Christian Sutter

List of Publications by Year
in descending order

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46 papers	4,234 citations	236612 25 h-index	276539 41 g-index
46 all docs	46 docs citations	46 times ranked	8364 citing authors

#	Article	IF	Citations
1	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
2	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
3	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
4	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
5	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
6	Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101.	1.3	262
7	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
8	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
9	Gene panel testing of 5589 <scp>BRCA</scp>1/2â€negative index patients with breast cancer in a routine diagnostic setting: results of the German Consortium for Hereditary Breast and Ovarian Cancer. Cancer Medicine, 2018, 7, 1349-1358.	1.3	126
10	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
11	The Pediatric Precision Oncology INFORM Registry: Clinical Outcome and Benefit for Patients with Very High-Evidence Targets. Cancer Discovery, 2021, 11, 2764-2779.	7.7	110
12	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
13	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	1.1	102
14	FANCMc.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	1.4	91
15	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	0.8	90
16	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88
17	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
18	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78

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19	Successful immune checkpoint blockade in a patient with advanced stage microsatellite-unstable biliary tract cancer. Journal of Physical Education and Sports Management, 2017, 3, a001974.	0.5	54
20	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
21	The association between breast cancer and S100P methylation in peripheral blood by multicenter caseâ€“control studies. Carcinogenesis, 2017, 38, 312-320.	1.3	41
22	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
23	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
24	DNA methylation array analysis identifies breast cancer associated RPTOR, MGRN1 and RAPSN hypomethylation in peripheral blood DNA. Oncotarget, 2016, 7, 64191-64202.	0.8	33
25	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	3.0	30
26	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
27	Performance of Breast Cancer Polygenic Risk Scores in 760 FemaleCHEK2Germline Mutation Carriers. Journal of the National Cancer Institute, 2021, 113, 893-899.	3.0	21
28	Cancer surveillance and distress among adult pathogenic TP53 germline variant carriers in Germany: A multicenter feasibility and acceptance survey. Cancer, 2020, 126, 4032-4041.	2.0	20
29	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
30	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18
31	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16
32	Periungual fibroma (Koenen tumors) as isolated sign of tuberous sclerosis complex with tuberous sclerosis complex 1 germline mutation. Journal of the American Academy of Dermatology, 2010, 62, 159-161.	0.6	13
33	Prevalence of Cancer Predisposition Germline Variants in Male Breast Cancer Patients: Results of the German Consortium for Hereditary Breast and Ovarian Cancer. Cancers, 2022, 14, 3292.	1.7	11
34	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
35	Investigating the effects of additional truncating variants in DNA-repair genes on breast cancer risk in BRCA1-positive women. BMC Cancer, 2019, 19, 787.	1.1	10
36	Molecular Diagnostics in Pediatric Brain Tumors: Impact on Diagnosis and Clinical Decision-Making â€” A Selected Case Series. Klinische Padiatrie, 2018, 230, 305-313.	0.2	8

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37	Germline testing for homologous recombination repair genesâ€"opportunities and challenges. Genes Chromosomes and Cancer, 2021, 60, 332-343.	1.5	7
38	Breast cancer characteristics and surgery among women with Liâ€Fraumeni syndrome in Germanyâ€"A retrospective cohort study. Cancer Medicine, 2021, 10, 7747-7758.	1.3	7
39	The GPRC5A frameshift variant c.183del is not associated with increased breast cancer risk in BRCA1 mutation carriers. International Journal of Cancer, 2019, 144, 1761-1763.	2.3	2
40	BRCA1/2 mutation prevalence in triple-negative breast cancer patients without family history of breast and ovarian cancer.. Journal of Clinical Oncology, 2016, 34, 1090-1090.	0.8	2
41	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. Cancers, 2022, 14, 3363.	1.7	2
42	MEDB-14. Clinical outcome of pediatric medulloblastoma patients with Li-Fraumeni syndrome. Neuro-Oncology, 2022, 24, i107-i107.	0.6	1
43	DNA methylation array analyses to identify HYAL2 methylation in peripheral blood as a marker for the detection of early breast cancer.. Journal of Clinical Oncology, 2014, 32, 26-26.	0.8	0
44	NGS-based multi-gene panel analysis in BRCA1/2-negative breast and ovarian cancer families.. Journal of Clinical Oncology, 2017, 35, 1526-1526.	0.8	0
45	OTHR-32. The Pediatric Targeted Therapy 2.0 registry: robust molecular diagnostics for precision oncology. Neuro-Oncology, 2022, 24, i154-i154.	0.6	0
46	HGG-61.Landscape of cancer predisposition in pediatric high-grade glioma. Neuro-Oncology, 2022, 24, i76-i76.	0.6	0