

Fran Supek

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.

59
papers

6,352
citations

24
h-index

65
g-index

65
ext. papers

8,843
ext. citations

13.1
avg, IF

6.18
L-index

#	Paper	IF	Citations
59	REVIGO summarizes and visualizes long lists of gene ontology terms. <i>PLoS ONE</i> , 2011 , 6, e21800	3.7	3264
58	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
57	Synonymous mutations frequently act as driver mutations in human cancers. <i>Cell</i> , 2014 , 156, 1324-1335	56.2	369
56	Differential DNA mismatch repair underlies mutation rate variation across the human genome. <i>Nature</i> , 2015 , 521, 81-4	50.4	224
55	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
54	The rules and impact of nonsense-mediated mRNA decay in human cancers. <i>Nature Genetics</i> , 2016 , 48, 1112-8	36.3	208
53	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
52	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
51	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. <i>Cell</i> , 2017 , 170, 534-547.e23	56.2	105
50	INCA: synonymous codon usage analysis and clustering by means of self-organizing map. <i>Bioinformatics</i> , 2004 , 20, 2329-30	7.2	90
49	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. <i>Genome Biology</i> , 2016 , 17, 129	18.3	85
48	Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. <i>BMC Bioinformatics</i> , 2005 , 6, 182	3.6	81
47	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. <i>Nature Genetics</i> , 2019 , 51, 1645-1651	36.3	77
46	Translational selection is ubiquitous in prokaryotes. <i>PLoS Genetics</i> , 2010 , 6, e1001004	6	64
45	On relevance of codon usage to expression of synthetic and natural genes in <i>Escherichia coli</i> . <i>Genetics</i> , 2010 , 185, 1129-34	4	54
44	The landscape of microbial phenotypic traits and associated genes. <i>Nucleic Acids Research</i> , 2016 , 44, 10074-10090	14.1	90
43	Antitumor potential of crown ethers: structure-activity relationships, cell cycle disturbances, and cell death studies of a series of ionophores. <i>Journal of Medicinal Chemistry</i> , 2007 , 50, 1007-18	8.3	48

42	The Code of Silence: Widespread Associations Between Synonymous Codon Biases and Gene Function. <i>Journal of Molecular Evolution</i> , 2016 , 82, 65-73	3.1	40
41	Inferring gene function from evolutionary change in signatures of translation efficiency. <i>Genome Biology</i> , 2014 , 15, R44	18.3	37
40	Accurate models for P-gp drug recognition induced from a cancer cell line cytotoxicity screen. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 5691-708	8.3	33
39	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. <i>Nature Communications</i> , 2018 , 9, 2601	17.4	32
38	Hydroxymethylated cytosines are associated with elevated C to G transversion rates. <i>PLoS Genetics</i> , 2014 , 10, e1004585	6	28
37	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. <i>Nature Cell Biology</i> , 2018 , 20, 1400-1409	23.4	27
36	Phyletic profiling with cliques of orthologs is enhanced by signatures of paralogy relationships. <i>PLoS Computational Biology</i> , 2013 , 9, e1002852	5	26
35	DNA mismatch repair promotes APOBEC3-mediated diffuse hypermutation in human cancers. <i>Nature Genetics</i> , 2020 , 52, 958-968	36.3	24
34	Whole genome DNA sequencing provides an atlas of somatic mutagenesis in healthy human cells and identifies a tumor-prone cell type. <i>Genome Biology</i> , 2019 , 20, 285	18.3	24
33	Atypical cytostatic mechanism of N-1-sulfonylcytosine derivatives determined by in vitro screening and computational analysis. <i>Investigational New Drugs</i> , 2008 , 26, 97-110	4.3	22
32	To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases. <i>Trends in Genetics</i> , 2021 , 37, 657-668	8.5	22
31	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020 , 7, 170	8.2	20
30	Could LogP be a principal determinant of biological activity in 18-crown-6 ethers? Synthesis of biologically active adamantane-substituted diaza-crowns. <i>European Journal of Medicinal Chemistry</i> , 2011 , 46, 3444-54	6.8	20
29	Enhanced analytical power of SDS-PAGE using machine learning algorithms. <i>Proteomics</i> , 2008 , 8, 28-31	4.8	20
28	Proteome sequence features carry signatures of the environmental niche of prokaryotes. <i>BMC Evolutionary Biology</i> , 2011 , 11, 26	3	19
27	Matching cell lines with cancer type and subtype of origin via mutational, epigenomic, and transcriptomic patterns. <i>Science Advances</i> , 2020 , 6,	14.3	18
26	Scales and mechanisms of somatic mutation rate variation across the human genome. <i>DNA Repair</i> , 2019 , 81, 102647	4.3	18
25	Global Shifts in Genome and Proteome Composition Are Very Tightly Coupled. <i>Genome Biology and Evolution</i> , 2015 , 7, 1519-32	3.9	17

