John A Capra

List of Publications by Year in Descending Order

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	Vascular alterations impede fragile tolerance to pregnancy in type 1 diabetes.. *F&S Science*, **2022**, 3, 148-158	3.4	
82	An association test of the spatial distribution of rare missense variants within protein structures identify Alzheimer's disease-related patterns.. *Genome Research*, **2022**,	9.7	1
81	Distinct Features of Probands With Early Repolarization and Brugada Syndromes Carrying SCN5A Pathogenic Variants. *Journal of the American College of Cardiology*, **2021**, 78, 1603-1617	15.1	2
80	Evaluating human autosomal loci for sexually antagonistic viability selection in two large biobanks. *Genetics*, **2021**, 217, 1-10	4	4
79	Modeling the Evolutionary Architectures of Transcribed Human Enhancer Sequences Reveals Distinct Origins, Functions, and Associations with Human Trait Variation. *Molecular Biology and Evolution*, **2021**, 38, 3681-3696	8.3	0
78	Familial Autonomic Ganglionopathy Caused by Rare Genetic Variants. *Neurology*, **2021**, 97, e145-e155	6.5	5
77	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits. *Nature Communications*, **2021**, 12, 4481	17.4	6
76	The influence of evolutionary history on human health and disease. *Nature Reviews Genetics*, **2021**, 22, 269-283	30.1	31
75	Genetics of agenesis/hypoplasia of the uterus and vagina: narrowing down the number of candidate genes for Mayer-Rokitansky-Küster-Hauser Syndrome. *Human Genetics*, **2021**, 140, 667-680	6.3	4
74	Topologically associating domain boundaries that are stable across diverse cell types are evolutionarily constrained and enriched for heritability. *American Journal of Human Genetics*, **2021**, 108, 269-283	11	23
73	A Multitask Deep-Learning Method for Predicting Membrane Associations and Secondary Structures of Proteins. *Journal of Proteome Research*, **2021**, 20, 4089-4100	5.6	2
72	Identifying digenic disease genes via machine learning in the Undiagnosed Diseases Network. *American Journal of Human Genetics*, **2021**, 108, 1946-1963	11	1
71	Structural characterization of rare missense variants within known neurodegenerative disease proteins. *Alzheimer's and Dementia*, **2020**, 16, e046405	1.2	
70	High-Throughput Reclassification of SCN5A Variants. *American Journal of Human Genetics*, **2020**, 107, 111-123	11	32
69	Functional annotation of rare structural variation in the human brain. *Nature Communications*, **2020**, 11, 2990	17.4	18
68	Predicting changes in protein thermodynamic stability upon point mutation with deep 3D convolutional neural networks. *PLoS Computational Biology*, **2020**, 16, e1008291	5	12
67	Learning and interpreting the gene regulatory grammar in a deep learning framework. *PLoS Computational Biology*, **2020**, 16, e1008334	5	7

