

Rapid and systematic analysis of the RNA recognition system

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Citation Report

#	ARTICLE	IF	CITATIONS
3	The Nuclear-Retained Noncoding RNA MALAT1 Regulates Alternative Splicing by Modulating SR Splicing Factor Phosphorylation. <i>Molecular Cell</i> , 2010, 39, 925-938.	4.5	1,906
4	Post-transcriptional control during chronic inflammation and cancer: a focus on AU-rich elements. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 2937-2955.	2.4	140
5	YB-1 Binds to GluR2 mRNA and CaM1 mRNA in the Brain and Regulates their Translational Levels in an Activity-Dependent Manner. <i>Cellular and Molecular Neurobiology</i> , 2010, 30, 1089-1100.	1.7	16
6	Systems analysis of alternative splicing and its regulation. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 550-565.	6.6	14
7	Alternative splicing: global insights. <i>FEBS Journal</i> , 2010, 277, 856-866.	2.2	128
8	Global analysis reveals SRp20- and SRp75-specific mRNPs in cycling and neural cells. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 962-970.	3.6	53
9	Deciphering the splicing code. <i>Nature</i> , 2010, 465, 53-59.	13.7	781
10	Systematic Analysis of Cis-Elements in Unstable mRNAs Demonstrates that CUGBP1 Is a Key Regulator of mRNA Decay in Muscle Cells. <i>PLoS ONE</i> , 2010, 5, e11201.	1.1	122
11	Predicting in vivo binding sites of RNA-binding proteins using mRNA secondary structure. <i>Rna</i> , 2010, 16, 1096-1107.	1.6	154
12	Sequence-non-specific effects of RNA interference triggers and microRNA regulators. <i>Nucleic Acids Research</i> , 2010, 38, 1-16.	6.5	485
13	Deciphering the role of RNA-binding proteins in the post-transcriptional control of gene expression. <i>Briefings in Functional Genomics</i> , 2010, 9, 391-404.	1.3	143
14	RNAcontext: A New Method for Learning the Sequence and Structure Binding Preferences of RNA-Binding Proteins. <i>PLoS Computational Biology</i> , 2010, 6, e1000832.	1.5	223
15	Regulation of Alternative Splicing by Histone Modifications. <i>Science</i> , 2010, 327, 996-1000.	6.0	931
16	In silico characterization and prediction of global protein-mRNA interactions in yeast. <i>Nucleic Acids Research</i> , 2011, 39, 5826-5836.	6.5	55
17	Construction, Structure and Dynamics of Post-Transcriptional Regulatory Network Directed by RNA-Binding Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2011, 722, 103-117.	0.8	22
18	Transcriptome-wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. <i>Molecular Cell</i> , 2011, 43, 340-352.	4.5	640
19	The Functional Consequences of Relative Substrate Specificity in Complex Biochemical Systems. <i>Frontiers in Genetics</i> , 2011, 2, 65.	1.1	6
20	A quantitative analysis of CLIP methods for identifying binding sites of RNA-binding proteins. <i>Nature Methods</i> , 2011, 8, 559-564.	9.0	460

