

# Eran Segal

## List of Publications by Year in descending order

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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	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
2	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
3	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
4	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. <i>Nature Medicine</i> , 2022, 28, 295-302.	30.7	74
5	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102
6	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
7	Soluble Receptor for Advanced Glycation End Products (sRAGE) Isoforms Predict Changes in Resting Energy Expenditure in Adults with Obesity during Weight Loss. <i>Current Developments in Nutrition</i> , 2022, 6, nzac046.	0.3	5
8	Whole-genome sequencing reveals that variants in the Interleukin 18 Receptor Accessory Protein 3â€™UTR protect against ALS. <i>Nature Neuroscience</i> , 2022, 25, 433-445.	14.8	16
9	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
10	Nowcasting the spread of SARS-CoV-2. <i>Nature Microbiology</i> , 2022, 7, 16-17.	13.3	8
11	Recording bacterial responses to changes in the gut environment. <i>Science</i> , 2022, 376, 697-698.	12.6	2
12	Antibody signatures in inflammatory bowel disease: current developments and future applications. <i>Trends in Molecular Medicine</i> , 2022, 28, 693-705.	6.7	8
13	New Approaches to Profile the Microbiome for Treatment of Neurodegenerative Disease. <i>Advances in Alzheimer's Disease</i> , 2022, , .	0.2	0
14	An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. <i>Nature Communications</i> , 2022, 13, .	12.8	31
15	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
16	The gut microbiome: a key player in the complexity of amyotrophic lateral sclerosis (ALS). <i>BMC Medicine</i> , 2021, 19, 13.	5.5	52
17	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
18	SARS-CoV-2 antibody testing for estimating COVID-19 prevalence in the population. <i>Cell Reports Medicine</i> , 2021, 2, 100191.	6.5	32

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19	Hospital load and increased COVID-19 related mortality in Israel. Nature Communications, 2021, 12, 1904.	12.8	64
20	Diversity and functional landscapes in the microbiota of animals in the wild. Science, 2021, 372, .	12.6	96
21	Identification of bacteria-derived HLA-bound peptides in melanoma. Nature, 2021, 592, 138-143.	27.8	187
22	Signals of hope: gauging the impact of a rapid national vaccination campaign. Nature Reviews Immunology, 2021, 21, 198-199.	22.7	48
23	The long-term genetic stability and individual specificity of the human gut microbiome. Cell, 2021, 184, 2302-2315.e12.	28.9	166
24	COVID-19 dynamics after a national immunization program in Israel. Nature Medicine, 2021, 27, 1055-1061.	30.7	183
25	Potential role of indolelactate and butyrate in multiple sclerosis revealed by integrated microbiome-metabolome analysis. Cell Reports Medicine, 2021, 2, 100246.	6.5	37
26	10ÂK: a large-scale prospective longitudinal study in Israel. European Journal of Epidemiology, 2021, 36, 1187-1194.	5.7	9
27	Prediction of Childhood Obesity from Nationwide Health Records. Journal of Pediatrics, 2021, 233, 132-140.e1.	1.8	12
28	Unified platform for genetic and serological detection of COVID-19 with single-molecule technology. PLoS ONE, 2021, 16, e0255096.	2.5	5
29	Population-wide diversity and stability of serum antibody epitope repertoires against human microbiota. Nature Medicine, 2021, 27, 1442-1450.	30.7	38
30	Cross-reactive antibodies against human coronaviruses and the animal coronavirome suggest diagnostics for future zoonotic spillovers. Science Immunology, 2021, 6, .	11.9	26
31	Personalized Postprandial Glucose Responseâ€Targeting Diet Versus Mediterranean Diet for Glycemic Control in Prediabetes. Diabetes Care, 2021, 44, 1980-1991.	8.6	55
32	Structured elements drive extensive circular RNA translation. Molecular Cell, 2021, 81, 4300-4318.e13.	9.7	108
33	New Approaches to Profile the Microbiome for Treatment of Neurodegenerative Disease. Journal of Alzheimer's Disease, 2021, 82, 1373-1401.	2.6	8
34	Stress-related emotional and behavioural impact following the first COVID-19 outbreak peak. Molecular Psychiatry, 2021, 26, 6149-6158.	7.9	19
35	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. The Lancet Digital Health, 2021, 3, e577-e586.	12.3	51
36	Challenges of conducting a remote behavioral weight loss study: Lessons learned and a practical guide. Contemporary Clinical Trials, 2021, 108, 106522.	1.8	4

