Mark B Gerstein

List of Publications by Year
in descending order

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494	121,510	209	148
papers	citations	147 h-index	326 g-index

545	545	545	123573
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RNA-Seq: a revolutionary tool for transcriptomics. Nature Reviews Genetics, 2009, 10, 57-63.	7.7	10,529
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
3	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
4	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
5	Functional profiling of the Saccharomyces cerevisiae genome. Nature, 2002, 418, 387-391.	13.7	3,938
6	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. Nature, 2006, 440, 637-643.	13.7	2,681
7	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
8	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. Science, 2008, 320, 1344-1349.	6.0	2,180
9	Global Analysis of Protein Activities Using Proteome Chips. Science, 2001, 293, 2101-2105.	6.0	2,082
10	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
11	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
12	A Map of the Interactome Network of the Metazoan C. elegans. Science, 2004, 303, 540-543.	6.0	1,587
13	Comparing protein abundance and mRNA expression levels on a genomic scale. Genome Biology, 2003, 4, 117.	13.9	1,453
14	CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. Genome Research, 2011, 21, 974-984.	2.4	1,387
15	Architecture of the human regulatory network derived from ENCODE data. Nature, 2012, 489, 91-100.	13.7	1,384
16	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
17	A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. Science, 2003, 302, 449-453.	6.0	1,183
18	Transcriptional landscape of the prenatal human brain. Nature, 2014, 508, 199-206.	13.7	1,147

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19	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. Cell, 2012, 148, 1293-1307.	13.5	1,134
20	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
21	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
22	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
23	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
24	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. Nature Communications, 2019, 10, 5029.	5.8	1,007
25	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. Science, 2007, 318, 420-426.	6.0	1,003
26	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
27	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. Science, 2004, 306, 2242-2246.	6.0	983
28	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	955
29	Genomic analysis of regulatory network dynamics reveals large topological changes. Nature, 2004, 431, 308-312.	13.7	921
30	Global analysis of protein phosphorylation in yeast. Nature, 2005, 438, 679-684.	13.7	915
31	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
32	FOXG1-Dependent Dysregulation of GABA/Glutamate Neuron Differentiation in Autism Spectrum Disorders. Cell, 2015, 162, 375-390.	13.5	894
33	The Importance of Bottlenecks in Protein Networks: Correlation with Gene Essentiality and Expression Dynamics. PLoS Computational Biology, 2007, 3, e59.	1.5	849
34	Analysis of yeast protein kinases using protein chips. Nature Genetics, 2000, 26, 283-289.	9.4	810
35	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
36	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744

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37	Molecular Characterization of Neuroendocrine Prostate Cancer and Identification of New Drug Targets. Cancer Discovery, 2011, 1, 487-495.	7.7	725
38	Subcellular localization of the yeast proteome. Genes and Development, 2002, 16, 707-719.	2.7	667
39	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
40	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
41	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
42	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
43	Relating Whole-Genome Expression Data with Protein-Protein Interactions. Genome Research, 2002, 12, 37-46.	2.4	605
44	Statistical analysis of amino acid patterns in transmembrane helices: the GxxxG motif occurs frequently and in association with Î²-branched residues at neighboring positions. Journal of Molecular Biology, 2000, 296, 921-936.	2.0	567
45	Volume changes on protein folding. Structure, 1994, 2, 641-649.	1.6	546
46	Spectral Biclustering of Microarray Data: Coclustering Genes and Conditions. Genome Research, 2003, 13, 703-716.	2.4	536
47	A standard reference frame for the description of nucleic acid base-pair geometry 1 1Edited by P. E. Wright 2 2This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton.. Journal of Molecular Biology, 2001, 313, 229-237.	2.0	533
48	What is a gene, post-ENCODE? History and updated definition. Genome Research, 2007, 17, 669-681.	2.4	530
49	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. Nature, 1999, 402, 413-418.	13.7	521
50	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	6.0	521
51	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. Genome Research, 2004, 14, 1107-1118.	2.4	516
52	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
53	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. Nature Biotechnology, 2009, 27, 66-75.	9.4	514
54	The packing density in proteins: standard radii and volumes 1 1Edited by J. M. Thornton. Journal of Molecular Biology, 1999, 290, 253-266.	2.0	482

