

Marc A MartÃ-â€renom

List of Publications by Year in descending order

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129
papers

17,303
citations

41344

49
h-index

16183

124
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156
all docs

156
docs citations

156
times ranked

26885
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Protein Structure Modeling Using Modeller. <i>Current Protocols in Bioinformatics</i> , 2006, 15, Unit-5.6.	25.8	2,858
2	Comparative Protein Structure Modeling of Genes and Genomes. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2000, 29, 291-325.	18.3	2,811
3	Vanilloid Receptor-Related Osmotically Activated Channel (VR-OAC), a Candidate Vertebrate Osmoreceptor. <i>Cell</i> , 2000, 103, 525-535.	28.9	1,237
4	Comparative Protein Structure Modeling Using MODELLER. <i>Current Protocols in Protein Science</i> , 2007, 50, Unit 2.9.	2.8	1,056
5	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. <i>Nature Reviews Genetics</i> , 2013, 14, 390-403.	16.3	963
6	Tools for comparative protein structure modeling and analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3375-3380.	14.5	406
7	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. <i>Nature Genetics</i> , 2018, 50, 238-249.	21.4	295
8	The three-dimensional folding of the β -globin gene domain reveals formation of chromatin globules. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 107-114.	8.2	274
9	Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation. <i>Genes and Development</i> , 2014, 28, 2151-2162.	5.9	270
10	MODBASE: a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2006, 34, D291-D295.	14.5	265
11	MODBASE, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2004, 32, 217D-222.	14.5	256
12	Automatic analysis and 3D-modelling of Hi-C data using TADbit reveals structural features of the fly chromatin colors. <i>PLoS Computational Biology</i> , 2017, 13, e1005665.	3.2	252
13	The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation. <i>Molecular Cell</i> , 2011, 44, 252-264.	9.7	249
14	Walking along chromosomes with super-resolution imaging, contact maps, and integrative modeling. <i>PLoS Genetics</i> , 2018, 14, e1007872.	3.5	209
15	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. <i>Nature Genetics</i> , 2019, 51, 1137-1148.	21.4	208
16	Protein structure modeling for structural genomics. <i>Nature Structural Biology</i> , 2000, 7, 986-990.	9.7	199
17	Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.	27.0	195
18	EVA: continuous automatic evaluation of protein structure prediction servers. <i>Bioinformatics</i> , 2001, 17, 1242-1243.	4.1	187

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19	Alignment of protein sequences by their profiles. <i>Protein Science</i> , 2004, 13, 1071-1087.	7.6	184
20	A composite score for predicting errors in protein structure models. <i>Protein Science</i> , 2006, 15, 1653-1666.	7.6	160
21	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
22	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
23	EVA: evaluation of protein structure prediction servers. <i>Nucleic Acids Research</i> , 2003, 31, 3311-3315.	14.5	154
24	MODBASE, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2009, 37, D347-D354.	14.5	154
25	Use of Single Point Mutations in Domain I of β 2-Glycoprotein I to Determine Fine Antigenic Specificity of Antiphospholipid Autoantibodies. <i>Journal of Immunology</i> , 2002, 169, 7097-7103.	0.8	137
26	Single-cell absolute contact probability detection reveals chromosomes are organized by multiple low-frequency yet specific interactions. <i>Nature Communications</i> , 2017, 8, 1753.	12.8	137
27	Distinct roles of cohesin-SA1 and cohesin-SA2 in 3D chromosome organization. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 496-504.	8.2	128
28	Promoter bivalency favors an open chromatin architecture in embryonic stem cells. <i>Nature Genetics</i> , 2018, 50, 1452-1462.	21.4	113
29	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. <i>Cell Reports</i> , 2019, 28, 352-367.e9.	6.4	112
30	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
31	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. <i>Molecular Cell</i> , 2020, 78, 522-538.e9.	9.7	107
32	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. <i>Journal of Molecular Biology</i> , 2006, 357, 1655-1668.	4.2	104
33	Structure-Based Assessment of Missense Mutations in Human BRCA1. <i>Cancer Research</i> , 2004, 64, 3790-3797.	0.9	103
34	3D mapping and accelerated super-resolution imaging of the human genome using in situ sequencing. <i>Nature Methods</i> , 2020, 17, 822-832.	19.0	99
35	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. <i>Nature Genetics</i> , 2020, 52, 655-661.	21.4	98
36	Reliability of Assessment of Protein Structure Prediction Methods. <i>Structure</i> , 2002, 10, 435-440.	3.3	95

