Thomas Schiex

List of Publications by Year
in descending order

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	Computational Design of Miniprotein Binders. Methods in Molecular Biology, 2022, 2405, 361-382.	0.9	2
2	Intracellular Salmonella Paratyphi A is motile and differs in the expression of flagella-chemotaxis, SPI-1 and carbon utilization pathways in comparison to intracellular S. Typhimurium. PLoS Pathogens, 2022, 18, e1010425.	4.7	4
3	A Comparative Study to Decipher the Structural and Dynamics Determinants Underlying the Activity and Thermal Stability of GH-11 Xylanases. International Journal of Molecular Sciences, 2021, 22, 5961.	4.1	9
4	Guaranteed Diversity and Optimality in Cost Function Network Based Computational Protein Design Methods. Algorithms, 2021, 14, 168.	2.1	6
5	Iterated local search with partition crossover for computational protein design. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1522-1529.	2.6	1
6	Seven Amino Acid Types Suffice to Create the Core Fold of RNA Polymerase. Journal of the American Chemical Society, 2021, 143, 15998-16006.	13.7	18
7	Molecular flexibility in computational protein design: an algorithmic perspective. Protein Engineering, Design and Selection, 2021, 34, .	2.1	8
8	Protein Design with Deep Learning. International Journal of Molecular Sciences, 2021, 22, 11741.	4.1	23
9	Cost Function Networks to Solve Large Computational Protein Design Problems. , 2021, , 81-102.		1
10	Positive multistate protein design. Bioinformatics, 2020, 36, 122-130.	4.1	17
11	Pushing Data into CP Models Using Graphical Model Learning and Solving. Lecture Notes in Computer Science, 2020, , 811-827.	1.3	2
12	Valued Constraint Satisfaction Problems. , 2020, , 185-207.		5
13	EuGene: An Automated Integrative Gene Finder for Eukaryotes and Prokaryotes. Methods in Molecular Biology, 2019, 1962, 97-120.	0.9	42
14	Guaranteed Diversity & Quality for the Weighted CSP. , 2019, , .		5
15	Variable Neighborhood Search with Cost Function Networks To Solve Large Computational Protein Design Problems. Journal of Chemical Information and Modeling, 2019, 59, 127-136.	5.4	9
16	A structural homology approach for computational protein design with flexible backbone. Bioinformatics, 2019, 35, 2418-2426.	4.1	6
17	Computational design of symmetrical eight-bladed Î²-propeller proteins. IUCrJ, 2019, 6, 46-55.	2.2	33
18	Cost function network-based design of protein–protein interactions: predicting changes in binding affinity. Bioinformatics, 2018, 34, 2581-2589.	4.1	10

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19	Fitness landscape analysis around the optimum in computational protein design. , 2018, , .		14
20	Balancing exploration and exploitation in population-based sampling improves fragment-based *de novo* protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2017, 85, 852-858.	2.6	20
21	Deterministic Search Methods for Computational Protein Design. Methods in Molecular Biology, 2017, 1529, 107-123.	0.9	7
22	The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. Nature, 2017, 546, 148-152.	27.8	579
23	Triangle-based consistencies for cost function networks. Constraints, 2017, 22, 230-264.	0.7	5
24	Hybridization and polyploidy enable genomic plasticity without sex in the most devastating plant-parasitic nematodes. PLoS Genetics, 2017, 13, e1006777.	3.5	150
25	Fast search algorithms for computational protein design. Journal of Computational Chemistry, 2016, 37, 1048-1058.	3.3	30
26	Multi-language evaluation of exact solvers in graphical model discrete optimization. Constraints, 2016, 21, 413-434.	0.7	38
27	Tractability-preserving transformations of global cost functions. Artificial Intelligence, 2016, 238, 166-189.	5.8	9
28	Guaranteed Weighted Counting for Affinity Computation: Beyond Determinism and Structure. Lecture Notes in Computer Science, 2016, , 733-750.	1.3	10
29	Strong consistencies for weighted constraint satisfaction problems. Constraints, 2015, 20, 471-472.	0.7	0
30	Guaranteed Discrete Energy Optimization on Large Protein Design Problems. Journal of Chemical Theory and Computation, 2015, 11, 5980-5989.	5.3	55
31	Approximate Counting with Deterministic Guarantees for Affinity Computation. Advances in Intelligent Systems and Computing, 2015, , 165-176.	0.6	3
32	Anytime Hybrid Best-First Search with Tree Decomposition for Weighted CSP. Lecture Notes in Computer Science, 2015, , 12-29.	1.3	18
33	Computational protein design as an optimization problem. Artificial Intelligence, 2014, 212, 59-79.	5.8	49
34	EuGene-PP: a next-generation automated annotation pipeline for prokaryotic genomes. Bioinformatics, 2014, 30, 2659-2661.	4.1	33
35	Maintaining Virtual Arc Consistency Dynamically during Search. , 2014, , .		1
36	Next-Generation Annotation of Prokaryotic Genomes with EuGene-P: Application to Sinorhizobium meliloti 2011. DNA Research, 2013, 20, 339-354.	3.4	90

