

Francisco Sanchez-Vega

List of Publications by Year in Descending Order

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Version: 2024-04-19

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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.

64
papers

10,692
citations

30
h-index

71
g-index

71
ext. papers

15,409
ext. citations

16.7
avg, IF

4.81
L-index

#	Paper	IF	Citations
64	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients.. <i>Cell</i> , 2022 , 185, 563-575.e11	56.2	11
63	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer.. <i>JCO Precision Oncology</i> , 2022 , 6, e2100365	3.6	
62	Molecular and phenotypic profiling of colorectal cancer patients in West Africa reveals biological insights. <i>Nature Communications</i> , 2021 , 12, 6821	17.4	2
61	Identifying Diagnostic MicroRNAs and Investigating Their Biological Implications in Rectal Cancer. <i>JAMA Network Open</i> , 2021 , 4, e2136913	10.4	0
60	Adoption of Organ Preservation and Surgeon Variability for Patients with Rectal Cancer Does Not Correlate with Worse Survival. <i>Annals of Surgical Oncology</i> , 2021 , 1	3.1	3
59	ASO Visual Abstract: Adoption of Organ Preservation and Surgeon Variability for Patients with Rectal Cancer Does Not Correlate with Worse Survival. <i>Annals of Surgical Oncology</i> , 2021 , 1	3.1	
58	A Randomized Phase II Trial of Adjuvant Hepatic Arterial Infusion and Systemic Therapy With or Without Panitumumab After Hepatic Resection of KRAS Wild-type Colorectal Cancer. <i>Annals of Surgery</i> , 2021 , 274, 248-254	7.8	1
57	Next-Generation Sequencing of 487 Esophageal Adenocarcinomas Reveals Independently Prognostic Genomic Driver Alterations and Pathways. <i>Clinical Cancer Research</i> , 2021 , 27, 3491-3498	12.9	1
56	The genomic landscape of carcinomas with mucinous differentiation. <i>Scientific Reports</i> , 2021 , 11, 9478	4.9	1
55	KRAS mutant rectal cancer cells interact with surrounding fibroblasts to deplete the extracellular matrix. <i>Molecular Oncology</i> , 2021 , 15, 2766-2781	7.9	0
54	Prevalence and Landscape of Actionable Genomic Alterations in Renal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2021 , 27, 5595-5606	12.9	3
53	Intraoperative opioid exposure, tumour genomic alterations, and survival differences in people with lung adenocarcinoma. <i>British Journal of Anaesthesia</i> , 2021 , 127, 75-84	5.4	12
52	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. <i>Blood</i> , 2021 , 137, 2103-2113	2.2	19
51	Mutation Is Associated with Increased Risk of Recurrence in Surgically Resected Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2021 , 27, 2604-2612	12.9	9
50	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. <i>JAMA Surgery</i> , 2021 , 156, e205601	5.4	16
49	The Emerging Importance of Tumor Genomics in Operable Non-Small Cell Lung Cancer. <i>Cancers</i> , 2021 , 13,	6.6	3
48	Intraoperative ketorolac may interact with patient-specific tumour genomics to modify recurrence risk in lung adenocarcinoma: an exploratory analysis. <i>British Journal of Anaesthesia</i> , 2021 , 127, e82-e85	5.4	0

