

Eran Segal

List of Publications by Year in descending order

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Version: 2024-02-01

191
papers

49,755
citations

5574

82
h-index

3407

183
g-index

223
all docs

223
docs citations

223
times ranked

59625
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs. <i>Cell</i> , 2007, 129, 1311-1323.	28.9	3,835
2	Long Noncoding RNA as Modular Scaffold of Histone Modification Complexes. <i>Science</i> , 2010, 329, 689-693.	12.6	2,976
3	The role of site accessibility in microRNA target recognition. <i>Nature Genetics</i> , 2007, 39, 1278-1284.	21.4	2,223
4	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. <i>Science</i> , 2003, 302, 249-255.	12.6	2,034
5	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018, 555, 210-215.	27.8	1,958
6	Personalized Nutrition by Prediction of Glycemic Responses. <i>Cell</i> , 2015, 163, 1079-1094.	28.9	1,816
7	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	21.4	1,543
8	Artificial sweeteners induce glucose intolerance by altering the gut microbiota. <i>Nature</i> , 2014, 514, 181-186.	27.8	1,529
9	A genomic code for nucleosome positioning. <i>Nature</i> , 2006, 442, 772-778.	27.8	1,333
10	Role of the gut microbiota in nutrition and health. <i>BMJ: British Medical Journal</i> , 2018, 361, k2179.	2.3	1,228
11	The human tumor microbiome is composed of tumor type-specific intracellular bacteria. <i>Science</i> , 2020, 368, 973-980.	12.6	1,077
12	The DNA-encoded nucleosome organization of a eukaryotic genome. <i>Nature</i> , 2009, 458, 362-366.	27.8	1,063
13	Personalized Gut Mucosal Colonization Resistance to Empiric Probiotics Is Associated with Unique Host and Microbiome Features. <i>Cell</i> , 2018, 174, 1388-1405.e21.	28.9	1,015
14	Transkingdom Control of Microbiota Diurnal Oscillations Promotes Metabolic Homeostasis. <i>Cell</i> , 2014, 159, 514-529.	28.9	984
15	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
16	Post-Antibiotic Gut Mucosal Microbiome Reconstitution Is Impaired by Probiotics and Improved by Autologous FMT. <i>Cell</i> , 2018, 174, 1406-1423.e16.	28.9	752
17	Microbiota-Modulated Metabolites Shape the Intestinal Microenvironment by Regulating NLRP6 Inflammasome Signaling. <i>Cell</i> , 2015, 163, 1428-1443.	28.9	728
18	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	27.8	713

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19	The pros, cons, and many unknowns of probiotics. Nature Medicine, 2019, 25, 716-729.	30.7	706
20	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
21	Module Map of Stem Cell Genes Guides Creation of Epithelial Cancer Stem Cells. Cell Stem Cell, 2008, 2, 333-344.	11.1	652
22	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	21.4	622
23	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
24	Microbiota Diurnal Rhythmicity Programs Host Transcriptome Oscillations. Cell, 2016, 167, 1495-1510.e12.	28.9	591
25	Determinants of nucleosome positioning. Nature Structural and Molecular Biology, 2013, 20, 267-273.	8.2	565
26	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	27.8	519
27	Decoding global gene expression programs in liver cancer by noninvasive imaging. Nature Biotechnology, 2007, 25, 675-680.	17.5	510
28	A module of negative feedback regulators defines growth factor signaling. Nature Genetics, 2007, 39, 503-512.	21.4	506
29	Evidence for an instructive mechanism of de novo methylation in cancer cells. Nature Genetics, 2006, 38, 149-153.	21.4	456
30	Potential roles of gut microbiome and metabolites in modulating ALS in mice. Nature, 2019, 572, 474-480.	27.8	454
31	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. Nature Biotechnology, 2012, 30, 521-530.	17.5	439
32	Predicting expression patterns from regulatory sequence in Drosophila segmentation. Nature, 2008, 451, 535-540.	27.8	434
33	Understanding the transcriptome through RNA structure. Nature Reviews Genetics, 2011, 12, 641-655.	16.3	411
34	Motif module map reveals enforcement of aging by continual NF- κ B activity. Genes and Development, 2007, 21, 000.1-000.	5.9	407
35	Distinct Modes of Regulation by Chromatin Encoded through Nucleosome Positioning Signals. PLoS Computational Biology, 2008, 4, e1000216.	3.2	393
36	Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. Science, 2015, 349, 1101-1106.	12.6	382

