

Thomas Schiex

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

10,408
citations

159585

30
h-index

95266

68
g-index

82
all docs

82
docs citations

82
times ranked

13469
citing authors

#	ARTICLE	IF	CITATIONS
1	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
2	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	27.8	1,166
3	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
4	Genome sequence of the plant pathogen <i>Ralstonia solanacearum</i> . <i>Nature</i> , 2002, 415, 497-502.	27.8	866
5	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	21.4	656
6	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. <i>Nature</i> , 2017, 546, 148-152.	27.8	579
7	CARHTA GENE: multipopulation integrated genetic and radiation hybrid mapping. <i>Bioinformatics</i> , 2005, 21, 1703-1704.	4.1	403
8	Current methods of gene prediction, their strengths and weaknesses. <i>Nucleic Acids Research</i> , 2002, 30, 4103-4117.	14.5	374
9	Legume genome evolution viewed through the <i>Medicago truncatula</i> and <i>Lotus japonicus</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14959-14964.	7.1	286
10	Exploring root symbiotic programs in the model legume <i>Medicago truncatula</i> using EST analysis. <i>Nucleic Acids Research</i> , 2002, 30, 5579-5592.	14.5	193
11	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. <i>PLoS Genetics</i> , 2017, 13, e1006777.	3.5	150
12	Solving weighted CSP by maintaining arc consistency. <i>Artificial Intelligence</i> , 2004, 159, 1-26.	5.8	112
13	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. <i>Current Bioinformatics</i> , 2008, 3, 87-97.	1.5	102
14	FrameDP: sensitive peptide detection on noisy matured sequences. <i>Bioinformatics</i> , 2009, 25, 670-671.	4.1	95
15	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to <i>Sinorhizobium meliloti</i> 2011. <i>DNA Research</i> , 2013, 20, 339-354.	3.4	90
16	FrameD: a flexible program for quality check and gene prediction in prokaryotic genomes and noisy matured eukaryotic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3738-3741.	14.5	85
17	NOGOOD RECORDING FOR STATIC AND DYNAMIC CONSTRAINT SATISFACTION PROBLEMS. <i>International Journal on Artificial Intelligence Tools</i> , 1994, 03, 187-207.	1.0	84
18	Gene Regulatory Network Reconstruction Using Bayesian Networks, the Dantzig Selector, the Lasso and Their Meta-Analysis. <i>PLoS ONE</i> , 2011, 6, e29165.	2.5	81

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19	Arc consistency for soft constraints. <i>Artificial Intelligence</i> , 2004, 154, 199-227.	5.8	80
20	Soft Constraints. <i>Foundations of Artificial Intelligence</i> , 2006, 2, 281-328.	0.9	73
21	A new framework for computational protein design through cost function network optimization. <i>Bioinformatics</i> , 2013, 29, 2129-2136.	4.1	65
22	Maintaining reversible DAC for Max-CSP. <i>Artificial Intelligence</i> , 1999, 107, 149-163.	5.8	59
23	Guaranteed Discrete Energy Optimization on Large Protein Design Problems. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5980-5989.	5.3	55
24	Computational protein design as an optimization problem. <i>Artificial Intelligence</i> , 2014, 212, 59-79.	5.8	49
25	Arc Consistency for Soft Constraints. <i>Lecture Notes in Computer Science</i> , 2000, , 411-425.	1.3	46
26	Solving Max-SAT as Weighted CSP. <i>Lecture Notes in Computer Science</i> , 2003, , 363-376.	1.3	43
27	EuGene: An Automated Integrative Gene Finder for Eukaryotes and Prokaryotes. <i>Methods in Molecular Biology</i> , 2019, 1962, 97-120.	0.9	42
28	Multi-language evaluation of exact solvers in graphical model discrete optimization. <i>Constraints</i> , 2016, 21, 413-434.	0.7	38
29	Integrating alternative splicing detection into gene prediction. <i>BMC Bioinformatics</i> , 2005, 6, 25.	2.6	37
30	Mendelian Error Detection in Complex Pedigrees Using Weighted Constraint Satisfaction Techniques. <i>Constraints</i> , 2008, 13, 130-154.	0.7	37
31	Nonmonotonic reasoning: from complexity to algorithms. <i>Annals of Mathematics and Artificial Intelligence</i> , 1998, 22, 207-236.	1.3	33
32	EUGENE'HOM: a generic similarity-based gene finder using multiple homologous sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3742-3745.	14.5	33
33	EuGene-PP: a next-generation automated annotation pipeline for prokaryotic genomes. <i>Bioinformatics</i> , 2014, 30, 2659-2661.	4.1	33
34	Computational design of symmetrical eight-bladed \hat{I}^2 -propeller proteins. <i>IUCr</i> , 2019, 6, 46-55.	2.2	33
35	A Composite Genetic Map of the Parasitoid Wasp <i>Trichogramma brassicae</i> Based on RAPD Markers. <i>Genetics</i> , 1998, 150, 275-282.	2.9	32
36	Rearranged gene order between pig and human in a QTL region on SSC 7. <i>Mammalian Genome</i> , 2003, 14, 71-80.	2.2	31

