Cedric Notredame

List of Publications by Year
in descending order

100 papers	40,423 citations	47006 47 h-index	37204 96 g-index
110 all docs	110 docs citations	110 times ranked	65411 citing authors

#	Article	IF	Citations
1	A long noncoding RNA promotes parasite differentiation in African trypanosomes. Science Advances, 2022, 8, .	10.3	12
2	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. Bioinformatics, 2021, 37, 1506-1514.	4.1	7
3	Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. Methods in Molecular Biology, 2021, 2231, 89-97.	0.9	6
4	A field guide for the compositional analysis of any-omics data. GigaScience, 2019, 8, .	6.4	187
5	Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards. Nucleic Acids Research, 2019, 47, W600-W604.	14.5	2
6	Large multiple sequence alignments with a root-to-leaf regressive method. Nature Biotechnology, 2019, 37, 1466-1470.	17.5	25
7	Protocol for Measuring Compulsive-like Feeding Behavior in Mice. Bio-protocol, 2019, 9, e3308.	0.4	1
8	Extinction and reinstatement of an operant responding maintained by food in different models of obesity. Addiction Biology, 2018, 23, 544-555.	2.6	11
9	Time‐course and dynamics of obesity‐related behavioral changes induced by energy‐dense foods in mice. Addiction Biology, 2018, 23, 531-543.	2.6	13
10	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. Systematic Biology, 2018, 67, 997-1009.	5.6	12
11	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. IScience, 2018, 9, 244-257.	4.1	5
12	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	4.1	36
13	Nextflow enables reproducible computational workflows. Nature Biotechnology, 2017, 35, 316-319.	17.5	1,867
14	Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. Plant Cell, 2017, 29, 1248-1261.	6.6	69
15	Haplotype selection as an adaptive mechanism in the protozoan pathogen Leishmania donovani. Nature Ecology and Evolution, 2017, 1, 1961-1969.	7.8	95
16	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
17	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	8.8	166
18	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	5.5	33

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19	How should we measure proportionality on relative gene expression data?. Theory in Biosciences, 2016, 135, 21-36.	1.4	77
20	PSI/TM-Coffee: a web server for fast and accurate multiple sequence alignments of regular and transmembrane proteins using homology extension on reduced databases. Nucleic Acids Research, 2016, 44, W339-W343.	14.5	55
21	Multiple sequence alignment modeling: methods and applications. Briefings in Bioinformatics, 2016, 17, 1009-1023.	6.5	153
22	Transcript profiling of jasmonateâ€elicited <i>Taxus</i> cells reveals a Î²â€phenylalanineâ€CoA ligase. Plant Biotechnology Journal, 2016, 14, 85-96.	8.3	41
23	Combined Treatment With Environmental Enrichment and (-)-Epigallocatechin-3-Gallate Ameliorates Learning Deficits and Hippocampal Alterations in a Mouse Model of Down Syndrome. ENeuro, 2016, 3, ENEURO.0103-16.2016.	1.9	42
24	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. Frontiers in Behavioral Neuroscience, 2015, 9, 330.	2.0	44
25	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction: Figure 1.. Nucleic Acids Research, 2015, 43, W3-W6.	14.5	44
26	Expression Divergence of Chemosensory Genes between<i>Drosophila sechellia</i>and Its Sibling Species and Its Implications for Host Shift. Genome Biology and Evolution, 2015, 7, 2843-2858.	2.5	51
27	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
28	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
29	Recovering accuracy methods for scalable consistency library. Journal of Supercomputing, 2015, 71, 1833-1845.	3.6	1
30	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	8.8	331
31	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. Journal of Molecular and Cellular Cardiology, 2015, 89, 98-112.	1.9	223
32	High Performance computing improvements on bioinformatics consistency-based multiple sequence alignment tools. Parallel Computing, 2015, 42, 18-34.	2.1	12
33	The impact of Docker containers on the performance of genomic pipelines. PeerJ, 2015, 3, e1273.	2.0	101
34	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. Nucleic Acids Research, 2014, 42, W356-W360.	14.5	3
35	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	5.5	102
36	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444