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55	Getting connected: analysis and principles of biological networks. Genes and Development, 2007, 21, 1010-1024.	2.7	477
56	A cis-regulatory map of the Drosophila genome. Nature, 2011, 471, 527-531.	13.7	477
57	New insights into Acinetobacter baumannii pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. Genes and Development, 2007, 21, 601-614.	2.7	455
58	Relating Three-Dimensional Structures to Protein Networks Provides Evolutionary Insights. Science, 2006, 314, 1938-1941.	6.0	447
59	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. Genes and Development, 2005, 19, 2816-2826.	2.7	443
60	MAPK target networks in Arabidopsis thaliana revealed using functional protein microarrays. Genes and Development, 2009, 23, 80-92.	2.7	438
61	Diverse Cellular Functions of the Hsp90 Molecular Chaperone Uncovered Using Systems Approaches. Cell, 2007, 131, 121-135.	13.5	437
62	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
63	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
64	Role of non-coding sequence variants in cancer. Nature Reviews Genetics, 2016, 17, 93-108.	7.7	420
65	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	7.7	398
66	The relationship between protein structure and function: a comprehensive survey with application to the yeast genome. Journal of Molecular Biology, 1999, 288, 147-164.	2.0	384
67	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	2.6	380
68	Millions of Years of Evolution Preserved: A Comprehensive Catalog of the Processed Pseudogenes in the Human Genome. Genome Research, 2003, 13, 2541-2558.	2.4	376
69	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
70	Differential binding of calmodulin-related proteins to their targets revealed through high-density Arabidopsis protein microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4730-4735.	3.3	369
71	A Single-Cell Transcriptomic Atlas of Human Neocortical Development during Mid-gestation. Neuron, 2019, 103, 785-801.e8.	3.8	361
72	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358

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73	Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells. Nature, 2012, 492, 438-442.	13.7	355
74	Assessing annotation transfer for genomics: quantifying the relations between protein sequence, structure and function through traditional and probabilistic scores. Journal of Molecular Biology, 2000, 297, 233-249.	2.0	345
75	The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12031-12036.	3.3	342
76	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. Science Signaling, 2010, 3, ra12.	1.6	341
77	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
78	Defining the TRiC/CCT interactome links chaperonin function to stabilization of newly made proteins with complex topologies. Nature Structural and Molecular Biology, 2008, 15, 1255-1262.	3.6	340
79	A database of macromolecular motions. Nucleic Acids Research, 1998, 26, 4280-4290.	6.5	333
80	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. Blood, 2009, 113, 2526-2534.	0.6	330
81	Identification of a Disease-Defining Gene Fusion in Epithelioid Hemangioendothelioma. Science Translational Medicine, 2011, 3, 98ra82.	5.8	328
82	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. Science, 2007, 317, 815-819.	6.0	320
83	Genomic analysis of essentiality within protein networks. Trends in Genetics, 2004, 20, 227-231.	2.9	303
84	Genomic analysis of the hierarchical structure of regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14724-14731.	3.3	299
85	The real cost of sequencing: higher than you think!. Genome Biology, 2011, 12, 125.	13.9	299
86	Distribution of NF-ÂB-binding sites across human chromosome 22. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12247-12252.	3.3	298
87	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. Genome Biology, 2014, 15, 480.	3.8	291
88	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
89	AlleleSeq: analysis of alleleâ€specific expression and binding in a network framework. Molecular Systems Biology, 2011, 7, 522.	3.2	284
90	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275

