

# Casey S. Greene

## List of Publications by Year in descending order

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Version: 2024-02-01

176  
papers

12,825  
citations

44066

48  
h-index

32838

100  
g-index

254  
all docs

254  
docs citations

254  
times ranked

23456  
citing authors

#	ARTICLE	IF	CITATIONS
1	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure". <i>MSystems</i> , 2022, , e0144721.	3.8	2
2	Computational audits combat disparities in recognition. <i>Nature Human Behaviour</i> , 2022, 6, 473-474.	12.0	2
3	Examining linguistic shifts between preprints and publications. <i>PLoS Biology</i> , 2022, 20, e3001470.	5.6	12
4	Ten simple rules for large-scale data processing. <i>PLoS Computational Biology</i> , 2022, 18, e1009757.	3.2	1
5	Ten quick tips for deep learning in biology. <i>PLoS Computational Biology</i> , 2022, 18, e1009803.	3.2	14
6	Long-Term Cellulose Enrichment Selects for Highly Cellulolytic Consortia and Competition for Public Goods. <i>MSystems</i> , 2022, 7, e0151921.	3.8	5
7	Widespread redundancy in -omics profiles of cancer mutation states. <i>Genome Biology</i> , 2022, 23, .	8.8	5
8	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. <i>Nature Communications</i> , 2022, 13, .	12.8	6
9	Expanding and Remixing the Metadata Landscape. <i>Trends in Cancer</i> , 2021, 7, 276-278.	7.4	5
10	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. <i>Genome Biology</i> , 2021, 22, 1.	8.8	239
11	Parameterized algorithms for identifying gene co-expression modules via weighted clique decomposition. , 2021, 2021, 111-122.		1
12	Induction of ADAM10 by Radiation Therapy Drives Fibrosis, Resistance, and Epithelial-to-Mesenchymal Transition in Pancreatic Cancer. <i>Cancer Research</i> , 2021, 81, 3255-3269.	0.9	37
13	Macrophages in SHH subgroup medulloblastoma display dynamic heterogeneity that varies with treatment modality. <i>Cell Reports</i> , 2021, 34, 108917.	6.4	27
14	Dietary Supplements and Nutraceuticals under Investigation for COVID-19 Prevention and Treatment. <i>MSystems</i> , 2021, 6, .	3.8	68
15	Reproducibility standards for machine learning in the life sciences. <i>Nature Methods</i> , 2021, 18, 1132-1135.	19.0	96
16	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	8.8	9
17	Cancer Informatics for Cancer Centers: Scientific Drivers for Informatics, Data Science, and Care in Pediatric, Adolescent, and Young Adult Cancer. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 881-896.	2.1	3
18	miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1009290.	3.2	38

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19	Analysis of scientific society honors reveals disparities. <i>Cell Systems</i> , 2021, 12, 900-906.e5.	6.2	10
20	Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design. <i>GigaScience</i> , 2021, 10, .	6.4	17
21	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	5.6	6
22	Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure. <i>MSystems</i> , 2021, 6, e0009521.	3.8	26
23	Identification and Development of Therapeutics for COVID-19. <i>MSystems</i> , 2021, 6, e0023321.	3.8	20
24	Human Intrigue: Meta-analysis approaches for big questions with big data while shaking up the peer review process. , 2021, , .		0
25	Characterizing Long COVID: Deep Phenotype of a Complex Condition. <i>EBioMedicine</i> , 2021, 74, 103722.	6.1	127
26	An Open-Publishing Response to the COVID-19 Infodemic.. <i>CEUR Workshop Proceedings</i> , 2021, 2976, 29-38.	2.3	2
27	Embracing study heterogeneity for finding genetic interactions in large-scale research consortia. <i>Genetic Epidemiology</i> , 2020, 44, 52-66.	1.3	4
28	Biologically Informed Neural Networks Predict Drug Responses. <i>Cancer Cell</i> , 2020, 38, 613-615.	16.8	8
29	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	27.8	233
30	Responsible, practical genomic data sharing that accelerates research. <i>Nature Reviews Genetics</i> , 2020, 21, 615-629.	16.3	66
31	Bacteria Contribute to Plant Secondary Compound Degradation in a Generalist Herbivore System. <i>MBio</i> , 2020, 11, .	4.1	30
32	Population-scale longitudinal mapping of COVID-19 symptoms, behaviour and testing. <i>Nature Human Behaviour</i> , 2020, 4, 972-982.	12.0	93
33	Compressing gene expression data using multiple latent space dimensionalities learns complementary biological representations. <i>Genome Biology</i> , 2020, 21, 109.	8.8	43
34	Recommendations to enhance rigor and reproducibility in biomedical research. <i>GigaScience</i> , 2020, 9, .	6.4	83
35	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
36	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). <i>Clinical Cancer Research</i> , 2020, 26, 5411-5423.	7.0	43

