Cedric Notredame

List of Publications by Year
in descending order

100 papers	40,423 citations	46984 47 h-index	37183 96 g-index
110 all docs	110 docs citations	110 times ranked	65411 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	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.	2.0	6,404
3	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
4	Nextflow enables reproducible computational workflows. Nature Biotechnology, 2017, 35, 316-319.	9.4	1,867
5	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
6	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
7	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.	6.5	982
8	M-Coffee: combining multiple sequence alignment methods with T-Coffee. Nucleic Acids Research, 2006, 34, 1692-1699.	6.5	533
9	Expresso: automatic incorporation of structural information in multiple sequence alignments using 3D-Coffee. Nucleic Acids Research, 2006, 34, W604-W608.	6.5	448
10	SAGA: sequence alignment by genetic algorithm. Nucleic Acids Research, 1996, 24, 1515-1524.	6.5	416
11	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
12	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
13	Epistasis as the primary factor in molecular evolution. Nature, 2012, 490, 535-538.	13.7	325
14	3DCoffee: Combining Protein Sequences and Structures within Multiple Sequence Alignments. Journal of Molecular Biology, 2004, 340, 385-395.	2.0	302
15	Recent progress in multiple sequence alignment: a survey. Pharmacogenomics, 2002, 3, 131-144.	0.6	289
16	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.	0.9	223
17	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.	3.5	221
18	Tcoffee@igs: a web server for computing, evaluating and combining multiple sequence alignments. Nucleic Acids Research, 2003, 31, 3503-3506.	6.5	214

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19	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.	6.5	209
20	A field guide for the compositional analysis of any-omics data. GigaScience, 2019, 8, .	3.3	187
21	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.	3.5	183
22	Upcoming challenges for multiple sequence alignment methods in the high-throughput era. Bioinformatics, 2009, 25, 2455-2465.	1.8	181
23	Recent Evolutions of Multiple Sequence Alignment Algorithms. PLoS Computational Biology, 2007, 3, e123.	1.5	171
24	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.	3.8	166
25	Multiple sequence alignment modeling: methods and applications. Briefings in Bioinformatics, 2016, 17, 1009-1023.	3.2	153
26	Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. BMC Bioinformatics, 2012, 13, S1.	1.2	148
27	3DCoffee@igs: a web server for combining sequences and structures into a multiple sequence alignment. Nucleic Acids Research, 2004, 32, W37-W40.	6.5	143
28	AMPA: an automated web server for prediction of protein antimicrobial regions. Bioinformatics, 2012, 28, 130-131.	1.8	140
29	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
30	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	1.2	127
31	R-Coffee: a method for multiple alignment of non-coding RNA. Nucleic Acids Research, 2008, 36, e52-e52.	6.5	116
32	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
33	The impact of Docker containers on the performance of genomic pipelines. PeerJ, 2015, 3, e1273.	0.9	101
34	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
35	Haplotype selection as an adaptive mechanism in the protozoan pathogen Leishmania donovani. Nature Ecology and Evolution, 2017, 1, 1961-1969.	3.4	95
36	CaspR: a web server for automated molecular replacement using homology modelling. Nucleic Acids Research, 2004, 32, W606-W609.	6.5	87

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37	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. Nature Protocols, 2011, 6, 1669-1682.	5.5	87
38	How should we measure proportionality on relative gene expression data?. Theory in Biosciences, 2016, 135, 21-36.	0.6	77
39	The Rhizome of Life: The Sympatric Rickettsia felis Paradigm Demonstrates the Random Transfer of DNA Sequences. Molecular Biology and Evolution, 2011, 28, 3213-3223.	3.5	73
40	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	5.8	73
41	Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. Plant Cell, 2017, 29, 1248-1261.	3.1	69
42	How Much Does It Cost?. Sociological Methods and Research, 2009, 38, 197-231.	4.3	67
43	APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. Bioinformatics, 2003, 19, i215-i221.	1.8	62
44	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
45	T-Coffee: Tree-Based Consistency Objective Function for Alignment Evaluation. Methods in Molecular Biology, 2014, 1079, 117-129.	0.4	56
46	Fibroblast-Derived Induced Pluripotent Stem Cells Show No Common Retroviral Vector Insertions. Stem Cells, 2009, 27, 300-306.	1.4	55
47	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.	6.5	55
48	R-Coffee: a web server for accurately aligning noncoding RNA sequences. Nucleic Acids Research, 2008, 36, W10-W13.	6.5	53
49	Expression Divergence of Chemosensory Genes between *Drosophila sechellia* and Its Sibling Species and Its Implications for Host Shift. Genome Biology and Evolution, 2015, 7, 2843-2858.	1.1	51
50	Segment-based multiple sequence alignment. Bioinformatics, 2008, 24, i187-i192.	1.8	44
51	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.	1.4	44
52	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.	1.0	44
53	TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction: Figure 1.. Nucleic Acids Research, 2015, 43, W3-W6.	6.5	44
54	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.	0.9	42