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91	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	9.4	274
92	The GENCODE pseudogene resource. Genome Biology, 2012, 13, R51.	13.9	273
93	Structural proteomics of an archaeon. Nature Structural Biology, 2000, 7, 903-909.	9.7	272
94	Bridging structural biology and genomics: assessing protein interaction data with known complexes. Trends in Genetics, 2002, 18, 529-536.	2.9	265
95	Characterization of stressâ€responsive lnc<scp>RNA</scp>s in <scp>A</scp>rabidopsis thaliana by integrating expression, epigenetic and structural features. Plant Journal, 2014, 80, 848-861.	2.8	264
96	The real cost of sequencing: scaling computation to keep pace with data generation. Genome Biology, 2016, 17, 53.	3.8	264
97	The transcriptional activity of human Chromosome 22. Genes and Development, 2003, 17, 529-540.	2.7	253
98	Normal mode analysis of macromolecular motions in a database framework: Developing mode concentration as a useful classifying statistic. Proteins: Structure, Function and Bioinformatics, 2002, 48, 682-695.	1.5	248
99	The Volume of Atoms on the Protein Surface: Calculated from Simulation, using Voronoi Polyhedra. Journal of Molecular Biology, 1995, 249, 955-966.	2.0	243
100	Genomic analysis of gene expression relationships in transcriptional regulatory networks. Trends in Genetics, 2003, 19, 422-427.	2.9	238
101	Protein family and fold occurrence in genomes: power-law behaviour and evolutionary model. Journal of Molecular Biology, 2001, 313, 673-681.	2.0	237
102	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. Genes and Development, 2002, 16, 3017-3033.	2.7	236
103	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
104	The Temporal Patterning MicroRNA let-7 Regulates Several Transcription Factors at the Larval to Adult Transition in C. elegans. Developmental Cell, 2005, 8, 321-330.	3.1	231
105	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
106	exRNA Atlas Analysis Reveals Distinct Extracellular RNA Cargo Types and Their Carriers Present across Human Biofluids. Cell, 2019, 177, 463-477.e15.	13.5	228
107	Gaining comprehensive biological insight into the transcriptome by performing a broad-spectrum RNA-seq analysis. Nature Communications, 2017, 8, 59.	5.8	225
108	Patterns of nucleotide substitution, insertion and deletion in the human genome inferred from pseudogenes. Nucleic Acids Research, 2003, 31, 5338-5348.	6.5	224

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109	Diverse transcription factor binding features revealed by genome-wide ChIP-seq in C. elegans. Genome Research, 2011, 21, 245-254.	2.4	224
110	Regulation of Gene Expression by a Metabolic Enzyme. Science, 2004, 306, 482-484.	6.0	223
111	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
112	TOS9 Regulates White-Opaque Switching in Candida albicans. Eukaryotic Cell, 2006, 5, 1674-1687.	3.4	207
113	The role of disorder in interaction networks: a structural analysis. Molecular Systems Biology, 2008, 4, 179.	3.2	206
114	The origin, evolution, and functional impact of short insertionâ€“deletion variants identified in 179 human genomes. Genome Research, 2013, 23, 749-761.	2.4	206
115	Computational analysis of membrane proteins: the largest class of drug targets. Drug Discovery Today, 2009, 14, 1130-1135.	3.2	204
116	Comparative analysis of processed pseudogenes in the mouse and human genomes. Trends in Genetics, 2004, 20, 62-67.	2.9	201
117	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. Cell, 2010, 143, 639-650.	13.5	200
118	Reconstruction of enhancerâ€“target networks in 935 samples of human primary cells, tissues and cell lines. Nature Genetics, 2017, 49, 1428-1436.	9.4	194
119	Molecular and cellular reorganization of neural circuits in the human lineage. Science, 2017, 358, 1027-1032.	6.0	192
120	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. Genome Research, 2007, 17, 839-851.	2.4	191
121	Comprehensive assessment of automatic structural alignment against a manual standard, the scop classification of proteins. Protein Science, 1998, 7, 445-456.	3.1	190
122	Mapping accessible chromatin regions using Sono-Seq. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14926-14931.	3.3	186
123	Diverse Roles and Interactions of the SWI/SNF Chromatin Remodeling Complex Revealed Using Global Approaches. PLoS Genetics, 2011, 7, e1002008.	1.5	185
124	PROTEIN FOLDING:The Endgame. Annual Review of Biochemistry, 1997, 66, 549-579.	5.0	184
125	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
126	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	2.9	183

