

Jacques van Helden

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90
papers

7,728
citations

39
h-index

87
g-index

117
ext. papers

8,984
ext. citations

11.5
avg, IF

5.95
L-index

#	Paper	IF	Citations
90	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005 , 23, 137-44	44.5	950
89	Evaluation of clustering algorithms for protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2006 , 7, 488	3.6	577
88	Extracting regulatory sites from the upstream region of yeast genes by computational analysis of oligonucleotide frequencies. <i>Journal of Molecular Biology</i> , 1998 , 281, 827-42	6.5	576
87	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. <i>Nature</i> , 2007 , 450, 219-32	50.4	506
86	Regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2003 , 31, 3593-6	20.1	336
85	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2005 , 33, D364-8	20.1	242
84	RSAT: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2008 , 36, W119-27	20.1	215
83	Discovering regulatory elements in non-coding sequences by analysis of spaced dyads. <i>Nucleic Acids Research</i> , 2000 , 28, 1808-18	20.1	207
82	In vitro screening of a FDA approved chemical library reveals potential inhibitors of SARS-CoV-2 replication. <i>Scientific Reports</i> , 2020 , 10, 13093	4.9	205
81	Using RSAT to scan genome sequences for transcription factor binding sites and cis-regulatory modules. <i>Nature Protocols</i> , 2008 , 3, 1578-88	18.8	200
80	RSAT 2015: Regulatory Sequence Analysis Tools. <i>Nucleic Acids Research</i> , 2015 , 43, W50-6	20.1	193
79	RSAT 2011: regulatory sequence analysis tools. <i>Nucleic Acids Research</i> , 2011 , 39, W86-91	20.1	192
78	Reticulate representation of evolutionary and functional relationships between phage genomes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 762-77	8.3	173
77	Prophinder: a computational tool for prophage prediction in prokaryotic genomes. <i>Bioinformatics</i> , 2008 , 24, 863-5	7.2	172
76	Effect of 21 different nitrogen sources on global gene expression in the yeast <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007 , 27, 3065-86	4.8	171
75	RSAT peak-motifs: motif analysis in full-size ChIP-seq datasets. <i>Nucleic Acids Research</i> , 2012 , 40, e31	20.1	159
74	A web site for the computational analysis of yeast regulatory sequences. <i>Yeast</i> , 2000 , 16, 177-87	3.4	152

73	Transcription factor regulation can be accurately predicted from the presence of target gene signatures in microarray gene expression data. <i>Nucleic Acids Research</i> , 2010 , 38, e120	20.1	150
72	Genome-wide characterization of mammalian promoters with distal enhancer functions. <i>Nature Genetics</i> , 2017 , 49, 1073-1081	36.3	143
71	The powerful law of the power law and other myths in network biology. <i>Molecular BioSystems</i> , 2009 , 5, 1482-93		133
70	The chromatin environment shapes DNA replication origin organization and defines origin classes. <i>Genome Research</i> , 2015 , 25, 1873-85	9.7	106
69	Statistical analysis of yeast genomic downstream sequences reveals putative polyadenylation signals. <i>Nucleic Acids Research</i> , 2000 , 28, 1000-10	20.1	105
68	RSAT 2018: regulatory sequence analysis tools 20th anniversary. <i>Nucleic Acids Research</i> , 2018 , 46, W209-W214	10.1	104
67	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003 , 31, 1121-35	20.1	101
66	Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , 2015 , 43, e27	20.1	95
65	Inferring meaningful pathways in weighted metabolic networks. <i>Journal of Molecular Biology</i> , 2006 , 356, 222-36	6.5	92
64	Network Analysis Tools: from biological networks to clusters and pathways. <i>Nature Protocols</i> , 2008 , 3, 1616-29	18.8	91
63	NeAT: a toolbox for the analysis of biological networks, clusters, classes and pathways. <i>Nucleic Acids Research</i> , 2008 , 36, W444-51	20.1	73
62	Metabolic PathFinding: inferring relevant pathways in biochemical networks. <i>Nucleic Acids Research</i> , 2005 , 33, W326-30	20.1	71
61	An overview of data models for the analysis of biochemical pathways. <i>Briefings in Bioinformatics</i> , 2003 , 4, 246-59	13.4	67
60	Pathway discovery in metabolic networks by subgraph extraction. <i>Bioinformatics</i> , 2010 , 26, 1211-8	7.2	66
59	A complete workflow for the analysis of full-size ChIP-seq (and similar) data sets using peak-motifs. <i>Nature Protocols</i> , 2012 , 7, 1551-68	18.8	64
58	Metrics for comparing regulatory sequences on the basis of pattern counts. <i>Bioinformatics</i> , 2004 , 20, 399-406	7.2	56
57	RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections. <i>Nucleic Acids Research</i> , 2017 , 45, e119	20.1	55
56	Establishment of the dorso-ventral pattern during embryonic development of drosophila melanogaster: a logical analysis. <i>Journal of Theoretical Biology</i> , 1997 , 189, 377-89	2.3	54