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37	Poly(dA:dT) tracts: major determinants of nucleosome organization. <i>Current Opinion in Structural Biology</i> , 2009, 19, 65-71.	5.7	376
38	Persistent microbiome alterations modulate the rate of post-dieting weight regain. <i>Nature</i> , 2016, 540, 544-551.	27.8	371
39	What controls nucleosome positions?. <i>Trends in Genetics</i> , 2009, 25, 335-343.	6.7	345
40	Monoubiquitinated H2B is associated with the transcribed region of highly expressed genes in human cells. <i>Nature Cell Biology</i> , 2008, 10, 483-488.	10.3	333
41	From signatures to models: understanding cancer using microarrays. <i>Nature Genetics</i> , 2005, 37, S38-S45.	21.4	331
42	A Transcriptional Profile of Aging in the Human Kidney. <i>PLoS Biology</i> , 2004, 2, e427.	5.6	281
43	Systematic discovery of cap-independent translation sequences in human and viral genomes. <i>Science</i> , 2016, 351, .	12.6	258
44	From DNA sequence to transcriptional behaviour: a quantitative approach. <i>Nature Reviews Genetics</i> , 2009, 10, 443-456.	16.3	249
45	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	27.8	245
46	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019, 568, 43-48.	27.8	244
47	Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses. <i>Cell Metabolism</i> , 2017, 25, 1243-1253.e5.	16.2	233
48	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
49	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	27.8	230
50	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. <i>Cell</i> , 2020, 182, 1460-1473.e17.	28.9	217
51	Axes of a revolution: challenges and promises of big data in healthcare. <i>Nature Medicine</i> , 2020, 26, 29-38.	30.7	206
52	In pursuit of design principles of regulatory sequences. <i>Nature Reviews Genetics</i> , 2014, 15, 453-468.	16.3	196
53	Genome-wide Measurement of RNA Folding Energies. <i>Molecular Cell</i> , 2012, 48, 169-181.	9.7	192
54	Taking it Personally: Personalized Utilization of the Human Microbiome in Health and Disease. <i>Cell Host and Microbe</i> , 2016, 19, 12-20.	11.0	192

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55	Identification of bacteria-derived HLA-bound peptides in melanoma. <i>Nature</i> , 2021, 592, 138-143.	27.8	187
56	Manipulating nucleosome disfavoring sequences allows fine-tune regulation of gene expression in yeast. <i>Nature Genetics</i> , 2012, 44, 743-750.	21.4	185
57	COVID-19 dynamics after a national immunization program in Israel. <i>Nature Medicine</i> , 2021, 27, 1055-1061.	30.7	183
58	Promoters maintain their relative activity levels under different growth conditions. <i>Molecular Systems Biology</i> , 2013, 9, 701.	7.2	181
59	Involvement of a gut-retina axis in protection against dietary glycemia-induced age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4472-E4481.	7.1	179
60	A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. <i>Molecular Cell</i> , 2018, 71, 178-190.e8.	9.7	177
61	Prediction of gestational diabetes based on nationwide electronic health records. <i>Nature Medicine</i> , 2020, 26, 71-76.	30.7	170
62	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
63	Transient transcriptional responses to stress are generated by opposing effects of mRNA production and degradation. <i>Molecular Systems Biology</i> , 2008, 4, 223.	7.2	169
64	Massively Parallel Interrogation of the Effects of Gene Expression Levels on Fitness. <i>Cell</i> , 2016, 166, 1282-1294.e18.	28.9	168
65	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021, 184, 2302-2315.e12.	28.9	166
66	High Nucleosome Occupancy Is Encoded at Human Regulatory Sequences. <i>PLoS ONE</i> , 2010, 5, e9129.	2.5	163
67	New insights into replication origin characteristics in metazoans. <i>Cell Cycle</i> , 2012, 11, 658-667.	2.6	162
68	Non-caloric artificial sweeteners and the microbiome: findings and challenges. <i>Gut Microbes</i> , 2015, 6, 149-155.	9.8	152
69	Unraveling determinants of transcription factor binding outside the core binding site. <i>Genome Research</i> , 2015, 25, 1018-1029.	5.5	146
70	Promoter Sequence Determines the Relationship between Expression Level and Noise. <i>PLoS Biology</i> , 2013, 11, e1001528.	5.6	143
71	Longitudinal symptom dynamics of COVID-19 infection. <i>Nature Communications</i> , 2020, 11, 6208.	12.8	141
72	Microbiome at the Frontier of Personalized Medicine. <i>Mayo Clinic Proceedings</i> , 2017, 92, 1855-1864.	3.0	138