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37	Back Cover Image. Genetic Epidemiology, 2020, 44, ii.	1.3	0
38	Constructing knowledge graphs and their biomedical applications. Computational and Structural Biotechnology Journal, 2020, 18, 1414-1428.	4.1	132
39	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. Genes, 2020, 11, 226.	2.4	11
40	<i>Pseudomonas aeruginosa</i> lasR mutant fitness in microoxia is supported by an Anr-regulated oxygen-binding hemerythrin. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3167-3173.	7.1	44
41	Incorporating biological structure into machine learning models in biomedicine. Current Opinion in Biotechnology, 2020, 63, 126-134.	6.6	26
42	Specific histone modifications associate with alternative exon selection during mammalian development. Nucleic Acids Research, 2020, 48, 4709-4724.	14.5	19
43	Correcting for experiment-specific variability in expression compendia can remove underlying signals. GigaScience, 2020, 9, .	6.4	17
44	Privacy-Preserving Generative Deep Neural Networks Support Clinical Data Sharing. Circulation: Cardiovascular Quality and Outcomes, 2019, 12, e005122.	2.2	172
45	Discovering Pathway and Cell Type Signatures in Transcriptomic Compendia with Machine Learning. Annual Review of Biomedical Data Science, 2019, 2, 1-17.	6.5	11
46	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9.	6.4	103
47	The antimicrobial potential of Streptomyces from insect microbiomes. Nature Communications, 2019, 10, 516.	12.8	222
48	MultiPLIER: A Transfer Learning Framework for Transcriptomics Reveals Systemic Features of Rare Disease. Cell Systems, 2019, 8, 380-394.e4.	6.2	92
49	Open collaborative writing with Manubot. PLoS Computational Biology, 2019, 15, e1007128.	3.2	51
50	Show me the models. Nature Biotechnology, 2019, 37, 623-625.	17.5	0
51	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
52	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5
53	Integrated phosphoproteomics and transcriptional classifiers reveal hidden RAS signaling dynamics in multiple myeloma. Blood Advances, 2019, 3, 3214-3227.	5.2	19
54	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261

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55	Immune landscapes associated with different glioblastoma molecular subtypes. <i>Acta Neuropathologica Communications</i> , 2019, 7, 203.	5.2	112
56	New <i>Drosophila</i> Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 251-267.	1.8	15
57	Learning and Imputation for Mass-spec Bias Reduction (LIMBR). <i>Bioinformatics</i> , 2019, 35, 1518-1526.	4.1	15
58	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 362-373.	0.7	23
59	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	3.4	1,282
60	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
61	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	119
62	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
63	Inclusion of Unstructured Clinical Text Improves Early Prediction of Death or Prolonged ICU Stay*. <i>Critical Care Medicine</i> , 2018, 46, 1125-1132.	0.9	61
64	A Multimodal Strategy Used by a Large c-di-GMP Network. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	52
65	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. , 2018, , .		101
66	Advances in Text Mining and Visualization for Precision Medicine. , 2018, , .		3
67	Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics. , 2018, , .		22
68	A parasite's perspective on data sharing. <i>GigaScience</i> , 2018, 7, .	6.4	5
69	Bayesian deep learning for single-cell analysis. <i>Nature Methods</i> , 2018, 15, 1009-1010.	19.0	21
70	Sci-Hub provides access to nearly all scholarly literature. <i>ELife</i> , 2018, 7, .	6.0	89
71	PathCORE-T: identifying and visualizing globally co-occurring pathways in large transcriptomic compendia. <i>BioData Mining</i> , 2018, 11, 14.	4.0	14
72	Metabolic pathways and immunometabolism in rare kidney diseases. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, annrheumdis-2017-212935.	0.9	101