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37	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
38	Estimating heritability of glycaemic response to metformin using nationwide electronic health records and population-sized pedigree. Communications Medicine, 2021, 1, .	4.2	1
39	Axes of a revolution: challenges and promises of big data in healthcare. Nature Medicine, 2020, 26, 29-38.	30.7	206
40	Longitudinal Multi-omics Reveals Subset-Specific Mechanisms Underlying Irritable Bowel Syndrome. Cell, 2020, 182, 1460-1473.e17.	28.9	217
41	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	27.8	230
42	The Gut Microbiome and Individual-Specific Responses to Diet. MSystems, 2020, 5, .	3.8	58
43	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	16.3	118
44	Longitudinal symptom dynamics of COVID-19 infection. Nature Communications, 2020, 11, 6208.	12.8	141
45	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
46	The human tumor microbiome is composed of tumor type-specific intracellular bacteria. Science, 2020, 368, 973-980.	12.6	1,077
47	High-throughput interrogation of programmed ribosomal frameshifting in human cells. Nature Communications, 2020, 11, 3061.	12.8	19
48	Gene Architecture and Sequence Composition Underpin Selective Dependency of Nuclear Export of Long RNAs on NXF1 and the TREX Complex. Molecular Cell, 2020, 79, 251-267.e6.	9.7	87
49	Prediction of gestational diabetes based on nationwide electronic health records. Nature Medicine, 2020, 26, 71-76.	30.7	170
50	Clinically Accurate Prediction of Glucose Levels in Patients with Type 1 Diabetes. Diabetes Technology and Therapeutics, 2020, 22, 562-569.	4.4	17
51	A framework for identifying regional outbreak and spread of COVID-19 from one-minute population-wide surveys. Nature Medicine, 2020, 26, 634-638.	30.7	122
52	Visualizing the structure and motion of the long noncoding RNA HOTAIR. Rna, 2020, 26, 629-636.	3.5	27
53	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
54	Potential roles of gut microbiome and metabolites in modulating ALS in mice. Nature, 2019, 572, 474-480.	27.8	454

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55	Dissecting splicing decisions and cell-to-cell variability with designed sequence libraries. Nature Communications, 2019, 10, 4572.	12.8	27
56	Sequence determinants of polyadenylation-mediated regulation. Genome Research, 2019, 29, 1635-1647.	5.5	19
57	The pros, cons, and many unknowns of probiotics. Nature Medicine, 2019, 25, 716-729.	30.7	706
58	Structural variation in the gut microbiome associates with host health. Nature, 2019, 568, 43-48.	27.8	244
59	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. Contemporary Clinical Trials, 2019, 79, 80-88.	1.8	18
60	A Significant Expansion of Our Understanding of the Composition of the Human Microbiome. MSystems, 2019, 4, .	3.8	0
61	Systematic interrogation of human promoters. Genome Research, 2019, 29, 171-183.	5.5	92
62	Environment dominates over host genetics in shaping human gut microbiota. Nature, 2018, 555, 210-215.	27.8	1,958
63	Unraveling the determinants of microRNA mediated regulation using a massively parallel reporter assay. Nature Communications, 2018, 9, 529.	12.8	36
64	Towards utilization of the human genome and microbiome for personalized nutrition. Current Opinion in Biotechnology, 2018, 51, 57-63.	6.6	101
65	Functional characterization of the p53 "mutome". Molecular and Cellular Oncology, 2018, 5, e1511207.	0.7	4
66	The Helix Twist: Damage and Repair Follows the DNA Minor Groove. Cell, 2018, 175, 902-904.	28.9	1
67	Personalized Gut Mucosal Colonization Resistance to Empiric Probiotics Is Associated with Unique Host and Microbiome Features. Cell, 2018, 174, 1388-1405.e21.	28.9	1,015
68	Post-Antibiotic Gut Mucosal Microbiome Reconstitution Is Impaired by Probiotics and Improved by Autologous FMT. Cell, 2018, 174, 1406-1423.e16.	28.9	752
69	A Systematic p53 Mutation Library Links Differential Functional Impact to Cancer Mutation Pattern and Evolutionary Conservation. Molecular Cell, 2018, 71, 178-190.e8.	9.7	177
70	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
71	Host genetics and microbiome associations through the lens of genome wide association studies. Current Opinion in Microbiology, 2018, 44, 9-19.	5.1	33
72	Role of the gut microbiota in nutrition and health. BMJ: British Medical Journal, 2018, 361, k2179.	2.3	1,228

