

Meagan Montesion

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,471
citations

687363

13
h-index

580821

25
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all docs

28
docs citations

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times ranked

2905
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of <i>CD274</i> (PD-L1) Copy Number Changes with Immune Checkpoint Inhibitor Clinical Benefit in Non-Squamous Non-Small Cell Lung Cancer. <i>Oncologist</i> , 2022, 27, 732-739.	3.7	5
2	Covalent ER α Antagonist H3B-6545 Demonstrates Encouraging Preclinical Activity in Therapy-Resistant Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 890-902.	4.1	12
3	Clinical, histopathologic, and molecular profiles of PRKAR1A-inactivated melanocytic neoplasms. <i>Journal of the American Academy of Dermatology</i> , 2021, 84, 1069-1071.	1.2	5
4	Somatic HLA Class I Loss Is a Widespread Mechanism of Immune Evasion Which Refines the Use of Tumor Mutational Burden as a Biomarker of Checkpoint Inhibitor Response. <i>Cancer Discovery</i> , 2021, 11, 282-292.	9.4	132
5	CYLD mutation characterizes a subset of HPV-positive head and neck squamous cell carcinomas with distinctive genomics and frequent cylindroma-like histologic features. <i>Modern Pathology</i> , 2021, 34, 358-370.	5.5	12
6	Pan-cancer landscape of <i>CD274</i> (PD-L1) copy number changes in 244 584 patient samples and the correlation with PD-L1 protein expression. , 2021, 9, e002680.		13
7	Genomic Profiling of Combined Hepatocellular Cholangiocarcinoma Reveals Genomics Similar to Either Hepatocellular Carcinoma or Cholangiocarcinoma. <i>JCO Precision Oncology</i> , 2021, 5, 1285-1296.	3.0	8
8	Budget Impact Analysis of Comprehensive Genomic Profiling in Patients With Advanced Non-Small-Cell Lung Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 1611-1624.	3.0	7
9	Pan-cancer landscape of <i>CD274</i> (PD-L1) rearrangements in 283,050 patient samples, its correlation with PD-L1 protein expression, and immunotherapy response. , 2021, 9, e003550.		8
10	<i>CDKN2C</i> -Null Leiomyosarcoma: A Novel, Genomically Distinct Class of <i>TP53</i> / <i>RB1</i> Wild-Type Tumor With Frequent <i>CIC</i> Genomic Alterations and 1p/19q-Codeletion. <i>JCO Precision Oncology</i> , 2020, 4, 955-971.	3.0	6
11	CYLD-mutant cylindroma-like basaloid carcinoma of the anus: a genetically and morphologically distinct class of HPV-related anal carcinoma. <i>Modern Pathology</i> , 2020, 33, 2614-2625.	5.5	9
12	Melanoma with in-frame deletion of MAP2K1: a distinct molecular subtype of cutaneous melanoma mutually exclusive from BRAF, NRAS, and NF1 mutations. <i>Modern Pathology</i> , 2020, 33, 2397-2406.	5.5	16
13	Vulvar Squamous Cell Carcinoma: Comprehensive Genomic Profiling of HPV+ Versus HPV- Forms Reveals Distinct Sets of Potentially Actionable Molecular Targets. <i>JCO Precision Oncology</i> , 2020, 4, 647-661.	3.0	21
14	Melanomas with activating RAF1 fusions: clinical, histopathologic, and molecular profiles. <i>Modern Pathology</i> , 2020, 33, 1466-1474.	5.5	28
15	Phenotypic and Genomic Determinants of Immunotherapy Response Associated with Squamousness. <i>Cancer Immunology Research</i> , 2019, 7, 866-873.	3.4	23
16	High-Grade Salivary Gland Ductal Carcinoma With Unusual EGFR Amplification Responsive to Afatinib. <i>JCO Precision Oncology</i> , 2019, 3, 1-5.	3.0	1
17	The Genomic Landscape of Merkel Cell Carcinoma and Clinicogenomic Biomarkers of Response to Immune Checkpoint Inhibitor Therapy. <i>Clinical Cancer Research</i> , 2019, 25, 5961-5971.	7.0	118
18	PD-L1 expression and tumor mutational burden are independent biomarkers in most cancers. <i>JCI Insight</i> , 2019, 4, .	5.0	345

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19	Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. <i>Journal of Clinical Investigation</i> , 2019, 129, 4276-4289.	8.2	134
20	Comprehensive Genomic Profiling of 104 Rare Histiocytic and Dendritic Cell Neoplasms Reveals Shared and Distinct Targetable Genomic Alterations. <i>Blood</i> , 2019, 134, 2541-2541.	1.4	2
21	Mechanisms of HERV-K (HML-2) Transcription during Human Mammary Epithelial Cell Transformation. <i>Journal of Virology</i> , 2018, 92, .	3.4	33
22	Multiple configurations of EGFR exon 20 resistance mutations after first- and third-generation EGFR TKI treatment affect treatment options in NSCLC. <i>PLoS ONE</i> , 2018, 13, e0208097.	2.5	17
23	Promoter expression of HERV-K (HML-2) provirus-derived sequences is related to LTR sequence variation and polymorphic transcription factor binding sites. <i>Retrovirology</i> , 2018, 15, 57.	2.0	33
24	A computational approach to distinguish somatic vs. germline origin of genomic alterations from deep sequencing of cancer specimens without a matched normal. <i>PLoS Computational Biology</i> , 2018, 14, e1005965.	3.2	191
25	A Next-Generation Sequencing-Based Karyotyping Algorithm Reveals the Genomic Structure of Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 2773-2773.	1.4	1
26	Discovery of unfixed endogenous retrovirus insertions in diverse human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2326-34.	7.1	225
27	Differential Expression of HERV-K (HML-2) Proviruses in Cells and Virions of the Teratocarcinoma Cell Line Tera-1. <i>Viruses</i> , 2015, 7, 939-968.	3.3	65