

# John A Capra

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83

papers

3,833

citations

28

h-index

61

g-index

111

ext. papers

5,036

ext. citations

9.5

avg, IF

5.73

L-index

#	Paper	IF	Citations
83	Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage. <i>Cell</i> , <b>2012</b> , 151, 206-20	56.2	458
82	Predicting functionally important residues from sequence conservation. <i>Bioinformatics</i> , <b>2007</b> , 23, 1875-82	22	439
81	DNA replication through G-quadruplex motifs is promoted by the <i>Saccharomyces cerevisiae</i> Pif1 DNA helicase. <i>Cell</i> , <b>2011</b> , 145, 678-91	56.2	408
80	Predicting protein ligand binding sites by combining evolutionary sequence conservation and 3D structure. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000585	5	283
79	SIRT4 Is a Lysine Deacetylase that Controls Leucine Metabolism and Insulin Secretion. <i>Cell Metabolism</i> , <b>2017</b> , 25, 838-855.e15	24.6	188
78	The phenotypic legacy of admixture between modern humans and Neandertals. <i>Science</i> , <b>2016</b> , 351, 737-43	31.3	172
77	G-quadruplex DNA sequences are evolutionarily conserved and associated with distinct genomic features in <i>Saccharomyces cerevisiae</i> . <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000861	5	170
76	Many human accelerated regions are developmental enhancers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20130025	5.8	117
75	Integrating diverse datasets improves developmental enhancer prediction. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003677	5	115
74	Folding and Misfolding of Human Membrane Proteins in Health and Disease: From Single Molecules to Cellular Proteostasis. <i>Chemical Reviews</i> , <b>2019</b> , 119, 5537-5606	68.1	93
73	Characterization and prediction of residues determining protein functional specificity. <i>Bioinformatics</i> , <b>2008</b> , 24, 1473-80	7.2	92
72	Joint mouse-human phenome-wide association to test gene function and disease risk. <i>Nature Communications</i> , <b>2016</b> , 7, 10464	17.4	91
71	Acetylation of RNA polymerase II regulates growth-factor-induced gene transcription in mammalian cells. <i>Molecular Cell</i> , <b>2013</b> , 52, 314-24	17.6	89
70	SIRT1 and SIRT3 deacetylate homologous substrates: AceCS1,2 and HMGCS1,2. <i>Aging</i> , <b>2011</b> , 3, 635-42	5.6	73
69	XPA: A key scaffold for human nucleotide excision repair. <i>DNA Repair</i> , <b>2016</b> , 44, 123-135	4.3	68
68	ProteinHistorian: tools for the comparative analysis of eukaryote protein origin. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002567	5	58
67	The essential <i>Schizosaccharomyces pombe</i> Pfh1 DNA helicase promotes fork movement past G-quadruplex motifs to prevent DNA damage. <i>BMC Biology</i> , <b>2014</b> , 12, 101	7.3	55

66	A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003684	6	52
65	Transposable Element Exaptation into Regulatory Regions Is Rare, Influenced by Evolutionary Age, and Subject to Pleiotropic Constraints. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2856-2869	8.3	46
64	Ongoing GC-biased evolution is widespread in the human genome and enriched near recombination hot spots. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 614-26	3.9	46
63	Informatics center for mouse genomics: the dissection of complex traits of the nervous system. <i>Neuroinformatics</i> , <b>2003</b> , 1, 327-42	3.2	41
62	How old is my gene?. <i>Trends in Genetics</i> , <b>2013</b> , 29, 659-68	8.5	40
61	Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 415-426	11	35
60	Prediction of gene regulatory enhancers across species reveals evolutionarily conserved sequence properties. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006484	5	33
59	High-Throughput Reclassification of SCN5A Variants. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 111-123	11	32
58	Are Interactions between cis-Regulatory Variants Evidence for Biological Epistasis or Statistical Artifacts?. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 817-830	11	32
57	The influence of evolutionary history on human health and disease. <i>Nature Reviews Genetics</i> , <b>2021</b> , 22, 269-283	30.1	31
56	Substitution patterns are GC-biased in divergent sequences across the metazoans. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 516-27	3.9	30
55	Pfh1 Is an Accessory Replicative Helicase that Interacts with the Replisome to Facilitate Fork Progression and Preserve Genome Integrity. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006238	6	25
54	Predicting susceptibility to SARS-CoV-2 infection based on structural differences in ACE2 across species. <i>FASEB Journal</i> , <b>2020</b> , 34, 15946-15960	0.9	24
53	Topologically associating domain boundaries that are stable across diverse cell types are evolutionarily constrained and enriched for heritability. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 269-283	11	23
52	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 1598-1606	12.3	22
51	Genome-wide enhancer annotations differ significantly in genomic distribution, evolution, and function. <i>BMC Genomics</i> , <b>2019</b> , 20, 511	4.5	19
50	Functional annotation of rare structural variation in the human brain. <i>Nature Communications</i> , <b>2020</b> , 11, 2990	17.4	18
49	Evolution of lysine acetylation in the RNA polymerase II C-terminal domain. <i>BMC Evolutionary Biology</i> , <b>2015</b> , 15, 35	3	17