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37	Restraint-based three-dimensional modeling of genomes and genomic domains. <i>FEBS Letters</i> , 2015, 589, 2987-2995.	2.8	93
38	The C-type lectin fold as an evolutionary solution for massive sequence variation. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 886-892.	8.2	92
39	Genome structure determination via 3C-based data integration by the Integrative Modeling Platform. <i>Methods</i> , 2012, 58, 300-306.	3.8	83
40	Alignment of multiple protein structures based on sequence and structure features. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 569-574.	2.1	82
41	Defined chromosome structure in the genome-reduced bacterium <i>Mycoplasma pneumoniae</i> . <i>Nature Communications</i> , 2017, 8, 14665.	12.8	81
42	Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization. <i>PLoS Computational Biology</i> , 2011, 7, e1002125.	3.2	76
43	Chromatin and RNA Maps Reveal Regulatory Long Noncoding RNAs in Mouse. <i>Molecular and Cellular Biology</i> , 2016, 36, 809-819.	2.3	75
44	All-atom knowledge-based potential for RNA structure prediction and assessment. <i>Bioinformatics</i> , 2011, 27, 1086-1093.	4.1	71
45	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. <i>Nature Communications</i> , 2021, 12, 651.	12.8	67
46	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. <i>Nucleic Acids Research</i> , 2015, 43, 3465-3477.	14.5	66
47	Lamin B1 mapping reveals the existence of dynamic and functional euchromatin lamin B1 domains. <i>Nature Communications</i> , 2018, 9, 3420.	12.8	66
48	Structure-based statistical analysis of transmembrane helices. <i>European Biophysics Journal</i> , 2013, 42, 199-207.	2.2	65
49	Chromatin globules: a common motif of higher order chromosome structure?. <i>Current Opinion in Cell Biology</i> , 2011, 23, 325-331.	5.4	63
50	Impact of <i>fgd1</i> and <i>ddn</i> Diversity in Mycobacterium tuberculosis Complex on <i>In Vitro</i> Susceptibility to PA-824. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5718-5722.	3.2	60
51	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. <i>Cell Reports</i> , 2019, 27, 3500-3510.e4.	6.4	60
52	Variable gap penalty for protein sequence-structure alignment. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 129-133.	2.1	58
53	<i>N</i> -glycosylation efficiency is determined by the distance to the C-terminus and the amino acid preceding an Ser-Thr sequon. <i>Protein Science</i> , 2011, 20, 179-186.	7.6	57
54	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. <i>PLoS Computational Biology</i> , 2007, 3, e178.	3.2	51

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55	Target Prediction for an Open Access Set of Compounds Active against Mycobacterium tuberculosis. PLoS Computational Biology, 2013, 9, e1003253.	3.2	51
56	OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes. Nucleic Acids Research, 2018, 46, e49-e49.	14.5	50
57	DBAli: a database of protein structure alignments. Bioinformatics, 2001, 17, 746-747.	4.1	49
58	Challenges and guidelines toward 4D nucleome data and model standards. Nature Genetics, 2018, 50, 1352-1358.	21.4	47
59	RNA structure alignment by a unit-vector approach. Bioinformatics, 2008, 24, i112-i118.	4.1	46
60	Accuracy of sequence alignment and fold assessment using reduced amino acid alphabets. Proteins: Structure, Function and Bioinformatics, 2006, 63, 986-995.	2.6	44
61	Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs. Nature Communications, 2020, 11, 2564.	12.8	41
62	Structure determination of genomic domains by satisfaction of spatial restraints. Chromosome Research, 2011, 19, 25-35.	2.2	39
63	Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. BMC Bioinformatics, 2010, 11, 322.	2.6	38
64	Release of 50 new, drug-like compounds and their computational target predictions for open source anti-tubercular drug discovery. PLoS ONE, 2015, 10, e0142293.	2.5	38
65	Use of estimated evolutionary strength at the codon level improves the prediction of disease-related protein mutations in humans. Human Mutation, 2008, 29, 198-204.	2.5	37
66	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
67	A Novel Family of Soluble Minimal Scaffolds Provides Structural Insight into the Catalytic Domains of Integral Membrane Metallopeptidases. Journal of Biological Chemistry, 2013, 288, 21279-21294.	3.4	35
68	Protein similarities beyond disulphide bridge topology. Journal of Molecular Biology, 1998, 284, 541-548.	4.2	34
69	4D nucleome modeling. Current Opinion in Genetics and Development, 2021, 67, 25-32.	3.3	34
70	The impact of chromosomal fusions on 3D genome folding and recombination in the germ line. Nature Communications, 2021, 12, 2981.	12.8	34
71	Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization in <i>Arabidopsis thaliana</i> . Nucleic Acids Research, 2021, 49, 1840-1858.	14.5	34
72	SARA: a server for function annotation of RNA structures. Nucleic Acids Research, 2009, 37, W260-W265.	14.5	33