66	Which animals are at risk? Predicting species susceptibility to Covid-19 **2020**,		7
65	Predicting susceptibility to SARS-CoV-2 infection based on structural differences in ACE2 across species. *FASEB Journal*, **2020**, 34, 15946-15960	0.9	24
64	Phenotypic Profiling in Subjects Heterozygous for 1 of 2 Rare Variants in the Hypophosphatasia Gene (). *Journal of the Endocrine Society*, **2020**, 4, bvaa084	0.4	3
63	Neanderthal introgression reintroduced functional ancestral alleles lost in Eurasian populations. *Nature Ecology and Evolution*, **2020**, 4, 1332-1341	12.3	12
62	Accounting for diverse evolutionary forces reveals mosaic patterns of selection on human preterm birth loci. *Nature Communications*, **2020**, 11, 3731	17.4	7
61	PSCAN: Spatial scan tests guided by protein structures improve complex disease gene discovery and signal variant detection. *Genome Biology*, **2020**, 21, 217	18.3	4
60	Integrating structural and evolutionary data to interpret variation and pathogenicity in adapter protein complex 4. *Protein Science*, **2020**, 29, 1535-1549	6.3	4
59	The Impact of Natural Selection on the Evolution and Function of Placentally Expressed Galectins. *Genome Biology and Evolution*, **2019**, 11, 2574-2592	3.9	2
58	Inferred divergent gene regulation in archaic hominins reveals potential phenotypic differences. *Nature Ecology and Evolution*, **2019**, 3, 1598-1606	12.3	22
57	Sequence Characteristics Distinguish Transcribed Enhancers from Promoters and Predict Their Breadth of Activity. *Genetics*, **2019**, 211, 1205-1217	4	5
56	Genome-wide enhancer annotations differ significantly in genomic distribution, evolution, and function. *BMC Genomics*, **2019**, 20, 511	4.5	19
55	IgG4-related disease: Association with a rare gene variant expressed in cytotoxic T cells. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e686	2.3	6
54	Protein structure aids predicting functional perturbation of missense variants in and. *Computational and Structural Biotechnology Journal*, **2019**, 17, 206-214	6.8	10
53	Immune Regulation in Eutherian Pregnancy: Live Birth Coevolved with Novel Immune Genes and Gene Regulation. *BioEssays*, **2019**, 41, e1900072	4.1	5
52	Genome-wide association analysis uncovers variants for reproductive variation across dog breeds and links to domestication. *Evolution, Medicine and Public Health*, **2019**, 2019, 93-103	3	4
51	Signatures of Recent Positive Selection in Enhancers Across 41 Human Tissues. *G3: Genes, Genomes, Genetics*, **2019**, 9, 2761-2774	3.2	8
50	Folding and Misfolding of Human Membrane Proteins in Health and Disease: From Single Molecules to Cellular Proteostasis. *Chemical Reviews*, **2019**, 119, 5537-5606	68.1	93
49	Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures. *American Journal of Human Genetics*, **2018**, 102, 415-426	11	35

48	Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia. *BMC Bioinformatics*, **2018**, 19, 18	3.6	6
47	Genome-wide maps of distal gene regulatory enhancers active in the human placenta. *PLoS ONE*, **2018**, 13, e0209611	3.7	5
46	Prediction of gene regulatory enhancers across species reveals evolutionarily conserved sequence properties. *PLoS Computational Biology*, **2018**, 14, e1006484	5	33
45	Mms1 binds to G-rich regions in Saccharomyces cerevisiae and influences replication and genome stability. *Nucleic Acids Research*, **2017**, 45, 7796-7806	20.1	15
44	SIRT4 Is a Lysine Deacylase that Controls Leucine Metabolism and Insulin Secretion. *Cell Metabolism* , **2017**, 25, 838-855.e15	24.6	188
43	Gene Regulatory Enhancers with Evolutionarily Conserved Activity Are More Pleiotropic than Those with Species-Specific Activity. *Genome Biology and Evolution*, **2017**, 9, 2615-2625	3.9	13
42	Short DNA sequence patterns accurately identify broadly active human enhancers. *BMC Genomics*, **2017**, 18, 536	4.5	16
41	The transformative potential of an integrative approach to pregnancy. *Placenta*, **2017**, 57, 204-215	3.4	7
40	Transposable Element Exaptation into Regulatory Regions Is Rare, Influenced by Evolutionary Age, and Subject to Pleiotropic Constraints. *Molecular Biology and Evolution*, **2017**, 34, 2856-2869	8.3	46
39	Ancient human miRNAs are more likely to have broad functions and disease associations than young miRNAs. *BMC Genomics*, **2017**, 18, 672	4.5	9
38	What is a placental mammal anyway?. *ELife*, **2017**, 6,	8.9	4
37	Heterozygosity Ratio, a Robust Global Genomic Measure of Autozygosity and Its Association with Height and Disease Risk. *Genetics*, **2016**, 204, 893-904	4	16
36	Are Interactions between cis-Regulatory Variants Evidence for Biological Epistasis or Statistical Artifacts?. *American Journal of Human Genetics*, **2016**, 99, 817-830	11	32
35	XPA: A key scaffold for human nucleotide excision repair. *DNA Repair*, **2016**, 44, 123-135	4.3	68
34	Joint mouse-human phenome-wide association to test gene function and disease risk. *Nature Communications*, **2016**, 7, 10464	17.4	91
33	The phenotypic legacy of admixture between modern humans and Neandertals. *Science*, **2016**, 351, 737-741	33.3	172
32	Pfh1 Is an Accessory Replicative Helicase that Interacts with the Replisome to Facilitate Fork Progression and Preserve Genome Integrity. *PLoS Genetics*, **2016**, 12, e1006238	6	25
31	Evolution of lysine acetylation in the RNA polymerase II C-terminal domain. *BMC Evolutionary Biology*, **2015**, 15, 35	3	17