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37	Fast search algorithms for computational protein design. <i>Journal of Computational Chemistry</i> , 2016, 37, 1048-1058.	3.3	30
38	Protein Design with Deep Learning. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11741.	4.1	23
39	Balancing exploration and exploitation in population-based sampling improves fragment-based <i>de novo</i> protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 852-858.	2.6	20
40	DARN! A Weighted Constraint Solver for RNA Motif Localization. <i>Constraints</i> , 2008, 13, 91-109.	0.7	18
41	Contribution of Radiation Hybrids to Genome Mapping in Domestic Animals. <i>Cytogenetic and Genome Research</i> , 2009, 126, 21-33.	1.1	18
42	Seven Amino Acid Types Suffice to Create the Core Fold of RNA Polymerase. <i>Journal of the American Chemical Society</i> , 2021, 143, 15998-16006.	13.7	18
43	Anytime Hybrid Best-First Search with Tree Decomposition for Weighted CSP. <i>Lecture Notes in Computer Science</i> , 2015, , 12-29.	1.3	18
44	Positive multistate protein design. <i>Bioinformatics</i> , 2020, 36, 122-130.	4.1	17
45	Bounding the optimum of constraint optimization problems. <i>Lecture Notes in Computer Science</i> , 1997, , 405-419.	1.3	16
46	High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. <i>BMC Genomics</i> , 2007, 8, 310.	2.8	16
47	Fitness landscape analysis around the optimum in computational protein design. , 2018, , .		14
48	2006 and 2007 Max-SAT Evaluations: Contributed Instances. <i>Journal of Satisfiability, Boolean Modeling and Computation</i> , 2008, 4, 239-250.	1.2	13
49	Analysis of CATMA transcriptome data identifies hundreds of novel functional genes and improves gene models in the <i>Arabidopsis</i> genome. <i>BMC Genomics</i> , 2007, 8, 401.	2.8	12
50	LeARN: a platform for detecting, clustering and annotating non-coding RNAs. <i>BMC Bioinformatics</i> , 2008, 9, 21.	2.6	12
51	Detecting long tandem duplications in genomic sequences. <i>BMC Bioinformatics</i> , 2012, 13, 83.	2.6	11
52	Cost function network-based design of protein-protein interactions: predicting changes in binding affinity. <i>Bioinformatics</i> , 2018, 34, 2581-2589.	4.1	10
53	Guaranteed Weighted Counting for Affinity Computation: Beyond Determinism and Structure. <i>Lecture Notes in Computer Science</i> , 2016, , 733-750.	1.3	10
54	Tractability-preserving transformations of global cost functions. <i>Artificial Intelligence</i> , 2016, 238, 166-189.	5.8	9

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55	Variable Neighborhood Search with Cost Function Networks To Solve Large Computational Protein Design Problems. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 127-136.	5.4	9
56	A Comparative Study to Decipher the Structural and Dynamics Determinants Underlying the Activity and Thermal Stability of GH-11 Xylanases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5961.	4.1	9
57	Computational Protein Design as a Cost Function Network Optimization Problem. <i>Lecture Notes in Computer Science</i> , 2012, , 840-849.	1.3	9
58	Molecular flexibility in computational protein design: an algorithmic perspective. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	2.1	8
59	A new local consistency for weighted CSP dedicated to long domains. , 2006, , .		7
60	Deterministic Search Methods for Computational Protein Design. <i>Methods in Molecular Biology</i> , 2017, 1529, 107-123.	0.9	7
61	A structural homology approach for computational protein design with flexible backbone. <i>Bioinformatics</i> , 2019, 35, 2418-2426.	4.1	6
62	Guaranteed Diversity and Optimality in Cost Function Network Based Computational Protein Design Methods. <i>Algorithms</i> , 2021, 14, 168.	2.1	6
63	Triangle-based consistencies for cost function networks. <i>Constraints</i> , 2017, 22, 230-264.	0.7	5
64	Guaranteed Diversity & Quality for the Weighted CSP. , 2019, , .		5
65	Decomposition of Multi-operator Queries on Semiring-Based Graphical Models. <i>Lecture Notes in Computer Science</i> , 2006, , 437-452.	1.3	5
66	A Panel of Learning Methods for the Reconstruction of Gene Regulatory Networks in a Systems Genetics Context. , 2013, , 9-31.		5
67	Valued Constraint Satisfaction Problems. , 2020, , 185-207.		5
68	Intracellular <i>Salmonella Paratyphi A</i> is motile and differs in the expression of flagella-chemotaxis, SPI-1 and carbon utilization pathways in comparison to intracellular <i>S. Typhimurium</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010425.	4.7	4
69	Approximate Counting with Deterministic Guarantees for Affinity Computation. <i>Advances in Intelligent Systems and Computing</i> , 2015, , 165-176.	0.6	3
70	Dynamic virtual arc consistency. , 2013, , .		2
71	Pushing Data into CP Models Using Graphical Model Learning and Solving. <i>Lecture Notes in Computer Science</i> , 2020, , 811-827.	1.3	2
72	Computational Design of Miniprotein Binders. <i>Methods in Molecular Biology</i> , 2022, 2405, 361-382.	0.9	2

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73	Maintaining Virtual Arc Consistency Dynamically during Search. , 2014, , .		1
74	Iterated local search with partition crossover for computational protein design. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1522-1529.	2.6	1
75	Cost Function Networks to Solve Large Computational Protein Design Problems. , 2021, , 81-102.		1
76	Introduction to the special issue on Constraint-based approaches to Preference Modelling and Reasoning. Constraints, 2010, 15, 453-455.	0.7	0
77	Strong consistencies for weighted constraint satisfaction problems. Constraints, 2015, 20, 471-472.	0.7	0