55	Representing and analysing molecular and cellular function using the computer. <i>Biological Chemistry</i> , 2000 , 381, 921-35	4.5	53
54	Metabolic pathfinding using RPAIR annotation. <i>Journal of Molecular Biology</i> , 2009 , 388, 390-414	6.5	52
53	Theoretical and empirical quality assessment of transcription factor-binding motifs. <i>Nucleic Acids Research</i> , 2011 , 39, 808-24	20.1	48
52	Redefining fundamental concepts of transcription initiation in bacteria. <i>Nature Reviews Genetics</i> , 2020 , 21, 699-714	30.1	41
51	Using RSAT oligo-analysis and dyad-analysis tools to discover regulatory signals in nucleic sequences. <i>Nature Protocols</i> , 2008 , 3, 1589-603	18.8	36
50	Clusters of conserved beta cell marker genes for assessment of beta cell phenotype. <i>PLoS ONE</i> , 2011 , 6, e24134	3.7	35
49	Evaluation of phylogenetic footprint discovery for predicting bacterial cis-regulatory elements and revealing their evolution. <i>BMC Bioinformatics</i> , 2008 , 9, 37	3.6	32
48	Interactive visualization and exploration of relationships between biological objects. <i>Trends in Biotechnology</i> , 2000 , 18, 487-94	15.1	32
47	Fine-tuning enhancer models to predict transcriptional targets across multiple genomes. <i>PLoS ONE</i> , 2007 , 2, e1115	3.7	31
46	Tracing the origins of SARS-COV-2 in coronavirus phylogenies: a review. <i>Environmental Chemistry Letters</i> , 2021 , 19, 1-17	13.3	31
45	RegulonDB (version 2.0): a database on transcriptional regulation in Escherichia coli. <i>Nucleic Acids Research</i> , 1999 , 27, 59-60	20.1	30
44	Transcriptional regulation of protein complexes in yeast. <i>Genome Biology</i> , 2004 , 5, R33	18.3	28
43	From molecular activities and processes to biological function. <i>Briefings in Bioinformatics</i> , 2001 , 2, 81-93	13.4	26
42	Combining pattern discovery and discriminant analysis to predict gene co-regulation. <i>Bioinformatics</i> , 2004 , 20, 2370-9	7.2	24
41	Prediction of metabolic pathways from genome-scale metabolic networks. <i>BioSystems</i> , 2011 , 105, 109-21.9	21.9	23
40	Unraveling networks of co-regulated genes on the sole basis of genome sequences. <i>Nucleic Acids Research</i> , 2011 , 39, 6340-58	20.1	23
39	info-gibbs: a motif discovery algorithm that directly optimizes information content during sampling. <i>Bioinformatics</i> , 2009 , 25, 2715-22	7.2	22
38	In silico identification of NF-kappaB-regulated genes in pancreatic beta-cells. <i>BMC Bioinformatics</i> , 2007 , 8, 55	3.6	21

