

# Franco J Vizeacoumar

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

939  
citations

623734

14  
h-index

501196

28  
g-index

30  
all docs

30  
docs citations

30  
times ranked

2082  
citing authors

#	ARTICLE	IF	CITATIONS
1	Essential Gene Profiles in Breast, Pancreatic, and Ovarian Cancer Cells. <i>Cancer Discovery</i> , 2012, 2, 172-189.	9.4	276
2	Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. <i>Journal of Cell Biology</i> , 2010, 188, 69-81.	5.2	100
3	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	7.2	90
4	Genome-wide synthetic lethal screen unveils novel CAIX-NFS1/xCT axis as a targetable vulnerability in hypoxic solid tumors. <i>Science Advances</i> , 2021, 7, .	10.3	65
5	Protein Tyrosine Kinases: Their Roles and Their Targeting in Leukemia. <i>Cancers</i> , 2021, 13, 184.	3.7	40
6	An integrated computational and experimental study uncovers <sc>FUT</sc> 9 as a metabolic driver of colorectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 956.	7.2	38
7	A picture is worth a thousand words: Genomics to phenomics in the yeast <i>Saccharomyces cerevisiae</i>. <i>FEBS Letters</i> , 2009, 583, 1656-1661.	2.8	32
8	EPHB6 augments both development and drug sensitivity of triple-negative breast cancer tumours. <i>Oncogene</i> , 2018, 37, 4073-4093.	5.9	30
9	Therapeutic relevance of the protein phosphatase 2A in cancer. <i>Oncotarget</i> , 2016, 7, 61544-61561.	1.8	27
10	Building high-resolution synthetic lethal networks: a "Google map"™ of the cancer cell. <i>Trends in Molecular Medicine</i> , 2014, 20, 704-715.	6.7	26
11	A Road Map to Personalizing Targeted Cancer Therapies Using Synthetic Lethality. <i>Trends in Cancer</i> , 2019, 5, 11-29.	7.4	21
12	The CINs of Polo-Like Kinase 1 in Cancer. <i>Cancers</i> , 2020, 12, 2953.	3.7	19
13	Estrogen receptor signaling regulates the expression of the breast tumor kinase in breast cancer cells. <i>BMC Cancer</i> , 2019, 19, 78.	2.6	18
14	APOBEC1 cytosine deaminase activity on single-stranded DNA is suppressed by replication protein A. <i>Nucleic Acids Research</i> , 2021, 49, 322-339.	14.5	18
15	Targeting synthetic lethality between the SRC kinase and the EPHB6 receptor may benefit cancer treatment. <i>Oncotarget</i> , 2016, 7, 50027-50042.	1.8	17
16	Biochemical characterization of INTS3 and C9ORF80, two subunits of hNABP1/2 heterotrimeric complex in nucleic acid binding. <i>Biochemical Journal</i> , 2018, 475, 45-60.	3.7	16
17	Targeting the CINful genome: Strategies to overcome tumor heterogeneity. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 147, 77-91.	2.9	14
18	FRK inhibits breast cancer cell migration and invasion by suppressing epithelial-mesenchymal transition. <i>Oncotarget</i> , 2017, 8, 113034-113065.	1.8	14

#	ARTICLE	IF	CITATIONS
19	The intrinsically kinase-inactive EPHB6 receptor predisposes cancer cells to DR5-induced apoptosis by promoting mitochondrial fragmentation. <i>Oncotarget</i> , 2016, 7, 77865-77877.	1.8	13
20	The EphB6 receptor is overexpressed in pediatric T cell acute lymphoblastic leukemia and increases its sensitivity to doxorubicin treatment. <i>Scientific Reports</i> , 2017, 7, 14767.	3.3	12
21	Highly Specific Sigma Receptor Ligands Exhibit Anti-Viral Properties in SARS-CoV-2 Infected Cells. <i>Pathogens</i> , 2021, 10, 1514.	2.8	12
22	Global phosphoproteomic analysis identifies SRMS-regulated secondary signaling intermediates. <i>Proteome Science</i> , 2018, 16, 16.	1.7	10
23	Humanized yeast genetic interaction mapping predicts synthetic lethal interactions of FBXW7 in breast cancer. <i>BMC Medical Genomics</i> , 2019, 12, 112.	1.5	10
24	Expression-based analyses indicate a central role for hypoxia in driving tumor plasticity through microenvironment remodeling and chromosomal instability. <i>Npj Systems Biology and Applications</i> , 2018, 4, 38.	3.0	8
25	Banding Together: A Systematic Comparison of The Cancer Genome Atlas and the Mitelman Databases. <i>Cancer Research</i> , 2019, 79, 5181-5190.	0.9	5
26	Enhancing the throughput and multiplexing capabilities of next generation sequencing for efficient implementation of pooled shRNA and CRISPR screens. <i>Scientific Reports</i> , 2017, 7, 1040.	3.3	4
27	Molecular characterization of an MLL1 fusion and its role in chromosomal instability. <i>Molecular Oncology</i> , 2019, 13, 422-440.	4.6	3
28	Differential expression of <i>HNF1A</i> and <i>HNF1A</i> â€‘ <i>CAS1</i> in colon cancer cells. <i>IUBMB Life</i> , 2022, 74, 496-507.	3.4	1
29	Computational Prediction of Chemical Tools for Identification and Validation of Synthetic Lethal Interaction Networks. <i>Methods in Molecular Biology</i> , 2021, 2381, 333-358.	0.9	0
30	Identification of novel genes involved in apoptosis of HIV-infected macrophages using unbiased genome-wide screening. <i>BMC Infectious Diseases</i> , 2021, 21, 655.	2.9	0