48	Short DNA sequence patterns accurately identify broadly active human enhancers. <i>BMC Genomics</i> , <b>2017</b> , 18, 536	4.5	16
47	Heterozygosity Ratio, a Robust Global Genomic Measure of Autozygosity and Its Association with Height and Disease Risk. <i>Genetics</i> , <b>2016</b> , 204, 893-904	4	16
46	Mms1 binds to G-rich regions in <i>Saccharomyces cerevisiae</i> and influences replication and genome stability. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 7796-7806	20.1	15
45	Modeling DNA methylation dynamics with approaches from phylogenetics. <i>Bioinformatics</i> , <b>2014</b> , 30, i408-14	7.2	14
44	Gene Regulatory Enhancers with Evolutionarily Conserved Activity Are More Pleiotropic than Those with Species-Specific Activity. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 2615-2625	3.9	13
43	Extrapolating histone marks across developmental stages, tissues, and species: an enhancer prediction case study. <i>BMC Genomics</i> , <b>2015</b> , 16, 104	4.5	12
42	Predicting changes in protein thermodynamic stability upon point mutation with deep 3D convolutional neural networks. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008291	5	12
41	Neanderthal introgression reintroduced functional ancestral alleles lost in Eurasian populations. <i>Nature Ecology and Evolution</i> , <b>2020</b> , 4, 1332-1341	12.3	12
40	The evolution of the human genome. <i>Current Opinion in Genetics and Development</i> , <b>2015</b> , 35, 9-15	4.9	11
39	Protein structure aids predicting functional perturbation of missense variants in and. <i>Computational and Structural Biotechnology Journal</i> , <b>2019</b> , 17, 206-214	6.8	10
38	Ancient human miRNAs are more likely to have broad functions and disease associations than young miRNAs. <i>BMC Genomics</i> , <b>2017</b> , 18, 672	4.5	9
37	Genome-wide association study of musical beat synchronization demonstrates high polygenicity		9
36	Log-odds sequence logos. <i>Bioinformatics</i> , <b>2015</b> , 31, 324-31	7.2	8
35	Signatures of Recent Positive Selection in Enhancers Across 41 Human Tissues. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 2761-2774	3.2	8
34	The transformative potential of an integrative approach to pregnancy. <i>Placenta</i> , <b>2017</b> , 57, 204-215	3.4	7
33	Learning and interpreting the gene regulatory grammar in a deep learning framework. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008334	5	7
32	Which animals are at risk? Predicting species susceptibility to Covid-19 <b>2020</b> ,		7
31	Accounting for diverse evolutionary forces reveals mosaic patterns of selection on human preterm birth loci. <i>Nature Communications</i> , <b>2020</b> , 11, 3731	17.4	7

