Marc A MartÃ-â€renom

List of Publications by Year
in descending order

129 papers	17,303 citations	41344 49 h-index	16183 124 g-index
156 all docs	156 docs citations	156 times ranked	26885 citing authors

#	Article	IF	Citations
1	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. Leukemia, 2022, 36, 583-587.	7.2	5
2	Identification of chromatin loops from Hi-C interaction matrices by CTCFâ€“CTCF topology classification. NAR Genomics and Bioinformatics, 2022, 4, lqac021.	3.2	13
3	Coordinated changes in gene expression, H1 variant distribution and genome 3D conformation in response to H1 depletion. Nucleic Acids Research, 2022, 50, 3892-3910.	14.5	10
4	In vivo temporal resolution of acute promyelocytic leukemia progression reveals a role of Klf4 in suppressing early leukemic transformation. Genes and Development, 2022, 36, 451-467.	5.9	1
5	TADs enriched in histone H1.2 strongly overlap with the B compartment, inaccessible chromatin, and ATâ€rich Giemsa bands. FEBS Journal, 2021, 288, 1989-2013.	4.7	10
6	4D nucleome modeling. Current Opinion in Genetics and Development, 2021, 67, 25-32.	3.3	34
7	OUP accepted manuscript. Nucleic Acids Research, 2021, 49, 11005-11021.	14.5	14
8	3D reconstruction of genomic regions from sparse interaction data. NAR Genomics and Bioinformatics, 2021, 3, lqab017.	3.2	2
9	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature Communications, 2021, 12, 651.	12.8	67
10	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. Genome Medicine, 2021, 13, 15.	8.2	15
11	Benchmarking experiments with polymer modeling. Nature Methods, 2021, 18, 456-457.	19.0	3
12	The impact of chromosomal fusions on 3D genome folding and recombination in the germ line. Nature Communications, 2021, 12, 2981.	12.8	34
13	Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization inArabidopsis thaliana. Nucleic Acids Research, 2021, 49, 1840-1858.	14.5	34
14	Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments. Methods in Molecular Biology, 2021, 2157, 35-63.	0.9	2
15	Three-dimensional genome organization via triplex-forming RNAs. Nature Structural and Molecular Biology, 2021, 28, 945-954.	8.2	18
16	CHESS enables quantitative comparison of chromatin contact data and automatic feature extraction. Nature Genetics, 2020, 52, 1247-1255.	21.4	32
17	Muscle progenitor specification and myogenic differentiation are associated with changes in chromatin topology. Nature Communications, 2020, 11, 6222.	12.8	28
18	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108

#	Article	IF	Citations
19	TADs without borders. Nature Genetics, 2020, 52, 752-753.	21.4	3
20	3D mapping and accelerated super-resolution imaging of the human genome using in situ sequencing. Nature Methods, 2020, 17, 822-832.	19.0	99
21	Hi-C chromosome conformation capture sequencing of avian genomes using the BGISEQ-500 platform. GigaScience, 2020, 9, .	6.4	6
22	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. Nature Genetics, 2020, 52, 655-661.	21.4	98
23	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. Molecular Cell, 2020, 78, 522-538.e9.	9.7	107
24	Hierarchical chromatin organization detected by TADpole. Nucleic Acids Research, 2020, 48, e39-e39.	14.5	22
25	Impact of Chromosome Fusions on 3D Genome Organization and Gene Expression in Budding Yeast. Genetics, 2020, 214, 651-667.	2.9	9
26	Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs. Nature Communications, 2020, 11, 2564.	12.8	41
27	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. Cell Reports, 2019, 28, 352-367.e9.	6.4	112
28	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. Nature Genetics, 2019, 51, 1137-1148.	21.4	208
29	RNA proximity sequencing reveals the spatial organization of the transcriptome in the nucleus. Nature Biotechnology, 2019, 37, 793-802.	17.5	30
30	Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells. Cell Reports, 2019, 27, 3500-3510.e4.	6.4	60
31	Binless normalization of Hi-C data provides significant interaction and difference detection independent of resolution. Nature Communications, 2019, 10, 1938.	12.8	12
32	Communicating Genome Architecture: Biovisualization of the Genome, from Data Analysis and Hypothesis Generation to Communication and Learning. Journal of Molecular Biology, 2019, 431, 1071-1087.	4.2	3
33	Restraint-Based Modeling of Genomes and Genomic Domains. , 2019, , 233-252.		1
34	OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes. Nucleic Acids Research, 2018, 46, e49-e49.	14.5	50
35	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	21.4	295
36	Walking along chromosomes with super-resolution imaging, contact maps, and integrative modeling. PLoS Genetics, 2018, 14, e1007872.	3.5	209