30	Extrapolating histone marks across developmental stages, tissues, and species: an enhancer prediction case study. *BMC Genomics*, **2015**, 16, 104	4.5	12
29	The evolution of the human genome. *Current Opinion in Genetics and Development*, **2015**, 35, 9-15	4.9	11
28	Log-odds sequence logos. *Bioinformatics*, **2015**, 31, 324-31	7.2	8
27	The essential Schizosaccharomyces pombe Pfh1 DNA helicase promotes fork movement past G-quadruplex motifs to prevent DNA damage. *BMC Biology*, **2014**, 12, 101	7.3	55
26	Integrating diverse datasets improves developmental enhancer prediction. *PLoS Computational Biology*, **2014**, 10, e1003677	5	115
25	Modeling DNA methylation dynamics with approaches from phylogenetics. *Bioinformatics*, **2014**, 30, i408-14	7.2	14
24	How old is my gene?. *Trends in Genetics*, **2013**, 29, 659-68	8.5	40
23	Acetylation of RNA polymerase II regulates growth-factor-induced gene transcription in mammalian cells. *Molecular Cell*, **2013**, 52, 314-24	17.6	89
22	Many human accelerated regions are developmental enhancers. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2013**, 368, 20130025	5.8	117
21	A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. *PLoS Genetics*, **2013**, 9, e1003684	6	52
20	Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage. *Cell*, **2012**, 151, 206-20	56.2	458
19	ProteinHistorian: tools for the comparative analysis of eukaryote protein origin. *PLoS Computational Biology*, **2012**, 8, e1002567	5	58
18	DNA replication through G-quadruplex motifs is promoted by the Saccharomyces cerevisiae Pif1 DNA helicase. *Cell*, **2011**, 145, 678-91	56.2	408
17	Substitution patterns are GC-biased in divergent sequences across the metazoans. *Genome Biology and Evolution*, **2011**, 3, 516-27	3.9	30
16	Ongoing GC-biased evolution is widespread in the human genome and enriched near recombination hot spots. *Genome Biology and Evolution*, **2011**, 3, 614-26	3.9	46
15	SIRT1 and SIRT3 deacetylate homologous substrates: AceCS1,2 and HMGCS1,2. *Aging*, **2011**, 3, 635-42	5.6	73
14	G-quadruplex DNA sequences are evolutionarily conserved and associated with distinct genomic features in Saccharomyces cerevisiae. *PLoS Computational Biology*, **2010**, 6, e1000861	5	170
13	Predicting protein ligand binding sites by combining evolutionary sequence conservation and 3D structure. *PLoS Computational Biology*, **2009**, 5, e1000585	5	283

12	Characterization and prediction of residues determining protein functional specificity. *Bioinformatics*, **2008**, 24, 1473-80	7.2	92
11	Predicting functionally important residues from sequence conservation. *Bioinformatics*, **2007**, 23, 1875-82	7.2	439
10	Informatics center for mouse genomics: the dissection of complex traits of the nervous system. *Neuroinformatics*, **2003**, 1, 327-42	3.2	41
9	Genome-wide Enhancer Maps Differ Significantly in Genomic Distribution, Evolution, and Function		4
8	Topologically associating domain (TAD) boundaries stable across diverse cell types are evolutionarily constrained and enriched for heritability		6
7	Identifying digenic disease genes using machine learning in the undiagnosed diseases network		1
6	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits		3
5	Dense phenotyping from electronic health records enables machine-learning-based prediction of preterm birth		3
4	Neanderthal introgression reintroduced functional alleles lost in the human out of Africa bottleneck		4
3	Accounting for diverse evolutionary forces reveals the mosaic nature of selection on genomic regions associated with human preterm birth		3
2	Genome-wide association study of musical beat synchronization demonstrates high polygenicity		9
1	Deep learning reveals evolutionary conservation and divergence of sequence properties underlying gene regulatory enhancers across mammals		2