Nidhi Sahni

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6776691/publications.pdf

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36 papers	4,543 citations	236925 25 h-index	361022 35 g-index
38 all docs	38 docs citations	38 times ranked	9102 citing authors

#	Article	IF	Citations
1	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	10.3	9
2	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
3	e-MutPath: computational modeling reveals the functional landscape of genetic mutations rewiring interactome networks. Nucleic Acids Research, 2021, 49, e2-e2.	14.5	10
4	Pathway perturbations in signaling networks: Linking genotype to phenotype. Seminars in Cell and Developmental Biology, 2020, 99, 3-11.	5.0	13
5	Integrated Genomic Characterization of the Human Immunome in Cancer. Cancer Research, 2020, 80, 4854-4867.	0.9	11
6	PBRM1 loss defines a nonimmunogenic tumor phenotype associated with checkpoint inhibitor resistance in renal carcinoma. Nature Communications, 2020, 11, 2135.	12.8	114
7	Proteome Instability Is a Therapeutic Vulnerability in Mismatch Repair-Deficient Cancer. Cancer Cell, 2020, 37, 371-386.e12.	16.8	68
8	Cellular origins and genetic landscape of cutaneous gamma delta T cell lymphomas. Nature Communications, 2020, 11, 1806.	12.8	62
9	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. Cancer Cell, 2019, 35, 851-867.e7.	16.8	156
10	MERIT: Systematic Analysis and Characterization of Mutational Effect on RNA Interactome Topology. Hepatology, 2019, 70, 532-546.	7.3	28
11	Multi-omics analysis reveals neoantigen-independent immune cell infiltration in copy-number driven cancers. Nature Communications, 2018, 9, 1317.	12.8	94
12	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. Nucleic Acids Research, 2018, 46, 1113-1123.	14.5	115
13	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	16.8	213
14	Neomorphic PDGFRA extracellular domain driver mutations are resistant to PDGFRA targeted therapies. Nature Communications, 2018, 9, 4583.	12.8	44
15	Gene Regulatory Network Perturbation by Genetic and Epigenetic Variation. Trends in Biochemical Sciences, 2018, 43, 576-592.	7.5	20
16	FACER: comprehensive molecular and functional characterization of epigenetic chromatin regulators. Nucleic Acids Research, 2018, 46, 10019-10033.	14.5	66
17	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. Cell Systems, 2017, 4, 242-250.e4.	6.2	91
18	HSP90 Shapes the Consequences of Human Genetic Variation. Cell, 2017, 168, 856-866.e12.	28.9	117

#	Article	IF	Citations
19	Regulome networks and mutational landscape in liver cancer: An informative path to precision medicine. Hepatology, 2017, 66, 280-282.	7.3	2
20	Functional variomics and network perturbation: connecting genotype to phenotype in cancer. Nature Reviews Genetics, 2017, 18, 395-410.	16.3	84
21	Base-resolution stratification of cancer mutations using functional variomics. Nature Protocols, 2017, 12, 2323-2341.	12.0	11
22	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. Cell Reports, 2017, 21, 798-812.	6.4	51
23	Signal Transduction and Regulation: Insights into Evolution. BioMed Research International, 2016, 2016, 1-2.	1.9	0
24	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. BioMed Research International, 2016, 2016, 1-14.	1.9	7
25	Pooledâ€matrix protein interaction screens using Barcode Fusion Genetics. Molecular Systems Biology, 2016, 12, 863.	7.2	102
26	An extended set of yeast-based functional assays accurately identifies human disease mutations. Genome Research, 2016, 26, 670-680.	5.5	116
27	Survey of variation in human transcription factors reveals prevalent DNA binding changes. Science, 2016, 351, 1450-1454.	12.6	114
28	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. Cell, 2016, 164, 805-817.	28.9	479
29	Comparative analysis of protein interactome networks prioritizes candidate genes with cancer signatures. Oncotarget, 2016, 7, 78841-78849.	1.8	14
30	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. Human Molecular Genetics, 2015, 24, 3005-3020.	2.9	162
31	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. Cell, 2015, 161, 661-673.	28.9	111
32	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. Cell, 2015, 161, 647-660.	28.9	482
33	Global Edgetic Rewiring in Cancer Networks. Cell Systems, 2015, 1, 251-253.	6.2	28
34	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. Genes and Development, 2014, 28, 1957-1975.	5.9	86
35	A Proteome-Scale Map of the Human Interactome Network. Cell, 2014, 159, 1212-1226.	28.9	1,199
36	Edgotype: a fundamental link between genotype and phenotype. Current Opinion in Genetics and Development, 2013, 23, 649-657.	3.3	129