#	Article	IF	Citations
37	Challenges and guidelines toward 4D nucleome data and model standards. Nature Genetics, 2018, 50, 1352-1358.	21.4	47
38	Promoter bivalency favors an open chromatin architecture in embryonic stem cells. Nature Genetics, 2018, 50, 1452-1462.	21.4	113
39	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
40	Lamin B1 mapping reveals the existence of dynamic and functional euchromatin lamin B1 domains. Nature Communications, 2018, 9, 3420.	12.8	66
41	Distinct roles of cohesin-SA1 and cohesin-SA2 in 3D chromosome organization. Nature Structural and Molecular Biology, 2018, 25, 496-504.	8.2	128
42	Defined chromosome structure in the genome-reduced bacterium Mycoplasma pneumoniae. Nature Communications, 2017, 8, 14665.	12.8	81
43	<scp>3D</scp> modeling of chromatin structure: is there a way to integrate and reconcile single cell and population experimental data?. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2017, 7, e1308.	14.6	11
44	Rational design of non-resistant targeted cancer therapies. Scientific Reports, 2017, 7, 46632.	3.3	11
45	Challenges for visualizing threeâ€dimensional data in genomic browsers. FEBS Letters, 2017, 591, 2505-2519.	2.8	11
46	Single-cell absolute contact probability detection reveals chromosomes are organized by multiple low-frequency yet specific interactions. Nature Communications, 2017, 8, 1753.	12.8	137
47	Parallel sequencing lives, or what makes large sequencing projects successful. GigaScience, 2017, 6, 1-6.	6.4	4
48	Automatic analysis and 3D-modelling of Hi-C data using TADbit reveals structural features of the fly chromatin colors. PLoS Computational Biology, 2017, 13, e1005665.	3.2	252
49	Biological insertion of computationally designed short transmembrane segments. Scientific Reports, 2016, 6, 23397.	3.3	18
50	Should network biology be used for drug discovery?. Expert Opinion on Drug Discovery, 2016, 11, 1135-1137.	5.0	4
51	Chromatin and RNA Maps Reveal Regulatory Long Noncoding RNAs in Mouse. Molecular and Cellular Biology, 2016, 36, 809-819.	2.3	75
52	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
53	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. Cell Reports, 2015, 13, 1855-1867.	6.4	33
54	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

#	Article	IF	Citations
55	On the demultiplexing of chromosome capture conformation data. FEBS Letters, 2015, 589, 3005-3013.	2.8	23
56	Ligand-Target Prediction by Structural Network Biology Using nAnnoLyze. PLoS Computational Biology, 2015, 11, e1004157.	3.2	16
57	Restraintâ€based threeâ€dimensional modeling of genomes and genomic domains. FEBS Letters, 2015, 589, 2987-2995.	2.8	93
58	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
59	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. Nucleic Acids Research, 2015, 43, 3465-3477.	14.5	66
60	Software for predicting the <scp>3D</scp> structure of <scp>RNA</scp> molecules. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2015, 5, 56-61.	14.6	5
61	Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation. Genes and Development, 2014, 28, 2151-2162.	5.9	270
62	Structure-based statistical analysis of transmembrane helices. European Biophysics Journal, 2013, 42, 199-207.	2.2	65
63	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
64	Whole-Genome Sequencing for Rapid Susceptibility Testing of M. tuberculosis. New England Journal of Medicine, 2013, 369, 290-292.	27.0	195
65	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. Nature Reviews Genetics, 2013, 14, 390-403.	16.3	963
66	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
67	Target Prediction for an Open Access Set of Compounds Active against Mycobacterium tuberculosis. PLoS Computational Biology, 2013, 9, e1003253.	3.2	51
68	Genome structure determination via 3C-based data integration by the Integrative Modeling Platform. Methods, 2012, 58, 300-306.	3.8	83
69	Polar/Ionizable Residues in Transmembrane Segments: Effects on Helix-Helix Packing. PLoS ONE, 2012, 7, e44263.	2.5	24
70	The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation. Molecular Cell, 2011, 44, 252-264.	9.7	249
71	Membrane protein integration into the endoplasmic reticulum. FEBS Journal, 2011, 278, 3846-3858.	4.7	32
72	The three-dimensional folding of the Î±-globin gene domain reveals formation of chromatin globules. Nature Structural and Molecular Biology, 2011, 18, 107-114.	8.2	274