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127	Assessing the limits of genomic data integration for predicting protein networks. Genome Research, 2005, 15, 945-953.	2.4	182
128	Mapping of transcription factor binding regions in mammalian cells by ChIP: Comparison of array- and sequencing-based technologies. Genome Research, 2007, 17, 898-909.	2.4	181
129	Identification and Analysis of Over 2000 Ribosomal Protein Pseudogenes in the Human Genome. Genome Research, 2002, 12, 1466-1482.	2.4	179
130	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. Genome Research, 2011, 21, 56-67.	2.4	179
131	Tracking Distinct RNA Populations Using Efficient and Reversible Covalent Chemistry. Molecular Cell, 2015, 59, 858-866.	4.5	179
132	Quantifying environmental adaptation of metabolic pathways in metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1374-1379.	3.3	177
133	Transcribed processed pseudogenes in the human genome: an intermediate form of expressed retrosequence lacking protein-coding ability. Nucleic Acids Research, 2005, 33, 2374-2383.	6.5	175
134	Studying Genomes Through the Aeons: Protein Families, Pseudogenes and Proteome Evolution. Journal of Molecular Biology, 2002, 318, 1155-1174.	2.0	174
135	A question of size: the eukaryotic proteome and the problems in defining it. Nucleic Acids Research, 2002, 30, 1083-1090.	6.5	172
136	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. PLoS Biology, 2009, 7, e1000218.	2.6	172
137	Beyond synexpression relationships: local clustering of time-shifted and inverted gene expression profiles identifies new, biologically relevant interactions. Journal of Molecular Biology, 2001, 314, 1053-1066.	2.0	171
138	Diverse human extracellular RNAs are widely detected in human plasma. Nature Communications, 2016, 7, 11106.	5.8	170
139	PseudoPipe: an automated pseudogene identification pipeline. Bioinformatics, 2006, 22, 1437-1439.	1.8	169
140	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
141	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5254-5259.	3.3	168
142	Molecular Fossils in the Human Genome: Identification and Analysis of the Pseudogenes in Chromosomes 21 and 22. Genome Research, 2002, 12, 272-280.	2.4	167
143	MolMovDB: analysis and visualization of conformational change and structural flexibility. Nucleic Acids Research, 2003, 31, 478-482.	6.5	167
144	Analyzing protein function on a genomic scale: the importance of gold-standard positives and negatives for network prediction. Current Opinion in Microbiology, 2004, 7, 535-545.	2.3	167

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145	Close association of RNA polymerase II and many transcription factors with Pol III genes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3639-3644.	3.3	167
146	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
147	Genome-Wide Identification of Binding Sites Defines Distinct Functions for Caenorhabditis elegans PHA-4/FOXA in Development and Environmental Response. PLoS Genetics, 2010, 6, e1000848.	1.5	165
148	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds ofDrosophilaandCaenorhabditis elegansTranscription Factors. Genetics, 2018, 208, 937-949.	1.2	164
149	Analysis of protein loop closure. Journal of Molecular Biology, 1991, 220, 133-149.	2.0	163
150	Interpretation of Genomic Variants Using a Unified Biological Network Approach. PLoS Computational Biology, 2013, 9, e1002886.	1.5	162
151	Insights into genetics, human biology and disease gleaned from family based genomic studies. Genetics in Medicine, 2019, 21, 798-812.	1.1	161
152	Domain Closure in Lactoferrin. Journal of Molecular Biology, 1993, 234, 357-372.	2.0	160
153	Volume changes in protein evolution. Journal of Molecular Biology, 1994, 236, 1067-1078.	2.0	160
154	CREB Binds to Multiple Loci on Human Chromosome 22. Molecular and Cellular Biology, 2004, 24, 3804-3814.	1.1	160
155	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nature Biotechnology, 2010, 28, 47-55.	9.4	158
156	Pseudogene.org: a comprehensive database and comparison platform for pseudogene annotation. Nucleic Acids Research, 2007, 35, D55-D60.	6.5	156
157	Interrelating Different Types of Genomic Data, from Proteome to Secretome: 'Oming in on Function. Genome Research, 2001, 11, 1463-1468.	2.4	155
158	Multi-species microarrays reveal the effect of sequence divergence on gene expression profiles. Genome Research, 2005, 15, 674-680.	2.4	155
159	Dermal Adipocyte Lipolysis and Myofibroblast Conversion Are Required for Efficient Skin Repair. Cell Stem Cell, 2020, 26, 880-895.e6.	5.2	154
160	A structural census of genomes: comparing bacterial, eukaryotic, and archaeal genomes in terms of protein structure. Journal of Molecular Biology, 1997, 274, 562-576.	2.0	153
161	Target hub proteins serve as master regulators of development in yeast. Genes and Development, 2006, 20, 435-448.	2.7	153
162	The Extracellular RNA Communication Consortium: Establishing Foundational Knowledge and Technologies for Extracellular RNA Research. Cell, 2019, 177, 231-242.	13.5	152

