Federica Piccioni

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7760300/publications.pdf

Version: 2024-02-01

20 papers 4,627 citations

567281 15 h-index 713466 21 g-index

24 all docs

24 docs citations

times ranked

24

9660 citing authors

#	Article	IF	CITATIONS
1	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. Cell, 2017, 171, 1437-1452.e17.	28.9	2,281
2	Optimized libraries for CRISPR-Cas9 genetic screens with multiple modalities. Nature Communications, 2018, 9, 5416.	12.8	535
3	A melanocyte lineage program confers resistance to MAP kinase pathway inhibition. Nature, 2013, 504, 138-142.	27.8	401
4	Mutational processes shape the landscape of TP53 mutations in human cancer. Nature Genetics, 2018, 50, 1381-1387.	21.4	334
5	A dominant-negative effect drives selection of <i>TP53</i> missense mutations in myeloid malignancies. Science, 2019, 365, 599-604.	12.6	265
6	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	16.8	171
7	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. Cancer Cell, 2015, 27, 397-408.	16.8	150
8	Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. Cell Reports, 2016, 17, 1171-1183.	6.4	119
9	Acquired FGFR and FGF Alterations Confer Resistance to Estrogen Receptor (ER) Targeted Therapy in ER+ Metastatic Breast Cancer. Clinical Cancer Research, 2020, 26, 5974-5989.	7.0	87
10	TRIM8 modulates the EWS/FLI oncoprotein to promote survival in Ewing sarcoma. Cancer Cell, 2021, 39, 1262-1278.e7.	16.8	49
11	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. Nature Communications, 2019, 10, 2400.	12.8	37
12	An <i>In Vivo</i> CRISPR Screening Platform for Prioritizing Therapeutic Targets in AML. Cancer Discovery, 2022, 12, 432-449.	9.4	32
13	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. Nature Structural and Molecular Biology, 2020, 27, 92-104.	8.2	30
14	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. Nature Communications, 2022, 13, 604.	12.8	22
15	Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. Nature Communications, 2021, 12, 4789.	12.8	21
16	Pooled Lentiviralâ€Delivery Genetic Screens. Current Protocols in Molecular Biology, 2018, 121, 32.1.1-32.1.21.	2.9	20
17	Comprehensive Mutational Analysis of the BRCA1-Associated DNA Helicase and Tumor-Suppressor FANCJ/BACH1/BRIP1. Molecular Cancer Research, 2021, 19, 1015-1025.	3.4	15
18	Allosteric inhibition of PPM1D serine/threonine phosphatase via an altered conformational state. Nature Communications, 2022, 13 , .	12.8	15

#	Article	lF	CITATION
19	A genome-wide gain-of-function screen identifies CDKN2C as a HBV host factor. Nature Communications, 2020, 11, 2707.	12.8	11
20	Considerations and practical implications of performing a phenotypic CRISPR/Cas survival screen. PLoS ONE, 2022, 17, e0263262.	2.5	4