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37	A new framework for computational protein design through cost function network optimization. Bioinformatics, 2013, 29, 2129-2136.	4.1	65
38	Dynamic virtual arc consistency. , 2013, , .		2
39	A Panel of Learning Methods for the Reconstruction of Gene Regulatory Networks in a Systems Genetics Context. , 2013, , 9-31.		5
40	Detecting long tandem duplications in genomic sequences. BMC Bioinformatics, 2012, 13, 83.	2.6	11
41	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
42	Computational Protein Design as a Cost Function Network Optimization Problem. Lecture Notes in Computer Science, 2012, , 840-849.	1.3	9
43	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	27.8	1,166
44	The genome of Theobroma cacao. Nature Genetics, 2011, 43, 101-108.	21.4	656
45	Gene Regulatory Network Reconstruction Using Bayesian Networks, the Dantzig Selector, the Lasso and Their Meta-Analysis. PLoS ONE, 2011, 6, e29165.	2.5	81
46	Introduction to the special issue on Constraint-based approaches to Preference Modelling and Reasoning. Constraints, 2010, 15, 453-455.	0.7	0
47	Contribution of Radiation Hybrids to Genome Mapping in Domestic Animals. Cytogenetic and Genome Research, 2009, 126, 21-33.	1.1	18
48	FrameDP: sensitive peptide detection on noisy matured sequences. Bioinformatics, 2009, 25, 670-671.	4.1	95
49	Mendelian Error Detection in Complex Pedigrees Using Weighted Constraint Satisfaction Techniques. Constraints, 2008, 13, 130-154.	0.7	37
50	DARN! A Weighted Constraint Solver for RNA Motif Localization. Constraints, 2008, 13, 91-109.	0.7	18
51	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. Nature Biotechnology, 2008, 26, 909-915.	17.5	1,012
52	LeARN: a platform for detecting, clustering and annotating non-coding RNAs. BMC Bioinformatics, 2008, 9, 21.	2.6	12
53	Genome Annotation in Plants and Fungi: EuGene as a Model Platform. Current Bioinformatics, 2008, 3, 87-97.	1.5	102
54	2006 and 2007 Max-SAT Evaluations: Contributed Instances. Journal of Satisfiability, Boolean Modeling and Computation, 2008, 4, 239-250.	1.2	13

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55	High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. BMC Genomics, 2007, 8, 310.	2.8	16
56	Analysis of CATMA transcriptome data identifies hundreds of novel functional genes and improves gene models in the Arabidopsis genome. BMC Genomics, 2007, 8, 401.	2.8	12
57	A new local consistency for weighted CSP dedicated to long domains. , 2006, , .		7
58	Legume genome evolution viewed through the Medicago truncatula and Lotus japonicus genomes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14959-14964.	7.1	286
59	Soft Constraints. Foundations of Artificial Intelligence, 2006, 2, 281-328.	0.9	73
60	Decomposition of Multi-operator Queries on Semiring-Based Graphical Models. Lecture Notes in Computer Science, 2006, , 437-452.	1.3	5
61	Integrating alternative splicing detection into gene prediction. BMC Bioinformatics, 2005, 6, 25.	2.6	37
62	CARHTA GENE: multipopulation integrated genetic and radiation hybrid mapping. Bioinformatics, 2005, 21, 1703-1704.	4.1	403
63	Arc consistency for soft constraints. Artificial Intelligence, 2004, 154, 199-227.	5.8	80
64	Solving weighted CSP by maintaining arc consistency. Artificial Intelligence, 2004, 159, 1-26.	5.8	112
65	Rearranged gene order between pig and human in a QTL region on SSC 7. Mammalian Genome, 2003, 14, 71-80.	2.2	31
66	FrameD: a flexible program for quality check and gene prediction in prokaryotic genomes and noisy matured eukaryotic sequences. Nucleic Acids Research, 2003, 31, 3738-3741.	14.5	85
67	EUGENE'HOM: a generic similarity-based gene finder using multiple homologous sequences. Nucleic Acids Research, 2003, 31, 3742-3745.	14.5	33
68	Solving Max-SAT as Weighted CSP. Lecture Notes in Computer Science, 2003, , 363-376.	1.3	43
69	Current methods of gene prediction, their strengths and weaknesses. Nucleic Acids Research, 2002, 30, 4103-4117.	14.5	374
70	Exploring root symbiotic programs in the model legume Medicago truncatula using EST analysis. Nucleic Acids Research, 2002, 30, 5579-5592.	14.5	193
71	Genome sequence of the plant pathogen Ralstonia solanacearum. Nature, 2002, 415, 497-502.	27.8	866
72	Arc Consistency for Soft Constraints. Lecture Notes in Computer Science, 2000, , 411-425.	1.3	46

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73	Maintaining reversible DAC for Max-CSP. Artificial Intelligence, 1999, 107, 149-163.	5.8	59
74	Nonmonotonic reasoning: from complexity to algorithms. Annals of Mathematics and Artificial Intelligence, 1998, 22, 207-236.	1.3	33
75	A Composite Genetic Map of the Parasitoid Wasp Trichogramma brassicae Based on RAPD Markers. Genetics, 1998, 150, 275-282.	2.9	32
76	Bounding the optimum of constraint optimization problems. Lecture Notes in Computer Science, 1997, , 405-419.	1.3	16
77	NOGOOD RECORDING FOR STATIC AND DYNAMIC CONSTRAINT SATISFACTION PROBLEMS. International Journal on Artificial Intelligence Tools, 1994, 03, 187-207.	1.0	84