

# Sharon R Grossman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/680294/publications.pdf>

Version: 2024-02-01

16  
papers

15,589  
citations

516710  
16  
h-index

940533  
16  
g-index

18  
all docs

18  
docs citations

18  
times ranked

30658  
citing authors

#	ARTICLE	IF	CITATIONS
1	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
2	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	27.8	2,625
3	Detecting Novel Associations in Large Data Sets. <i>Science</i> , 2011, 334, 1518-1524.	12.6	2,252
4	Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. <i>Nature Genetics</i> , 2019, 51, 1664-1669.	21.4	631
5	Detecting Natural Selection in Genomic Data. <i>Annual Review of Genetics</i> , 2013, 47, 97-120.	7.6	584
6	Systematic mapping of functional enhancer-promoter connections with CRISPR interference. <i>Science</i> , 2016, 354, 769-773.	12.6	512
7	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. <i>Science</i> , 2010, 327, 883-886.	12.6	457
8	RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites. <i>Cell</i> , 2014, 159, 188-199.	28.9	425
9	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	28.9	325
10	Systematic dissection of genomic features determining transcription factor binding and enhancer function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1291-E1300.	7.1	150
11	Genome-wide scans provide evidence for positive selection of genes implicated in Lassa fever. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 868-877.	4.0	93
12	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in <i>Plasmodium falciparum</i> . <i>PLoS Genetics</i> , 2011, 7, e1001383.	3.5	85
13	Positional specificity of different transcription factor classes within enhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7222-E7230.	7.1	72
14	Compatibility rules of human enhancer and promoter sequences. <i>Nature</i> , 2022, 607, 176-184.	27.8	67
15	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	21.4	55
16	Ancient and Recent Adaptive Evolution of Primate Non-Homologous End Joining Genes. <i>PLoS Genetics</i> , 2010, 6, e1001169.	3.5	28