#	ARTICLE	IF	CITATIONS
21	MicroRNA regulation by RNA-binding proteins and its implications for cancer. <i>Nature Reviews Cancer</i> , 2011, 11, 644-656.	12.8	555
22	Understanding the transcriptome through RNA structure. <i>Nature Reviews Genetics</i> , 2011, 12, 641-655.	7.7	411
23	A quantitative RNA code for mRNA target selection by the germline fate determinant GLD-1. <i>EMBO Journal</i> , 2011, 30, 533-545.	3.5	81
24	Crystallographic Analysis of Polypyrimidine Tract-Binding Protein-Raver1 Interactions Involved in Regulation of Alternative Splicing. <i>Structure</i> , 2011, 19, 1816-1825.	1.6	37
25	Predicting RNA-Protein Interactions Using Only Sequence Information. <i>BMC Bioinformatics</i> , 2011, 12, 489.	1.2	399
26	Prioritizing single-nucleotide variations that potentially regulate alternative splicing. <i>BMC Proceedings</i> , 2011, 5, S40.	1.8	5
27	Predicting sequence and structural specificities of RNA binding regions recognized by splicing factor SRSF1. <i>BMC Genomics</i> , 2011, 12, S8.	1.2	26
28	RBPDDB: a database of RNA-binding specificities. <i>Nucleic Acids Research</i> , 2011, 39, D301-D308.	6.5	477
29	Quantitative evaluation of all hexamers as exonic splicing elements. <i>Genome Research</i> , 2011, 21, 1360-1374.	2.4	207
30	Identification of RNA recognition elements in the <i>Saccharomyces cerevisiae</i> transcriptome. <i>Nucleic Acids Research</i> , 2011, 39, 1501-1509.	6.5	67
31	Genomic Analyses of the RNA-binding Protein Hu Antigen R (HuR) Identify a Complex Network of Target Genes and Novel Characteristics of Its Binding Sites. <i>Journal of Biological Chemistry</i> , 2011, 286, 37063-37066.	1.6	68
32	Bayesian prediction of tissue-regulated splicing using RNA sequence and cellular context. <i>Bioinformatics</i> , 2011, 27, 2554-2562.	1.8	77
33	Role of AUF1 and HuR in the pH-responsive stabilization of phosphoenolpyruvate carboxykinase mRNA in LLC-PK ₁ -F ⁺ cells. <i>American Journal of Physiology - Renal Physiology</i> , 2011, 301, F1066-F1077.	1.3	14
34	Identification of Evolutionarily Conserved Exons as Regulated Targets for the Splicing Activator Tra2 ¹² in Development. <i>PLoS Genetics</i> , 2011, 7, e1002390.	1.5	65
35	Dissecting the protein-RNA interface: the role of protein surface shapes and RNA secondary structures in protein-RNA recognition. <i>Nucleic Acids Research</i> , 2012, 40, 3299-3306.	6.5	50
36	YB-1 binds to CAUC motifs and stimulates exon inclusion by enhancing the recruitment of U2AF to weak polypyrimidine tracts. <i>Nucleic Acids Research</i> , 2012, 40, 8622-8636.	6.5	88
37	Versatility of the translational machinery during stress: changing partners to keep dancing. <i>Cell Research</i> , 2012, 22, 1634-1636.	5.7	3
38	Sequence requirements for RNA binding by HuR and AUF1. <i>Journal of Biochemistry</i> , 2012, 151, 423-437.	0.9	60

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39	RNA-binding protein HuR autoregulates its expression by promoting alternative polyadenylation site usage. <i>Nucleic Acids Research</i> , 2012, 40, 787-800.	6.5	123
40	From specific to global analysis of posttranscriptional regulation in eukaryotes: posttranscriptional regulatory networks. <i>Briefings in Functional Genomics</i> , 2012, 11, 505-521.	1.3	16
41	Cooperativity in RNA-Protein Interactions: Global Analysis of RNA Binding Specificity. <i>Cell Reports</i> , 2012, 1, 570-581.	2.9	106
42	Insights from the HuR-interacting transcriptome: ncRNAs, ubiquitin pathways, and patterns of secondary structure dependent RNA interactions. <i>Molecular Genetics and Genomics</i> , 2012, 287, 867-879.	1.0	8
43	Functional Interactions Between microRNAs and RNA Binding Proteins. <i>MicroRNA (Shariqah, United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	8.6	54
44	Identification of RNA-protein interaction networks using PAR-CLIP. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 159-177.	3.2	192
45	The RNA-binding landscapes of two SR proteins reveal unique functions and binding to diverse RNA classes. <i>Genome Biology</i> , 2012, 13, R17.	13.9	229
46	An oxygen-regulated switch in the protein synthesis machinery. <i>Nature</i> , 2012, 486, 126-129.	13.7	266
47	Spatial arrangement of an RNA zipcode identifies mRNAs under post-transcriptional control. <i>Genes and Development</i> , 2012, 26, 43-53.	2.7	127
48	RNA-protein interactions in vivo: global gets specific. <i>Trends in Biochemical Sciences</i> , 2012, 37, 255-262.	3.7	85
49	Post-transcriptional regulation of mu-opioid receptor: role of the RNA-binding proteins heterogeneous nuclear ribonucleoprotein H1 and F. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 599-610.	2.4	18
50	A compendium of RNA-binding motifs for decoding gene regulation. <i>Nature</i> , 2013, 499, 172-177.	13.7	1,281
51	Analysis of base-pairing probabilities of RNA molecules involved in protein-RNA interactions. <i>Bioinformatics</i> , 2013, 29, 2524-2528.	1.8	10
52	New Insights into Functional Roles of the Polypyrimidine Tract-Binding Protein. <i>International Journal of Molecular Sciences</i> , 2013, 14, 22906-22932.	1.8	100
53	Hidden specificity in an apparently nonspecific RNA-binding protein. <i>Nature</i> , 2013, 502, 385-388.	13.7	85
54	Learning the language of post-transcriptional gene regulation. <i>Genome Biology</i> , 2013, 14, 130.	3.8	18
55	Toward a Genome-Wide Landscape of Translational Control. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012302-a012302.	2.3	50
56	Computational biology of RNA interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 107-120.	3.2	24

