

# Yves Moreau

## List of Publications by Year in descending order

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Version: 2024-02-01

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	From genotype to phenotype in <i>Arabidopsis thaliana</i> : <i>in-silico</i> genome interpretation predicts 288 phenotypes from sequencing data. <i>Nucleic Acids Research</i> , 2022, 50, e16-e16.	14.5	6
2	PyUUL provides an interface between biological structures and deep learning algorithms. <i>Nature Communications</i> , 2022, 13, 961.	12.8	10
3	Multiple Sclerosis Data Alliance – A global multi-stakeholder collaboration to scale-up real world data research. <i>Multiple Sclerosis and Related Disorders</i> , 2021, 47, 102634.	2.0	11
4	Complicated legacies: The human genome at 20. <i>Science</i> , 2021, 371, 564-569.	12.6	11
5	Two-level preconditioning for Ridge Regression. <i>Numerical Linear Algebra With Applications</i> , 2021, 28, e2371.	1.6	1
6	<i>In silico</i> prediction of <i>in vitro</i> protein liquid-liquid phase separation experiments outcomes with multi-head neural attention. <i>Bioinformatics</i> , 2021, 37, 3473-3479.	4.1	14
7	Current cancer driver variant predictors learn to recognize driver genes instead of functional variants. <i>BMC Biology</i> , 2021, 19, 3.	3.8	14
8	ChemGrapher: Optical Graph Recognition of Chemical Compounds by Deep Learning. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4506-4517.	5.4	35
9	Insight into the protein solubility driving forces with neural attention. <i>PLoS Computational Biology</i> , 2020, 16, e1007722.	3.2	25
10	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
11	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
12	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
13	Insight into the protein solubility driving forces with neural attention. , 2020, 16, e1007722.		0
14	Fast semi-supervised discriminant analysis for binary classification of large data sets. <i>Pattern Recognition</i> , 2019, 91, 86-99.	8.1	9
15	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. <i>Scientific Reports</i> , 2019, 9, 16932.	3.3	19
16	Peripheral Blood RNA Levels of <i>QSOX1</i> and <i>PLBD1</i> Are New Independent Predictors of Left Ventricular Dysfunction After Acute Myocardial Infarction. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002656.	3.6	37
17	Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery. <i>Cell Chemical Biology</i> , 2018, 25, 611-618.e3.	5.2	176
18	ACE-inhibition induces a cardioprotective transcriptional response in the metabolic syndrome heart. <i>Scientific Reports</i> , 2018, 8, 16169.	3.3	8

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19	ECCB 2018: The 17th European Conference on Computational Biology. <i>Bioinformatics</i> , 2018, 34, i595-i598.	4.1	1
20	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. <i>Bioinformatics</i> , 2018, 34, 3118-3125.	4.1	13
21	Gene prioritization using Bayesian matrix factorization with genomic and phenotypic side information. <i>Bioinformatics</i> , 2018, 34, i447-i456.	4.1	32
22	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017, 8, 1221.	12.8	75
23	Viva Europa, a Land of Excellence in Research and Innovation for Health and Wellbeing. <i>Progress in Preventive Medicine (New York, N Y)</i> , 2017, 2, e006.	0.7	6
24	Topic modeling of biomedical text. , 2016, , .		3
25	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. <i>Clinical Epigenetics</i> , 2016, 8, 108.	4.1	18
26	A Comprehensive Comparison of Two MEDLINE Annotators for Disease and Gene Linkage: Sometimes Less is More. <i>Lecture Notes in Computer Science</i> , 2016, , 765-778.	1.3	2
27	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
28	Candidate gene prioritization with Endeavour. <i>Nucleic Acids Research</i> , 2016, 44, W117-W121.	14.5	111
29	<i>Beegle:</i>from literature mining to disease-gene discovery. <i>Nucleic Acids Research</i> , 2016, 44, e18-e18.	14.5	30
30	Concurrent Whole-Genome Haplotyping and Copy-Number Profiling of Single Cells. <i>American Journal of Human Genetics</i> , 2015, 96, 894-912.	6.2	110
31	Gene prioritization through geometric-inspired kernel data fusion. , 2015, , .		5
32	Galahad: a web server for drug effect analysis from gene expression. <i>Nucleic Acids Research</i> , 2015, 43, W208-W212.	14.5	8
33	NGS-Logistics: federated analysis of NGS sequence variants across multiple locations. <i>Genome Medicine</i> , 2014, 6, 71.	8.2	16
34	Effective diagnosis of genetic disease by computational phenotype analysis of the disease-associated genome. <i>Science Translational Medicine</i> , 2014, 6, 252ra123.	12.4	223
35	Protein fold recognition using geometric kernel data fusion. <i>Bioinformatics</i> , 2014, 30, 1850-1857.	4.1	27
36	A Self-Tuning Genetic Algorithm with Applications in Biomarker Discovery. , 2014, , .		3

