Ekta Khurana

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4479347/publications.pdf

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33 papers	9,751 citations	257101 24 h-index	433756 31 g-index
47 all docs	47 docs citations	47 times ranked	21848 citing authors

#	Article	IF	Citations
1	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
2	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
3	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
4	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
5	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
6	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
7	Role of non-coding sequence variants in cancer. Nature Reviews Genetics, 2016, 17, 93-108.	7.7	420
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
9	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. Genome Biology, 2014, 15, 480.	3.8	291
10	Interpretation of Genomic Variants Using a Unified Biological Network Approach. PLoS Computational Biology, 2013, 9, e1002886.	1.5	162
11	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. Cell, 2020, 180, 915-927.e16.	13.5	98
12	Developmental chromatin programs determine oncogenic competence in melanoma. Science, 2021, 373, eabc1048.	6.0	80
13	FUN-LDA: A Latent Dirichlet Allocation Model for Predicting Tissue-Specific Functional Effects of Noncoding Variation: Methods and Applications. American Journal of Human Genetics, 2018, 102, 920-942.	2.6	75
14	Chromatin profiles classify castration-resistant prostate cancers suggesting therapeutic targets. Science, 2022, 376, .	6.0	75
15	MYBL1 rearrangements and MYB amplification in breast adenoid cystic carcinomas lacking the MYBâ€“NFIB fusion gene. Journal of Pathology, 2018, 244, 143-150.	2.1	74
16	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
17	LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations. Nucleic Acids Research, 2015, 43, 8123-8134.	6.5	72
18	Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes. Cell Systems, 2019, 8, 446-455.e8.	2.9	65

#	Article	IF	Citations
19	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. Nature Genetics, 2017, 49, 825-833.	9.4	55
20	Lineage Reversion Drives WNT Independence in Intestinal Cancer. Cancer Discovery, 2020, 10, 1590-1609.	7.7	52
21	Non-coding genetic variation in cancer. Current Opinion in Systems Biology, 2017, 1, 9-15.	1.3	42
22	DeepMILO: a deep learning approach to predict the impact of non-coding sequence variants on 3D chromatin structure. Genome Biology, 2020, 21, 79.	3.8	32
23	Identification of novel prostate cancer drivers using RegNetDriver: a framework for integration of genetic and epigenetic alterations with tissue-specific regulatory network. Genome Biology, 2017, 18, 141.	3.8	31
24	Segmental duplications in the human genome reveal details of pseudogene formation. Nucleic Acids Research, 2010, 38, 6997-7007.	6.5	26
25	Inherited determinants of early recurrent somatic mutations in prostate cancer. Nature Communications, 2017, 8, 48.	5.8	23
26	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	2.9	16
27	Loss-of-function tolerance of enhancers in the human genome. PLoS Genetics, 2020, 16, e1008663.	1.5	12
28	CNCDatabase: a database of non-coding cancer drivers. Nucleic Acids Research, 2021, 49, D1094-D1101.	6.5	12
29	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
30	Hard-to-reach repairs. Nature, 2016, 532, 181-182.	13.7	5
31	Using FunSeq2 for Coding and Nonâ€Coding Variant Annotation and Prioritization. Current Protocols in Bioinformatics, 2017, 57, 15.11.1-15.11.17.	25.8	5
32	Abstract 235: Identifying potential drug targets using patient-derived, tissue specific, gene regulatory networks. , 2021, , .		0
33	Abstract 2034: Patient-specific enhancer-gene networks for hundreds of primary cancer samples. , 2021, , .		0