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73	Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. <i>Nature Genetics</i> , 2009, 41, 438-445.	21.4	132
74	A framework for identifying regional outbreak and spread of COVID-19 from one-minute population-wide surveys. <i>Nature Medicine</i> , 2020, 26, 634-638.	30.7	122
75	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
76	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 581-596.	16.3	118
77	Computational prediction of RNA structural motifs involved in posttranscriptional regulatory processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14885-14890.	7.1	109
78	Structured elements drive extensive circular RNA translation. <i>Molecular Cell</i> , 2021, 81, 4300-4318.e13.	9.7	108
79	Reversal of aging by NF κ B blockade. <i>Cell Cycle</i> , 2008, 7, 556-559.	2.6	103
80	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102
81	Towards utilization of the human genome and microbiome for personalized nutrition. <i>Current Opinion in Biotechnology</i> , 2018, 51, 57-63.	6.6	101
82	EGF Decreases the Abundance of MicroRNAs That Restrain Oncogenic Transcription Factors. <i>Science Signaling</i> , 2010, 3, ra43.	3.6	100
83	Diversity and functional landscapes in the microbiota of animals in the wild. <i>Science</i> , 2021, 372, .	12.6	96
84	Nucleosome sequence preferences influence in vivo nucleosome organization. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 918-920.	8.2	95
85	Core promoter sequence in yeast is a major determinant of expression level. <i>Genome Research</i> , 2015, 25, 1008-1017.	5.5	94
86	Systematic interrogation of human promoters. <i>Genome Research</i> , 2019, 29, 171-183.	5.5	92
87	A Feature-Based Approach to Modeling Protein-DNA Interactions. <i>PLoS Computational Biology</i> , 2008, 4, e1000154.	3.2	89
88	Incorporating nucleosomes into thermodynamic models of transcription regulation. <i>Genome Research</i> , 2009, 19, 1480-1496.	5.5	87
89	Gene Architecture and Sequence Composition Underpin Selective Dependency of Nuclear Export of Long RNAs on NXF1 and the TREX Complex. <i>Molecular Cell</i> , 2020, 79, 251-267.e6.	9.7	87
90	p53 binds preferentially to genomic regions with high DNA-encoded nucleosome occupancy. <i>Genome Research</i> , 2010, 20, 1361-1368.	5.5	86

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91	Sequence features of yeast and human core promoters that are predictive of maximal promoter activity. Nucleic Acids Research, 2013, 41, 5569-5581.	14.5	84
92	Noise in gene expression is coupled to growth rate. Genome Research, 2015, 25, 1893-1902.	5.5	83
93	The grammar of transcriptional regulation. Human Genetics, 2014, 133, 701-711.	3.8	78
94	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. Nature Medicine, 2022, 28, 295-302.	30.7	74
95	Disruption of Yeast Forkhead-associated Cell Cycle Transcription by Oxidative Stress. Molecular Biology of the Cell, 2004, 15, 5659-5669.	2.1	71
96	Systematic Dissection of the Sequence Determinants of Gene 3â€™ End Mediated Expression Control. PLoS Genetics, 2015, 11, e1005147.	3.5	70
97	A Transcriptional Program Mediating Entry into Cellular Quiescence. PLoS Genetics, 2007, 3, e91.	3.5	67
98	Preferentially Quantized Linker DNA Lengths in Saccharomyces cerevisiae. PLoS Computational Biology, 2008, 4, e1000175.	3.2	65
99	Overlapping codes within protein-coding sequences. Genome Research, 2010, 20, 1582-1589.	5.5	65
100	From promoter sequence to expression. , 2002, , .		64
101	Hospital load and increased COVID-19 related mortality in Israel. Nature Communications, 2021, 12, 1904.	12.8	64
102	Cell Lineage Analysis of the Mammalian Female Germline. PLoS Genetics, 2012, 8, e1002477.	3.5	60
103	A day in the life of the meta-organism: diurnal rhythms of the intestinal microbiome and its host. Gut Microbes, 2015, 6, 137-142.	9.8	59
104	Revealing Targeted Therapy for Human Cancer by Gene Module Maps. Cancer Research, 2008, 68, 369-378.	0.9	58
105	The Gut Microbiome and Individual-Specific Responses to Diet. MSystems, 2020, 5, .	3.8	58
106	Systematic functional characterization of cis-regulatory motifs in human core promoters. Genome Research, 2008, 18, 477-488.	5.5	57
107	Two DNA-encoded strategies for increasing expression with opposing effects on promoter dynamics and transcriptional noise. Genome Research, 2013, 23, 966-976.	5.5	57
108	Personalized Postprandial Glucose Responseâ€”Targeting Diet Versus Mediterranean Diet for Glycemic Control in Prediabetes. Diabetes Care, 2021, 44, 1980-1991.	8.6	55

