

Cedric Notredame

List of Publications by Citations

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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 | An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74 | 50.4 | 11449 |
| 102 | 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 |
| 101 | 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 |
| 100 | Long noncoding RNAs with enhancer-like function in human cells. <i>Cell</i> , 2010 , 143, 46-58 | 56.2 | 1422 |
| 99 | A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64 | 50.4 | 1026 |
| 98 | 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 |
| 97 | Nextflow enables reproducible computational workflows. <i>Nature Biotechnology</i> , 2017 , 35, 316-319 | 44.5 | 588 |
| 96 | M-Coffee: combining multiple sequence alignment methods with T-Coffee. <i>Nucleic Acids Research</i> , 2006 , 34, 1692-9 | 20.1 | 414 |
| 95 | 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 |
| 94 | 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 |
| 93 | SAGA: sequence alignment by genetic algorithm. <i>Nucleic Acids Research</i> , 1996 , 24, 1515-24 | 20.1 | 285 |
| 92 | 3DCoffee: combining protein sequences and structures within multiple sequence alignments. <i>Journal of Molecular Biology</i> , 2004 , 340, 385-95 | 6.5 | 271 |
| 91 | Epistasis as the primary factor in molecular evolution. <i>Nature</i> , 2012 , 490, 535-8 | 50.4 | 246 |
| 90 | Recent progress in multiple sequence alignment: a survey. <i>Pharmacogenomics</i> , 2002 , 3, 131-44 | 2.6 | 227 |
| 89 | 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 |
| 88 | 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 |
| 87 | Identification of a novel microRNA (miRNA) from rice that targets an alternatively spliced transcript of the Nrmp6 (Natural resistance-associated macrophage protein 6) gene involved in pathogen resistance. <i>New Phytologist</i> , 2013 , 199, 212-227 | 9.8 | 175 |

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| 86 | 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 |
| 85 | 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 |
| 84 | Upcoming challenges for multiple sequence alignment methods in the high-throughput era. <i>Bioinformatics</i> , 2009 , 25, 2455-65 | 7.2 | 153 |
| 83 | Recent evolutions of multiple sequence alignment algorithms. <i>PLoS Computational Biology</i> , 2007 , 3, e123 | 3 | 146 |
| 82 | 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 |
| 81 | 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 |
| 80 | 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 |
| 79 | Accurate multiple sequence alignment of transmembrane proteins with PSI-Coffee. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 4, S1 | 3.6 | 99 |
| 78 | AMPA: an automated web server for prediction of protein antimicrobial regions. <i>Bioinformatics</i> , 2012 , 28, 130-1 | 7.2 | 90 |
| 77 | R-Coffee: a method for multiple alignment of non-coding RNA. <i>Nucleic Acids Research</i> , 2008 , 36, e52 | 20.1 | 88 |
| 76 | Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1009-1023 | 13.4 | 85 |
| 75 | Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016 , 17, 251 | 18.3 | 85 |
| 74 | CaspR: a web server for automated molecular replacement using homology modelling. <i>Nucleic Acids Research</i> , 2004 , 32, W606-9 | 20.1 | 81 |
| 73 | 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 |
| 72 | The impact of Docker containers on the performance of genomic pipelines. <i>PeerJ</i> , 2015 , 3, e1273 | 3.1 | 77 |
| 71 | Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014 , 24, 2077-89 | 9.7 | 74 |
| 70 | Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011 , 12, 552 | 4.5 | 72 |
| 69 | A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019 , 8, | 7.6 | 66 |

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| 68 | 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 |
| 67 | Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015 , 145, 78-179 | 1.9 | 57 |
| 66 | Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015 , 6, 5903 | 17.4 | 56 |
| 65 | 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 |
| 64 | Fibroblast-derived induced pluripotent stem cells show no common retroviral vector insertions. <i>Stem Cells</i> , 2009 , 27, 300-6 | 5.8 | 51 |
| 63 | 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 |
| 62 | R-Coffee: a web server for accurately aligning noncoding RNA sequences. <i>Nucleic Acids Research</i> , 2008 , 36, W10-3 | 20.1 | 51 |
| 61 | How should we measure proportionality on relative gene expression data?. <i>Theory in Biosciences</i> , 2016 , 135, 21-36 | 1.3 | 50 |
| 60 | APDB: a novel measure for benchmarking sequence alignment methods without reference alignments. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i215-21 | 7.2 | 45 |
| 59 | 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 |
| 58 | T-Coffee: Tree-based consistency objective function for alignment evaluation. <i>Methods in Molecular Biology</i> , 2014 , 1079, 117-29 | 1.4 | 41 |
| 57 | Evolutionary Footprints Reveal Insights into Plant MicroRNA Biogenesis. <i>Plant Cell</i> , 2017 , 29, 1248-1261 | 11.6 | 40 |
| 56 | Segment-based multiple sequence alignment. <i>Bioinformatics</i> , 2008 , 24, i187-92 | 7.2 | 39 |
| 55 | 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 |
| 54 | 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 |
| 53 | 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 |
| 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. <i>Frontiers in Behavioral Neuroscience</i> , 2015 , 9, 330 | 3.5 | 32 |
| 51 | TCS: a web server for multiple sequence alignment evaluation and phylogenetic reconstruction. <i>Nucleic Acids Research</i> , 2015 , 43, W3-6 | 20.1 | 30 |