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73	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	6.7	181
74	Abstract 5318: High-grade serous ovarian cancer DNA methylation and survival in African-American women. , 2018, , .		0
75	PSB 2019 Workshop on Text Mining and Visualization for Precision Medicine. , 2018, , .		0
76	Integrating Phosphoproteomics and Transcriptional Classifiers Reveals "Hidden Signaling" in Multiple Myeloma Including Differential KRAS and NRAS Mutant Effects. Blood, 2018, 132, 469-469.	1.4	8
77	Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 80-91.	0.7	66
78	Functional network community detection can disaggregate and filter multiple underlying pathways in enrichment analyses. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 157-167.	0.7	0
79	Data-Sharing Models. New England Journal of Medicine, 2017, 376, 2305-2306.	27.0	11
80	Tissue-specific network-based genome wide study of amygdala imaging phenotypes to identify functional interaction modules. Bioinformatics, 2017, 33, 3250-3257.	4.1	23
81	A novel multi-network approach reveals tissue-specific cellular modulators of fibrosis in systemic sclerosis. Genome Medicine, 2017, 9, 27.	8.2	92
82	Celebrating parasites. Nature Genetics, 2017, 49, 483-484.	21.4	25
83	Reproducibility of computational workflows is automated using continuous analysis. Nature Biotechnology, 2017, 35, 342-346.	17.5	111
84	Machine Learning Analysis Identifies <i>Drosophila Grunge/Atrophin</i> as an Important Learning and Memory Gene Required for Memory Retention and Social Learning. G3: Genes, Genomes, Genetics, 2017, 7, 3705-3718.	1.8	7
85	Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks. Cell Systems, 2017, 5, 63-71.e6.	6.2	84
86	Implicating candidate genes at GWAS signals by leveraging topologically associating domains. European Journal of Human Genetics, 2017, 25, 1286-1289.	2.8	18
87	Challenges and Opportunities in Studying the Epidemiology of Ovarian Cancer Subtypes. Current Epidemiology Reports, 2017, 4, 211-220.	2.4	56
88	A Pilot Characterization of the Human Chronobiome. Scientific Reports, 2017, 7, 17141.	3.3	70
89	A machine learning classifier trained on cancer transcriptomes detects NF1 inactivation signal in glioblastoma. BMC Genomics, 2017, 18, 127.	2.8	30
90	NO-BOUNDARY THINKING IN BIOINFORMATICS. , 2017, 22, 646-648.		1

