Fran Supek

List of Publications by Year
in descending order

55 papers	10,217 citations	186209 28 h-index	149623 56 g-index
65 all docs	65 docs citations	65 times ranked	22673 citing authors

#	Article	IF	Citations
1	REVIGO Summarizes and Visualizes Long Lists of Gene Ontology Terms. PLoS ONE, 2011, 6, e21800.	1.1	5,347
2	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
3	Synonymous Mutations Frequently Act as Driver Mutations in Human Cancers. Cell, 2014, 156, 1324-1335.	13.5	482
4	The rules and impact of nonsense-mediated mRNA decay in human cancers. Nature Genetics, 2016, 48, 1112-1118.	9.4	340
5	Differential DNA mismatch repair underlies mutation rate variation across the human genome. Nature, 2015, 521, 81-84.	13.7	310
6	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
7	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
8	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
9	Clustered Mutation Signatures Reveal that Error-Prone DNA Repair Targets Mutations to Active Genes. Cell, 2017, 170, 534-547.e23.	13.5	173
10	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. Nature Genetics, 2019, 51, 1645-1651.	9.4	171
11	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. Genome Biology, 2016, 17, 129.	3.8	126
12	To NMD or Not To NMD: Nonsense-Mediated mRNA Decay in Cancer and Other Genetic Diseases. Trends in Genetics, 2021, 37, 657-668.	2.9	124
13	Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. BMC Bioinformatics, 2005, 6, 182.	1.2	109
14	INCA: synonymous codon usage analysis and clustering by means of self-organizing map. Bioinformatics, 2004, 20, 2329-2330.	1.8	103
15	Translational Selection Is Ubiquitous in Prokaryotes. PLoS Genetics, 2010, 6, e1001004.	1.5	76
16	DNA mismatch repair promotes APOBEC3-mediated diffuse hypermutation in human cancers. Nature Genetics, 2020, 52, 958-968.	9.4	76
17	The landscape of microbial phenotypic traits and associated genes. Nucleic Acids Research, 2016, 44, gkw964.	6.5	71
18	The Code of Silence: Widespread Associations Between Synonymous Codon Biases and Gene Function. Journal of Molecular Evolution, 2016, 82, 65-73.	0.8	60

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19	Antitumor Potential of Crown Ethers: Structure–Activity Relationships, Cell Cycle Disturbances, and Cell Death Studies of a Series of Ionophores. Journal of Medicinal Chemistry, 2007, 50, 1007-1018.	2.9	59
20	Scales and mechanisms of somatic mutation rate variation across the human genome. DNA Repair, 2019, 81, 102647.	1.3	59
21	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	2.4	59
22	On Relevance of Codon Usage to Expression of Synthetic and Natural Genes in <i>Escherichia coli</i>. Genetics, 2010, 185, 1129-1134.	1.2	57
23	Inferring gene function from evolutionary change in signatures of translation efficiency. Genome Biology, 2014, 15, R44.	13.9	53
24	Matching cell lines with cancer type and subtype of origin via mutational, epigenomic, and transcriptomic patterns. Science Advances, 2020, 6, .	4.7	53
25	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. Nature Communications, 2018, 9, 2601.	5.8	47
26	Whole genome DNA sequencing provides an atlas of somatic mutagenesis in healthy human cells and identifies a tumor-prone cell type. Genome Biology, 2019, 20, 285.	3.8	46
27	Accurate Models for P-gp Drug Recognition Induced from a Cancer Cell Line Cytotoxicity Screen. Journal of Medicinal Chemistry, 2013, 56, 5691-5708.	2.9	45
28	Passenger mutations accurately classify human tumors. PLoS Computational Biology, 2019, 15, e1006953.	1.5	39
29	Loss of G9a preserves mutation patterns but increases chromatin accessibility, genomic instability and aggressiveness in skin tumours. Nature Cell Biology, 2018, 20, 1400-1409.	4.6	35
30	Hydroxymethylated Cytosines Are Associated with Elevated C to G Transversion Rates. PLoS Genetics, 2014, 10, e1004585.	1.5	31
31	Global Shifts in Genome and Proteome Composition Are Very Tightly Coupled. Genome Biology and Evolution, 2015, 7, 1519-1532.	1.1	31
32	Phyletic Profiling with Cliques of Orthologs Is Enhanced by Signatures of Paralogy Relationships. PLoS Computational Biology, 2013, 9, e1002852.	1.5	29
33	Mutational signatures are markers of drug sensitivity of cancer cells. Nature Communications, 2022, 13, .	5.8	29
34	Could LogP be a principal determinant of biological activity in 18-crown-6 ethers? Synthesis of biologically active adamantane-substituted diaza-crowns. European Journal of Medicinal Chemistry, 2011, 46, 3444-3454.	2.6	26
35	Proteome sequence features carry signatures of the environmental niche of prokaryotes. BMC Evolutionary Biology, 2011, 11, 26.	3.2	25
36	Loss of the abasic site sensor HMCES is synthetic lethal with the activity of the APOBEC3A cytosine deaminase in cancer cells. PLoS Biology, 2021, 19, e3001176.	2.6	25