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37	Pharmacological Assessment Defines Leishmania donovani Casein Kinase 1 as a Drug Target and Reveals Important Functions in Parasite Viability and Intracellular Infection. Antimicrobial Agents and Chemotherapy, 2014, 58, 1501-1515.	3.2	44
38	TCS: A New Multiple Sequence Alignment Reliability Measure to Estimate Alignment Accuracy and Improve Phylogenetic Tree Reconstruction. Molecular Biology and Evolution, 2014, 31, 1625-1637.	8.9	183
39	T-Coffee: Tree-Based Consistency Objective Function for Alignment Evaluation. Methods in Molecular Biology, 2014, 1079, 117-129.	0.9	56
40	Improving multiple sequence alignment biological accuracy through genetic algorithms. Journal of Supercomputing, 2013, 65, 1076-1088.	3.6	9
41	Performance analysis of computational approaches to solve Multiple Sequence Alignment. Journal of Supercomputing, 2013, 64, 69-78.	3.6	4
42	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. Bioinformatics, 2013, 29, 1112-1119.	4.1	20
43	Scalability and accuracy improvements of consistency-based multiple sequence alignment tools. , 2013, , .		5
44	Breen et al. reply. Nature, 2013, 497, E2-E3.	27.8	11
45	Identification of a novel micro<scp>RNA</scp> (mi<scp>RNA</scp>) from rice that targets an alternatively spliced transcript of the <i><scp>N</scp>ramp6</i> (<i><scp>N</scp>atural) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Phytologist, 2013, 199, 212-227.	7.3	221
46	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. International Journal of Molecular Sciences, 2013, 14, 15423-15458.	4.1	22
47	T-RMSD: a web server for automated fine-grained protein structural classification. Nucleic Acids Research, 2013, 41, W358-W362.	14.5	3
48	Efficient and Interpretable Prediction of Protein Functional Classes by Correspondence Analysis and Compact Set Relations. PLoS ONE, 2013, 8, e75542.	2.5	7
49	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. Nucleic Acids Research, 2012, 40, e52-e52.	14.5	23
50	AMPA: an automated web server for prediction of protein antimicrobial regions. Bioinformatics, 2012, 28, 130-131.	4.1	140
51	Epistasis as the primary factor in molecular evolution. Nature, 2012, 490, 535-538.	27.8	325
52	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
53	Enhancing the Scalability of Consistency-based Progressive Multiple Sequences Alignment Applications. , 2012, , .		6
54	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	5.5	4,428

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55	Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. BMC Bioinformatics, 2012, 13, S1.	2.6	148
56	An improved understanding of TNFL/TNFR interactions using structure-based classifications. Trends in Biochemical Sciences, 2012, 37, 353-363.	7.5	31
57	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. Nature Protocols, 2011, 6, 1669-1682.	12.0	87
58	T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. Nucleic Acids Research, 2011, 39, W13-W17.	14.5	982
59	Exploiting parallelism on progressive alignment methods. Journal of Supercomputing, 2011, 58, 186-194.	3.6	7
60	A user-friendly web portal for T-Coffee on supercomputers. BMC Bioinformatics, 2011, 12, 150.	2.6	5
61	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	2.8	127
62	The Rhizome of Life: The Sympatric Rickettsia felis Paradigm Demonstrates the Random Transfer of DNA Sequences. Molecular Biology and Evolution, 2011, 28, 3213-3223.	8.9	73
63	BlastR—fast and accurate database searches for non-coding RNAs. Nucleic Acids Research, 2011, 39, 6886-6895.	14.5	28
64	STRIKE: evaluation of protein MSAs using a single 3D structure. Bioinformatics, 2011, 27, 3385-3391.	4.1	23
65	Improving the Alignment Quality of Consistency Based Aligners with an Evaluation Function Using Synonymous Protein Words. PLoS ONE, 2011, 6, e27872.	2.5	4
66	Predicting phenotypic traits of prokaryotes from protein domain frequencies. BMC Bioinformatics, 2010, 11, 481.	2.6	14
67	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in <i>Drosophila</i> embryogenesis. Genes and Development, 2010, 24, 129-134.	5.9	30
68	Cloud-Coffee: implementation of a parallel consistency-based multiple alignment algorithm in the T-Coffee package and its benchmarking on the Amazon Elastic-Cloud. Bioinformatics, 2010, 26, 1903-1904.	4.1	30
69	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	5.6	348
70	Cyclosporin A Treatment of Leishmania donovani Reveals Stage-Specific Functions of Cyclophilins in Parasite Proliferation and Viability. PLoS Neglected Tropical Diseases, 2010, 4, e729.	3.0	34
71	T-RMSD: A Fine-grained, Structure-based Classification Method and its Application to the Functional Characterization of TNF Receptors. Journal of Molecular Biology, 2010, 400, 605-617.	4.2	5
72	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	28.9	1,664