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91	ADAGE signature analysis: differential expression analysis with data-defined gene sets. BMC Bioinformatics, 2017, 18, 512.	2.6	17
92	Tell me your neighbors, and I will tell you what you are. Science Translational Medicine, 2017, 9, .	12.4	1
93	Comprehensive Cross-Population Analysis of High-Grade Serous Ovarian Cancer Supports No More Than Three Subtypes. G3: Genes, Genomes, Genetics, 2016, 6, 4097-4103.	1.8	31
94	COMPUTATIONAL APPROACHES TO STUDY MICROBES AND MICROBIOMES. , 2016, , .		7
95	Genetic Associationâ€“Guided Analysis of Gene Networks for the Study of Complex Traits. Circulation: Cardiovascular Genetics, 2016, 9, 179-184.	5.1	9
96	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
97	Integrative Networks Illuminate Biological Factors Underlying Geneâ€“Disease Associations. Current Genetic Medicine Reports, 2016, 4, 155-162.	1.9	7
98	Semi-supervised learning of the electronic health record for phenotype stratification. Journal of Biomedical Informatics, 2016, 64, 168-178.	4.3	135
99	Pathway and network-based strategies to translate genetic discoveries into effective therapies. Human Molecular Genetics, 2016, 25, R94-R98.	2.9	33
100	Network-based analysis of genetic variants associated with hippocampal volume in Alzheimerâ€™s disease: a study of ADNI cohorts. BioData Mining, 2016, 9, 3.	4.0	28
101	ADAGE-Based Integration of Publicly Available Pseudomonas aeruginosa Gene Expression Data with Denoising Autoencoders Illuminates Microbe-Host Interactions. MSystems, 2016, 1, .	3.8	116
102	Recent Advances and Emerging Applications in Text and Data Mining for Biomedical Discovery. Briefings in Bioinformatics, 2016, 17, 33-42.	6.5	131
103	Adapting bioinformatics curricula for big data. Briefings in Bioinformatics, 2016, 17, 43-50.	6.5	44
104	Evolution of High Cellulolytic Activity in Symbiotic Streptomyces through Selection of Expanded Gene Content and Coordinated Gene Expression. PLoS Biology, 2016, 14, e1002475.	5.6	68
105	Cellulose-Enriched Microbial Communities from Leaf-Cutter Ant (Atta colombica) Refuse Dumps Vary in Taxonomic Composition and Degradation Ability. PLoS ONE, 2016, 11, e0151840.	2.5	29
106	Genomic characterization of patient-derived xenograft models established from fine needle aspirate biopsies of a primary pancreatic ductal adenocarcinoma and from patient-matched metastatic sites. Oncotarget, 2016, 7, 17087-17102.	1.8	40
107	Cross-platform normalization of microarray and RNA-seq data for machine learning applications. PeerJ, 2016, 4, e1621.	2.0	78
108	CoINCLIDE: All together now. Science Translational Medicine, 2016, 8, .	12.4	0

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109	Nothing but a hound dog. Science Translational Medicine, 2016, 8, .	12.4	0
110	Abstract 3407: Gene expression subtypes of high grade serous ovarian cancer in African American women. , 2016, , .		0
111	Abstract 815: Patterns of metagene activation in ovarian cancer subtypes. , 2016, , .		0
112	The future is unsupervised. Science Translational Medicine, 2016, 8, .	12.4	0
113	Gut check. Science Translational Medicine, 2016, 8, .	12.4	0
114	A stromal focus reveals tumor immune signatures. Science Translational Medicine, 2016, 8, .	12.4	0
115	How to know what we donâ€™t. Science Translational Medicine, 2016, 8, .	12.4	0
116	Cheap-seq. Science Translational Medicine, 2016, 8, 370ec203.	12.4	0
117	Leveraging global gene expression patterns to predict expression of unmeasured genes. BMC Genomics, 2015, 16, 1065.	2.8	3
118	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. BioData Mining, 2015, 8, 17.	4.0	2
119	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. Nature Methods, 2015, 12, 211-214.	19.0	137
120	Systems Level Analysis of Systemic Sclerosis Shows a Network of Immune and Profibrotic Pathways Connected with Genetic Polymorphisms. PLoS Computational Biology, 2015, 11, e1004005.	3.2	115
121	Understanding multicellular function and disease with human tissue-specific networks. Nature Genetics, 2015, 47, 569-576.	21.4	738
122	International genome-wide meta-analysis identifies new primary biliary cirrhosis risk loci and targetable pathogenic pathways. Nature Communications, 2015, 6, 8019.	12.8	245
123	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. Human Molecular Genetics, 2015, 24, 7406-7420.	2.9	17
124	Identification of Novel Genetic Models of Glaucoma Using the â€œEMERGENTâ€•Genetic Programming-Based Artificial Intelligence System. Genetic and Evolutionary Computation, 2015, , 17-35.	1.0	4
125	Abstract 1928: High-grade serous ovarian cancer subtypes are similar across diverse populations. , 2015, , .		0
126	Abstract 2171: Leveraging global gene expression patterns to identify gene sets that predict expression of large numbers of unmeasured genes. , 2015, , .		0