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73	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , 2015, 13, 1855-1867.	6.4	33
74	Membrane protein integration into the endoplasmic reticulum. <i>FEBS Journal</i> , 2011, 278, 3846-3858.	4.7	32
75	CHESS enables quantitative comparison of chromatin contact data and automatic feature extraction. <i>Nature Genetics</i> , 2020, 52, 1247-1255.	21.4	32
76	RNA proximity sequencing reveals the spatial organization of the transcriptome in the nucleus. <i>Nature Biotechnology</i> , 2019, 37, 793-802.	17.5	30
77	Muscle progenitor specification and myogenic differentiation are associated with changes in chromatin topology. <i>Nature Communications</i> , 2020, 11, 6222.	12.8	28
78	Prediction of enzyme function by combining sequence similarity and protein interactions. <i>BMC Bioinformatics</i> , 2008, 9, 249.	2.6	27
79	Detecting remotely related proteins by their interactions and sequence similarity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7151-7156.	7.1	26
80	DBAli tools: mining the protein structure space. <i>Nucleic Acids Research</i> , 2007, 35, W393-W397.	14.5	25
81	Polar/Ionizable Residues in Transmembrane Segments: Effects on Helix-Helix Packing. <i>PLoS ONE</i> , 2012, 7, e44263.	2.5	24
82	A Kernel for Open Source Drug Discovery in Tropical Diseases. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e418.	3.0	23
83	On the demultiplexing of chromosome capture conformation data. <i>FEBS Letters</i> , 2015, 589, 3005-3013.	2.8	23
84	Protein translocation into peroxisomes by ring-shaped import receptors. <i>FEBS Letters</i> , 2007, 581, 4795-4802.	2.8	22
85	Hierarchical chromatin organization detected by TADpole. <i>Nucleic Acids Research</i> , 2020, 48, e39-e39.	14.5	22
86	Open Source Research – the Power of Us. <i>Australian Journal of Chemistry</i> , 2006, 59, 291.	0.9	21
87	Localization of binding sites in protein structures by optimization of a composite scoring function. <i>Protein Science</i> , 2006, 15, 2366-2380.	7.6	21
88	Using tertiary structure for the computation of highly accurate multiple RNA alignments with the SARA-Coffee package. <i>Bioinformatics</i> , 2013, 29, 1112-1119.	4.1	20
89	ModView, visualization of multiple protein sequences and structures. <i>Bioinformatics</i> , 2003, 19, 165-166.	4.1	18
90	Biological insertion of computationally designed short transmembrane segments. <i>Scientific Reports</i> , 2016, 6, 23397.	3.3	18

