Ekta Khurana

List of Publications by Year in Descending Order

33 papers	6,366 citations	20 h-index	47 g-index
47 ext. papers	8,418 ext. citations	25.9 avg, IF	4.74 L-index

#	Paper	IF	Citations
33	CNCDatabase: a database of non-coding cancer drivers. *Nucleic Acids Research*, **2021**, 49, D1094-D1101	20.1	4
32	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. *Cell Reports*, **2021**, 34, 108707	10.6	7
31	Developmental chromatin programs determine oncogenic competence in melanoma. *Science*, **2021**, 373, eabc1048	33.3	13
30	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,	11.5	3
29	Lineage Reversion Drives WNT Independence in Intestinal Cancer. *Cancer Discovery*, **2020**, 10, 1590-1609	24.4	16
28	Passenger Mutations in More Than 2,500 Cancer Genomes: Overall Molecular Functional Impact and Consequences. *Cell*, **2020**, 180, 915-927.e16	56.2	38
27	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
26	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
25	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
24	DeepMILO: a deep learning approach to predict the impact of non-coding sequence variants on 3D chromatin structure. *Genome Biology*, **2020**, 21, 79	18.3	11
23	Loss-of-function tolerance of enhancers in the human genome. *PLoS Genetics*, **2020**, 16, e1008663	6	4
22	Identification of Cancer Drivers at CTCF Insulators in 1,962 Whole Genomes. *Cell Systems*, **2019**, 8, 446-455.e8	10.68	29
21	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
20	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	11	49
19	MYBL1 rearrangements and MYB amplification in breast adenoid cystic carcinomas lacking the MYB-NFIB fusion gene. *Journal of Pathology*, **2018**, 244, 143-150	9.4	46
18	Non-coding genetic variation in cancer. *Current Opinion in Systems Biology*, **2017**, 1, 9-15	3.2	23
17	Using FunSeq2 for Coding and Non-Coding Variant Annotation and Prioritization. *Current Protocols in Bioinformatics*, **2017**, 57, 15.11.1-15.11.17	24.2	2

List of Publications

16	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. *Nature Genetics*, **2017**, 49, 825-833	36.3	41
15	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	18.3	20
14	Inherited determinants of early recurrent somatic mutations in prostate cancer. *Nature Communications*, **2017**, 8, 48	17.4	16
13	Role of non-coding sequence variants in cancer. *Nature Reviews Genetics*, **2016**, 17, 93-108	30.1	301
12	Cancer genomics: Hard-to-reach repairs. *Nature*, **2016**, 532, 181-2	50.4	4
11	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
10	LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations. *Nucleic Acids Research*, **2015**, 43, 8123-34	20.1	48
9	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. *Genome Biology*, **2014**, 15, 480	18.3	209
8	Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science*, **2013** , 342, 1235587	33.3	281
7	Interpretation of genomic variants using a unified biological network approach. *PLoS Computational Biology*, **2013**, 9, e1002886	5	116
6	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
5	A systematic survey of loss-of-function variants in human protein-coding genes. *Science*, **2012**, 335, 823-8	33.3	880
4	Segmental duplications in the human genome reveal details of pseudogene formation. *Nucleic Acids Research*, **2010**, 38, 6997-7007	20.1	21
3	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
2	Passenger mutations in 2500 cancer genomes: Overall molecular functional impact and consequences		4
1	Pathway and network analysis of more than 2,500 whole cancer genomes		4