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73	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
74	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
75	Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses. <i>Cell Metabolism</i> , 2017, 25, 1243-1253.e5.	16.2	233
76	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
77	Microbiome at the Frontier of Personalized Medicine. <i>Mayo Clinic Proceedings</i> , 2017, 92, 1855-1864.	3.0	138
78	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
79	Microbiota Diurnal Rhythmicity Programs Host Transcriptome Oscillations. <i>Cell</i> , 2016, 167, 1495-1510.e12.	28.9	591
80	Massively Parallel Interrogation of the Effects of Gene Expression Levels on Fitness. <i>Cell</i> , 2016, 166, 1282-1294.e18.	28.9	168
81	Persistent microbiome alterations modulate the rate of post-dieting weight regain. <i>Nature</i> , 2016, 540, 544-551.	27.8	371
82	Toward a systematic understanding of translational regulatory elements in human and viruses. <i>RNA Biology</i> , 2016, 13, 927-933.	3.1	8
83	Systematic discovery of cap-independent translation sequences in human and viral genomes. <i>Science</i> , 2016, 351, .	12.6	258
84	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	19.0	44
85	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
86	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
87	Microbiota-Modulated Metabolites Shape the Intestinal Microenvironment by Regulating NLRP6 Inflammasome Signaling. <i>Cell</i> , 2015, 163, 1428-1443.	28.9	728
88	GenoExp: a web tool for predicting gene expression levels from single nucleotide polymorphisms. <i>Bioinformatics</i> , 2015, 31, 1848-1850.	4.1	8
89	Growth dynamics of gut microbiota in health and disease inferred from single metagenomic samples. <i>Science</i> , 2015, 349, 1101-1106.	12.6	382
90	Editorial overview: Genome architecture and expression. <i>Current Opinion in Genetics and Development</i> , 2015, 31, v-vi.	3.3	1