47	Therapeutic Implications of Detecting MAPK-Activating Alterations in Cutaneous and Unknown Primary Melanomas. <i>Clinical Cancer Research</i> , 2021 , 27, 2226-2235	12.9	6
46	Mismatch Repair-Deficient Rectal Cancer and Resistance to Neoadjuvant Chemotherapy. <i>Clinical Cancer Research</i> , 2020 , 26, 3271-3279	12.9	41
45	Lung-only melanoma: UV mutational signature supports origin from occult cutaneous primaries and argues against the concept of primary pulmonary melanoma. <i>Modern Pathology</i> , 2020 , 33, 2244-2255	9.8	12
44	Early TP53 alterations engage environmental exposures to promote gastric premalignancy in an integrative mouse model. <i>Nature Genetics</i> , 2020 , 52, 219-230	36.3	15
43	Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma: A Phase 2 Clinical Trial. <i>JAMA Oncology</i> , 2020 , 6, 60-67	13.4	55
42	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2020 , 15, 1844-1856	8.9	20
41	Rb and p53-Deficient Myxofibrosarcoma and Undifferentiated Pleomorphic Sarcoma Require Skp2 for Survival. <i>Cancer Research</i> , 2020 , 80, 2461-2471	10.1	10
40	Analysis of Tumor Genomic Pathway Alterations Using Broad-Panel Next-Generation Sequencing in Surgically Resected Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2019 , 25, 7475-7484	12.9	14
39	A rectal cancer organoid platform to study individual responses to chemoradiation. <i>Nature Medicine</i> , 2019 , 25, 1607-1614	50.5	149
38	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with -Mutant Lung Cancers. <i>Clinical Cancer Research</i> , 2019 , 25, 1063-1069	12.9	156
37	Phase II study of trastuzumab with modified docetaxel, cisplatin, and 5 fluorouracil in metastatic HER2-positive gastric cancer. <i>Gastric Cancer</i> , 2019 , 22, 355-362	7.6	9
36	Genomic stratification beyond Ras/B-Raf in colorectal liver metastasis patients treated with hepatic arterial infusion. <i>Cancer Medicine</i> , 2019 , 8, 6538-6548	4.8	5
35	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. <i>ELife</i> , 2019 , 8,	8.9	17
34	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. <i>Blood</i> , 2019 , 134, 633-633	2.2	
33	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Non-Small-Cell Lung Cancer. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	27
32	and Amplifications Determine Response to HER2 Inhibition in -Amplified Esophagogastric Cancer. <i>Cancer Discovery</i> , 2019 , 9, 199-209	24.4	79
31	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. <i>Cancer Cell</i> , 2018 , 33, 527-541.e855	14.5	855
30	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854

29	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
28	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
27	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
26	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
25	Genomic Features of Response to Combination Immunotherapy in Patients with Advanced Non-Small-Cell Lung Cancer. <i>Cancer Cell</i> , 2018 , 33, 843-852.e4	24.3	525
24	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2018 , 33, 125-136.e3	24.3	338
23	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
22	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
21	Effects of Co-occurring Genomic Alterations on Outcomes in Patients with -Mutant Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 334-340	12.9	173
20	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10	10.6	200
19	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , 2018 , 8, 49-58	24.4	180
18	Molecular Determinants of Response to Anti-Programmed Cell Death (PD)-1 and Anti-Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Non-Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. <i>Journal of Clinical Oncology</i> , 2018 , 36, 633-641	2.2	730
17	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. <i>Cancer Cell</i> , 2018 , 34, 893-905.e8	24.3	166
16	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
15	KMT2C mediates the estrogen dependence of breast cancer through regulation of ER α enhancer function. <i>Oncogene</i> , 2018 , 37, 4692-4710	9.2	48
14	CDK4/6 or MAPK blockade enhances efficacy of EGFR inhibition in oesophageal squamous cell carcinoma. <i>Nature Communications</i> , 2017 , 8, 13897	17.4	42
13	ARF Confers a Context-Dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. <i>Cancer Research</i> , 2017 , 77, 1035-1046	10.1	12
12	Transposon mutagenesis identifies chromatin modifiers cooperating with in thyroid tumorigenesis and detects as a cancer gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E4951-E4960	11.5	9

11	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	9.75	961
10	The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing. <i>Science Signaling</i> , 2017 , 10,	8.8	33
9	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. <i>Cancer Cell</i> , 2017 , 32, 155-168.e6	24.3	61
8	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
7	Recurrent, truncating SOX9 mutations are associated with SOX9 overexpression, KRAS mutation, and TP53 wild type status in colorectal carcinoma. <i>Oncotarget</i> , 2016 , 7, 50875-50882	3.3	15
6	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. <i>Biomolecules</i> , 2016 , 6,	5.9	16
5	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. <i>PLoS Computational Biology</i> , 2016 , 12, e1004765	5	23
4	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
3	Pan-cancer stratification of solid human epithelial tumors and cancer cell lines reveals commonalities and tissue-specific features of the CpG island methylator phenotype. <i>Epigenetics and Chromatin</i> , 2015 , 8, 14	5.8	27
2	Learning multivariate distributions by competitive assembly of marginals. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2013 , 35, 398-410	13.3	2
1	Recurrent patterns of DNA methylation in the ZNF154, CASP8, and VHL promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. <i>Epigenetics</i> , 2013 , 8, 1355-72	5.7	40