30	IgG4-related disease: Association with a rare gene variant expressed in cytotoxic T cells. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2019</b> , 7, e686	2.3	6
29	Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 18	3.6	6
28	Topologically associating domain (TAD) boundaries stable across diverse cell types are evolutionarily constrained and enriched for heritability		6
27	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits. <i>Nature Communications</i> , <b>2021</b> , 12, 4481	17.4	6
26	Sequence Characteristics Distinguish Transcribed Enhancers from Promoters and Predict Their Breadth of Activity. <i>Genetics</i> , <b>2019</b> , 211, 1205-1217	4	5
25	Immune Regulation in Eutherian Pregnancy: Live Birth Coevolved with Novel Immune Genes and Gene Regulation. <i>BioEssays</i> , <b>2019</b> , 41, e1900072	4.1	5
24	Familial Autonomic Ganglionopathy Caused by Rare Genetic Variants. <i>Neurology</i> , <b>2021</b> , 97, e145-e155	6.5	5
23	Genome-wide maps of distal gene regulatory enhancers active in the human placenta. <i>PLoS ONE</i> , <b>2018</b> , 13, e0209611	3.7	5
22	Genome-wide association analysis uncovers variants for reproductive variation across dog breeds and links to domestication. <i>Evolution, Medicine and Public Health</i> , <b>2019</b> , 2019, 93-103	3	4
21	What is a placental mammal anyway?. <i>ELife</i> , <b>2017</b> , 6,	8.9	4
20	Evaluating human autosomal loci for sexually antagonistic viability selection in two large biobanks. <i>Genetics</i> , <b>2021</b> , 217, 1-10	4	4
19	Genome-wide Enhancer Maps Differ Significantly in Genomic Distribution, Evolution, and Function		4
18	Neanderthal introgression reintroduced functional alleles lost in the human out of Africa bottleneck		4
17	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. <i>Genome Biology</i> , <b>2020</b> , 21, 217	18.3	4
16	Integrating structural and evolutionary data to interpret variation and pathogenicity in adapter protein complex 4. <i>Protein Science</i> , <b>2020</b> , 29, 1535-1549	6.3	4
15	Genetics of agenesis/hypoplasia of the uterus and vagina: narrowing down the number of candidate genes for Mayer-Rokitansky-Küster-Hauser Syndrome. <i>Human Genetics</i> , <b>2021</b> , 140, 667-680	6.3	4
14	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits		3
13	Dense phenotyping from electronic health records enables machine-learning-based prediction of preterm birth		3

12	Accounting for diverse evolutionary forces reveals the mosaic nature of selection on genomic regions associated with human preterm birth		3
11	Phenotypic Profiling in Subjects Heterozygous for 1 of 2 Rare Variants in the Hypophosphatasia Gene (). <i>Journal of the Endocrine Society</i> , <b>2020</b> , 4, bvaa084	0.4	3
10	The Impact of Natural Selection on the Evolution and Function of Placentally Expressed Galectins. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 2574-2592	3.9	2
9	Distinct Features of Proband With Early Repolarization and Brugada Syndromes Carrying SCN5A Pathogenic Variants. <i>Journal of the American College of Cardiology</i> , <b>2021</b> , 78, 1603-1617	15.1	2
8	Deep learning reveals evolutionary conservation and divergence of sequence properties underlying gene regulatory enhancers across mammals		2
7	A Multitask Deep-Learning Method for Predicting Membrane Associations and Secondary Structures of Proteins. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 4089-4100	5.6	2
6	Identifying digenic disease genes using machine learning in the undiagnosed diseases network		1
5	Identifying digenic disease genes via machine learning in the Undiagnosed Diseases Network. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1946-1963	11	1
4	An association test of the spatial distribution of rare missense variants within protein structures identify Alzheimer's disease-related patterns.. <i>Genome Research</i> , <b>2022</b> ,	9.7	1
3	Modeling the Evolutionary Architectures of Transcribed Human Enhancer Sequences Reveals Distinct Origins, Functions, and Associations with Human Trait Variation. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 3681-3696	8.3	0
2	Structural characterization of rare missense variants within known neurodegenerative disease proteins. <i>Alzheimer's and Dementia</i> , <b>2020</b> , 16, e046405	1.2	
1	Vascular alterations impede fragile tolerance to pregnancy in type 1 diabetes.. <i>F&amp;S Science</i> , <b>2022</b> , 3, 148-158		1