#	Article	IF	Citations
73	Chromatin globules: a common motif of higher order chromosome structure?. Current Opinion in Cell Biology, 2011, 23, 325-331.	5.4	63
74	Structure determination of genomic domains by satisfaction of spatial restraints. Chromosome Research, 2011, 19, 25-35.	2.2	39
75	Nâ€glycosylation efficiency is determined by the distance to the Câ€terminus and the amino acid preceding an Asnâ€Serâ€Thr sequon. Protein Science, 2011, 20, 179-186.	7.6	57
76	Impact of fgd1 and ddn Diversity in Mycobacterium tuberculosis Complex on In Vitro Susceptibility to PA-824. Antimicrobial Agents and Chemotherapy, 2011, 55, 5718-5722.	3.2	60
77	All-atom knowledge-based potential for RNA structure prediction and assessment. Bioinformatics, 2011, 27, 1086-1093.	4.1	71
78	Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization. PLoS Computational Biology, 2011, 7, e1002125.	3.2	76
79	Quantifying the relationship between sequence and three-dimensional structure conservation in RNA. BMC Bioinformatics, 2010, 11, 322.	2.6	38
80	SARA: a server for function annotation of RNA structures. Nucleic Acids Research, 2009, 37, W260-W265.	14.5	33
81	MODBASE, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2009, 37, D347-D354.	14.5	154
82	ModLink+: improving fold recognition by using proteinâ€“protein interactions. Bioinformatics, 2009, 25, 1506-1512.	4.1	14
83	A Kernel for Open Source Drug Discovery in Tropical Diseases. PLoS Neglected Tropical Diseases, 2009, 3, e418.	3.0	23
84	Alignment of multiple protein structures based on sequence and structure features. Protein Engineering, Design and Selection, 2009, 22, 569-574.	2.1	82
85	A kernel for the Tropical Disease Initiative. Nature Biotechnology, 2009, 27, 320-321.	17.5	7
86	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
87	Prediction of enzyme function by combining sequence similarity and protein interactions. BMC Bioinformatics, 2008, 9, 249.	2.6	27
88	Evolutionary potentials: structure specific knowledge-based potentials exploiting the evolutionary record of sequence homologs. Genome Biology, 2008, 9, R68.	9.6	7
89	RNA structure alignment by a unit-vector approach. Bioinformatics, 2008, 24, i112-i118.	4.1	46
90	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. PLoS Computational Biology, 2007, 3, e178.	3.2	51

#	Article	IF	Citations
91	DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397.	14.5	25
92	Protein translocation into peroxisomes by ringâ€shaped import receptors. FEBS Letters, 2007, 581, 4795-4802.	2.8	22
93	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
94	Comparative Protein Structure Modeling Using MODELLER. Current Protocols in Protein Science, 2007, 50, Unit 2.9.	2.8	1,056
95	Variable gap penalty for protein sequenceâ€“structure alignment. Protein Engineering, Design and Selection, 2006, 19, 129-133.	2.1	58
96	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
97	Refinement of Protein Structures by Iterative Comparative Modeling and CryoEM Density Fitting. Journal of Molecular Biology, 2006, 357, 1655-1668.	4.2	104
98	Open Source Research â€” the Power of Us. Australian Journal of Chemistry, 2006, 59, 291.	0.9	21
99	Accuracy of sequence alignment and fold assessment using reduced amino acid alphabets. Proteins: Structure, Function and Bioinformatics, 2006, 63, 986-995.	2.6	44
100	A composite score for predicting errors in protein structure models. Protein Science, 2006, 15, 1653-1666.	7.6	160
101	Localization of binding sites in protein structures by optimization of a composite scoring function. Protein Science, 2006, 15, 2366-2380.	7.6	21
102	MODBASE: a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2006, 34, D291-D295.	14.5	265
103	Comparative Protein Structure Modeling. , 2005, , 831-860.		15
104	The C-type lectin fold as an evolutionary solution for massive sequence variation. Nature Structural and Molecular Biology, 2005, 12, 886-892.	8.2	92
105	Detecting remotely related proteins by their interactions and sequence similarity. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7151-7156.	7.1	26
106	Structure-Based Assessment of Missense Mutations in Human BRCA1. Cancer Research, 2004, 64, 3790-3797.	0.9	103
107	Alignment of protein sequences by their profiles. Protein Science, 2004, 13, 1071-1087.	7.6	184
108	MODBASE, a database of annotated comparative protein structure models, and associated resources. Nucleic Acids Research, 2004, 32, 217D-222.	14.5	256

