Eric M Sanford

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6813408/publications.pdf

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25 papers 3,552 citations

687363 13 h-index 713466 21 g-index

30 all docs 30 docs citations

30 times ranked

7302 citing authors

#	Article	IF	CITATIONS
1	Gene Networks with Transcriptional Bursting Recapitulate Rare Transient Coordinated High Expression States in Cancer. Cell Systems, 2020, 10, 363-378.e12.	6.2	54
2	Gene regulation gravitates toward either addition or multiplication when combining the effects of two signals. ELife, 2020, 9, .	6.0	13
3	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
4	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
5	HER2-Overexpressing Breast Cancers Amplify FGFR Signaling upon Acquisition of Resistance to Dual Therapeutic Blockade of HER2. Clinical Cancer Research, 2017, 23, 4323-4334.	7.0	64
6	Antitumor Response of VEGFR2- and VEGFR3-Amplified Angiosarcoma to Pazopanib. Journal of the National Comprehensive Cancer Network: JNCCN, 2016, 14, 499-502.	4.9	32
7	Genomic Alterations Observed in Colitis-Associated Cancers Are Distinct From Those Found in Sporadic Colorectal Cancers and Vary by Type of Inflammatory Bowel Disease. Gastroenterology, 2016, 151, 278-287.e6.	1.3	147
8	Comprehensive Genomic Profiling Identifies a Subset of Crizotinib-Responsive <i>ALK</i> Rearranged Non-Small Cell Lung Cancer Not Detected by Fluorescence In Situ Hybridization. Oncologist, 2016, 21, 762-770.	3.7	119
9	Comprehensive Genomic Profiling of Advanced Penile Carcinoma Suggests a High Frequency of Clinically Relevant Genomic Alterations. Oncologist, 2016, 21, 33-39.	3.7	69
10	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
11	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
12	Enrichment of Targetable Mutations in the Relapsed Neuroblastoma Genome. PLoS Genetics, 2016, 12, e1006501.	3.5	98
13	Activation of MET via Diverse Exon 14 Splicing Alterations Occurs in Multiple Tumor Types and Confers Clinical Sensitivity to MET Inhibitors. Cancer Discovery, 2015, 5, 850-859.	9.4	632
14	Prospective Comprehensive Genomic Profiling of Advanced Gastric Carcinoma Cases Reveals Frequent Clinically Relevant Genomic Alterations and New Routes for Targeted Therapies. Oncologist, 2015, 20, 499-507.	3.7	64
15	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
16	Identification and characterization of <i>RET</i> fusions in advanced colorectal cancer. Oncotarget, 2015, 6, 28929-28937.	1.8	94
17	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
18	Genomic analysis of colitis-associated cancers Journal of Clinical Oncology, 2015, 33, 3566-3566.	1.6	0

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19	Comprehensive genomic profiling identifies clinically relevant genomic alterations in relapsed and metastatic penile squamous cell carcinoma Journal of Clinical Oncology, 2015, 33, e15628-e15628.	1.6	0
20	Patient Derived Xenograft (PDX) Models Recapitulate the Genomic-Driver Composition of Acute Leukemia Samples. Blood, 2014, 124, 286-286.	1.4	4
21	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
22	Patient Derived Xenograft (PDX) Models Faithfully Recapitulate The Genetic Composition Of Primary AML. Blood, 2013, 122, 1328-1328.	1.4	2
23	Identification Of Actionable Genomic Alterations In Hematologic Malignancies By a Clinical Next Generation Sequencing-Based Assay. Blood, 2013, 122, 230-230.	1.4	2
24	Pilot Study To Evaluate The Prevalence Of Actionable Oncogenic Mutations In Patients With Relapsed Refractory Multiple Myeloma. Blood, 2013, 122, 755-755.	1.4	1
25	Comprehensive Mutational Profiling In Myelodysplastic Syndromes Treated With Decitabine and Tretinoin. Blood, 2013, 122, 2791-2791.	1.4	0