

Eilon Sharon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2999573/publications.pdf>

Version: 2024-02-01

20
papers

4,498
citations

471509

17
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

6654
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic interrogation of human promoters. <i>Genome Research</i> , 2019, 29, 171-183.	5.5	92
2	Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing. <i>Cell</i> , 2018, 175, 544-557.e16.	28.9	166
3	Large-scale mapping of gene regulatory logic reveals context-dependent repression by transcriptional activators. <i>Genome Research</i> , 2017, 27, 87-94.	5.5	28
4	Quantification of transplant-derived circulating cell-free DNA in absence of a donor genotype. <i>PLoS Computational Biology</i> , 2017, 13, e1005629.	3.2	60
5	Genetic variation in MHC proteins is associated with T cell receptor expression biases. <i>Nature Genetics</i> , 2016, 48, 995-1002.	21.4	151
6	Systematic Dissection of the Sequence Determinants of Gene 3' End Mediated Expression Control. <i>PLoS Genetics</i> , 2015, 11, e1005147.	3.5	70
7	Unraveling determinants of transcription factor binding outside the core binding site. <i>Genome Research</i> , 2015, 25, 1018-1029.	5.5	146
8	Probing the effect of promoters on noise in gene expression using thousands of designed sequences. <i>Genome Research</i> , 2014, 24, 1698-1706.	5.5	118
9	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013, 23, 1928-1937.	5.5	12
10	Deciphering the rules by which 5' UTR sequences affect protein expression in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2792-801.	7.1	231
11	Measurements of the Impact of 3' End Sequences on Gene Expression Reveal Wide Range and Sequence Dependent Effects. <i>PLoS Computational Biology</i> , 2013, 9, e1002934.	3.2	31
12	Manipulating nucleosome disfavoring sequences allows fine-tune regulation of gene expression in yeast. <i>Nature Genetics</i> , 2012, 44, 743-750.	21.4	185
13	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. <i>Nature Biotechnology</i> , 2012, 30, 521-530.	17.5	439
14	Compensation for differences in gene copy number among yeast ribosomal proteins is encoded within their promoters. <i>Genome Research</i> , 2011, 21, 2114-2128.	5.5	51
15	How Transcription Factors Identify Regulatory Sites in Genomic Sequence. <i>Sub-Cellular Biochemistry</i> , 2011, 52, 193-204.	2.4	2
16	A Feature-Based Approach to Modeling Protein-DNA Interactions. <i>PLoS Computational Biology</i> , 2008, 4, e1000154.	3.2	89
17	Distinct Modes of Regulation by Chromatin Encoded through Nucleosome Positioning Signals. <i>PLoS Computational Biology</i> , 2008, 4, e1000216.	3.2	393
18	A Feature-Based Approach to Modeling Protein-DNA Interactions. , 2007, , 77-91.		4

#	ARTICLE	IF	CITATIONS
19	Identification of hundreds of conserved and nonconserved human microRNAs. <i>Nature Genetics</i> , 2005, 37, 766-770.	21.4	1,720
20	MicroRNA expression detected by oligonucleotide microarrays: System establishment and expression profiling in human tissues. <i>Genome Research</i> , 2004, 14, 2486-2494.	5.5	495