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127	Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 132-43.	0.7	45
128	Testing multiple hypotheses through IMP weighted FDR based on a genetic functional network with application to a new zebrafish transcriptome study. , 2014, , .		0
129	Evolution of substrate specificity in bacterial AA10 lytic polysaccharide monooxygenases. Biotechnology for Biofuels, 2014, 7, 109.	6.2	69
130	Predicting targeted drug combinations based on Pareto optimal patterns of coexpression network connectivity. Genome Medicine, 2014, 6, 33.	8.2	10
131	Cellulolytic Streptomyces Strains Associated with Herbivorous Insects Share a Phylogenetically Linked Capacity To Degrade Lignocellulose. Applied and Environmental Microbiology, 2014, 80, 4692-4701.	3.1	70
132	Computational genetics analysis of grey matter density in Alzheimer's disease. BioData Mining, 2014, 7, 17.	4.0	6
133	Big Data Bioinformatics. Journal of Cellular Physiology, 2014, 229, 1896-1900.	4.1	161
134	UNSUPERVISED FEATURE CONSTRUCTION AND KNOWLEDGE EXTRACTION FROM GENOME-WIDE ASSAYS OF BREAST CANCER WITH DENOISING AUTOENCODERS. , 2014, , .		79
135	Biochemical Properties and Atomic Resolution Structure of a Proteolytically Processed $\beta$ -Mannanase from Cellulolytic Streptomyces sp. SirexAA-E. PLoS ONE, 2014, 9, e94166.	2.5	18
136	Aerobic deconstruction of cellulosic biomass by an insect-associated Streptomyces. Scientific Reports, 2013, 3, 1030.	3.3	107
137	Defining cell-type specificity at the transcriptional level in human disease. Genome Research, 2013, 23, 1862-1873.	5.5	196
138	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. PLoS Computational Biology, 2013, 9, e1002957.	3.2	62
139	APPLICATIONS OF BIOINFORMATICS TO NON-CODING RNAs IN THE ERA OF NEXT-GENERATION SEQUENCING. , 2013, , .		4
140	Time-Point Specific Weighting Improves Coexpression Networks from Time-Course Experiments. Lecture Notes in Computer Science, 2013, , 11-22.	1.3	1
141	LT-IIB(T13I), a Non-Toxic Type II Heat-Labile Enterotoxin, Augments the Capacity of a Ricin Toxin Subunit Vaccine to Evoke Neutralizing Antibodies and Protective Immunity. PLoS ONE, 2013, 8, e69678.	2.5	16
142	Abstract A28: Identification of HDAC inhibitor potentiating targets in acute myeloid leukemia cells by large-scale RNA-interference. , 2013, , .		0
143	Pharmacological Validation Of Potentiating Targets From SAHA RNA-Interference Modifier Screens In Acute Myeloid Leukemia. Blood, 2013, 122, 3832-3832.	1.4	3
144	Chapter 2: Data-Driven View of Disease Biology. PLoS Computational Biology, 2012, 8, e1002816.	3.2	15

