

# Shane Neph

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10844817/publications.pdf>

Version: 2024-02-01

21  
papers

16,815  
citations

430442

18  
h-index

713013

21  
g-index

22  
all docs

22  
docs citations

22  
times ranked

28583  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping and Dynamics of Regulatory DNA in Maturing Arabidopsis thaliana Siliques. <i>Frontiers in Plant Science</i> , 2019, 10, 1434.	1.7	13
2	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
3	Operating on Genomic Ranges Using BEDOPS. <i>Methods in Molecular Biology</i> , 2016, 1418, 267-281.	0.4	8
4	Mapping and Dynamics of Regulatory DNA and Transcription Factor Networks in Arabidopsis thaliana. <i>Cell Reports</i> , 2014, 8, 2015-2030.	2.9	249
5	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	13.7	211
6	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
7	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	13.5	329
8	Personal and population genomics of human regulatory variation. <i>Genome Research</i> , 2012, 22, 1689-1697.	2.4	98
9	BEDOPS: high-performance genomic feature operations. <i>Bioinformatics</i> , 2012, 28, 1919-1920.	1.8	840
10	Foxp3 Exploits a Pre-Existent Enhancer Landscape for Regulatory T Cell Lineage Specification. <i>Cell</i> , 2012, 151, 153-166.	13.5	411
11	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	13.7	715
12	Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. <i>Science</i> , 2012, 337, 1190-1195.	6.0	3,129
13	Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. <i>Cell</i> , 2012, 150, 1274-1286.	13.5	451
14	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	13.7	2,434
15	The Human Mitochondrial Transcriptome. <i>Cell</i> , 2011, 146, 645-658.	13.5	716
16	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. <i>Nature Methods</i> , 2009, 6, 283-289.	9.0	533
17	Assaying the regulatory potential of mammalian conserved non-coding sequences in human cells. <i>Genome Biology</i> , 2008, 9, R168.	13.9	18
18	A Computational Pipeline for High-Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. <i>PLoS Computational Biology</i> , 2007, 3, e126.	1.5	77

#	ARTICLE	IF	CITATIONS
19	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. <i>Nucleic Acids Research</i> , 2007, 35, 4809-4819.	6.5	292
20	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
21	MicroFootPrinter: a tool for phylogenetic footprinting in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2006, 34, W366-W368.	6.5	25