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| 50 | The iRMSD: a local measure of sequence alignment accuracy using structural information. <i>Bioinformatics</i> , 2006 , 22, e35-9 | 7.2 | 29 |
| 49 | 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 |
| 48 | An improved understanding of TNFL/TNFR interactions using structure-based classifications. <i>Trends in Biochemical Sciences</i> , 2012 , 37, 353-63 | 10.3 | 28 |
| 47 | 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 |
| 46 | BlastR--fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , 2011 , 39, 6886-95 | 20.1 | 26 |
| 45 | 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 |
| 44 | Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329 | 7.2 | 25 |
| 43 | 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 |
| 42 | Improved definition of the mouse transcriptome via targeted RNA sequencing. <i>Genome Research</i> , 2016 , 26, 705-16 | 9.7 | 23 |
| 41 | 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 |
| 40 | 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 |
| 39 | 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 |
| 38 | STRIKE: evaluation of protein MSAs using a single 3D structure. <i>Bioinformatics</i> , 2011 , 27, 3385-91 | 7.2 | 17 |
| 37 | 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 |
| 36 | Differential proportionality - a normalization-free approach to differential gene expression | | 15 |
| 35 | 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 |
| 34 | PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments. <i>Nucleic Acids Research</i> , 2006 , 34, W600-3 | 20.1 | 13 |
| 33 | Large multiple sequence alignments with a root-to-leaf regressive method. <i>Nature Biotechnology</i> , 2019 , 37, 1466-1470 | 44.5 | 13 |

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| 32 | 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 |
| 31 | Lessons Learned: Recommendations for Establishing Critical Periodic Scientific Benchmarking | | 12 |
| 30 | High Performance computing improvements on bioinformatics consistency-based multiple sequence alignment tools. <i>Parallel Computing</i> , 2015 , 42, 18-34 | 1 | 9 |
| 29 | 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 |
| 28 | Predicting phenotypic traits of prokaryotes from protein domain frequencies. <i>BMC Bioinformatics</i> , 2010 , 11, 481 | 3.6 | 9 |
| 27 | 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 |
| 26 | Generalized Bootstrap Supports for Phylogenetic Analyses of Protein Sequences Incorporating Alignment Uncertainty. <i>Systematic Biology</i> , 2018 , 67, 997-1009 | 8.4 | 8 |
| 25 | Improving multiple sequence alignment biological accuracy through genetic algorithms. <i>Journal of Supercomputing</i> , 2013 , 65, 1076-1088 | 2.5 | 7 |
| 24 | Breen et al. reply. <i>Nature</i> , 2013 , 497, E2-E3 | 50.4 | 7 |
| 23 | Enhancing the Scalability of Consistency-based Progressive Multiple Sequences Alignment Applications 2012 , | | 5 |
| 22 | 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 |
| 21 | Computing multiple sequence/structure alignments with the T-coffee package. <i>Current Protocols in Bioinformatics</i> , 2004 , Chapter 3, Unit3.8 | 24.2 | 5 |
| 20 | Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. <i>IScience</i> , 2018 , 9, 244-257 | 6.1 | 5 |
| 19 | Scalability and accuracy improvements of consistency-based multiple sequence alignment tools 2013 , | | 4 |
| 18 | Exploiting parallelism on progressive alignment methods. <i>Journal of Supercomputing</i> , 2011 , 58, 186-194 | 2.5 | 4 |
| 17 | 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 |
| 16 | Performance analysis of computational approaches to solve Multiple Sequence Alignment. <i>Journal of Supercomputing</i> , 2013 , 64, 69-78 | 2.5 | 3 |
| 15 | 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 |

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| 14 | T-RMSD: a web server for automated fine-grained protein structural classification. <i>Nucleic Acids Research</i> , 2013 , 41, W358-62 | 20.1 | 3 |
| 13 | 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 |
| 12 | 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 |
| 11 | Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. <i>Bioinformatics</i> , 2019 , | 7.2 | 2 |
| 10 | A field guide for the compositional analysis of any-omics data | | 2 |
| 9 | Recovering accuracy methods for scalable consistency library. <i>Journal of Supercomputing</i> , 2015 , 71, 1833-1845 | 13.45 | 1 |
| 8 | A user-friendly web portal for T-Coffee on supercomputers. <i>BMC Bioinformatics</i> , 2011 , 12, 150 | 3.6 | 1 |
| 7 | APDB: a web server to evaluate the accuracy of sequence alignments using structural information. <i>Bioinformatics</i> , 2006 , 22, 2439-40 | 7.2 | 1 |
| 6 | Fast and accurate large multiple sequence alignments using root-to-leave regressive computation | | 1 |
| 5 | Four layer multi-omics reveals molecular responses to aneuploidy in Leishmania | | 1 |
| 4 | Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. <i>Methods in Molecular Biology</i> , 2021 , 2231, 89-97 | 1.4 | 1 |
| 3 | Approaches for containerized scientific workflows in cloud environments with applications in life science. <i>F1000Research</i> , 10, 513 | 3.6 | 0 |
| 2 | Using Genetic Algorithms for Pairwise and Multiple Sequence Alignments 2003 , 87-111 | | |
| 1 | Protocol for Measuring Compulsive-like Feeding Behavior in Mice. <i>Bio-protocol</i> , 2019 , 9, e3308 | 0.9 | |