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37	Gene interaction networks boost genetic algorithm performance in biomarker discovery. , 2014, , .		0
38	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research, 2013, 41, 6119-6138.	14.5	142
39	eXtasy: variant prioritization by genomic data fusion. Nature Methods, 2013, 10, 1083-1084.	19.0	153
40	A Hybrid Approach to Feature Ranking for Microarray Data Classification. Communications in Computer and Information Science, 2013, , 241-248.	0.5	2
41	A Genetic Algorithm for Pancreatic Cancer Diagnosis. Communications in Computer and Information Science, 2013, , 222-230.	0.5	5
42	eXtasy simplified-towards opening the black box. , 2013, , .		0
43	An ontology describing congenital heart defects data. EMBnet Journal, 2013, 19, 76.	0.6	0
44	An unbiased evaluation of gene prioritization tools. Bioinformatics, 2012, 28, 3081-3088.	4.1	79
45	Chromosome Instability Is Common in Human Cleavage-Stage Embryos. Obstetrical and Gynecological Survey, 2012, 67, 787-788.	0.4	1
46	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
47	Computational tools for prioritizing candidate genes: boosting disease gene discovery. Nature Reviews Genetics, 2012, 13, 523-536.	16.3	387
48	A Simple Genetic Algorithm for Biomarker Mining. Lecture Notes in Computer Science, 2012, , 222-232.	1.3	4
49	Towards Better Prioritization of Epigenetically Modified DNA Regions. Lecture Notes in Computer Science, 2012, , 270-277.	1.3	0
50	Applying Kernel Methods on Protein Complexes Detection Problem. Communications in Computer and Information Science, 2012, , 463-471.	0.5	0
51	Kernel-based Data Fusion for Machine Learning. Studies in Computational Intelligence, 2011, , .	0.9	14
52	Weighted hybrid clustering by combining text mining and bibliometrics on a large-scale journal database. Journal of the Association for Information Science and Technology, 2010, 61, 1105-1119.	2.6	19
53	Hybrid Clustering by Integrating Text and Citation Based Graphs in Journal Database Analysis. , 2009, , .		2
54	Hybrid Clustering of Text Mining and Bibliometrics Applied to Journal Sets. , 2009, , .		24

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55	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
56	Kernel-based data fusion for gene prioritization. Bioinformatics, 2007, 23, i125-i132.	4.1	116
57	Gene prioritization through genomic data fusion. Nature Biotechnology, 2006, 24, 537-544.	17.5	787
58	Advances in Cluster Analysis of Microarray Data. , 2005, , 153-173.		7
59	Benchmarking the CATMA Microarray. A Novel Tool for Arabidopsis Transcriptome Analysis. Plant Physiology, 2005, 137, 588-601.	4.8	91
60	Comparison and meta-analysis of microarray data: from the bench to the computer desk. Trends in Genetics, 2003, 19, 570-577.	6.7	169
61	Gene profiling of hippocampal neuronal culture. Journal of Neurochemistry, 2003, 85, 1279-1288.	3.9	36
62	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. European Journal of Control, 2003, 9, 237-278.	2.6	10
63	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. Nucleic Acids Research, 2003, 31, 3468-3470.	14.5	46
64	Toucan: deciphering the cis-regulatory logic of coregulated genes. Nucleic Acids Research, 2003, 31, 1753-1764.	14.5	167
65	Adaptive quality-based clustering of gene expression profiles. Bioinformatics, 2002, 18, 735-746.	4.1	170
66	INCLUSive: INtegrated Clustering, Upstream sequence retrieval and motif Sampling. Bioinformatics, 2002, 18, 331-332.	4.1	78
67	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
68	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
69	mRNA profiling of pancreatic beta-cells: investigating mechanisms of diabetes. , 2001, , 187-211.		2
70	A higher-order background model improves the detection of promoter regulatory elements by Gibbs sampling. Bioinformatics, 2001, 17, 1113-1122.	4.1	344
71	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
72	Embedding recurrent neural networks into predator-prey models. Neural Networks, 1999, 12, 237-245.	5.9	19

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73	Representation of neural networks as Lotka-Volterra systems. , 1999, , .		0
74	Gene Regulation Bioinformatics of Microarray Data. , 0, , 55-98.		0
75	Guest Commentary on Chapter 8: Data Integration: The Next Big Hope?. , 0, , 155-158.		0