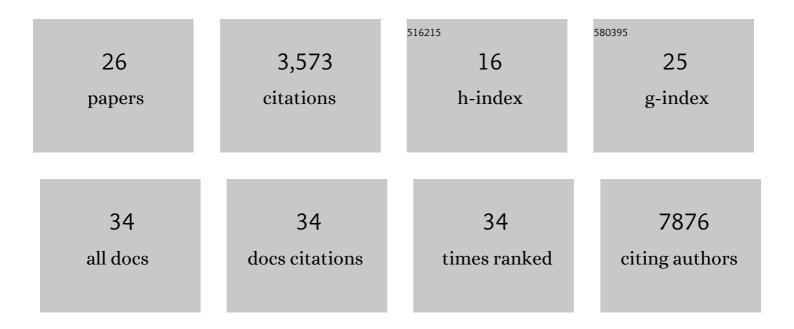
Franu00e7ois Jose Serra

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. Molecular Biology and Evolution, 2016, 33, 1635-1638.	3.5	1,692
2	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	9.4	295
3	Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation. Genes and Development, 2014, 28, 2151-2162.	2.7	270
4	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.	1.5	252
5	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	6.5	182
6	Role of tomato <i>BRANCHED1</i> â€like genes in the control of shoot branching. Plant Journal, 2011, 67, 701-714.	2.8	179
7	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
8	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. Molecular Cell, 2020, 78, 522-538.e9.	4.5	107
9	Restraintâ€based threeâ€dimensional modeling of genomes and genomic domains. FEBS Letters, 2015, 589, 2987-2995.	1.3	93
10	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. Nucleic Acids Research, 2015, 43, 3465-3477.	6.5	66
11	Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs. Nature Communications, 2020, 11, 2564.	5.8	41
12	Evolution of the biosynthesis of diâ€ <i>myo</i> â€inositol phosphate, a marker of adaptation to hot marine environments. Environmental Microbiology, 2012, 14, 691-701.	1.8	28
13	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	1.2	27
14	Evolutionary Genomics of Genes Involved in Olfactory Behavior in the <i>Drosophila melanogaster</i> Species Group. Evolutionary Bioinformatics, 2012, 8, EBO.S8484.	0.6	24
15	Selective constraints on protamine 2 in primates and rodents. BMC Evolutionary Biology, 2016, 16, 21.	3.2	20
16	Sexual Selection Halts the Relaxation of Protamine 2 among Rodents. PLoS ONE, 2011, 6, e29247.	1.1	17
17	OUP accepted manuscript. Nucleic Acids Research, 2021, 49, 11005-11021.	6.5	14
18	Identification of chromatin loops from Hi-C interaction matrices by CTCF–CTCF topology classification. NAR Genomics and Bioinformatics, 2022, 4, lqac021.	1.5	13

#	Article	IF	CITATIONS
19	Natural Selection on Functional Modules, a Genome-Wide Analysis. PLoS Computational Biology, 2011, 7, e1001093.	1.5	12
20	Positive Selection in Nucleoporins Challenges Constraints on Early Expressed Genes in Drosophila Development. Genome Biology and Evolution, 2013, 5, 2231-2241.	1.1	11
21	<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.	6.2	11
22	Neutral Theory Predicts the Relative Abundance and Diversity of Genetic Elements in a Broad Array of Eukaryotic Genomes. PLoS ONE, 2013, 8, e63915.	1.1	10
23	Parallel sequencing lives, or what makes large sequencing projects successful. GigaScience, 2017, 6, 1-6.	3.3	4
24	Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments. Methods in Molecular Biology, 2021, 2157, 35-63.	0.4	2
25	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. Genome Biology and Evolution, 2015, 7, 1490-1505.	1.1	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. Blood, 2016, 128, 459-459.	0.6	0