

Cedric Notredame

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

103
papers

30,015
citations

45
h-index

110
g-index

110
ext. papers

36,568
ext. citations

12.3
avg, IF

8.23
L-index

#	Paper	IF	Citations
103	Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. <i>Methods in Molecular Biology</i> , 2021 , 2231, 89-97	1.4	1
102	A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019 , 8,	7.6	66
101	Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards. <i>Nucleic Acids Research</i> , 2019 , 47, W600-W604	20.1	2
100	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2019 ,	7.2	2
99	Protocol for Measuring Compulsive-like Feeding Behavior in Mice. <i>Bio-protocol</i> , 2019 , 9, e3308	0.9	
98	Large multiple sequence alignments with a root-to-leaf regressive method. <i>Nature Biotechnology</i> , 2019 , 37, 1466-1470	44.5	13
97	Extinction and reinstatement of an operant responding maintained by food in different models of obesity. <i>Addiction Biology</i> , 2018 , 23, 544-555	4.6	9
96	Time-course and dynamics of obesity-related behavioral changes induced by energy-dense foods in mice. <i>Addiction Biology</i> , 2018 , 23, 531-543	4.6	8
95	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018 , 67, 997-1009	8.4	8
94	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. <i>IScience</i> , 2018 , 9, 244-257	6.1	5
93	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329		25
92	Nextflow enables reproducible computational workflows. <i>Nature Biotechnology</i> , 2017 , 35, 316-319	44.5	588
91	Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. <i>Plant Cell</i> , 2017 , 29, 1248-1261	11.6	40
90	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , 2017 , 1, 1961-1969	12.3	65
89	Transcript profiling of jasmonate-elicited <i>Taxus</i> cells reveals a β -phenylalanine-CoA ligase. <i>Plant Biotechnology Journal</i> , 2016 , 14, 85-96	11.6	33
88	How should we measure proportionality on relative gene expression data?. <i>Theory in Biosciences</i> , 2016 , 135, 21-36	1.3	50
87	PSI/TM-Coffee: a web server for fast and accurate multiple sequence alignments of regular and transmembrane proteins using homology extension on reduced databases. <i>Nucleic Acids Research</i> , 2016 , 44, W339-43	20.1	28

86	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1009-1023	13.4	85
85	Combined Treatment With Environmental Enrichment and (-)-Epigallocatechin-3-Gallate Ameliorates Learning Deficits and Hippocampal Alterations in a Mouse Model of Down Syndrome. <i>ENeuro</i> , 2016 , 3,	3.9	26
84	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016 , 17, 251	18.3	85
83	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016 , 17, 32	18.3	124
82	Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016 , 26, 705-16	9.7	23
81	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015 , 145, 78-179	1.9	57
80	Recovering accuracy methods for scalable consistency library. <i>Journal of Supercomputing</i> , 2015 , 71, 1833-1845	1.9	1
79	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
78	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. <i>Journal of Molecular and Cellular Cardiology</i> , 2015 , 89, 98-112	5.8	173
77	High Performance computing improvements on bioinformatics consistency-based multiple sequence alignment tools. <i>Parallel Computing</i> , 2015 , 42, 18-34	1	9
76	Principal Component Analysis of the Effects of Environmental Enrichment and (-)-epigallocatechin-3-gallate on Age-Associated Learning Deficits in a Mouse Model of Down Syndrome. <i>Frontiers in Behavioral Neuroscience</i> , 2015 , 9, 330	3.5	32
75	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction. <i>Nucleic Acids Research</i> , 2015 , 43, W3-6	20.1	30
74	Expression Divergence of Chemosensory Genes between <i>Drosophila sechellia</i> and Its Sibling Species and Its Implications for Host Shift. <i>Genome Biology and Evolution</i> , 2015 , 7, 2843-58	3.9	34
73	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903	17.4	56
72	The impact of Docker containers on the performance of genomic pipelines. <i>PeerJ</i> , 2015 , 3, e1273	3.1	77
71	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
70	Pharmacological assessment defines <i>Leishmania donovani</i> casein kinase 1 as a drug target and reveals important functions in parasite viability and intracellular infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1501-15	5.9	34
69	TCS: a new multiple sequence alignment reliability measure to estimate alignment accuracy and improve phylogenetic tree reconstruction. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1625-37	8.3	132

