David Juan

List of Publications by Year
in descending order

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51 papers	4,392 citations	257450 24 h-index	161849 54 g-index
66 all docs	66 docs citations	66 times ranked	10281 citing authors

#	Article	IF	Citations
1	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
2	Emerging methods in protein co-evolution. Nature Reviews Genetics, 2013, 14, 249-261.	16.3	553
3	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. Human Molecular Genetics, 2014, 23, 5866-5878.	2.9	463
4	Spatiotemporal transcriptomic divergence across human and macaque brain development. Science, 2018, 362, .	12.6	279
5	A comparative genomics multitool for scientific discovery and conservation. Nature, 2020, 587, 240-245.	27.8	216
6	Identification of amino acid residues crucial for chemokine receptor dimerization. Nature Immunology, 2004, 5, 216-223.	14.5	176
7	High-confidence prediction of global interactomes based on genome-wide coevolutionary networks. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 934-939.	7.1	172
8	Protein interactions and ligand binding: From protein subfamilies to functional specificity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1995-2000.	7.1	132
9	Assessing Protein Co-evolution in the Context of the Tree of Life Assists in the Prediction of the Interactome. Journal of Molecular Biology, 2005, 352, 1002-1015.	4.2	128
10	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
11	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	12.8	90
12	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. Nature Neuroscience, 2021, 24, 176-185.	14.8	73
13	Loose ends: almost one in five human genes still have unresolved coding status. Nucleic Acids Research, 2018, 46, 7070-7084.	14.5	62
14	Intronic CNVs and gene expression variation in human populations. PLoS Genetics, 2019, 15, e1007902.	3.5	61
15	Subfunctionalization via Adaptive Evolution Influenced by Genomic Context: The Case of Histone Chaperones ASF1a and ASF1b. Molecular Biology and Evolution, 2013, 30, 1853-1866.	8.9	60
16	Reconstructing Denisovan Anatomy Using DNA Methylation Maps. Cell, 2019, 179, 180-192.e10.	28.9	51
17	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Genome Biology, 2016, 17, 152.	8.8	46
18	Scoring docking models with evolutionary information. Proteins: Structure, Function and Bioinformatics, 2005, 60, 275-280.	2.6	41

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19	Transcriptional dissection of pancreatic tumors engrafted in mice. Genome Medicine, 2014, 6, 27.	8.2	41
20	Coâ€evolution and coâ€adaptation in protein networks. FEBS Letters, 2008, 582, 1225-1230.	2.8	40
21	Conservation of coevolving protein interfaces bridges prokaryoteâ€“eukaryote homologies in the twilight zone. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15018-15023.	7.1	40
22	Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Cell Reports, 2016, 14, 1246-1257.	6.4	38
23	Detection of significant protein coevolution. Bioinformatics, 2015, 31, 2166-2173.	4.1	32
24	EcID. A database for the inference of functional interactions in E. coli. Nucleic Acids Research, 2009, 37, D629-D635.	14.5	28
25	Comprehensive identification of somatic nucleotide variants in human brain tissue. Genome Biology, 2021, 22, 92.	8.8	26
26	Somatic mosaicism reveals clonal distributions of neocortical development. Nature, 2022, 604, 689-696.	27.8	26
27	TSEMA: interactive prediction of protein pairings between interacting families. Nucleic Acids Research, 2006, 34, W315-W319.	14.5	25
28	TreeDet: a web server to explore sequence space. Nucleic Acids Research, 2006, 34, W110-W115.	14.5	24
29	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. Nature Neuroscience, 2021, 24, 186-196.	14.8	22
30	Enhancing the prediction of protein pairings between interacting families using orthology information. BMC Bioinformatics, 2008, 9, 35.	2.6	21
31	Prediction of Protein Interaction Based on Similarity of Phylogenetic Trees. Methods in Molecular Biology, 2008, 484, 523-535.	0.9	20
32	JDet: interactive calculation and visualization of function-related conservation patterns in multiple sequence alignments and structures. Bioinformatics, 2012, 28, 584-586.	4.1	20
33	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. Nature Communications, 2020, 11, 2854.	12.8	20
34	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. Nucleic Acids Research, 2017, 45, 9244-9259.	14.5	19
35	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	12.8	19
36	A neural network approach to evaluate fold recognition results. Proteins: Structure, Function and Bioinformatics, 2003, 50, 600-608.	2.6	16

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37	Uncovering the Molecular Machinery of the Human Spindleâ€"An Integration of Wet and Dry Systems Biology. PLoS ONE, 2012, 7, e31813.	2.5	14
38	Selection of organisms for the co-evolution-based study of protein interactions. BMC Bioinformatics, 2011, 12, 363.	2.6	13
39	Copy number variation underlies complex phenotypes in domestic dog breeds and other canids. Genome Research, 2021, 31, 762-774.	5.5	12
40	Inference of Functional Relations in Predicted Protein Networks with a Machine Learning Approach. PLoS ONE, 2010, 5, e9969.	2.5	11
41	Expanding the Geographic Characterisation of Epsteinâ€"Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686.	3.6	10
42	Copy number variantsÂand fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS Genetics, 2020, 16, e1008742.	3.5	10
43	A framework for computational and experimental methods: Identifying dimerization residues in CCR chemokine receptors. Bioinformatics, 2005, 21, ii13-ii18.	4.1	9
44	Late-replicating CNVs as a source of new genes. Biology Open, 2013, 2, 1402-1411.	1.2	9
45	Extreme differences between human germline and tumor mutation densities are driven by ancestral human-specific deviations. Nature Communications, 2020, 11, 2512.	12.8	9
46	Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions. Molecular BioSystems, 2013, 9, 70-76.	2.9	8
47	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
48	Somatic Mutations Detected in Parkinson Disease Could Affect Genes With a Role in Synaptic and Neuronal Processes. Frontiers in Aging, 2022, 3, .	2.6	7
49	Transcriptome innovations in primates revealed by single-molecule long-read sequencing. Genome Research, 2022, 32, 1448-1462.	5.5	6
50	Mirroring co-evolving trees in the light of their topologies. Bioinformatics, 2012, 28, 1202-1208.	4.1	4
51	Accessible Protein Interaction Data for Network Modeling. Structure of the Information and Available Repositories. Lecture Notes in Computer Science, 2005, , 1-13.	1.3	3