Francisco Sanchez-Vega

List of Publications by Year
in descending order

68 papers	18,893 citations	101543 36 h-index	98798 67 g-index
71 all docs	71 docs citations	71 times ranked	29360 citing authors

#	Article	IF	Citations
1	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
2	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
3	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
4	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
5	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
6	Molecular Determinants of Response to Antiâ€"Programmed Cell Death (PD)-1 and Antiâ€"Programmed Death-Ligand 1 (PD-L1) Blockade in Patients With Nonâ€"Small-Cell Lung Cancer Profiled With Targeted Next-Generation Sequencing. Journal of Clinical Oncology, 2018, 36, 633-641.	1.6	1,109
7	Genomic Features of Response to Combination Immunotherapy in Patients with Advanced Non-Small-Cell Lung Cancer. Cancer Cell, 2018, 33, 843-852.e4.	16.8	827
8	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
9	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
10	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	16.8	589
11	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
12	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
13	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
14	Effects of Co-occurring Genomic Alterations on Outcomes in Patients withKRAS-Mutant Nonâ€"Small Cell Lung Cancer. Clinical Cancer Research, 2018, 24, 334-340.	7.0	323
15	A rectal cancer organoid platform to study individual responses to chemoradiation. Nature Medicine, 2019, 25, 1607-1614.	30.7	320
16	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. Cancer Cell, 2018, 34, 893-905.e8.	16.8	307
17	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	9.4	275
18	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272

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19	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with EGFR-Mutant Lung Cancers. Clinical Cancer Research, 2019, 25, 1063-1069.	7.0	257
20	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	28.9	223
21	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
22	Mismatch Repairâ€"Deficient Rectal Cancer and Resistance to Neoadjuvant Chemotherapy. Clinical Cancer Research, 2020, 26, 3271-3279.	7.0	118
23	EGFR and MET Amplifications Determine Response to HER2 Inhibition in ERBB2-Amplified Esophagogastric Cancer. Cancer Discovery, 2019, 9, 199-209.	9.4	115
24	Assessment of Hepatic Arterial Infusion of Floxuridine in Combination With Systemic Gemcitabine and Oxaliplatin in Patients With Unresectable Intrahepatic Cholangiocarcinoma. JAMA Oncology, 2020, 6, 60.	7.1	112
25	KMT2C mediates the estrogen dependence of breast cancer through regulation of ERÎ± enhancer function. Oncogene, 2018, 37, 4692-4710.	5.9	102
26	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. Cancer Cell, 2018, 33, 527-541.e8.	16.8	99
27	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. Cancer Cell, 2017, 32, 155-168.e6.	16.8	93
28	The Underlying Tumor Genomics of Predominant Histologic Subtypes in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2020, 15, 1844-1856.	1.1	83
29	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. Nature Communications, 2022, 13, .	12.8	63
30	Harmonization of Tumor Mutational Burden Quantification and Association With Response to Immune Checkpoint Blockade in Nonâ€"Small-Cell Lung Cancer. JCO Precision Oncology, 2019, 3, 1-12.	3.0	58
31	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. Blood, 2021, 137, 2103-2113.	1.4	57
32	CDK4/6 or MAPK blockade enhances efficacy of EGFR inhibition in oesophageal squamous cell carcinoma. Nature Communications, 2017, 8, 13897.	12.8	54
33	Recurrent patterns of DNA methylation in theZNF154,CASP8, andVHLpromoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. Epigenetics, 2013, 8, 1355-1372.	2.7	52
34	The RNA-editing enzyme ADAR promotes lung adenocarcinoma migration and invasion by stabilizing FAK. Science Signaling, 2017, 10, .	3.6	52
35	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	4.3	52
36	Pan-cancer stratification of solid human epithelial tumors and cancer cell lines reveals commonalities and tissue-specific features of the CpG island methylator phenotype. Epigenetics and Chromatin, 2015, 8, 14.	3.9	42

