## James X Sun

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotechnology, 2013, 31, 1023-1031.	17.5	1,785
2	Rucaparib maintenance treatment for recurrent ovarian carcinoma after response to platinum therapy (ARIEL3): a randomised, double-blind, placebo-controlled, phase 3 trial. Lancet, The, 2017, 390, 1949-1961.	13.7	1,261
3	Rucaparib in relapsed, platinum-sensitive high-grade ovarian carcinoma (ARIEL2 Part 1): an international, multicentre, open-label, phase 2 trial. Lancet Oncology, The, 2017, 18, 75-87.	10.7	975
4	Emergence of Constitutively Active Estrogen Receptor-α Mutations in Pretreated Advanced Estrogen Receptor–Positive Breast Cancer. Clinical Cancer Research, 2014, 20, 1757-1767.	7.0	529
5	Secondary Somatic Mutations Restoring <i>RAD51C</i> and <i>RAD51D</i> Associated with Acquired Resistance to the PARP Inhibitor Rucaparib in High-Grade Ovarian Carcinoma. Cancer Discovery, 2017, 7, 984-998.	9.4	310
6	<i>BRCA</i> Reversion Mutations in Circulating Tumor DNA Predict Primary and Acquired Resistance to the PARP Inhibitor Rucaparib in High-Grade Ovarian Carcinoma. Cancer Discovery, 2019, 9, 210-219.	9.4	278
7	<sup>Non-V600</sup> <i>BRAF</i> Mutations Define a Clinically Distinct Molecular Subtype of Metastatic Colorectal Cancer. Journal of Clinical Oncology, 2017, 35, 2624-2630.	1.6	267
8	Antitumor activity and safety of the PARP inhibitor rucaparib in patients with high-grade ovarian carcinoma and a germline or somatic BRCA1 or BRCA2 mutation: Integrated analysis of data from Study 10 and ARIEL2. Gynecologic Oncology, 2017, 147, 267-275.	1.4	222
9	Beyond microsatellite testing: assessment of tumor mutational burden identifies subsets of colorectal cancer who may respond to immune checkpoint inhibition. Journal of Gastrointestinal Oncology, 2018, 9, 610-617.	1.4	192
10	A computational approach to distinguish somatic vs. germline origin of genomic alterations from deep sequencing of cancer specimens without a matched normal. PLoS Computational Biology, 2018, 14, e1005965.	3.2	191
11	ALK, ROS1, and NTRK Rearrangements in Metastatic Colorectal Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	183
12	Comprehensive Genomic Profiling of 282 Pediatric Low- and High-Grade Gliomas Reveals Genomic Drivers, Tumor Mutational Burden, and Hypermutation Signatures. Oncologist, 2017, 22, 1478-1490.	3.7	176
13	Genomic Profiling of Small-Bowel Adenocarcinoma. JAMA Oncology, 2017, 3, 1546.	7.1	154
14	A Novel Next-Generation Sequencing Approach to Detecting Microsatellite Instability and Pan-Tumor Characterization of 1000 Microsatellite Instability–High Cases in 67,000 Patient Samples. Journal of Molecular Diagnostics, 2019, 21, 1053-1066.	2.8	147
15	Total mutation burden (TMB) in lung cancer (LC) and relationship with response to PD-1/PD-L1 targeted therapies Journal of Clinical Oncology, 2016, 34, 9017-9017.	1.6	129
16	Biological and clinical evidence for somatic mutations in <i>BRCA1</i> and <i>BRCA2</i> as predictive markers for olaparib response in high-grade serous ovarian cancers in the maintenance setting. Oncotarget, 2017, 8, 43653-43661.	1.8	85
17	Genomic Profiling of a Large Set of Diverse Pediatric Cancers Identifies Known and Novel Mutations across Tumor Spectra. Cancer Research, 2017, 77, 509-519.	0.9	75
18	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or Refractory Cancers. Oncologist, 2016, 21, 1315-1325.	3.7	64

