

Fran Supek

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6133688/fran-supek-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	A framework for mutational signature analysis based on DNA shape parameters.. <i>PLoS ONE</i> , 2022 , 17, e0262495	3.7	0
58	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
57	Mutational signatures are markers of drug sensitivity of cancer cells. <i>Nature Communications</i> , 2022 , 13,	17.4	2
56	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
55	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
54	Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers. <i>Nature Communications</i> , 2021 , 12, 7051	17.4	1
53	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020 , 7, 170	8.2	20
52	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
51	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
50	DNA mismatch repair promotes APOBEC3-mediated diffuse hypermutation in human cancers. <i>Nature Genetics</i> , 2020 , 52, 958-968	36.3	24
49	Passenger mutations accurately classify human tumors. <i>PLoS Computational Biology</i> , 2019 , 15, e1006953	5	14
48	Integrated Analysis of Germline and Tumor DNA Identifies New Candidate Genes Involved in Familial Colorectal Cancer. <i>Cancers</i> , 2019 , 11,	6.6	8
47	Scales and mechanisms of somatic mutation rate variation across the human genome. <i>DNA Repair</i> , 2019 , 81, 102647	4.3	18
46	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
45	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype. <i>Scientific Reports</i> , 2019 , 9, 19537	4.9	7
44	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
43	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

42	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
41	The evolutionary signal in metagenome phyletic profiles predicts many gene functions. <i>Microbiome</i> , 2018 , 6, 129	16.6	2
40	Systematic discovery of germline cancer predisposition genes through the identification of somatic second hits. <i>Nature Communications</i> , 2018 , 9, 2601	17.4	32
39	Phenotype Prediction with Semi-supervised Classification Trees. <i>Lecture Notes in Computer Science</i> , 2018 , 138-150	0.9	1
38	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
37	Elevated Rate of Genome Rearrangements in Radiation-Resistant Bacteria. <i>Genetics</i> , 2017 , 205, 1677-1689		10
36	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
35	Visualizing GO Annotations. <i>Methods in Molecular Biology</i> , 2017 , 1446, 207-220	1.4	6
34	Phenotype Inference from Text and Genomic Data. <i>Lecture Notes in Computer Science</i> , 2017 , 373-377	0.9	1
33	Extensive complementarity between gene function prediction methods. <i>Bioinformatics</i> , 2016 , 32, 3645-3653		8
32	The rules and impact of nonsense-mediated mRNA decay in human cancers. <i>Nature Genetics</i> , 2016 , 48, 1112-8	36.3	208
31	The landscape of microbial phenotypic traits and associated genes. <i>Nucleic Acids Research</i> , 2016 , 44, 10074-10090		10
30	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. <i>Genome Biology</i> , 2016 , 17, 129	18.3	85
29	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
28	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
27	Differential DNA mismatch repair underlies mutation rate variation across the human genome. <i>Nature</i> , 2015 , 521, 81-4	50.4	224
26	Global Shifts in Genome and Proteome Composition Are Very Tightly Coupled. <i>Genome Biology and Evolution</i> , 2015 , 7, 1519-32	3.9	17
25	Synonymous mutations frequently act as driver mutations in human cancers. <i>Cell</i> , 2014 , 156, 1324-1335	56.2	369

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	Hydroxymethylated cytosines are associated with elevated C to G transversion rates. <i>PLoS Genetics</i> , 2014 , 10, e1004585	6	28
22	Inferring gene function from evolutionary change in signatures of translation efficiency. <i>Genome Biology</i> , 2014 , 15, R44	18.3	37
21	Phyletic profiling with cliques of orthologs is enhanced by signatures of paralogy relationships. <i>PLoS Computational Biology</i> , 2013 , 9, e1002852	5	26
20	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
19	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
18	Putative mechanisms of antitumor activity of cyano-substituted heteroaryles in HeLa cells. <i>Investigational New Drugs</i> , 2012 , 30, 450-67	4.3	2
17	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
16	Proteome sequence features carry signatures of the environmental niche of prokaryotes. <i>BMC Evolutionary Biology</i> , 2011 , 11, 26	3	19
15	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
14	REVIGO summarizes and visualizes long lists of gene ontology terms. <i>PLoS ONE</i> , 2011 , 6, e21800	3.7	3264
13	Translational selection is ubiquitous in prokaryotes. <i>PLoS Genetics</i> , 2010 , 6, e1001004	6	64
12	On relevance of codon usage to expression of synthetic and natural genes in Escherichia coli. <i>Genetics</i> , 2010 , 185, 1129-34	4	54
11	Computational structure-activity study directs synthesis of novel antitumor enkephalin analogs. <i>Amino Acids</i> , 2010 , 38, 1185-91	3.5	15
10	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
9	Enhanced analytical power of SDS-PAGE using machine learning algorithms. <i>Proteomics</i> , 2008 , 8, 28-31	4.8	20
8	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
7	Comparison of codon usage measures and their applicability in prediction of microbial gene expressivity. <i>BMC Bioinformatics</i> , 2005 , 6, 182	3.6	81

6	INCA: synonymous codon usage analysis and clustering by means of self-organizing map. <i>Bioinformatics</i> , 2004 , 20, 2329-30	7.2	90
5	Patterns of diverse gene functions in genomic neighborhoods predict gene function and phenotype		1
4	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
3	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
2	Mutational signatures are markers of drug sensitivity of cancer cells		2
1	Loss of HMCES is synthetic lethal with APOBEC activity in cancer cells		1