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109	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	9.6	53
110	Contribution of histone sequence preferences to nucleosome organization: proposed definitions and methodology. <i>Genome Biology</i> , 2010, 11, 140.	8.8	53
111	The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). <i>BMC Medicine</i> , 2021, 19, 13.	5.5	52
112	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
113	Anosmia, ageusia, and other COVID-19-like symptoms in association with a positive SARS-CoV-2 test, across six national digital surveillance platforms: an observational study. <i>The Lancet Digital Health</i> , 2021, 3, e577-e586.	12.3	51
114	Host-parasite network structure is associated with community-level immunogenetic diversity. <i>Nature Communications</i> , 2014, 5, 5172.	12.8	49
115	Systematic Investigation of Transcription Factor Activity in the Context of Chromatin Using Massively Parallel Binding and Expression Assays. <i>Molecular Cell</i> , 2017, 65, 604-617.e6.	9.7	48
116	Signals of hope: gauging the impact of a rapid national vaccination campaign. <i>Nature Reviews Immunology</i> , 2021, 21, 198-199.	22.7	48
117	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	19.0	44
118	Effects of personalized diets by prediction of glycemic responses on glycemic control and metabolic health in newly diagnosed T2DM: a randomized dietary intervention pilot trial. <i>BMC Medicine</i> , 2022, 20, 56.	5.5	44
119	Nucleosome maps of the human cytomegalovirus genome reveal a temporal switch in chromatin organization linked to a major IE protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13126-13131.	7.1	43
120	Reconstruction of Cell Lineage Trees in Mice. <i>PLoS ONE</i> , 2008, 3, e1939.	2.5	43
121	Stemness, cancer, and cancer stem cells. <i>Cell Cycle</i> , 2008, 7, 3622-3624.	2.6	39
122	Population-wide diversity and stability of serum antibody epitope repertoires against human microbiota. <i>Nature Medicine</i> , 2021, 27, 1442-1450.	30.7	38
123	Potential role of indolelactate and butyrate in multiple sclerosis revealed by integrated microbiome-metabolome analysis. <i>Cell Reports Medicine</i> , 2021, 2, 100246.	6.5	37
124	Widespread Compensatory Evolution Conserves DNA-Encoded Nucleosome Organization in Yeast. <i>PLoS Computational Biology</i> , 2010, 6, e1001039.	3.2	36
125	Unraveling the determinants of microRNA mediated regulation using a massively parallel reporter assay. <i>Nature Communications</i> , 2018, 9, 529.	12.8	36
126	Estimating Cell Depth from Somatic Mutations. <i>PLoS Computational Biology</i> , 2008, 4, e1000058.	3.2	35