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55	Transcript profiling of jasmonateâ€elicited <i>Taxus</i> cells reveals a Î²â€phenylalanineâ€CoA ligase. Plant Biotechnology Journal, 2016, 14, 85-96.	4.1	41
56	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
57	The iRMSD: a local measure of sequence alignment accuracy using structural information. Bioinformatics, 2006, 22, e35-e39.	1.8	34
58	Cyclosporin A Treatment of Leishmania donovani Reveals Stage-Specific Functions of Cyclophilins in Parasite Proliferation and Viability. PLoS Neglected Tropical Diseases, 2010, 4, e729.	1.3	34
59	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
60	An improved understanding of TNFL/TNFR interactions using structure-based classifications. Trends in Biochemical Sciences, 2012, 37, 353-363.	3.7	31
61	A novel, noncanonical mechanism of cytoplasmic polyadenylation operates in <i>Drosophila</i> embryogenesis. Genes and Development, 2010, 24, 129-134.	2.7	30
62	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.	1.8	30
63	BlastRâ€"fast and accurate database searches for non-coding RNAs. Nucleic Acids Research, 2011, 39, 6886-6895.	6.5	28
64	Computing Multiple Sequence/Structure Alignments with the Tâ€Coffee Package. Current Protocols in Bioinformatics, 2010, 29, Unit 3.8.1-25.	25.8	25
65	Large multiple sequence alignments with a root-to-leaf regressive method. Nature Biotechnology, 2019, 37, 1466-1470.	9.4	25
66	STRIKE: evaluation of protein MSAs using a single 3D structure. Bioinformatics, 2011, 27, 3385-3391.	1.8	23
67	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. Nucleic Acids Research, 2012, 40, e52-e52.	6.5	23
68	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. International Journal of Molecular Sciences, 2013, 14, 15423-15458.	1.8	22
69	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. Bioinformatics, 2013, 29, 1112-1119.	1.8	20
70	Predicting phenotypic traits of prokaryotes from protein domain frequencies. BMC Bioinformatics, 2010, 11, 481.	1.2	14
71	PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments. Nucleic Acids Research, 2006, 34, W600-W603.	6.5	13
72	Vertebrate conserved non coding DNA regions have a high persistence length and a short persistence time. BMC Genomics, 2007, 8, 398.	1.2	13

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73	Time‐course and dynamics of obesity‐related behavioral changes induced by energy‐dense foods in mice. Addiction Biology, 2018, 23, 531-543.	1.4	13
74	High Performance computing improvements on bioinformatics consistency-based multiple sequence alignment tools. Parallel Computing, 2015, 42, 18-34.	1.3	12
75	Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. Systematic Biology, 2018, 67, 997-1009.	2.7	12
76	A long noncoding RNA promotes parasite differentiation in African trypanosomes. Science Advances, 2022, 8, .	4.7	12
77	Breen et al. reply. Nature, 2013, 497, E2-E3.	13.7	11
78	Extinction and reinstatement of an operant responding maintained by food in different models of obesity. Addiction Biology, 2018, 23, 544-555.	1.4	11
79	Improving multiple sequence alignment biological accuracy through genetic algorithms. Journal of Supercomputing, 2013, 65, 1076-1088.	2.4	9
80	Exploiting parallelism on progressive alignment methods. Journal of Supercomputing, 2011, 58, 186-194.	2.4	7
81	Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. Bioinformatics, 2021, 37, 1506-1514.	1.8	7
82	Efficient and Interpretable Prediction of Protein Functional Classes by Correspondence Analysis and Compact Set Relations. PLoS ONE, 2013, 8, e75542.	1.1	7
83	Enhancing the Scalability of Consistency-based Progressive Multiple Sequences Alignment Applications. , 2012, , .		6
84	Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. Methods in Molecular Biology, 2021, 2231, 89-97.	0.4	6
85	Computing Multiple Sequence/Structure Alignments with the T‐Coffee Package. Current Protocols in Bioinformatics, 2003, 4, Unit3.8.	25.8	5
86	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.	2.0	5
87	A user-friendly web portal for T-Coffee on supercomputers. BMC Bioinformatics, 2011, 12, 150.	1.2	5
88	Scalability and accuracy improvements of consistency-based multiple sequence alignment tools. , 2013, , .		5
89	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. IScience, 2018, 9, 244-257.	1.9	5
90	Performance analysis of computational approaches to solve Multiple Sequence Alignment. Journal of Supercomputing, 2013, 64, 69-78.	2.4	4

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91	Improving the Alignment Quality of Consistency Based Aligners with an Evaluation Function Using Synonymous Protein Words. PLoS ONE, 2011, 6, e27872.	1.1	4
92	T-RMSD: a web server for automated fine-grained protein structural classification. Nucleic Acids Research, 2013, 41, W358-W362.	6.5	3
93	SARA-Coffee web server, a tool for the computation of RNA sequence and structure multiple alignments. Nucleic Acids Research, 2014, 42, W356-W360.	6.5	3
94	Using Genetic Algorithms for Pairwise and Multiple Sequence Alignments. , 2003, , 87-111.		2
95	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.	6.5	2
96	APDB: a web server to evaluate the accuracy of sequence alignments using structural information. Bioinformatics, 2006, 22, 2439-2440.	1.8	1
97	Recovering accuracy methods for scalable consistency library. Journal of Supercomputing, 2015, 71, 1833-1845.	2.4	1
98	Approaches for containerized scientific workflows in cloud environments with applications in life science. F1000Research, 0, 10, 513.	0.8	1
99	Computing Multiple Sequence Alignment with Template-Based Methods. , 2009, , 54-69.		1
100	Protocol for Measuring Compulsive-like Feeding Behavior in Mice. Bio-protocol, 2019, 9, e3308.	0.2	1