68	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. <i>Nucleic Acids Research</i> , 2014 , 42, W356-60	20.1	3
67	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014 , 24, 2077-89	9.7	74
66	T-Coffee: Tree-based consistency objective function for alignment evaluation. <i>Methods in Molecular Biology</i> , 2014 , 1079, 117-29	1.4	41
65	Improving multiple sequence alignment biological accuracy through genetic algorithms. <i>Journal of Supercomputing</i> , 2013 , 65, 1076-1088	2.5	7
64	Performance analysis of computational approaches to solve Multiple Sequence Alignment. <i>Journal of Supercomputing</i> , 2013 , 64, 69-78	2.5	3
63	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. <i>Bioinformatics</i> , 2013 , 29, 1112-9	7.2	18
62	Scalability and accuracy improvements of consistency-based multiple sequence alignment tools 2013 ,		4
61	Breen et al. reply. <i>Nature</i> , 2013 , 497, E2-E3	50.4	7
60	Identification of a novel microRNA (miRNA) from rice that targets an alternatively spliced transcript of the Nramp6 (Natural resistance-associated macrophage protein 6) gene involved in pathogen resistance. <i>New Phytologist</i> , 2013 , 199, 212-227	9.8	175
59	Detecting and comparing non-coding RNAs in the high-throughput era. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 15423-58	6.3	16
58	T-RMSD: a web server for automated fine-grained protein structural classification. <i>Nucleic Acids Research</i> , 2013 , 41, W358-62	20.1	3
57	Efficient and interpretable prediction of protein functional classes by correspondence analysis and compact set relations. <i>PLoS ONE</i> , 2013 , 8, e75542	3.7	3
56	AMPA: an automated web server for prediction of protein antimicrobial regions. <i>Bioinformatics</i> , 2012 , 28, 130-1	7.2	90
55	Epistasis as the primary factor in molecular evolution. <i>Nature</i> , 2012 , 490, 535-8	50.4	246
54	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
53	Enhancing the Scalability of Consistency-based Progressive Multiple Sequences Alignment Applications 2012 ,		5
52	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
51	Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 4, S1	3.6	99

50	An improved understanding of TNFL/TNFR interactions using structure-based classifications. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 353-63	10.3	28
49	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. <i>Nucleic Acids Research</i> , 2012 , 40, e52	20.1	14
48	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , 2011 , 6, 1669-82	18.8	80
47	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. <i>Nucleic Acids Research</i> , 2011 , 39, W13-7	20.1	692
46	Exploiting parallelism on progressive alignment methods. <i>Journal of Supercomputing</i> , 2011 , 58, 186-194	2.5	4
45	A user-friendly web portal for T-Coffee on supercomputers. <i>BMC Bioinformatics</i> , 2011 , 12, 150	3.6	1
44	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011 , 12, 552	4.5	72
43	The rhizome of life: the sympatric <i>Rickettsia felis</i> paradigm demonstrates the random transfer of DNA sequences. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3213-23	8.3	51
42	BlastR--fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , 2011 , 39, 6886-2051	2.5	26
41	STRIKE: evaluation of protein MSAs using a single 3D structure. <i>Bioinformatics</i> , 2011 , 27, 3385-91	7.2	17
40	Improving the alignment quality of consistency based aligners with an evaluation function using synonymous protein words. <i>PLoS ONE</i> , 2011 , 6, e27872	3.7	4
39	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in <i>Drosophila</i> embryogenesis. <i>Genes and Development</i> , 2010 , 24, 129-34	12.6	22
38	Cloud-Coffee: implementation of a parallel consistency-based multiple alignment algorithm in the T-Coffee package and its benchmarking on the Amazon Elastic-Cloud. <i>Bioinformatics</i> , 2010 , 26, 1903-4	7.2	23
37	Multi-platform next-generation sequencing of the domestic turkey (<i>Meleagris gallopavo</i>): genome assembly and analysis. <i>PLoS Biology</i> , 2010 , 8, e1000475	9.7	311
36	Cyclosporin A treatment of <i>Leishmania donovani</i> reveals stage-specific functions of cyclophilins in parasite proliferation and viability. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e729	4.8	26
35	T-RMSD: a fine-grained, structure-based classification method and its application to the functional characterization of TNF receptors. <i>Journal of Molecular Biology</i> , 2010 , 400, 605-17	6.5	5
34	Long noncoding RNAs with enhancer-like function in human cells. <i>Cell</i> , 2010 , 143, 46-58	56.2	1422
33	Computing multiple sequence/structure alignments with the T-coffee package. <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 3, Unit 3.8.1-25	24.2	22

