Yves Moreau

List of Publications by Year in descending order

75 papers	9,467 citations	218677 26 h-index	133252 59 g-index
85 all docs	85 docs citations	85 times ranked	11629 citing authors

#	Article	IF	Citations
1	PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. Nucleic Acids Research, 2002, 30, 325-327.	14.5	4,875
2	Gene prioritization through genomic data fusion. Nature Biotechnology, 2006, 24, 537-544.	17.5	787
3	Computational tools for prioritizing candidate genes: boosting disease gene discovery. Nature Reviews Genetics, 2012, 13, 523-536.	16.3	387
4	A higher-order background model improves the detection of promoter regulatory elements by Gibbs sampling. Bioinformatics, 2001, 17, 1113-1122.	4.1	344
5	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
6	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. Journal of Computational Biology, 2002, 9, 447-464.	1.6	301
7	Effective diagnosis of genetic disease by computational phenotype analysis of the disease-associated genome. Science Translational Medicine, 2014, 6, 252ra123.	12.4	223
8	Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery. Cell Chemical Biology, 2018, 25, 611-618.e3.	5.2	176
9	Adaptive quality-based clustering of gene expression profiles. Bioinformatics, 2002, 18, 735-746.	4.1	170
10	Comparison and meta-analysis of microarray data: from the bench to the computer desk. Trends in Genetics, 2003, 19, 570-577.	6.7	169
11	Toucan: deciphering the cis-regulatory logic of coregulated genes. Nucleic Acids Research, 2003, 31, 1753-1764.	14.5	167
12	eXtasy: variant prioritization by genomic data fusion. Nature Methods, 2013, 10, 1083-1084.	19.0	153
13	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research, 2013, 41, 6119-6138.	14.5	142
14	Kernel-based data fusion for gene prioritization. Bioinformatics, 2007, 23, i125-i132.	4.1	116
15	Candidate gene prioritization with Endeavour. Nucleic Acids Research, 2016, 44, W117-W121.	14.5	111
16	Concurrent Whole-Genome Haplotyping and Copy-Number Profiling of Single Cells. American Journal of Human Genetics, 2015, 96, 894-912.	6.2	110
17	Benchmarking the CATMA Microarray. A Novel Tool forArabidopsis Transcriptome Analysis. Plant Physiology, 2005, 137, 588-601.	4.8	91
18	An unbiased evaluation of gene prioritization tools. Bioinformatics, 2012, 28, 3081-3088.	4.1	79

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19	INCLUSive: INtegrated Clustering, Upstream sequence retrieval and motif Sampling. Bioinformatics, 2002, 18, 331-332.	4.1	78
20	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	12.8	75
21	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. Nucleic Acids Research, 2003, 31, 3468-3470.	14.5	46
22	Peripheral Blood RNA Levels of QSOX1 and PLBD1 Are New Independent Predictors of Left Ventricular Dysfunction After Acute Myocardial Infarction. Circulation Genomic and Precision Medicine, 2019, 12, e002656.	3.6	37
23	Gene profiling of hippocampal neuronal culture. Journal of Neurochemistry, 2003, 85, 1279-1288.	3.9	36
24	ChemGrapher: Optical Graph Recognition of Chemical Compounds by Deep Learning. Journal of Chemical Information and Modeling, 2020, 60, 4506-4517.	5.4	35
25	Gene prioritization using Bayesian matrix factorization with genomic and phenotypic side information. Bioinformatics, 2018, 34, i447-i456.	4.1	32
26	Beegle:from literature mining to disease-gene discovery. Nucleic Acids Research, 2016, 44, e18-e18.	14.5	30
27	Annotate-it: a Swiss-knife approach to annotation, analysis and interpretation of single nucleotide variation in human disease. Genome Medicine, 2012, 4, 73.	8.2	28
28	Protein fold recognition using geometric kernel data fusion. Bioinformatics, 2014, 30, 1850-1857.	4.1	27
29	Insight into the protein solubility driving forces with neural attention. PLoS Computational Biology, 2020, 16, e1007722.	3.2	25
30	Hybrid Clustering of Text Mining and Bibliometrics Applied to Journal Sets. , 2009, , .		24
31	Embedding recurrent neural networks into predatorâ€“prey models. Neural Networks, 1999, 12, 237-245.	5.9	19
32	Weighted hybrid clustering by combining text mining and bibliometrics on a largeâ€scale journal database. Journal of the Association for Information Science and Technology, 2010, 61, 1105-1119.	2.6	19
33	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	3.3	19
34	Methylome analysis for spina bifida shows SOX18 hypomethylation as a risk factor with evidence for a complex (epi)genetic interplay to affect neural tube development. Clinical Epigenetics, 2016, 8, 108.	4.1	18
35	NGS-Logistics: federated analysis of NGS sequence variants across multiple locations. Genome Medicine, 2014, 6, 71.	8.2	16
36	Kernel-based Data Fusion for Machine Learning. Studies in Computational Intelligence, 2011, , .	0.9	14

