

Nicholas A Sinnott-Armstrong

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9331205/publications.pdf>

Version: 2024-02-01

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	A conserved YAP/Notch/REST network controls the neuroendocrine cell fate in the lungs. <i>Nature Communications</i> , 2022, 13, 2690.	5.8	19
2	Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. <i>American Journal of Human Genetics</i> , 2022, 109, 1286-1297.	2.6	30
3	Systematic discovery and perturbation of regulatory genes in human T cells reveals the architecture of immune networks. <i>Nature Genetics</i> , 2022, 54, 1133-1144.	9.4	31
4	SARS-CoV-2 RNA in Wastewater Settled Solids Is Associated with COVID-19 Cases in a Large Urban Sewershed. <i>Environmental Science & Technology</i> , 2021, 55, 488-498.	4.6	286
5	Sex-specific genetic effects across biomarkers. <i>European Journal of Human Genetics</i> , 2021, 29, 154-163.	1.4	48
6	Genetics of 35 blood and urine biomarkers in the UK Biobank. <i>Nature Genetics</i> , 2021, 53, 185-194.	9.4	377
7	Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. <i>Nature Communications</i> , 2021, 12, 350.	5.8	13
8	Tracing DNA paths and RNA profiles in cultured cells and tissues with ORCA. <i>Nature Protocols</i> , 2021, 16, 1647-1713.	5.5	26
9	GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. <i>ELife</i> , 2021, 10, .	2.8	77
10	p53 is a central regulator driving neurodegeneration caused by C9orf72 poly(PR). <i>Cell</i> , 2021, 184, 689-708.e20.	13.5	104
11	A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. <i>Cell Metabolism</i> , 2021, 33, 615-628.e13.	7.2	28
12	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , 2021, 53, 638-649.	9.4	86
13	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. <i>Environmental Science and Technology Letters</i> , 2021, 8, 398-404.	3.9	89
14	Extensive pleiotropism and allelic heterogeneity mediate metabolic effects of <i>IRX3</i> and <i>IRX5</i> . <i>Science</i> , 2021, 372, 1085-1091.	6.0	66
15	A MicroRNA Linking Human Positive Selection and Metabolic Disorders. <i>Cell</i> , 2020, 183, 684-701.e14.	13.5	46
16	Multi-faceted epigenetic dysregulation of gene expression promotes esophageal squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 3675.	5.8	63
17	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743.	13.7	134
18	Multiomic blood correlates of genetic risk identify presymptomatic disease alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21813-21820.	3.3	22

#	ARTICLE	IF	CITATIONS
19	Long-range single-molecule mapping of chromatin accessibility in eukaryotes. <i>Nature Methods</i> , 2020, 17, 319-327.	9.0	93
20	Chromatin accessibility dynamics in a model of human forebrain development. <i>Science</i> , 2020, 367, .	6.0	187
21	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
22	The origins of specialized pottery and diverse alcohol fermentation techniques in Early Neolithic China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12767-12774.	3.3	63
23	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	9.4	592
24	Homogeneity in the association of body mass index with type 2 diabetes across the UK Biobank: A Mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002982.	3.9	34
25	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	9.4	377
26	Reduced signal for polygenic adaptation of height in UK Biobank. <i>ELife</i> , 2019, 8, .	2.8	283
27	Title is missing!. , 2019, 16, e1002982.		0
28	Title is missing!. , 2019, 16, e1002982.		0
29	Title is missing!. , 2019, 16, e1002982.		0
30	Title is missing!. , 2019, 16, e1002982.		0
31	Title is missing!. , 2019, 16, e1002982.		0
32	Pan-cancer screen for mutations in non-coding elements with conservation and cancer specificity reveals correlations with expression and survival. <i>Npj Genomic Medicine</i> , 2018, 3, 1.	1.7	79
33	Diff-seq: A high throughput sequencing-based mismatch detection assay for DNA variant enrichment and discovery. <i>Nucleic Acids Research</i> , 2018, 46, e42-e42.	6.5	7
34	Super-resolution chromatin tracing reveals domains and cooperative interactions in single cells. <i>Science</i> , 2018, 362, .	6.0	700
35	Loss of <i>LDAH</i> associated with prostate cancer and hearing loss. <i>Human Molecular Genetics</i> , 2018, 27, 4194-4203.	1.4	14
36	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	1.1	39

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37	An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. Nature Methods, 2017, 14, 959-962.	9.0	1,653
38	Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. Nature Genetics, 2016, 48, 1260-1266.	9.4	75
39	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
40	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
41	Omni-ATAC-seq: Improved ATAC-seq protocol. Protocol Exchange, 0, , .	0.3	21