32	Predicting phenotypic traits of prokaryotes from protein domain frequencies. <i>BMC Bioinformatics</i> , 2010 , 11, 481	3.6	9
31	How Much Does It Cost?: Optimization of Costs in Sequence Analysis of Social Science Data. <i>Sociological Methods and Research</i> , 2009 , 38, 197-231	2.9	44
30	Fibroblast-derived induced pluripotent stem cells show no common retroviral vector insertions. <i>Stem Cells</i> , 2009 , 27, 300-6	5.8	51
29	Upcoming challenges for multiple sequence alignment methods in the high-throughput era. <i>Bioinformatics</i> , 2009 , 25, 2455-65	7.2	153
28	Segment-based multiple sequence alignment. <i>Bioinformatics</i> , 2008 , 24, i187-92	7.2	39
27	R-Coffee: a method for multiple alignment of non-coding RNA. <i>Nucleic Acids Research</i> , 2008 , 36, e52	20.1	88
26	R-Coffee: a web server for accurately aligning noncoding RNA sequences. <i>Nucleic Acids Research</i> , 2008 , 36, W10-3	20.1	51
25	Vertebrate conserved non coding DNA regions have a high persistence length and a short persistence time. <i>BMC Genomics</i> , 2007 , 8, 398	4.5	12
24	Recent evolutions of multiple sequence alignment algorithms. <i>PLoS Computational Biology</i> , 2007 , 3, e123	3	146
23	The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods. <i>Nucleic Acids Research</i> , 2007 , 35, W645-8	20.1	170
22	Expresso: automatic incorporation of structural information in multiple sequence alignments using 3D-Coffee. <i>Nucleic Acids Research</i> , 2006 , 34, W604-8	20.1	383
21	PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments. <i>Nucleic Acids Research</i> , 2006 , 34, W600-3	20.1	13
20	APDB: a web server to evaluate the accuracy of sequence alignments using structural information. <i>Bioinformatics</i> , 2006 , 22, 2439-40	7.2	1
19	The iRMSD: a local measure of sequence alignment accuracy using structural information. <i>Bioinformatics</i> , 2006 , 22, e35-9	7.2	29
18	M-Coffee: combining multiple sequence alignment methods with T-Coffee. <i>Nucleic Acids Research</i> , 2006 , 34, 1692-9	20.1	414
17	3DCoffee@igs: a web server for combining sequences and structures into a multiple sequence alignment. <i>Nucleic Acids Research</i> , 2004 , 32, W37-40	20.1	139
16	CaspR: a web server for automated molecular replacement using homology modelling. <i>Nucleic Acids Research</i> , 2004 , 32, W606-9	20.1	81
15	Computing multiple sequence/structure alignments with the T-coffee package. <i>Current Protocols in Bioinformatics</i> , 2004 , Chapter 3, Unit3.8	24.2	5

14	3DCoffee: combining protein sequences and structures within multiple sequence alignments. <i>Journal of Molecular Biology</i> , 2004 , 340, 385-95	6.5	271
13	APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i215-21	7.2	45
12	Using Genetic Algorithms for Pairwise and Multiple Sequence Alignments 2003 , 87-111		
11	Structural genomics of highly conserved microbial genes of unknown function in search of new antibacterial targets. <i>Journal of Structural and Functional Genomics</i> , 2003 , 4, 141-57		52
10	Tcoffee@igs: A web server for computing, evaluating and combining multiple sequence alignments. <i>Nucleic Acids Research</i> , 2003 , 31, 3503-6	20.1	203
9	Recent progress in multiple sequence alignment: a survey. <i>Pharmacogenomics</i> , 2002 , 3, 131-44	2.6	227
8	T-Coffee: A novel method for fast and accurate multiple sequence alignment. <i>Journal of Molecular Biology</i> , 2000 , 302, 205-17	6.5	5330
7	SAGA: sequence alignment by genetic algorithm. <i>Nucleic Acids Research</i> , 1996 , 24, 1515-24	20.1	285
6	Fast and accurate large multiple sequence alignments using root-to-leave regressive computation		1
5	Differential proportionality - a normalization-free approach to differential gene expression		15
4	Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking		12
3	A field guide for the compositional analysis of any-omics data		2
2	Approaches for containerized scientific workflows in cloud environments with applications in life science. <i>F1000Research</i> , 10, 513	3.6	0
1	Four layer multi-omics reveals molecular responses to aneuploidy in Leishmania		1