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57	Targeting the Y/CCAAT box in cancer: YB-1 (YBX1) or NF-Y?. <i>Cell Death and Differentiation</i> , 2013, 20, 676-685.	5.0	96
58	The many functions of mRNA localization during normal development and disease: from pillar to post. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2013, 2, 781-796.	5.9	42
59	IGF-I 3' Untranslated Region: Strain-Specific Polymorphisms and Motifs Regulating IGF-I in Osteoblasts. <i>Endocrinology</i> , 2013, 154, 253-262.	1.4	21
60	Hyper conserved elements in vertebrate mRNA 3'-UTRs reveal a translational network of RNA-binding proteins controlled by HuR. <i>Nucleic Acids Research</i> , 2013, 41, 3201-3216.	6.5	38
61	Modeling the binding specificity of the RNA-binding protein GLD-1 suggests a function of coding region-located sites in translational repression. <i>Rna</i> , 2013, 19, 1317-1326.	1.6	21
62	Hsp70 Is a Novel Posttranscriptional Regulator of Gene Expression That Binds and Stabilizes Selected mRNAs Containing AU-Rich Elements. <i>Molecular and Cellular Biology</i> , 2013, 33, 71-84.	1.1	54
63	Computational Assessment of the Cooperativity between RNA Binding Proteins and MicroRNAs in Transcript Decay. <i>PLoS Computational Biology</i> , 2013, 9, e1003075.	1.5	30
64	Connecting cis-elements and trans-factors with mechanisms of developmental regulation of mRNA translation in meiotic and haploid mammalian spermatogenic cells. <i>Reproduction</i> , 2013, 146, R1-R19.	1.1	55
65	RBPmotif: a web server for the discovery of sequence and structure preferences of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2013, 41, W180-W186.	6.5	25
66	Structural insights into the targeting of mRNA GU-rich elements by the three RRM domains of CELF1. <i>Nucleic Acids Research</i> , 2013, 41, 7153-7166.	6.5	26
67	Vimentin interacts with the 5'-untranslated region of mouse mu opioid receptor (MOR) and is required for post-transcriptional regulation. <i>RNA Biology</i> , 2013, 10, 256-266.	1.5	8
68	A Biophysical Model for Identifying Splicing Regulatory Elements and Their Interactions. <i>PLoS ONE</i> , 2013, 8, e54885.	1.1	5
69	RNA-binding proteins in pluripotency, differentiation, and reprogramming. <i>Frontiers in Biology</i> , 2014, 9, 389-409.	0.7	31
70	De Novo Prediction of PTBP1 Binding and Splicing Targets Reveals Unexpected Features of Its RNA Recognition and Function. <i>PLoS Computational Biology</i> , 2014, 10, e1003442.	1.5	56
71	Hu Antigen R (HuR) Is a Positive Regulator of the RNA-binding Proteins TDP-43 and FUS/TLS. <i>Journal of Biological Chemistry</i> , 2014, 289, 31792-31804.	1.6	29
72	Predicting protein-RNA interaction amino acids using random forest based on submodularity subset selection. <i>Computational Biology and Chemistry</i> , 2014, 53, 324-330.	1.1	38
73	Analysis for co-occurring sequence features identifies link between common synonymous variant and an early-terminated NPC1 isoform. <i>Journal of Clinical Bioinformatics</i> , 2014, 4, 14.	1.2	0
74	RBPmap: a web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, W361-W367.	6.5	409