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73	Computing Multiple Sequence/Structure Alignments with the T‐Coffee Package. Current Protocols in Bioinformatics, 2010, 29, Unit 3.8.1-25.	25.8	25
74	How Much Does It Cost?. Sociological Methods and Research, 2009, 38, 197-231.	6.8	67
75	Fibroblast-Derived Induced Pluripotent Stem Cells Show No Common Retroviral Vector Insertions. Stem Cells, 2009, 27, 300-306.	3.2	55
76	Upcoming challenges for multiple sequence alignment methods in the high-throughput era. Bioinformatics, 2009, 25, 2455-2465.	4.1	181
77	Computing Multiple Sequence Alignment with Template-Based Methods. , 2009, , 54-69.		1
78	Segment-based multiple sequence alignment. Bioinformatics, 2008, 24, i187-i192.	4.1	44
79	R-Coffee: a method for multiple alignment of non-coding RNA. Nucleic Acids Research, 2008, 36, e52-e52.	14.5	116
80	R-Coffee: a web server for accurately aligning noncoding RNA sequences. Nucleic Acids Research, 2008, 36, W10-W13.	14.5	53
81	Recent Evolutions of Multiple Sequence Alignment Algorithms. PLoS Computational Biology, 2007, 3, e123.	3.2	171
82	The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods. Nucleic Acids Research, 2007, 35, W645-W648.	14.5	209
83	Vertebrate conserved non coding DNA regions have a high persistence length and a short persistence time. BMC Genomics, 2007, 8, 398.	2.8	13
84	M-Coffee: combining multiple sequence alignment methods with T-Coffee. Nucleic Acids Research, 2006, 34, 1692-1699.	14.5	533
85	Expresso: automatic incorporation of structural information in multiple sequence alignments using 3D-Coffee. Nucleic Acids Research, 2006, 34, W604-W608.	14.5	448
86	PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments. Nucleic Acids Research, 2006, 34, W600-W603.	14.5	13
87	APDB: a web server to evaluate the accuracy of sequence alignments using structural information. Bioinformatics, 2006, 22, 2439-2440.	4.1	1
88	The iRMSD: a local measure of sequence alignment accuracy using structural information. Bioinformatics, 2006, 22, e35-e39.	4.1	34
89	3DCoffee@igs: a web server for combining sequences and structures into a multiple alignment. Nucleic Acids Research, 2004, 32, W37-W40.	14.5	143
90	CaspR: a web server for automated molecular replacement using homology modelling. Nucleic Acids Research, 2004, 32, W606-W609.	14.5	87

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91	3DCoffee: Combining Protein Sequences and Structures within Multiple Sequence Alignments. Journal of Molecular Biology, 2004, 340, 385-395.	4.2	302
92	Structural genomics of highly conserved microbial genes of unknown function in search of new antibacterial targets. Journal of Structural and Functional Genomics, 2003, 4, 141-157.	1.2	56
93	Tcoffee@igs: a web server for computing, evaluating and combining multiple sequence alignments. Nucleic Acids Research, 2003, 31, 3503-3506.	14.5	214
94	Computing Multiple Sequence/Structure Alignments with the T â€Coffee Package. Current Protocols in Bioinformatics, 2003, 4, Unit3.8.	25.8	5
95	APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. Bioinformatics, 2003, 19, i215-i221.	4.1	62
96	Using Genetic Algorithms for Pairwise and Multiple Sequence Alignments. , 2003, , 87-111.		2
97	Recent progress in multiple sequence alignment: a survey. Pharmacogenomics, 2002, 3, 131-144.	1.3	289
98	T-coffee: a novel method for fast and accurate multiple sequence alignment 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 302, 205-217.	4.2	6,404
99	SAGA: sequence alignment by genetic algorithm. Nucleic Acids Research, 1996, 24, 1515-1524.	14.5	416
100	Approaches for containerized scientific workflows in cloud environments with applications in life science. F1000Research, 0, 10, 513.	1.6	1