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19	Loss of heterozygosity as a marker of homologous repair deficiency in multiple myeloma: a role for PARP inhibition?. Leukemia, 2018, 32, 1561-1566.	7.2	39
20	First-in-human trial of multikinase VEGF inhibitor regorafenib and anti-EGFR antibody cetuximab in advanced cancer patients. JCI Insight, 2017, 2, .	5.0	26
21	Tumor mutational burden as a potential biomarker for PD1/PD-L1 therapy in colorectal cancer Journal of Clinical Oncology, 2016, 34, 3587-3587.	1.6	26
22	Evaluation of microsatellite instability (MSI) status in 11,573 diverse solid tumors using comprehensive genomic profiling (CGP) Journal of Clinical Oncology, 2016, 34, 1523-1523.	1.6	10
23	Comprehensive genomic profiling (CGP) with loss of heterozygosity (LOH) to identify therapeutically relevant subsets of ovarian cancer (OC) Journal of Clinical Oncology, 2017, 35, 5512-5512.	1.6	10
24	Concomitant targeting of the mTOR/MAPK pathways: novel therapeutic strategy in subsets of <i>RICTOR/KRAS</i> -altered non-small cell lung cancer. Oncotarget, 2018, 9, 33995-34008.	1.8	9
25	Evaluation of microsatellite instability (MSI) status in gastrointestinal (GI) tumor samples tested with comprehensive genomic profiling (CGP) Journal of Clinical Oncology, 2016, 34, 528-528.	1.6	6
26	Mutational burden of tumors with primary site unknown Journal of Clinical Oncology, 2017, 35, 3039-3039.	1.6	6
27	Germline variants in cancer risk genes detected by NGS-based comprehensive tumor genomic profiling (CGP) Journal of Clinical Oncology, 2015, 33, 11084-11084.	1.6	5
28	Analysis of candidate homologous repair deficiency genes in a clinical trial of olaparib in patients (pts) with platinum-sensitive, relapsed serous ovarian cancer (PSR SOC) Journal of Clinical Oncology, 2014, 32, 5536-5536.	1.6	2
29	BRCA1/2 reversion mutations revealed in breast and gynecologic cancers sequenced during routine clinical care using tissue or liquid biopsy Journal of Clinical Oncology, 2017, 35, 5551-5551.	1.6	2
30	Exploratory analysis of percentage of genomic loss of heterozygosity (LOH) in patients with platinum-sensitive recurrent ovarian carcinoma (rOC) in ARIEL3 Journal of Clinical Oncology, 2018, 36, 5545-5545.	1.6	2
31	Immunotherapy (IO) versus targeted therapy triage in endometrial adenocarcinoma (EA) by concurrent assessment of tumor mutation burden (TMB), microsatellite instability (MSI) status, and targetable genomic alterations (GA) Journal of Clinical Oncology, 2016, 34, 5591-5591.	1.6	2
32	Effect of mutations in distinct components of the PI3K/AKT/mTOR pathway on sensitivity to endocrine therapy in estrogen receptor (ER)-positive breast cancer Journal of Clinical Oncology, 2015, 33, 532-532.	1.6	1
33	Loss of heterozygosity in multiple myeloma: A role for PARP inhibition?. Journal of Clinical Oncology, 2017, 35, 8026-8026.	1.6	1
34	Comprehensive genomic profiling (CGP) to assess mutational load in gastric and esophageal adenocarcinomas: Implications for immunotherapies Journal of Clinical Oncology, 2016, 34, 66-66.	1.6	1
35	<i>BRCA1/2</i> reversion mutations in prostate cancer identified from clinical tissue and liquid biopsy samples Journal of Clinical Oncology, 2017, 35, 5024-5024.	1.6	1
36	Frequent LOH of CYP2D6 in ER+ breast cancer determined by next-generation sequencing (NGS) Journal of Clinical Oncology, 2013, 31, 534-534.	1.6	0

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37	Comprehensive genomic profiling of anal squamous cell carcinoma to reveal frequency of clinically relevant genomic alterations in the PI3K/mTOR pathway Journal of Clinical Oncology, 2015, 33, 3522-3522.	1.6	0
38	Evaluation of possible linkage between everolimus benefit in estrogen receptor (ER)-positive breast cancer and genomic alterations of the PI3K/AKT/mTOR pathway Journal of Clinical Oncology, 2015, 33, 530-530.	1.6	0
39	Intratumoral heterogeneity of cancer driver genomic alterations across several tumor types Journal of Clinical Oncology, 2015, 33, 1558-1558.	1.6	0
40	BRCA1/2 reversion mutations in pancreatobiliary cancer identified from patient biopsies Journal of Clinical Oncology, 2017, 35, 4130-4130.	1.6	0