

# Nidhi Sahni

## List of Publications by Year in descending order

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

Version: 2024-02-01

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 Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	28.9	1,199
2	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
3	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
4	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018, 33, 450-462.e10.	16.8	213
5	A disease module in the interactome explains disease heterogeneity, drug response and captures novel pathways and genes in asthma. <i>Human Molecular Genetics</i> , 2015, 24, 3005-3020.	2.9	162
6	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. <i>Cancer Cell</i> , 2019, 35, 851-867.e7.	16.8	156
7	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	28.9	135
8	Edgotype: a fundamental link between genotype and phenotype. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 649-657.	3.3	129
9	HSP90 Shapes the Consequences of Human Genetic Variation. <i>Cell</i> , 2017, 168, 856-866.e12.	28.9	117
10	An extended set of yeast-based functional assays accurately identifies human disease mutations. <i>Genome Research</i> , 2016, 26, 670-680.	5.5	116
11	LncMAP: Pan-cancer atlas of long noncoding RNA-mediated transcriptional network perturbations. <i>Nucleic Acids Research</i> , 2018, 46, 1113-1123.	14.5	115
12	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	12.6	114
13	PBRM1 loss defines a nonimmunogenic tumor phenotype associated with checkpoint inhibitor resistance in renal carcinoma. <i>Nature Communications</i> , 2020, 11, 2135.	12.8	114
14	Human Gene-Centered Transcription Factor Networks for Enhancers and Disease Variants. <i>Cell</i> , 2015, 161, 661-673.	28.9	111
15	Pooled matrix protein interaction screens using Barcode Fusion Genetics. <i>Molecular Systems Biology</i> , 2016, 12, 863.	7.2	102
16	Multi-omics analysis reveals neoantigen-independent immune cell infiltration in copy-number driven cancers. <i>Nature Communications</i> , 2018, 9, 1317.	12.8	94
17	In Situ Peroxidase Labeling and Mass-Spectrometry Connects Alpha-Synuclein Directly to Endocytic Trafficking and mRNA Metabolism in Neurons. <i>Cell Systems</i> , 2017, 4, 242-250.e4.	6.2	91
18	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014, 28, 1957-1975.	5.9	86

#	ARTICLE	IF	CITATIONS
19	Functional variomics and network perturbation: connecting genotype to phenotype in cancer. <i>Nature Reviews Genetics</i> , 2017, 18, 395-410.	16.3	84
20	Proteome Instability Is a Therapeutic Vulnerability in Mismatch Repair-Deficient Cancer. <i>Cancer Cell</i> , 2020, 37, 371-386.e12.	16.8	68
21	FACER: comprehensive molecular and functional characterization of epigenetic chromatin regulators. <i>Nucleic Acids Research</i> , 2018, 46, 10019-10033.	14.5	66
22	Cellular origins and genetic landscape of cutaneous gamma delta T cell lymphomas. <i>Nature Communications</i> , 2020, 11, 1806.	12.8	62
23	Revealing the Determinants of Widespread Alternative Splicing Perturbation in Cancer. <i>Cell Reports</i> , 2017, 21, 798-812.	6.4	51
24	Neomorphic PDGFRA extracellular domain driver mutations are resistant to PDGFRA targeted therapies. <i>Nature Communications</i> , 2018, 9, 4583.	12.8	44
25	Global Edgetic Rewiring in Cancer Networks. <i>Cell Systems</i> , 2015, 1, 251-253.	6.2	28
26	MERIT: Systematic Analysis and Characterization of Mutational Effect on RNA Interactome Topology. <i>Hepatology</i> , 2019, 70, 532-546.	7.3	28
27	Gene Regulatory Network Perturbation by Genetic and Epigenetic Variation. <i>Trends in Biochemical Sciences</i> , 2018, 43, 576-592.	7.5	20
28	Comparative analysis of protein interactome networks prioritizes candidate genes with cancer signatures. <i>Oncotarget</i> , 2016, 7, 78841-78849.	1.8	14
29	Pathway perturbations in signaling networks: Linking genotype to phenotype. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 3-11.	5.0	13
30	Base-resolution stratification of cancer mutations using functional variomics. <i>Nature Protocols</i> , 2017, 12, 2323-2341.	12.0	11
31	Integrated Genomic Characterization of the Human Immunome in Cancer. <i>Cancer Research</i> , 2020, 80, 4854-4867.	0.9	11
32	e-MutPath: computational modeling reveals the functional landscape of genetic mutations rewiring interactome networks. <i>Nucleic Acids Research</i> , 2021, 49, e2-e2.	14.5	10
33	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	10.3	9
34	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. <i>BioMed Research International</i> , 2016, 2016, 1-14.	1.9	7
35	Regulome networks and mutational landscape in liver cancer: An informative path to precision medicine. <i>Hepatology</i> , 2017, 66, 280-282.	7.3	2
36	Signal Transduction and Regulation: Insights into Evolution. <i>BioMed Research International</i> , 2016, 2016, 1-2.	1.9	0