#	Article	IF	Citations
109	Modeling Protein Structure from its Sequence. Current Protocols in Bioinformatics, 2003, 3, 5.1.1.	25.8	6
110	Tools for comparative protein structure modeling and analysis. Nucleic Acids Research, 2003, 31, 3375-3380.	14.5	406
111	EVA: evaluation of protein structure prediction servers. Nucleic Acids Research, 2003, 31, 3311-3315.	14.5	154
112	ModView, visualization of multiple protein sequences and structures. Bioinformatics, 2003, 19, 165-166.	4.1	18
113	Use of Single Point Mutations in Domain I of Î²2-Glycoprotein I to Determine Fine Antigenic Specificity of Antiphospholipid Autoantibodies. Journal of Immunology, 2002, 169, 7097-7103.	0.8	137
114	Comparative Protein Structure Prediction. Current Protocols in Protein Science, 2002, 28, 2.9.1-2.9.22.	2.8	6
115	Reply to Moult et al.. Structure, 2002, 10, 292-293.	3.3	0
116	Reliability of Assessment of Protein Structure Prediction Methods. Structure, 2002, 10, 435-440.	3.3	95
117	Classification of protein disulphide-bridge topologies. Journal of Computer-Aided Molecular Design, 2001, 15, 477-487.	2.9	16
118	EVA: continuous automatic evaluation of protein structure prediction servers. Bioinformatics, 2001, 17, 1242-1243.	4.1	187
119	DBAli: a database of protein structure alignments. Bioinformatics, 2001, 17, 746-747.	4.1	49
120	Structures of scrambled disulfide forms of the potato carboxypeptidase inhibitor predicted by molecular dynamics simulations with constraints. Proteins: Structure, Function and Bioinformatics, 2000, 40, 482-493.	2.6	7
121	Protein structure modeling for structural genomics. Nature Structural Biology, 2000, 7, 986-990.	9.7	199
122	Refinement of modelled structures by knowledge-based energy profiles and secondary structure prediction: application to the human procarboxypeptidase A2. Journal of Computer-Aided Molecular Design, 2000, 14, 83-92.	2.9	8
123	Comparative Protein Structure Modeling of Genes and Genomes. Annual Review of Biophysics and Biomolecular Structure, 2000, 29, 291-325.	18.3	2,811
124	ASAP: analysis of peptide composition. Bioinformatics, 2000, 16, 1153-1154.	4.1	1
125	Vanilloid Receptorâ€“Related Osmotically Activated Channel (VR-OAC), a Candidate Vertebrate Osmoreceptor. Cell, 2000, 103, 525-535.	28.9	1,237
126	Statistical Analysis of the Loop-Geometry on a Non-Redundant Database of Proteins. Journal of Molecular Modeling, 1998, 4, 347-354.	1.8	4

#	Article	IF	Citations
127	Protein similarities beyond disulphide bridge topology. Journal of Molecular Biology, 1998, 284, 541-548.	4.2	34
128	Effects of counter-ions and volume on the simulated dynamics of solvated proteins. Application to the activation domain of procarboxypeptidase B. Protein Engineering, Design and Selection, 1998, 11, 881-890.	2.1	4
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