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127	High nucleosome occupancy is encoded at X-linked gene promoters in <i>C. elegans</i> . <i>Genome Research</i> , 2011, 21, 237-244.	5.5	35
128	Robust Prediction of Expression Differences among Human Individuals Using Only Genotype Information. <i>PLoS Genetics</i> , 2013, 9, e1003396.	3.5	34
129	Host genetics and microbiome associations through the lens of genome wide association studies. <i>Current Opinion in Microbiology</i> , 2018, 44, 9-19.	5.1	33
130	Using Expression Profiles of <i>Caenorhabditis elegans</i> Neurons To Identify Genes That Mediate Synaptic Connectivity. <i>PLoS Computational Biology</i> , 2008, 4, e1000120.	3.2	32
131	SARS-CoV-2 antibody testing for estimating COVID-19 prevalence in the population. <i>Cell Reports Medicine</i> , 2021, 2, 100191.	6.5	32
132	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
133	An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. <i>Nature Communications</i> , 2022, 13, .	12.8	31
134	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
135	Clinical efficacy of fecal microbial transplantation treatment in adults with moderate-to-severe atopic dermatitis. <i>Immunity, Inflammation and Disease</i> , 2022, 10, .	2.7	28
136	A Discriminative Model for Identifying Spatial cis-Regulatory Modules. <i>Journal of Computational Biology</i> , 2005, 12, 822-834.	1.6	27
137	Dissecting splicing decisions and cell-to-cell variability with designed sequence libraries. <i>Nature Communications</i> , 2019, 10, 4572.	12.8	27
138	Visualizing the structure and motion of the long noncoding RNA HOTAIR. <i>Rna</i> , 2020, 26, 629-636.	3.5	27
139	Cross-reactive antibodies against human coronaviruses and the animal coronavirome suggest diagnostics for future zoonotic spillovers. <i>Science Immunology</i> , 2021, 6, .	11.9	26
140	Probabilistic Discovery of Overlapping Cellular Processes and Their Regulation. <i>Journal of Computational Biology</i> , 2005, 12, 909-927.	1.6	24
141	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	30.7	23
142	A Prediction Model to Prioritize Individuals for a SARS-CoV-2 Test Built from National Symptom Surveys. <i>Med</i> , 2021, 2, 196-208.e4.	4.4	23
143	Sequence features of viral and human Internal Ribosome Entry Sites predictive of their activity. <i>PLoS Computational Biology</i> , 2017, 13, e1005734.	3.2	23
144	Predicting Disease Risk Using Bootstrap Ranking and Classification Algorithms. <i>PLoS Computational Biology</i> , 2013, 9, e1003200.	3.2	20

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145	Sequence determinants of polyadenylation-mediated regulation. <i>Genome Research</i> , 2019, 29, 1635-1647.	5.5	19
146	High-throughput interrogation of programmed ribosomal frameshifting in human cells. <i>Nature Communications</i> , 2020, 11, 3061.	12.8	19
147	Stress-related emotional and behavioural impact following the first COVID-19 outbreak peak. <i>Molecular Psychiatry</i> , 2021, 26, 6149-6158.	7.9	19
148	The Gut Microbiome of Adults With Type 1 Diabetes and Its Association With the Host Glycemic Control. <i>Diabetes Care</i> , 2022, 45, 555-563.	8.6	19
149	Probabilistic hierarchical clustering for biological data. , 2002, , .		18
150	A shared architecture for promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1253-1254.	21.4	18
151	The rationale and design of the personal diet study, a randomized clinical trial evaluating a personalized approach to weight loss in individuals with pre-diabetes and early-stage type 2 diabetes. <i>Contemporary Clinical Trials</i> , 2019, 79, 80-88.	1.8	18
152	A Minimalistic Resource Allocation Model to Explain Ubiquitous Increase in Protein Expression with Growth Rate. <i>PLoS ONE</i> , 2016, 11, e0153344.	2.5	18
153	Modeling interactions between adjacent nucleosomes improves genome-wide predictions of nucleosome occupancy. <i>Bioinformatics</i> , 2009, 25, i348-i355.	4.1	17
154	Molecular dissection of the genetic mechanisms that underlie expression conservation in orthologous yeast ribosomal promoters. <i>Genome Research</i> , 2014, 24, 1991-1999.	5.5	17
155	Clinically Accurate Prediction of Glucose Levels in Patients with Type 1 Diabetes. <i>Diabetes Technology and Therapeutics</i> , 2020, 22, 562-569.	4.4	17
156	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3'UTR protect against ALS. <i>Nature Neuroscience</i> , 2022, 25, 433-445.	14.8	16
157	Prediction of Personal Glycemic Responses to Food for Individuals With Type 1 Diabetes Through Integration of Clinical and Microbial Data. <i>Diabetes Care</i> , 2022, 45, 502-511.	8.6	15
158	An atlas of robust microbiome associations with phenotypic traits based on large-scale cohorts from two continents. <i>PLoS ONE</i> , 2022, 17, e0265756.	2.5	15
159	Probabilistic discovery of overlapping cellular processes and their regulation. , 2004, , .		14
160	Computational Prediction of RNA Structural Motifs Involved in Post-Transcriptional Regulatory Processes. <i>Methods in Molecular Biology</i> , 2011, 714, 467-479.	0.9	14
161	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. <i>Genome Research</i> , 2013, 23, 1928-1937.	5.5	12
162	Prediction of Childhood Obesity from Nationwide Health Records. <i>Journal of Pediatrics</i> , 2021, 233, 132-140.e1.	1.8	12

