

# Franu00e7ois Jose Serra

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

3,573  
citations

516710

16  
h-index

580821

25  
g-index

34  
all docs

34  
docs citations

34  
times ranked

7876  
citing authors

#	ARTICLE	IF	CITATIONS
1	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1635-1638.	8.9	1,692
2	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
3	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
4	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
5	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011, 39, W470-W474.	14.5	182
6	Role of tomato <i>BRANCHED1</i> -like genes in the control of shoot branching. <i>Plant Journal</i> , 2011, 67, 701-714.	5.7	179
7	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
8	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. <i>Molecular Cell</i> , 2020, 78, 522-538.e9.	9.7	107
9	Restraint-based three-dimensional modeling of genomes and genomic domains. <i>FEBS Letters</i> , 2015, 589, 2987-2995.	2.8	93
10	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
11	Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs. <i>Nature Communications</i> , 2020, 11, 2564.	12.8	41
12	Evolution of the biosynthesis of diacylglycerol inositol phosphate, a marker of adaptation to hot marine environments. <i>Environmental Microbiology</i> , 2012, 14, 691-701.	3.8	28
13	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , 2011, 12, 55.	2.8	27
14	Evolutionary Genomics of Genes Involved in Olfactory Behavior in the <i>Drosophila melanogaster</i> Species Group. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8484.	1.2	24
15	Selective constraints on protamine 2 in primates and rodents. <i>BMC Evolutionary Biology</i> , 2016, 16, 21.	3.2	20
16	Sexual Selection Halts the Relaxation of Protamine 2 among Rodents. <i>PLoS ONE</i> , 2011, 6, e29247.	2.5	17
17	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2021, 49, 11005-11021.	14.5	14
18	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

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19	Natural Selection on Functional Modules, a Genome-Wide Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001093.	3.2	12
20	Positive Selection in Nucleoporins Challenges Constraints on Early Expressed Genes in <i>Drosophila</i> Development. <i>Genome Biology and Evolution</i> , 2013, 5, 2231-2241.	2.5	11
21	<scp>3D</scp> 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
22	Neutral Theory Predicts the Relative Abundance and Diversity of Genetic Elements in a Broad Array of Eukaryotic Genomes. <i>PLoS ONE</i> , 2013, 8, e63915.	2.5	10
23	Parallel sequencing lives, or what makes large sequencing projects successful. <i>GigaScience</i> , 2017, 6, 1-6.	6.4	4
24	Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments. <i>Methods in Molecular Biology</i> , 2021, 2157, 35-63.	0.9	2
25	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. <i>Genome Biology and Evolution</i> , 2015, 7, 1490-1505.	2.5	1
26	Aberrant Expression of the SOX11 Oncogene in Mantle Cell Lymphoma Is Associated with Activation and De Novo 3D Looping of a Distant Enhancer Element. <i>Blood</i> , 2016, 128, 459-459.	1.4	0