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91	Three-dimensional genome organization via triplex-forming RNAs. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 945-954.	8.2	18
92	Classification of protein disulphide-bridge topologies. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 477-487.	2.9	16
93	Ligand-Target Prediction by Structural Network Biology Using nAnnoLyze. <i>PLoS Computational Biology</i> , 2015, 11, e1004157.	3.2	16
94	Comparative Protein Structure Modeling. , 2005, , 831-860.		15
95	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. <i>Genome Medicine</i> , 2021, 13, 15.	8.2	15
96	ModLink+: improving fold recognition by using protein-protein interactions. <i>Bioinformatics</i> , 2009, 25, 1506-1512.	4.1	14
97	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2021, 49, 11005-11021.	14.5	14
98	Identification of chromatin loops from Hi-C interaction matrices by CTCF-CTCF topology classification. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac021.	3.2	13
99	Binless normalization of Hi-C data provides significant interaction and difference detection independent of resolution. <i>Nature Communications</i> , 2019, 10, 1938.	12.8	12
100	<sc>3D</sc> modeling of chromatin structure: is there a way to integrate and reconcile single cell and population experimental data?. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2017, 7, e1308.	14.6	11
101	Rational design of non-resistant targeted cancer therapies. <i>Scientific Reports</i> , 2017, 7, 46632.	3.3	11
102	Challenges for visualizing three-dimensional data in genomic browsers. <i>FEBS Letters</i> , 2017, 591, 2505-2519.	2.8	11
103	TADs enriched in histone H1.2 strongly overlap with the B compartment, inaccessible chromatin, and AT-rich Giemsa bands. <i>FEBS Journal</i> , 2021, 288, 1989-2013.	4.7	10
104	Coordinated changes in gene expression, H1 variant distribution and genome 3D conformation in response to H1 depletion. <i>Nucleic Acids Research</i> , 2022, 50, 3892-3910.	14.5	10
105	Impact of Chromosome Fusions on 3D Genome Organization and Gene Expression in Budding Yeast. <i>Genetics</i> , 2020, 214, 651-667.	2.9	9
106	Refinement of modelled structures by knowledge-based energy profiles and secondary structure prediction: application to the human procarboxypeptidase A2. <i>Journal of Computer-Aided Molecular Design</i> , 2000, 14, 83-92.	2.9	8
107	Structures of scrambled disulfide forms of the potato carboxypeptidase inhibitor predicted by molecular dynamics simulations with constraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 482-493.	2.6	7
108	Evolutionary potentials: structure specific knowledge-based potentials exploiting the evolutionary record of sequence homologs. <i>Genome Biology</i> , 2008, 9, R68.	9.6	7

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109	A kernel for the Tropical Disease Initiative. <i>Nature Biotechnology</i> , 2009, 27, 320-321.	17.5	7
110	Comparative Protein Structure Prediction. <i>Current Protocols in Protein Science</i> , 2002, 28, 2.9.1-2.9.22.	2.8	6
111	Modeling Protein Structure from its Sequence. <i>Current Protocols in Bioinformatics</i> , 2003, 3, 5.1.1.	25.8	6
112	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. <i>GigaScience</i> , 2020, 9, .	6.4	6
113	Software for predicting the <scp>3D</scp> structure of <scp>RNA</scp> molecules. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2015, 5, 56-61.	14.6	5
114	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. <i>Leukemia</i> , 2022, 36, 583-587.	7.2	5
115	Statistical Analysis of the Loop-Geometry on a Non-Redundant Database of Proteins. <i>Journal of Molecular Modeling</i> , 1998, 4, 347-354.	1.8	4
116	Effects of counter-ions and volume on the simulated dynamics of solvated proteins. Application to the activation domain of procarboxypeptidase B. <i>Protein Engineering, Design and Selection</i> , 1998, 11, 881-890.	2.1	4
117	Should network biology be used for drug discovery?. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 1135-1137.	5.0	4
118	Parallel sequencing lives, or what makes large sequencing projects successful. <i>GigaScience</i> , 2017, 6, 1-6.	6.4	4
119	Communicating Genome Architecture: Biovisualization of the Genome, from Data Analysis and Hypothesis Generation to Communication and Learning. <i>Journal of Molecular Biology</i> , 2019, 431, 1071-1087.	4.2	3
120	TADs without borders. <i>Nature Genetics</i> , 2020, 52, 752-753.	21.4	3
121	Benchmarking experiments with polymer modeling. <i>Nature Methods</i> , 2021, 18, 456-457.	19.0	3
122	3D reconstruction of genomic regions from sparse interaction data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab017.	3.2	2
123	Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments. <i>Methods in Molecular Biology</i> , 2021, 2157, 35-63.	0.9	2
124	ASAP: analysis of peptide composition. <i>Bioinformatics</i> , 2000, 16, 1153-1154.	4.1	1
125	Restraint-Based Modeling of Genomes and Genomic Domains. , 2019, , 233-252.		1
126	In vivo temporal resolution of acute promyelocytic leukemia progression reveals a role of <i>Klf4</i> in suppressing early leukemic transformation. <i>Genes and Development</i> , 2022, 36, 451-467.	5.9	1

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127	Reply to Moulton et al.. Structure, 2002, 10, 292-293.	3.3	0
128	Aberrant Expression of the SOX11 Oncogene in Mantle Cell Lymphoma Is Associated with Activation and De Novo 3D Looping of a Distant Enhancer Element. Blood, 2016, 128, 459-459.	1.4	0
129	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. SSRN Electronic Journal, 0, , .	0.4	0