Franu00e7ois Jose Serra

List of Publications by Year
in descending order

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	Identification of chromatin loops from Hi-C interaction matrices by CTCF–CTCF topology classification. NAR Genomics and Bioinformatics, 2022, 4, lqac021.	3.2	13
2	OUP accepted manuscript. Nucleic Acids Research, 2021, 49, 11005-11021.	14.5	14
3	Analysis, Modeling, and Visualization of Chromosome Conformation Capture Experiments. Methods in Molecular Biology, 2021, 2157, 35-63.	0.9	2
4	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. Molecular Cell, 2020, 78, 522-538.e9.	9.7	107
5	Transcriptional activation during cell reprogramming correlates with the formation of 3D open chromatin hubs. Nature Communications, 2020, 11, 2564.	12.8	41
6	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	21.4	295
7	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
8	<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
9	Parallel sequencing lives, or what makes large sequencing projects successful. GigaScience, 2017, 6, 1-6.	6.4	4
10	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
11	Selective constraints on protamine 2 in primates and rodents. BMC Evolutionary Biology, 2016, 16, 21.	3.2	20
12	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. Molecular Biology and Evolution, 2016, 33, 1635-1638.	8.9	1,692
13	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
14	Restraint-based three-dimensional modeling of genomes and genomic domains. FEBS Letters, 2015, 589, 2987-2995.	2.8	93
15	Assessing the limits of restraint-based 3D modeling of genomes and genomic domains. Nucleic Acids Research, 2015, 43, 3465-3477.	14.5	66
16	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.	2.5	1
17	Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation. Genes and Development, 2014, 28, 2151-2162.	5.9	270
18	Positive Selection in Nucleoporins Challenges Constraints on Early Expressed Genes in Drosophila Development. Genome Biology and Evolution, 2013, 5, 2231-2241.	2.5	11

#	Article	IF	Citations
19	Neutral Theory Predicts the Relative Abundance and Diversity of Genetic Elements in a Broad Array of Eukaryotic Genomes. PLoS ONE, 2013, 8, e63915.	2.5	10
20	Evolutionary Genomics of Genes Involved in Olfactory Behavior in the *Drosophila melanogaster* Species Group. Evolutionary Bioinformatics, 2012, 8, EBO.S8484.	1.2	24
21	Evolution of the biosynthesis of di‐*myo*‐inositol phosphate, a marker of adaptation to hot marine environments. Environmental Microbiology, 2012, 14, 691-701.	3.8	28
22	Sexual Selection Halts the Relaxation of Protamine 2 among Rodents. PLoS ONE, 2011, 6, e29247.	2.5	17
23	Role of tomato *BRANCHED1*‐like genes in the control of shoot branching. Plant Journal, 2011, 67, 701-714.	5.7	179
24	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	2.8	27
25	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	14.5	182
26	Natural Selection on Functional Modules, a Genome-Wide Analysis. PLoS Computational Biology, 2011, 7, e1001093.	3.2	12