Dong Shen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11834372/publications.pdf

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20 papers	15,332 citations	516710 16 h-index	839539 18 g-index
20 all docs	20 docs citations	20 times ranked	28205 citing authors

#	Article	IF	Citations
1	Landscape of IDH1/2 mutations in Chinese patients with solid tumors: A panâ€cancer analysis. Molecular Genetics & Genomic Medicine, 2021, 9, e1697.	1.2	8
2	Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers. Nature Communications, 2016, 7, 12498.	12.8	69
3	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood, 2015, 126, 2484-2490.	1.4	207
4	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
5	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
6	Acquired copy number alterations of miRNA genes in acute myeloid leukemia are uncommon. Blood, 2013, 122, e44-e51.	1.4	13
7	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. Cancer Discovery, 2013, 3, 224-237.	9.4	697
8	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
9	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
10	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. Nature Genetics, 2012, 44, 53-57.	21.4	513
11	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
12	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
13	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	5.5	4,086
14	Whole genome sequencing to characterize luminal-type breast cancer.. Journal of Clinical Oncology, 2012, 30, 503-503.	1.6	1
15	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	1.4	0
16	Identification of a Novel <emph type="ital">TP53</emph> Cancer Susceptibility Mutation Through Whole-Genome Sequencing of a Patient With Therapy-Related AML. JAMA - Journal of the American Medical Association, 2011, 305, 1568.	7.4	146
17	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
18	Chromatid cohesion defects may underlie chromosome instability in human colorectal cancers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3443-3448.	7.1	361

#	Article	IF	Citations
19	The Genomic Landscapes of Human Breast and Colorectal Cancers. Science, 2007, 318, 1108-1113.	12.6	3,049
20	Three Classes of Genes Mutated In Colorectal Cancers with Chromosomal Instability. Cancer Research, 2004, 64, 2998-3001.	0.9	174