Anne-Ruxandra Carvunis

List of Publications by Year
in descending order

31 papers	6,208 citations	331670 21 h-index	414414 32 g-index
47 all docs	47 docs citations	47 times ranked	10528 citing authors

#	Article	IF	Citations
1	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	1,199
2	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. Science, 2011, 333, 601-607.	12.6	838
3	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. Science, 2011, 333, 596-601.	12.6	776
4	Proto-genes and de novo gene birth. Nature, 2012, 487, 370-374.	27.8	555
5	Integrative approaches for finding modular structure in biological networks. Nature Reviews Genetics, 2013, 14, 719-732.	16.3	512
6	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. Nature, 2012, 487, 491-495.	27.8	349
7	Literature-curated protein interaction datasets. Nature Methods, 2009, 6, 39-46.	19.0	288
8	Genome-scale analysis of in vivo spatiotemporal promoter activity in Caenorhabditis elegans. Nature Biotechnology, 2007, 25, 663-668.	17.5	286
9	Empirically controlled mapping of the Caenorhabditis elegans protein-protein interactome network. Nature Methods, 2009, 6, 47-54.	19.0	260
10	De novo gene birth. PLoS Genetics, 2019, 15, e1008160.	3.5	233
11	Genome-Wide Identification of Pseudomonas aeruginosa Virulence-Related Genes Using a Caenorhabditis elegans Infection Model. PLoS Pathogens, 2012, 8, e1002813.	4.7	153
12	Synteny-based analyses indicate that sequence divergence is not the main source of orphan genes. ELife, 2020, 9, .	6.0	104
13	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	17.5	86
14	De novo emergence of adaptive membrane proteins from thymine-rich genomic sequences. Nature Communications, 2020, 11, 781.	12.8	84
15	No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. Molecular Biology and Evolution, 2017, 34, msw284.	8.9	74
16	Mapping transcription factor interactome networks using HaloTag protein arrays. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4238-47.	7.1	67
17	Quantitative Translation of Dog-to-Human Aging by Conserved Remodeling of the DNA Methylome. Cell Systems, 2020, 11, 176-185.e6.	6.2	67
18	The meanings of 'function' in biology and the problematic case of de novo gene emergence. ELife, 2019, 8, .	6.0	56

#	Article	IF	Citations
19	Siri of the Cell: What Biology Could Learn from the iPhone. Cell, 2014, 157, 534-538.	28.9	31
20	Revisiting the <i>Saccharomyces cerevisiae</i> predicted ORFeome. Genome Research, 2008, 18, 1294-1303.	5.5	30
21	Of mice, men and immunity: a case for evolutionary systems biology. Nature Immunology, 2018, 19, 421-425.	14.5	26
22	Evidence for a common evolutionary rate in metazoan transcriptional networks. ELife, 2015, 4, .	6.0	26
23	A UV-Induced Genetic Network Links the RSC Complex to Nucleotide Excision Repair and Shows Dose-Dependent Rewiring. Cell Reports, 2013, 5, 1714-1724.	6.4	18
24	Dynamics of three-state excitable units on Poisson vs. power-law random networks. Physica A: Statistical Mechanics and Its Applications, 2006, 367, 595-612.	2.6	12
25	LI Detector: a framework for sensitive colony-based screens regardless of the distribution of fitness effects. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	7
26	New genes from borrowed parts. Science, 2021, 371, 779-780.	12.6	6
27	Interactome Networks. , 2013, , 45-63.		5
28	Evolutionary Characterization of the Short Protein SPAAR. Genes, 2021, 12, 1864.	2.4	3
29	RNF219 regulates CCR4-NOT function in mRNA translation and deadenylation. Scientific Reports, 2022, 12, .	3.3	3
30	The Recalcitrance and Resilience of Scientific Function. Poroi, 2020, 15, .	0.1	0
31	Elastic network modeling of cellular networks unveils sensor and effector genes that control information flow. PLoS Computational Biology, 2022, 18, e1010181.	3.2	0