	ProCKSI: a decision support system for Protein (Structure) Comparison, Knowledge, Similarity and Information. BMC Bioinformatics, 2007, 8, 416.	2.6	48
126	The imitation gameâ€"a computational chemical approach to recognizing life. Nature Biotechnology, 2006, 24, 1203-1206.	17.5	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.	2.7	19
130	A Study on the use of ``self-generation'' in memetic algorithms. Natural Computing, 2004, 3, 53-76.	3.0	83
131	Real-Coded Memetic Algorithms with Crossover Hill-Climbing. Evolutionary Computation, 2004, 12, 273-302.	3.0	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