Nicholas A Sinnott-Armstrong

List of Publications by Year
in descending order

41 papers	12,207 citations	218592 26 h-index	345118 36 g-index
60 all docs	60 docs citations	60 times ranked	26675 citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
3	Super-resolution chromatin tracing reveals domains and cooperative interactions in single cells. Science, 2018, 362, .	6.0	700
4	Opportunities and challenges for transcriptome-wide association studies. Nature Genetics, 2019, 51, 592-599.	9.4	592
5	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
6	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
7	Genetics of 35 blood and urine biomarkers in the UK Biobank. Nature Genetics, 2021, 53, 185-194.	9.4	377
8	SARS-CoV-2 RNA in Wastewater Settled Solids Is Associated with COVID-19 Cases in a Large Urban Sewershed. Environmental Science & Technology, 2021, 55, 488-498.	4.6	286
9	Reduced signal for polygenic adaptation of height in UK Biobank. ELife, 2019, 8, .	2.8	283
10	Chromatin accessibility dynamics in a model of human forebrain development. Science, 2020, 367, .	6.0	187
11	Landscape of cohesin-mediated chromatin loops in the human genome. Nature, 2020, 583, 737-743.	13.7	134
12	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
13	p53 is a central regulator driving neurodegeneration caused by C9orf72 poly(PR). Cell, 2021, 184, 689-708.e20.	13.5	104
14	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. Nature Methods, 2020, 17, 319-327.	9.0	93
15	Scaling of SARS-CoV-2 RNA in Settled Solids from Multiple Wastewater Treatment Plants to Compare Incidence Rates of Laboratory-Confirmed COVID-19 in Their Sewersheds. Environmental Science and Technology Letters, 2021, 8, 398-404.	3.9	89
16	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. Nature Genetics, 2021, 53, 638-649.	9.4	86
17	Pan-cancer screen for mutations in non-coding elements with conservation and cancer specificity reveals correlations with expression and survival. Npj Genomic Medicine, 2018, 3, 1.	1.7	79
18	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. ELife, 2021, 10, .	2.8	77

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19	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. Nature Genetics, 2016, 48, 1260-1266.	9.4	75
20	Extensive pleiotropism and allelic heterogeneity mediate metabolic effects of IRX3 and IRX5. Science, 2021, 372, 1085-1091.	6.0	66
21	The origins of specialized pottery and diverse alcohol fermentation techniques in Early Neolithic China. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12767-12774.	3.3	63
22	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. Nature Communications, 2020, 11, 3675.	5.8	63
23	Sex-specific genetic effects across biomarkers. European Journal of Human Genetics, 2021, 29, 154-163.	1.4	48
24	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. Cell, 2020, 183, 684-701.e14.	13.5	46
25	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
26	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002982.	3.9	34
27	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. Nature Genetics, 2022, 54, 1133-1144.	9.4	31
28	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. American Journal of Human Genetics, 2022, 109, 1286-1297.	2.6	30
29	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. Cell Metabolism, 2021, 33, 615-628.e13.	7.2	28
30	Tracing DNA paths and RNA profiles in cultured cells and tissues with ORCA. Nature Protocols, 2021, 16, 1647-1713.	5.5	26
31	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21813-21820.	3.3	22
32	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21
33	A conserved YAP/Notch/REST network controls the neuroendocrine cell fate in the lungs. Nature Communications, 2022, 13, 2690.	5.8	19
34	Loss of LDAH associated with prostate cancer and hearing loss. Human Molecular Genetics, 2018, 27, 4194-4203.	1.4	14
35	Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. Nature Communications, 2021, 12, 350.	5.8	13
36	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. Nucleic Acids Research, 2018, 46, e42-e42.	6.5	7

#	Article	IF	Citations
37	Title is missing!. , 2019, 16, e1002982.		0
38	Title is missing!. , 2019, 16, e1002982.		0
39	Title is missing!. , 2019, 16, e1002982.		0
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