24	Signatures of conformational stability and oxidation resistance in proteomes of pathogenic bacteria. <i>Cell Reports</i> , 2014 , 7, 1393-1400	10.6	17
23	Computational structure-activity study directs synthesis of novel antitumor enkephalin analogs. <i>Amino Acids</i> , 2010 , 38, 1185-91	3.5	15
22	Passenger mutations accurately classify human tumors. <i>PLoS Computational Biology</i> , 2019 , 15, e1006953	5	14
21	Nucleoid-associated proteins affect mutation dynamics in E. coli in a growth phase-specific manner. <i>PLoS Computational Biology</i> , 2012 , 8, e1002846	5	13
20	Elevated Rate of Genome Rearrangements in Radiation-Resistant Bacteria. <i>Genetics</i> , 2017 , 205, 1677-1689	4.9	10
19	Machine learning prioritizes synthesis of primaquine ureidoamides with high antimalarial activity and attenuated cytotoxicity. <i>European Journal of Medicinal Chemistry</i> , 2018 , 146, 651-667	6.8	10
18	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
17	Integrated Analysis of Germline and Tumor DNA Identifies New Candidate Genes Involved in Familial Colorectal Cancer. <i>Cancers</i> , 2019 , 11,	6.6	8
16	Extensive complementarity between gene function prediction methods. <i>Bioinformatics</i> , 2016 , 32, 3645-3653	3.5	8
15	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
14	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype. <i>Scientific Reports</i> , 2019 , 9, 19537	4.9	7
13	Visualizing GO Annotations. <i>Methods in Molecular Biology</i> , 2017 , 1446, 207-220	1.4	6
12	The evolutionary signal in metagenome phyletic profiles predicts many gene functions. <i>Microbiome</i> , 2018 , 6, 129	16.6	2
11	Putative mechanisms of antitumor activity of cyano-substituted heteroaryles in HeLa cells. <i>Investigational New Drugs</i> , 2012 , 30, 450-67	4.3	2
10	Loss of the abasic site sensor HMCES is synthetic lethal with the activity of the APOBEC3A cytosine deaminase in cancer cells. <i>PLoS Biology</i> , 2021 , 19, e3001176	9.7	2
9	Mutational signatures are markers of drug sensitivity of cancer cells		2
8	Mutational signatures are markers of drug sensitivity of cancer cells. <i>Nature Communications</i> , 2022 , 13,	17.4	2
7	Phenotype Prediction with Semi-supervised Classification Trees. <i>Lecture Notes in Computer Science</i> , 2018 , 138-150	0.9	1

6	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype		1
5	Phenotype Inference from Text and Genomic Data. <i>Lecture Notes in Computer Science</i> , 2017 , 373-377	0.9	1
4	Loss of HMCES is synthetic lethal with APOBEC activity in cancer cells		1
3	Spectrum of DNA mismatch repair failures viewed through the lens of cancer genomics and implications for therapy.. <i>Clinical Science</i> , 2022 , 136, 383-404	6.5	1
2	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. <i>Nature Communications</i> , 2021 , 12, 7051	17.4	1
1	A framework for mutational signature analysis based on DNA shape parameters.. <i>PLoS ONE</i> , 2022 , 17, e0262495	3.7	0