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37	Atypical cytostatic mechanism of N-1-sulfonylcytosine derivatives determined by in vitro screening and computational analysis. Investigational New Drugs, 2008, 26, 97-110.	1.2	23
38	Enhanced analytical power of SDS‐PAGE using machine learning algorithms. Proteomics, 2008, 8, 28-31.	1.3	22
39	Nucleoid-Associated Proteins Affect Mutation Dynamics in E. coli in a Growth Phase-Specific Manner. PLoS Computational Biology, 2012, 8, e1002846.	1.5	21
40	Signatures of Conformational Stability and Oxidation Resistance in Proteomes of Pathogenic Bacteria. Cell Reports, 2014, 7, 1393-1400.	2.9	19
41	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype. Scientific Reports, 2019, 9, 19537.	1.6	19
42	Computational structure‐activity study directs synthesis of novel antitumor enkephalin analogs. Amino Acids, 2010, 38, 1185-1191.	1.2	17
43	Integrated Analysis of Germline and Tumor DNA Identifies New Candidate Genes Involved in Familial Colorectal Cancer. Cancers, 2019, 11, 362.	1.7	16
44	Elevated Rate of Genome Rearrangements in Radiation-Resistant Bacteria. Genetics, 2017, 205, 1677-1689.	1.2	14
45	The impact of rare germline variants on human somatic mutation processes. Nature Communications, 2022, 13, .	5.8	13
46	Extensive complementarity between gene function prediction methods. Bioinformatics, 2016, 32, 3645-3653.	1.8	12
47	Visualizing GO Annotations. Methods in Molecular Biology, 2017, 1446, 207-220.	0.4	12
48	Machine learning prioritizes synthesis of primaquine ureidoamides with high antimalarial activity and attenuated cytotoxicity. European Journal of Medicinal Chemistry, 2018, 146, 651-667.	2.6	11
49	Spectrum of DNA mismatch repair failures viewed through the lens of cancer genomics and implications for therapy. Clinical Science, 2022, 136, 383-404.	1.8	8
50	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. Nature Communications, 2021, 12, 7051.	5.8	5
51	A framework for mutational signature analysis based on DNA shape parameters. PLoS ONE, 2022, 17, e0262495.	1.1	4
52	Putative mechanisms of antitumor activity of cyano-substituted heteroaryles in HeLa cells. Investigational New Drugs, 2012, 30, 450-467.	1.2	3
53	The evolutionary signal in metagenome phyletic profiles predicts many gene functions. Microbiome, 2018, 6, 129.	4.9	3
54	Phenotype Inference from Text and Genomic Data. Lecture Notes in Computer Science, 2017, , 373-377.	1.0	2

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55	Phenotype Prediction with Semi-supervised Classification Trees. Lecture Notes in Computer Science, 2018, , 138-150.	1.0	1