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91	Systematic Dissection of the Sequence Determinants of Gene 3â€™ End Mediated Expression Control. PLoS Genetics, 2015, 11, e1005147.	3.5	70
92	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
93	Unraveling determinants of transcription factor binding outside the core binding site. Genome Research, 2015, 25, 1018-1029.	5.5	146
94	Core promoter sequence in yeast is a major determinant of expression level. Genome Research, 2015, 25, 1008-1017.	5.5	94
95	Non-caloric artificial sweeteners and the microbiome: findings and challenges. Gut Microbes, 2015, 6, 149-155.	9.8	152
96	Artificial Sweeteners Induce Glucose Intolerance by Altering the Gut Microbiota. Obstetrical and Gynecological Survey, 2015, 70, 31-32.	0.4	6
97	Noise in gene expression is coupled to growth rate. Genome Research, 2015, 25, 1893-1902.	5.5	83
98	Personalized Nutrition by Prediction of Glycemic Responses. Cell, 2015, 163, 1079-1094.	28.9	1,816
99	Molecular dissection of the genetic mechanisms that underlie expression conservation in orthologous yeast ribosomal promoters. Genome Research, 2014, 24, 1991-1999.	5.5	17
100	A shared architecture for promoters and enhancers. Nature Genetics, 2014, 46, 1253-1254.	21.4	18
101	The grammar of transcriptional regulation. Human Genetics, 2014, 133, 701-711.	3.8	78
102	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	27.8	519
103	Transkingdom Control of Microbiota Diurnal Oscillations Promotes Metabolic Homeostasis. Cell, 2014, 159, 514-529.	28.9	984
104	Probing the effect of promoters on noise in gene expression using thousands of designed sequences. Genome Research, 2014, 24, 1698-1706.	5.5	118
105	Hostâ€™parasite network structure is associated with community-level immunogenetic diversity. Nature Communications, 2014, 5, 5172.	12.8	49
106	Artificial sweeteners induce glucose intolerance by altering the gut microbiota. Nature, 2014, 514, 181-186.	27.8	1,529
107	In pursuit of design principles of regulatory sequences. Nature Reviews Genetics, 2014, 15, 453-468.	16.3	196
108	Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. Genome Research, 2013, 23, 1928-1937.	5.5	12

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109	Fixated on fixation - using ChIP to interrogate the dynamics of chromatin interactions. Genome Biology, 2013, 14, 138.	9.6	3
110	Determinants of nucleosome positioning. Nature Structural and Molecular Biology, 2013, 20, 267-273.	8.2	565
111	Promoter Sequence Determines the Relationship between Expression Level and Noise. PLoS Biology, 2013, 11, e1001528.	5.6	143
112	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
113	Deciphering the rules by which 5' UTR sequences affect protein expression in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2792-801.	7.1	231
114	Predicting Disease Risk Using Bootstrap Ranking and Classification Algorithms. PLoS Computational Biology, 2013, 9, e1003200.	3.2	20
115	Robust Prediction of Expression Differences among Human Individuals Using Only Genotype Information. PLoS Genetics, 2013, 9, e1003396.	3.5	34
116	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
117	Nucleosome maps of the human cytomegalovirus genome reveal a temporal switch in chromatin organization linked to a major IE protein. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13126-13131.	7.1	43
118	Promoters maintain their relative activity levels under different growth conditions. Molecular Systems Biology, 2013, 9, 701.	7.2	181
119	Measurements of the Impact of 3' End Sequences on Gene Expression Reveal Wide Range and Sequence Dependent Effects. PLoS Computational Biology, 2013, 9, e1002934.	3.2	31
120	Cell Lineage Analysis of the Mammalian Female Germline. PLoS Genetics, 2012, 8, e1002477.	3.5	60
121	New insights into replication origin characteristics in metazoans. Cell Cycle, 2012, 11, 658-667.	2.6	162
122	Genome-wide Measurement of RNA Folding Energies. Molecular Cell, 2012, 48, 169-181.	9.7	192
123	ENCODE explained. Nature, 2012, 489, 52-54.	27.8	245
124	Manipulating nucleosome disfavoring sequences allows fine-tune regulation of gene expression in yeast. Nature Genetics, 2012, 44, 743-750.	21.4	185
125	Inferring gene regulatory logic from high-throughput measurements of thousands of systematically designed promoters. Nature Biotechnology, 2012, 30, 521-530.	17.5	439
126	Strengths and Weaknesses of Selected Modeling Methods Used in Systems Biology. , 2011, , .		2