37	Modularity of the transcriptional response of protein complexes in yeast. <i>Journal of Molecular Biology</i> , 2006 , 363, 589-610	6.5	21
36	Coordinated response of the <i>Desulfovibrio desulfuricans</i> 27774 transcriptome to nitrate, nitrite and nitric oxide. <i>Scientific Reports</i> , 2017 , 7, 16228	4.9	20
35	In silico identification of putative regulatory sequence elements in the 5' untranslated region of genes that are expressed during male gametogenesis. <i>Plant Physiology</i> , 2003 , 132, 75-83	6.6	20
34	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019 , 20, 164	18.3	19
33	Integrating sequence, evolution and functional genomics in regulatory genomics. <i>Genome Biology</i> , 2009 , 10, 202	18.3	17
32	Deciphering the adaptation strategies of <i>Desulfovibrio piezophilus</i> to hydrostatic pressure through metabolic and transcriptional analyses. <i>Environmental Microbiology Reports</i> , 2016 , 8, 520-6	3.7	14
31	Retrieve-ensembl-seq: user-friendly and large-scale retrieval of single or multi-genome sequences from Ensembl. <i>Bioinformatics</i> , 2009 , 25, 2739-40	7.2	12
30	Sequanix: a dynamic graphical interface for Snakemake workflows. <i>Bioinformatics</i> , 2018 , 34, 1934-1936	7.2	11
29	Transcriptional and epigenetic signatures of zygotic genome activation during early <i>Drosophila</i> embryogenesis. <i>BMC Genomics</i> , 2013 , 14, 226	4.5	9
28	In response to αCan sugars be produced from fatty acids? A test case for pathway analysis toolsα <i>Bioinformatics</i> , 2009 , 25, 3202-5	7.2	9
27	Analyzing multiple data sets by interconnecting RSAT programs via SOAP Web services: an example with CHIP-chip data. <i>Nature Protocols</i> , 2008 , 3, 1604-15	18.8	9
26	Discrimination of yeast genes involved in methionine and phosphate metabolism on the basis of upstream motifs. <i>Bioinformatics</i> , 2005 , 21, 3490-500	7.2	9
25	Contribution of the gene extramacrochaetae to the precise positioning of bristles in <i>Drosophila</i> . <i>Roux's Archives of Developmental Biology</i> , 1995 , 204, 336-343		8
24	Discovery of conserved motifs in promoters of orthologous genes in prokaryotes. <i>Methods in Molecular Biology</i> , 2007 , 395, 293-308	1.4	8
23	Predicting metabolic pathways by sub-network extraction. <i>Methods in Molecular Biology</i> , 2012 , 804, 107-120		7
22	Confidence intervals are no salvation from the alleged fickleness of the P value. <i>Nature Methods</i> , 2016 , 13, 605-6	21.6	7
21	Tuning promoter boundaries improves regulatory motif discovery in nonmodel plants: the peach example. <i>Plant Physiology</i> , 2021 , 185, 1242-1258	6.6	7
20	Transcriptional Profiling of Midguts Prepared from αPositive Collected from Two Distinct Cameroonian Foci: Coordinated Signatures of the Midgutsα Remodeling As αSupportive Niches. <i>Frontiers in Immunology</i> , 2017 , 8, 876	8.4	6

19	Approaches to visualisation in bioinformatics: from dendrograms to Space Explorer. <i>Information Sciences</i> , 2001 , 139, 19-57	7.7	6
18	RSAT::Plants: Motif Discovery Within Clusters of Upstream Sequences in Plant Genomes. <i>Methods in Molecular Biology</i> , 2016 , 1482, 279-95	1.4	5
17	An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. <i>Lancet, The</i> , 2021 , 398, 1402-1404	4.0	5
16	Application of Regulatory Sequence Analysis and Metabolic Network Analysis to the Interpretation of Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2001 , 147-163	0.9	5
15	Bacterial molecular networks: bridging the gap between functional genomics and dynamical modelling. <i>Methods in Molecular Biology</i> , 2012 , 804, 1-11	1.4	4
14	Discovery of motifs in promoters of coregulated genes. <i>Methods in Molecular Biology</i> , 2007 , 395, 329-48	1.4	4
13	RSAT variation-tools: An accessible and flexible framework to predict the impact of regulatory variants on transcription factor binding. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 1415-1428	6.8	4
12	biotoolsSchema: a formalized schema for bioinformatics software description. <i>GigaScience</i> , 2021 , 10,	7.6	4
11	RSAT::Plants: Motif Discovery in ChIP-Seq Peaks of Plant Genomes. <i>Methods in Molecular Biology</i> , 2016 , 1482, 297-322	1.4	3
10	An Overview of Data Models for the Analysis of Biochemical Pathways. <i>Lecture Notes in Computer Science</i> , 2003 , 174-174	0.9	3
9	Sub-microscopic Plasmodium falciparum infections in matched peripheral, placental and umbilical cord blood samples from asymptomatic Congolese women at delivery. <i>Acta Tropica</i> , 2019 , 193, 142-147	3.2	2
8	Investigating transcriptional regulation: from analysis of complex networks to discovery of cis-regulatory elements. <i>Methods</i> , 2009 , 48, 277-86	4.6	2
7	Machine learning techniques to identify putative genes involved in nitrogen catabolite repression in the yeast <i>Saccharomyces cerevisiae</i> . <i>BMC Proceedings</i> , 2008 , 2 Suppl 4, S5	2.3	2
6	Motif analysis in co-expression networks reveals regulatory elements in plants: The peach as a model		1
5	RSAT matrix-clustering: dynamic exploration and redundancy reduction of transcription factor binding motif collections		1
4	An integrated analysis tool reveals intrinsic biases in gene set enrichment		1
3	RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach. <i>Frontiers in Microbiology</i> , 2020 , 11, 567471	5.7	0
2	Integrating Bacterial ChIP-seq and RNA-seq Data With SnakeChunks. <i>Current Protocols in Bioinformatics</i> , 2019 , 66, e72	24.2	0

- 1 Gaussian Graphical Models to Infer Putative Genes Involved in Nitrogen Catabolite Repression in *S. cerevisiae*. *Lecture Notes in Computer Science*, **2009**, 13-24 0.9