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37	Early TP53 alterations engage environmental exposures to promote gastric premalignancy in an integrative mouse model. Nature Genetics, 2020, 52, 219-230.	21.4	37
38	Intraoperative opioid exposure, tumour genomic alterations, and survival differences in people with lung adenocarcinoma. British Journal of Anaesthesia, 2021, 127, 75-84.	3.4	33
39	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. PLoS Computational Biology, 2016, 12, e1004765.	3.2	32
40	Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. ELife, 2019, 8, .	6.0	31
41	Analysis of Tumor Genomic Pathway Alterations Using Broad-Panel Next-Generation Sequencing in Surgically Resected Lung Adenocarcinoma. Clinical Cancer Research, 2019, 25, 7475-7484.	7.0	30
42	Recurrent, truncating SOX9 mutations are associated with SOX9 overexpression, KRAS mutation, and TP53 wild type status in colorectal carcinoma. Oncotarget, 2016, 7, 50875-50882.	1.8	26
43	Therapeutic Implications of Detecting MAPK-Activating Alterations in Cutaneous and Unknown Primary Melanomas. Clinical Cancer Research, 2021, 27, 2226-2235.	7.0	25
44	Lung-only melanoma: UV mutational signature supports origin from occult cutaneous primaries and argues against the concept of primary pulmonary melanoma. Modern Pathology, 2020, 33, 2244-2255.	5.5	23
45	The Emergence of Pan-Cancer CIMP and Its Elusive Interpretation. Biomolecules, 2016, 6, 45.	4.0	22
46	Rb and p53-Deficient Myxofibrosarcoma and Undifferentiated Pleomorphic Sarcoma Require Skp2 for Survival. Cancer Research, 2020, 80, 2461-2471.	0.9	22
47	KRAS G12C Mutation Is Associated with Increased Risk of Recurrence in Surgically Resected Lung Adenocarcinoma. Clinical Cancer Research, 2021, 27, 2604-2612.	7.0	20
48	Transposon mutagenesis identifies chromatin modifiers cooperating with Ras in thyroid tumorigenesis and detects ATXN7 as a cancer gene. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4951-E4960.	7.1	17
49	ARF Confers a Context-Dependent Response to Chemotherapy in Muscle-Invasive Bladder Cancer. Cancer Research, 2017, 77, 1035-1046.	0.9	15
50	Molecular and phenotypic profiling of colorectal cancer patients in West Africa reveals biological insights. Nature Communications, 2021, 12, 6821.	12.8	15
51	Prevalence and Landscape of Actionable Genomic Alterations in Renal Cell Carcinoma. Clinical Cancer Research, 2021, 27, 5595-5606.	7.0	12
52	Phase II study of trastuzumab with modified docetaxel, cisplatin, and 5 fluorouracil in metastatic HER2-positive gastric cancer. Gastric Cancer, 2019, 22, 355-362.	5.3	11
53	The genomic landscape of carcinomas with mucinous differentiation. Scientific Reports, 2021, 11, 9478.	3.3	9
54	CpG island methylator phenotype in adenocarcinomas from the digestive tract: Methods, conclusions, and controversies. World Journal of Gastrointestinal Oncology, 2017, 9, 105.	2.0	9

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55	Genomic stratification beyond Ras/Bâ€Raf in colorectal liver metastasis patients treated with hepatic arterial infusion. Cancer Medicine, 2019, 8, 6538-6548.	2.8	8
56	Next-Generation Sequencing of 487 Esophageal Adenocarcinomas Reveals Independently Prognostic Genomic Driver Alterations and Pathways. Clinical Cancer Research, 2021, 27, 3491-3498.	7.0	8
57	The Emerging Importance of Tumor Genomics in Operable Non-Small Cell Lung Cancer. Cancers, 2021, 13, 3656.	3.7	8
58	KRAS mutant rectal cancer cells interact with surrounding fibroblasts to deplete the extracellular matrix. Molecular Oncology, 2021, 15, 2766-2781.	4.6	7
59	Intraoperative ketorolac may interact with patient-specific tumour genomics to modify recurrence risk in lung adenocarcinoma: an exploratory analysis. British Journal of Anaesthesia, 2021, 127, e82-e85.	3.4	5
60	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. Annals of Surgery, 2021, 274, 248-254.	4.2	4
61	Adoption of Organ Preservation and Surgeon Variability for Patients with Rectal Cancer Does Not Correlate with Worse Survival. Annals of Surgical Oncology, 2021, , 1.	1.5	4
62	Association of genomic profiles and survival in early onset and screeningâ€age colorectal cancer patients with liver metastases resected over 15 years. Journal of Surgical Oncology, 2022, 125, 880-888.	1.7	4
63	Learning Multivariate Distributions by Competitive Assembly of Marginals. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 398-410.	13.9	3
64	Identifying Diagnostic MicroRNAs and Investigating Their Biological Implications in Rectal Cancer. JAMA Network Open, 2021, 4, e2136913.	5.9	3
65	Computational methods and translational applications for targeted nextâ€generation sequencing platforms. Genes Chromosomes and Cancer, 2022, 61, 322-331.	2.8	3
66	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. Blood, 2019, 134, 633-633.	1.4	1
67	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100365.	3.0	1
68	ASO Visual Abstract: Adoption of Organ Preservation and Surgeon Variability for Patients with Rectal Cancer Does Not Correlate with Worse Survival. Annals of Surgical Oncology, 2021, , 1.	1.5	0