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37	In silico prediction of in vitro protein liquidâ€“liquid phase separation experiments outcomes with multi-head neural attention. Bioinformatics, 2021, 37, 3473-3479.	4.1	14
38	Current cancer driver variant predictors learn to recognize driver genes instead of functional variants. BMC Biology, 2021, 19, 3.	3.8	14
39	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	4.1	13
40	Multiple Sclerosis Data Alliance â€“ A global multi-stakeholder collaboration to scale-up real world data research. Multiple Sclerosis and Related Disorders, 2021, 47, 102634.	2.0	11
41	Complicated legacies: The human genome at 20. Science, 2021, 371, 564-569.	12.6	11
42	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. European Journal of Control, 2003, 9, 237-278.	2.6	10
43	PyUUL provides an interface between biological structures and deep learning algorithms. Nature Communications, 2022, 13, 961.	12.8	10
44	Fast semi-supervised discriminant analysis for binary classification of large data sets. Pattern Recognition, 2019, 91, 86-99.	8.1	9
45	Galahad: a web server for drug effect analysis from gene expression. Nucleic Acids Research, 2015, 43, W208-W212.	14.5	8
46	ACE-inhibition induces a cardioprotective transcriptional response in the metabolic syndrome heart. Scientific Reports, 2018, 8, 16169.	3.3	8
47	Advances in Cluster Analysis of Microarray Data. , 2005, , 153-173.		7
48	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. Progress in Preventive Medicine (New York, N Y), 2017, 2, e006.	0.7	6
49	From genotype to phenotype inArabidopsis thaliana:in-silicogenome interpretation predicts 288 phenotypes from sequencing data. Nucleic Acids Research, 2022, 50, e16-e16.	14.5	6
50	Learning with Heterogenous Data Sets by Weighted Multiple Kernel Canonical Correlation Analysis. IEEE International Workshop on Machine Learning for Signal Processing, 2007, , .	0.0	5
51	A Genetic Algorithm for Pancreatic Cancer Diagnosis. Communications in Computer and Information Science, 2013, , 222-230.	0.5	5
52	Gene prioritization through geometric-inspired kernel data fusion. , 2015, , .		5
53	A Simple Genetic Algorithm for Biomarker Mining. Lecture Notes in Computer Science, 2012, , 222-232.	1.3	4
54	A Self-Tuning Genetic Algorithm with Applications in Biomarker Discovery. , 2014, , .		3

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55	Topic modeling of biomedical text. , 2016, , .		3
56	mRNA profiling of pancreatic beta-cells: investigating mechanisms of diabetes. , 2001, , 187-211.		2
57	Hybrid Clustering by Integrating Text and Citation Based Graphs in Journal Database Analysis. , 2009, , .		2
58	A Hybrid Approach to Feature Ranking for Microarray Data Classification. Communications in Computer and Information Science, 2013, , 241-248.	0.5	2
59	A Comprehensive Comparison of Two MEDLINE Annotators for Disease and Gene Linkage: Sometimes Less is More. Lecture Notes in Computer Science, 2016, , 765-778.	1.3	2
60	Chromosome Instability Is Common in Human Cleavage-Stage Embryos. Obstetrical and Gynecological Survey, 2012, 67, 787-788.	0.4	1
61	ECCB 2018: The 17th European Conference on Computational Biology. Bioinformatics, 2018, 34, i595-i598.	4.1	1
62	Twoâ€level preconditioning for Ridge Regression. Numerical Linear Algebra With Applications, 2021, 28, e2371.	1.6	1
63	COMPOSITION METHODS FOR THE SIMULATION OF ARRAYS OF CHUA'S CIRCUITS. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 1999, 09, 723-733.	1.7	0
64	Representation of neural networks as Lotka-Volterra systems. , 1999, , .		0
65	Gene Regulation Bioinformatics of Microarray Data. , 0, , 55-98.		0
66	Guest Commentary on Chapter 8: Data Integration: The Next Big Hope?. , 0, , 155-158.		0
67	eXtasy simplified-towards opening the black box. , 2013, , .		0
68	Gene interaction networks boost genetic algorithm performance in biomarker discovery. , 2014, , .		0
69	Towards Better Prioritization of Epigenetically Modified DNA Regions. Lecture Notes in Computer Science, 2012, , 270-277.	1.3	0
70	Applying Kernel Methods on Protein Complexes Detection Problem. Communications in Computer and Information Science, 2012, , 463-471.	0.5	0
71	An ontology describing congenital heart defects data. EMBnet Journal, 2013, 19, 76.	0.6	0
72	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0

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73	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
74	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
75	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0