

Anne-Ruxandra Carvunis

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.

33 papers	4,542 citations	19 h-index	47 g-index
47 ext. papers	5,659 ext. citations	20.1 avg, IF	4.98 L-index

#	Paper	IF	Citations
33	A proteome-scale map of the human interactome network. <i>Cell</i> , 2014 , 159, 1212-1226	56.2	898
32	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689
31	Independently evolved virulence effectors converge onto hubs in a plant immune system network. <i>Science</i> , 2011 , 333, 596-601	33.3	601
30	Integrative approaches for finding modular structure in biological networks. <i>Nature Reviews Genetics</i> , 2013 , 14, 719-32	30.1	390
29	Proto-genes and de novo gene birth. <i>Nature</i> , 2012 , 487, 370-4	50.4	379
28	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
27	Genome-scale analysis of in vivo spatiotemporal promoter activity in <i>Caenorhabditis elegans</i> . <i>Nature Biotechnology</i> , 2007 , 25, 663-8	44.5	250
26	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009 , 6, 39-46	21.6	237
25	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009 , 6, 47-54	21.6	224
24	Genome-wide identification of <i>Pseudomonas aeruginosa</i> virulence-related genes using a <i>Caenorhabditis elegans</i> infection model. <i>PLoS Pathogens</i> , 2012 , 8, e1002813	7.6	112
23	De novo gene birth. <i>PLoS Genetics</i> , 2019 , 15, e1008160	6	99
22	Mapping transcription factor interactome networks using HaloTag protein arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4238-47	11.5	52
21	No Evidence for Phylostratigraphic Bias Impacting Inferences on Patterns of Gene Emergence and Evolution. <i>Molecular Biology and Evolution</i> , 2017 , 34, 843-856	8.3	51
20	Synteny-based analyses indicate that sequence divergence is not the main source of orphan genes. <i>eLife</i> , 2020 , 9,	8.9	38
19	Quantitative Translation of Dog-to-Human Aging by Conserved Remodeling of the DNA Methylome. <i>Cell Systems</i> , 2020 , 11, 176-185.e6	10.6	32
18	De novo emergence of adaptive membrane proteins from thymine-rich genomic sequences. <i>Nature Communications</i> , 2020 , 11, 781	17.4	26
17	Siri of the cell: what biology could learn from the iPhone. <i>Cell</i> , 2014 , 157, 534-8	56.2	25

16	The meanings of function in biology and the problematic case of de novo gene emergence. <i>ELife</i> , 2019 , 8,	8.9	23
15	Revisiting the <i>Saccharomyces cerevisiae</i> predicted ORFeome. <i>Genome Research</i> , 2008 , 18, 1294-303	9.7	22
14	Evidence for a common evolutionary rate in metazoan transcriptional networks. <i>ELife</i> , 2015 , 4,	8.9	19
13	A UV-induced genetic network links the RSC complex to nucleotide excision repair and shows dose-dependent rewiring. <i>Cell Reports</i> , 2013 , 5, 1714-24	10.6	18
12	Of mice, men and immunity: a case for evolutionary systems biology. <i>Nature Immunology</i> , 2018 , 19, 421-425	12.5	14
11	Dynamics of three-state excitable units on Poisson vs. power-law random networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2006 , 367, 595-612	3.3	10
10	Interactome Networks 2013 , 45-63		4
9	A community-driven roadmap to advance research on translated open reading frames detected by Ribo-seq		4
8	Quantitative translation of dog-to-human aging by conserved remodeling of epigenetic networks		3
7	New genes from borrowed parts. <i>Science</i> , 2021 , 371, 779-780	33.3	3
6	Syntenic-based analyses indicate that sequence divergence is not the main source of orphan genes		2
5	No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution		2
4	A reference translome map reveals two modes of protein evolution		2
3	Evolutionary Characterization of the Short Protein SPAAR.. <i>Genes</i> , 2021 , 12,	4.2	1
2	De novo emergence of adaptive membrane proteins from thymine-rich intergenic sequences		1
1	LI Detector: a framework for sensitive colony-based screens regardless of the distribution of fitness effects. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	1