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127	Understanding the transcriptome through RNA structure. <i>Nature Reviews Genetics</i> , 2011, 12, 641-655.	16.3	411
128	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
129	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
130	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
131	How Transcription Factors Identify Regulatory Sites in Genomic Sequence. <i>Sub-Cellular Biochemistry</i> , 2011, 52, 193-204.	2.4	2
132	Nucleosome sequence preferences influence in vivo nucleosome organization. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 918-920.	8.2	95
133	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	27.8	713
134	Journal club. <i>Nature</i> , 2010, 464, 329-329.	27.8	0
135	High Nucleosome Occupancy Is Encoded at Human Regulatory Sequences. <i>PLoS ONE</i> , 2010, 5, e9129.	2.5	163
136	p53 binds preferentially to genomic regions with high DNA-encoded nucleosome occupancy. <i>Genome Research</i> , 2010, 20, 1361-1368.	5.5	86
137	Overlapping codes within protein-coding sequences. <i>Genome Research</i> , 2010, 20, 1582-1589.	5.5	65
138	Widespread Compensatory Evolution Conserves DNA-Encoded Nucleosome Organization in Yeast. <i>PLoS Computational Biology</i> , 2010, 6, e1001039.	3.2	36
139	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
140	EGF Decreases the Abundance of MicroRNAs That Restrain Oncogenic Transcription Factors. <i>Science Signaling</i> , 2010, 3, ra43.	3.6	100
141	Long Noncoding RNA as Modular Scaffold of Histone Modification Complexes. <i>Science</i> , 2010, 329, 689-693.	12.6	2,976
142	Contribution of histone sequence preferences to nucleosome organization: proposed definitions and methodology. <i>Genome Biology</i> , 2010, 11, 140.	8.8	53
143	Incorporating nucleosomes into thermodynamic models of transcription regulation. <i>Genome Research</i> , 2009, 19, 1480-1496.	5.5	87
144	Modeling interactions between adjacent nucleosomes improves genome-wide predictions of nucleosome occupancy. <i>Bioinformatics</i> , 2009, 25, i348-i355.	4.1	17

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145	Poly(dA:dT) tracts: major determinants of nucleosome organization. <i>Current Opinion in Structural Biology</i> , 2009, 19, 65-71.	5.7	376
146	The DNA-encoded nucleosome organization of a eukaryotic genome. <i>Nature</i> , 2009, 458, 362-366.	27.8	1,063
147	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
148	From DNA sequence to transcriptional behaviour: a quantitative approach. <i>Nature Reviews Genetics</i> , 2009, 10, 443-456.	16.3	249
149	What controls nucleosome positions?. <i>Trends in Genetics</i> , 2009, 25, 335-343.	6.7	345
150	Incorporating Nucleosomes into Thermodynamic Models of Transcription Regulation. <i>Lecture Notes in Computer Science</i> , 2009, , 217-217.	1.3	2
151	Predicting expression patterns from regulatory sequence in <i>Drosophila</i> segmentation. <i>Nature</i> , 2008, 451, 535-540.	27.8	434
152	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
153	Module Map of Stem Cell Genes Guides Creation of Epithelial Cancer Stem Cells. <i>Cell Stem Cell</i> , 2008, 2, 333-344.	11.1	652
154	Stemness, cancer, and cancer stem cells. <i>Cell Cycle</i> , 2008, 7, 3622-3624.	2.6	39
155	Systematic functional characterization of <i>cis</i> -regulatory motifs in human core promoters. <i>Genome Research</i> , 2008, 18, 477-488.	5.5	57
156	Reversal of aging by NF- $\kappa$ B blockade. <i>Cell Cycle</i> , 2008, 7, 556-559.	2.6	103
157	Estimating Cell Depth from Somatic Mutations. <i>PLoS Computational Biology</i> , 2008, 4, e1000058.	3.2	35
158	A Feature-Based Approach to Modeling Protein-DNA Interactions. <i>PLoS Computational Biology</i> , 2008, 4, e1000154.	3.2	89
159	Distinct Modes of Regulation by Chromatin Encoded through Nucleosome Positioning Signals. <i>PLoS Computational Biology</i> , 2008, 4, e1000216.	3.2	393
160	Revealing Targeted Therapy for Human Cancer by Gene Module Maps. <i>Cancer Research</i> , 2008, 68, 369-378.	0.9	58
161	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
162	Preferentially Quantized Linker DNA Lengths in <i>Saccharomyces cerevisiae</i> . <i>PLoS Computational Biology</i> , 2008, 4, e1000175.	3.2	65