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163	Major Molecular Differences between Mammalian Sexes Are Involved in Drug Metabolism and Renal Function. Developmental Cell, 2004, 6, 791-800.	3.1	151
164	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
165	Identification and analysis of unitary pseudogenes: historic and contemporary gene losses in humans and other primates. Genome Biology, 2010, 11, R26.	13.9	150
166	Epigenetic Repression of miR-31 Disrupts Androgen Receptor Homeostasis and Contributes to Prostate Cancer Progression. Cancer Research, 2013, 73, 1232-1244.	0.4	150
167	GATA-1 binding sites mapped in the Â-globin locus by using mammalian chIp-chip analysis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2924-2929.	3.3	149
168	Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. Genes and Development, 2009, 23, 619-632.	2.7	149
169	Large-scale analysis of pseudogenes in the human genome. Current Opinion in Genetics and Development, 2004, 14, 328-335.	1.5	147
170	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. Nucleic Acids Research, 2012, 40, 553-568.	6.5	145
171	A Bayesian system integrating expression data with sequence patterns for localizing proteins: comprehensive application to the yeast genome 1 1Edited by F. Cohen. Journal of Molecular Biology, 2000, 301, 1059-1075.	2.0	142
172	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. PLoS Computational Biology, 2010, 6, e1000730.	1.5	140
173	Whole-genome Trees Based on the Occurrence of Folds and Orthologs: Implications for Comparing Genomes on Different Levels. Genome Research, 2000, 10, 808-818.	2.4	139
174	Mining the Structural Genomics Pipeline: Identification of Protein Properties that Affect High-throughput Experimental Analysis. Journal of Molecular Biology, 2004, 336, 115-130.	2.0	138
175	A multiregional proteomic survey of the postnatal human brain. Nature Neuroscience, 2017, 20, 1787-1795.	7.1	138
176	Normal modes for predicting protein motions: A comprehensive database assessment and associated Web tool. Protein Science, 2005, 14, 633-643.	3.1	137
177	Revisiting the codon adaptation index from a whole-genome perspective: analyzing the relationship between gene expression and codon occurrence in yeast using a variety of models. Nucleic Acids Research, 2003, 31, 2242-2251.	6.5	136
178	Analyzing Cellular Biochemistry in Terms of Molecular Networks. Annual Review of Biochemistry, 2004, 73, 1051-1087.	5.0	133
179	Positive selection at the protein network periphery: Evaluation in terms of structural constraints and cellular context. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20274-20279.	3.3	132
180	MetaSV: an accurate and integrative structural-variant caller for next generation sequencing. Bioinformatics, 2015, 31, 2741-2744.	1.8	131

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181	Use of Thioredoxin as a Reporter To Identify a Subset of Escherichia coli Signal Sequences That Promote Signal Recognition Particle-Dependent Translocation. Journal of Bacteriology, 2005, 187, 2983-2991.	1.0	128
182	Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. Genome Research, 2008, 18, 1865-1874.	2.4	126
183	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4534-4539.	3.3	125
184	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	3.8	125
185	RNA expression patterns change dramatically in human neutrophils exposed to bacteria. Blood, 2001, 97, 2457-2468.	0.6	124
186	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
187	Comprehensive analysis of amino acid and nucleotide composition in eukaryotic genomes, comparing genes and pseudogenes. Nucleic Acids Research, 2002, 30, 2515-2523.	6.5	121
188	DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17771-17776.	3.3	121
189	Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. Genome Research, 2012, 22, 1069-1080.	2.4	121
190	Domain Closure in Adenylate Kinase. Journal of Molecular Biology, 1993, 229, 494-501.	2.0	119
191	Personal genome sequencing: current approaches and challenges. Genes and Development, 2010, 24, 423-431.	2.7	119
192	How representative are the known structures of the proteins in a complete genome? A comprehensive structural census. Folding & Design, 1998, 3, 497-512.	4.5	118
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