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163	Efficient Bundle Sorting. SIAM Journal on Computing, 2006, 36, 394-410.	1.0	11
164	10ÂK: a large-scale prospective longitudinal study in Israel. European Journal of Epidemiology, 2021, 36, 1187-1194.	5.7	9
165	GenoExp: a web tool for predicting gene expression levels from single nucleotide polymorphisms. Bioinformatics, 2015, 31, 1848-1850.	4.1	8
166	Toward a systematic understanding of translational regulatory elements in human and viruses. RNA Biology, 2016, 13, 927-933.	3.1	8
167	New Approaches to Profile the Microbiome for Treatment of Neurodegenerative Disease. Journal of Alzheimer's Disease, 2021, 82, 1373-1401.	2.6	8
168	Nowcasting the spread of SARS-CoV-2. Nature Microbiology, 2022, 7, 16-17.	13.3	8
169	Antibody signatures in inflammatory bowel disease: current developments and future applications. Trends in Molecular Medicine, 2022, 28, 693-705.	6.7	8
170	Prediction of type 2 diabetes mellitus onset using logistic regression-based scorecards. ELife, 0, 11, .	6.0	7
171	Artificial Sweeteners Induce Glucose Intolerance by Altering the Gut Microbiota. Obstetrical and Gynecological Survey, 2015, 70, 31-32.	0.4	6
172	A discriminative model for identifying spatial cis-regulatory modules. , 2004, , .		5
173	Unified platform for genetic and serological detection of COVID-19 with single-molecule technology. PLoS ONE, 2021, 16, e0255096.	2.5	5
174	Soluble Receptor for Advanced Glycation End Products (sRAGE) Isoforms Predict Changes in Resting Energy Expenditure in Adults with Obesity during Weight Loss. Current Developments in Nutrition, 2022, 6, nza046.	0.3	5
175	Functional characterization of the p53 -mutome-. Molecular and Cellular Oncology, 2018, 5, e1511207.	0.7	4
176	Challenges of conducting a remote behavioral weight loss study: Lessons learned and a practical guide. Contemporary Clinical Trials, 2021, 108, 106522.	1.8	4
177	A Feature-Based Approach to Modeling Protein-DNA Interactions. , 2007, , 77-91.		4
178	Rationale and design of a randomised controlled trial testing the effect of personalised diet in individuals with pre-diabetes or type 2 diabetes mellitus treated with metformin. BMJ Open, 2020, 10, e037859.	1.9	4
179	Fixated on fixation - using ChIP to interrogate the dynamics of chromatin interactions. Genome Biology, 2013, 14, 138.	9.6	3
180	COVID-19 and beyond:Âa call for action andÂaudacious solidarity to all the citizens and nations,Âit is humanity's fight. F1000Research, 0, 9, 1130.	1.6	3

#	ARTICLE	IF	CITATIONS
181	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology. , 2011, , .		2
182	How Transcription Factors Identify Regulatory Sites in Genomic Sequence. Sub-Cellular Biochemistry, 2011, 52, 193-204.	2.4	2
183	Incorporating Nucleosomes into Thermodynamic Models of Transcription Regulation. Lecture Notes in Computer Science, 2009, , 217-217.	1.3	2
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