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163	Computational prediction of RNA structural motifs involved in posttranscriptional regulatory processes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14885-14890.	7.1	109
164	Transient transcriptional responses to stress are generated by opposing effects of mRNA production and degradation. Molecular Systems Biology, 2008, 4, 223.	7.2	169
165	Reconstruction of Cell Lineage Trees in Mice. PLoS ONE, 2008, 3, e1939.	2.5	43
166	A Transcriptional Program Mediating Entry into Cellular Quiescence. PLoS Genetics, 2007, 3, e91.	3.5	67
167	Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs. Cell, 2007, 129, 1311-1323.	28.9	3,835
168	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. Genome Biology, 2007, 8, R192.	9.6	53
169	Motif module map reveals enforcement of aging by continual NF- $\kappa$ B activity. Genes and Development, 2007, 21, 000.1-000.	5.9	407
170	Decoding global gene expression programs in liver cancer by noninvasive imaging. Nature Biotechnology, 2007, 25, 675-680.	17.5	510
171	A module of negative feedback regulators defines growth factor signaling. Nature Genetics, 2007, 39, 503-512.	21.4	506
172	The role of site accessibility in microRNA target recognition. Nature Genetics, 2007, 39, 1278-1284.	21.4	2,223
173	A Feature-Based Approach to Modeling Protein-DNA Interactions. , 2007, , 77-91.		4
174	Evidence for an instructive mechanism of de novo methylation in cancer cells. Nature Genetics, 2006, 38, 149-153.	21.4	456
175	A genomic code for nucleosome positioning. Nature, 2006, 442, 772-778.	27.8	1,333
176	Efficient Bundle Sorting. SIAM Journal on Computing, 2006, 36, 394-410.	1.0	11
177	From signatures to models: understanding cancer using microarrays. Nature Genetics, 2005, 37, S38-S45.	21.4	331
178	A Discriminative Model for Identifying Spatial cis-Regulatory Modules. Journal of Computational Biology, 2005, 12, 822-834.	1.6	27
179	Probabilistic Discovery of Overlapping Cellular Processes and Their Regulation. Journal of Computational Biology, 2005, 12, 909-927.	1.6	24
180	A discriminative model for identifying spatial cis-regulatory modules. , 2004, , .		5

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181	Probabilistic discovery of overlapping cellular processes and their regulation. , 2004, , .		14
182	Disruption of Yeast Forkhead-associated Cell Cycle Transcription by Oxidative Stress. Molecular Biology of the Cell, 2004, 15, 5659-5669.	2.1	71
183	A Transcriptional Profile of Aging in the Human Kidney. PLoS Biology, 2004, 2, e427.	5.6	281
184	A module map showing conditional activity of expression modules in cancer. Nature Genetics, 2004, 36, 1090-1098.	21.4	622
185	Session Introduction. , 2004, , .		1
186	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543
187	A Gene-Coexpression Network for Global Discovery of Conserved Genetic Modules. Science, 2003, 302, 249-255.	12.6	2,034
188	From promoter sequence to expression. , 2002, , .		64
189	Probabilistic hierarchical clustering for biological data. , 2002, , .		18
190	COVID-19 and beyond:Âa call for action andÂaudacious solidarity to all the citizens and nations,Âit is humanityâ€™s fight. F1000Research, 0, 9, 1130.	1.6	3
191	Prediction of type 2 diabetes mellitus onset using logistic regression-based scorecards. ELife, 0, 11, .	6.0	7