

Hannes Ponstingl

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1231932/publications.pdf>

Version: 2024-02-01

14
papers

2,875
citations

687363

13
h-index

1058476

14
g-index

20
all docs

20
docs citations

20
times ranked

6533
citing authors

#	ARTICLE	IF	CITATIONS
1	Promoter-bound METTL3 maintains myeloid leukaemia by m6A-dependent translation control. <i>Nature</i> , 2017, 552, 126-131.	27.8	833
2	A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2016, 17, 1193-1205.	6.4	556
3	Leukemia-Associated Somatic Mutations Drive Distinct Patterns of Age-Related Clonal Hemopoiesis. <i>Cell Reports</i> , 2015, 10, 1239-1245.	6.4	443
4	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
5	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. <i>Cancer Cell</i> , 2013, 24, 15-29.	16.8	183
6	ATM orchestrates the DNA-damage response to counter toxic non-homologous end-joining at broken replication forks. <i>Nature Communications</i> , 2019, 10, 87.	12.8	133
7	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , 2015, 47, 47-56.	21.4	77
8	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. <i>Nature Communications</i> , 2018, 9, 5378.	12.8	60
9	A single-copy Sleeping Beauty transposon mutagenesis screen identifies new PTEN-cooperating tumor suppressor genes. <i>Nature Genetics</i> , 2017, 49, 730-741.	21.4	53
10	Genome-wide transposon screening and quantitative insertion site sequencing for cancer gene discovery in mice. <i>Nature Protocols</i> , 2017, 12, 289-309.	12.0	41
11	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. <i>Nature Communications</i> , 2021, 12, 2298.	12.8	32
12	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. <i>Nature Genetics</i> , 2022, 54, 251-262.	21.4	23
13	PiggyBac mutagenesis and exome sequencing identify genetic driver landscapes and potential therapeutic targets of EGFR-mutant gliomas. <i>Genome Biology</i> , 2020, 21, 181.	8.8	18
14	SETBP1 overexpression acts in the place of class-defining mutations to drive FLT3-ITD mutant AML. <i>Blood Advances</i> , 2021, 5, 2412-2425.	5.2	10