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75	Expression of Glutamine Transporter Slc38a3 (SNAT3) During Acidosis is Mediated by a Different Mechanism than Tissue-Specific Expression. Cellular Physiology and Biochemistry, 2014, 33, 1591-1606.	1.1	11
76	Dissecting the expression landscape of RNA-binding proteins in human cancers. Genome Biology, 2014, 15, R14.	13.9	208
77	Differential protein occupancy profiling of the mRNA transcriptome. Genome Biology, 2014, 15, R15.	13.9	72
78	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. , 2014, , .		0
79	Long non-coding RNAs: modulators of nuclear structure and function. Current Opinion in Cell Biology, 2014, 26, 10-18.	2.6	219
80	Systematic Identification of Regulatory Elements in Conserved 3' UTRs of Human Transcripts. Cell Reports, 2014, 7, 281-292.	2.9	58
81	ncRNA-Protein Interactions in Development and Disease from the Perspective of High-Throughput Studies. , 2014, , 87-115.		0
82	Global regulation of mRNA translation and stability in the early Drosophila embryo by the Smaug RNA-binding protein. Genome Biology, 2014, 15, R4.	13.9	89
83	Identifying mRNA sequence elements for target recognition by human Argonaute proteins. Genome Research, 2014, 24, 775-785.	2.4	34
84	GraphProt: modeling binding preferences of RNA-binding proteins. Genome Biology, 2014, 15, R17.	13.9	247
85	Cluster based prediction of PDZ-peptide interactions. BMC Genomics, 2014, 15, S5.	1.2	16
86	RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods. Methods in Molecular Biology, 2014, , .	0.4	14
87	Emerging Functions of SRSF1, Splicing Factor and Oncoprotein, in RNA Metabolism and Cancer. Molecular Cancer Research, 2014, 12, 1195-1204.	1.5	215
89	Quantitative analysis of RNA-protein interactions on a massively parallel array reveals biophysical and evolutionary landscapes. Nature Biotechnology, 2014, 32, 562-568.	9.4	202
90	Screening protein-RNA complexes by NMR spectroscopy for structure determination. Methods, 2014, 65, 288-301.	1.9	13
91	Enzymatic combinatorial nucleoside deletion scanning mutagenesis of functional RNA. Chemical Communications, 2014, 50, 10937.	2.2	4
92	Finding the target sites of RNA-binding proteins. Wiley Interdisciplinary Reviews RNA, 2014, 5, 111-130.	3.2	89
93	Non-coding RNA: a new frontier in regulatory biology. National Science Review, 2014, 1, 190-204.	4.6	175