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145	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2012, 40, W484-W490.	14.5	105
146	TEXT AND DATA MINING FOR BIOMEDICAL DISCOVERY. , 2012, , .		2
147	Accurate evaluation and analysis of functional genomics data and methods. <i>Annals of the New York Academy of Sciences</i> , 2012, 1260, 95-100.	3.8	20
148	Evolving hard problems: Generating human genetics datasets with a complex etiology. <i>BioData Mining</i> , 2011, 4, 21.	4.0	19
149	PILGRM: an interactive data-driven discovery platform for expert biologists. <i>Nucleic Acids Research</i> , 2011, 39, W368-W374.	14.5	27
150	An Analysis of New Expert Knowledge Scaling Methods for Biologically Inspired Computing. <i>Lecture Notes in Computer Science</i> , 2011, , 286-293.	1.3	2
151	An Open-Ended Computational Evolution Strategy for Evolving Parsimonious Solutions to Human Genetics Problems. <i>Lecture Notes in Computer Science</i> , 2011, , 313-320.	1.3	1
152	Multifactor dimensionality reduction for graphics processing units enables genome-wide testing of epistasis in sporadic ALS. <i>Bioinformatics</i> , 2010, 26, 694-695.	4.1	76
153	Fast genome-wide epistasis analysis using ant colony optimization for multifactor dimensionality reduction analysis on graphics processing units. , 2010, , .		10
154	Integrative Systems Biology for Data-Driven Knowledge Discovery. <i>Seminars in Nephrology</i> , 2010, 30, 443-454.	1.6	20
155	Environmental Sensing of Expert Knowledge in a Computational Evolution System for Complex Problem Solving in Human Genetics. <i>Genetic and Evolutionary Computation</i> , 2010, , 19-36.	1.0	11
156	The Informative Extremes: Using Both Nearest and Farthest Individuals Can Improve Relief Algorithms in the Domain of Human Genetics. <i>Lecture Notes in Computer Science</i> , 2010, , 182-193.	1.3	24
157	Artificial Immune Systems for Epistasis Analysis in Human Genetics. <i>Lecture Notes in Computer Science</i> , 2010, , 194-204.	1.3	3
158	A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships. <i>Lecture Notes in Computer Science</i> , 2010, , 74-85.	1.3	2
159	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. <i>Adaptation, Learning, and Optimization</i> , 2010, , 215-226.	0.6	9
160	Failure to Replicate a Genetic Association May Provide Important Clues About Genetic Architecture. <i>PLoS ONE</i> , 2009, 4, e5639.	2.5	227
161	Development and evaluation of an open-ended computational evolution system for the creation of digital organisms with complex genetic architecture. , 2009, , .		1
162	Nature-inspired algorithms for the genetic analysis of epistasis in common human diseases: Theoretical assessment of wrapper vs. filter approaches. , 2009, , .		1

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163	Sensible initialization using expert knowledge for genome-wide analysis of epistasis using genetic programming. , 2009, 2009, 1289-1296.		14
164	Environmental noise improves epistasis models of genetic data discovered using a computational evolution system. , 2009, , .		6
165	Accelerating epistasis analysis in human genetics with consumer graphics hardware. BMC Research Notes, 2009, 2, 149.	1.4	36
166	Spatially Uniform ReliefF (SURF) for computationally-efficient filtering of gene-gene interactions. BioData Mining, 2009, 2, 5.	4.0	129
167	ENABLING PERSONAL GENOMICS WITH AN EXPLICIT TEST OF EPISTASIS. , 2009, , 327-336.		35
168	Optimal Use of Expert Knowledge in Ant Colony Optimization for the Analysis of Epistasis in Human Disease. Lecture Notes in Computer Science, 2009, , 92-103.	1.3	21
169	Ability of epistatic interactions of cytokine single-nucleotide polymorphisms to predict susceptibility to disease subsets in systemic sclerosis patients. Arthritis and Rheumatism, 2008, 59, 974-983.	6.7	35
170	Using expert knowledge in initialization for genome-wide analysis of epistasis using genetic programming. , 2008, , .		5
171	Solving complex problems in human genetics using GP. ACM SIGEVolution, 2008, 3, 2-8.	0.5	4
172	Ant Colony Optimization for Genome-Wide Genetic Analysis. Lecture Notes in Computer Science, 2008, , 37-47.	1.3	38
173	An Expert Knowledge-Guided Mutation Operator for Genome-Wide Genetic Analysis Using Genetic Programming. Lecture Notes in Computer Science, 2007, , 30-40.	1.3	17
174	LTR Retrotransposon-Gene Associations in Drosophila melanogaster. Journal of Molecular Evolution, 2006, 62, 111-120.	1.8	21
175	Solving Complex Problems in Human Genetics Using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 1867-1881.		0
176	Solving Complex Problems in Human Genetics using Nature-Inspired Algorithms Requires Strategies which Exploit Domain-Specific Knowledge. , 0, , 166-180.		0