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94	The Role of Mammalian MAPK Signaling in Regulation of Cytokine mRNA Stability and Translation. <i>Journal of Interferon and Cytokine Research</i> , 2014, 34, 220-232.	0.5	69
95	Spliceosomal Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	6
96	Metastasis-suppressor transcript destabilization through TARBP2 binding of mRNA hairpins. <i>Nature</i> , 2014, 513, 256-260.	13.7	76
97	The multiplicity of alternative splicing decisions in <i>Caenorhabditis elegans</i> is linked to specific intronic regulatory motifs and minisatellites. <i>BMC Genomics</i> , 2014, 15, 364.	1.2	0
98	Ribonomic approaches to study the RNA-binding proteome. <i>FEBS Letters</i> , 2014, 588, 3649-3664.	1.3	40
99	RNA Bind-n-Seq: Quantitative Assessment of the Sequence and Structural Binding Specificity of RNA Binding Proteins. <i>Molecular Cell</i> , 2014, 54, 887-900.	4.5	346
100	Computational Methods for CLIP-Seq Data Processing. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S16803.	1.0	21
101	The Crystal Structure of the NHL Domain in Complex with RNA Reveals the Molecular Basis of <i>Drosophila</i> Brain-Tumor-Mediated Gene Regulation. <i>Cell Reports</i> , 2015, 13, 1206-1220.	2.9	79
102	The potential of the <scp>riboSNitch</scp> in personalized medicine. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 517-532.	3.2	42
103	Suppression of miR-199a maturation by HuR is crucial for hypoxia-induced glycolytic switch in hepatocellular carcinoma. <i>EMBO Journal</i> , 2015, 34, 2671-2685.	3.5	84
104	Brain tumor is a sequence-specific RNA-binding protein that directs maternal mRNA clearance during the <i>Drosophila</i> maternal-to-zygotic transition. <i>Genome Biology</i> , 2015, 16, 94.	3.8	80
105	A Quantitative Profiling Tool for Diverse Genomic Data Types Reveals Potential Associations between Chromatin and Pre-mRNA Processing. <i>PLoS ONE</i> , 2015, 10, e0132448.	1.1	5
106	Deciphering RNA Regulatory Elements Involved in the Developmental and Environmental Gene Regulation of <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2015, 10, e0142342.	1.1	2
107	Biochemical and bioinformatic methods for elucidating the role of RNA-protein interactions in posttranscriptional regulation. <i>Briefings in Functional Genomics</i> , 2015, 14, 102-114.	1.3	10
108	High-throughput characterization of protein-RNA interactions. <i>Briefings in Functional Genomics</i> , 2015, 14, 74-89.	1.3	83
109	RNA structure generates natural cooperativity between single-stranded RNA binding proteins targeting 5' and 3' UTRs. <i>Nucleic Acids Research</i> , 2015, 43, 1160-1169.	6.5	10
110	Starcode: sequence clustering based on all-pairs search. <i>Bioinformatics</i> , 2015, 31, 1913-1919.	1.8	164
111	Dissecting the target specificity of RNase H recruiting oligonucleotides using massively parallel reporter analysis of short RNA motifs. <i>Nucleic Acids Research</i> , 2015, 43, 8476-8487.	6.5	7

#	ARTICLE	IF	CITATIONS
112	mRNA and DNA selection via protein multimerization: YB-1 as a case study. <i>Nucleic Acids Research</i> , 2015, 43, 9457-9473.	6.5	35
113	Analysis of sequencing data for probing RNA secondary structures and protein-RNA binding in studying posttranscriptional regulations. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv106.	3.2	6
114	Deciphering the protein-RNA recognition code: Combining large-scale quantitative methods with structural biology. <i>BioEssays</i> , 2015, 37, 899-908.	1.2	26
115	Probing RNA-protein networks: biochemistry meets genomics. <i>Trends in Biochemical Sciences</i> , 2015, 40, 157-164.	3.7	39
116	Transcriptome-wide ribonuclease-mediated protein footprinting to identify RNA-protein interaction sites. <i>Methods</i> , 2015, 72, 76-85.	1.9	12
117	RPI-Pred: predicting ncRNA-protein interaction using sequence and structural information. <i>Nucleic Acids Research</i> , 2015, 43, 1370-1379.	6.5	178
118	RNA Bind-n-Seq. <i>Methods in Enzymology</i> , 2015, 558, 465-493.	0.4	27
119	Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. <i>Nature Biotechnology</i> , 2015, 33, 831-838.	9.4	2,206
120	Leveraging cross-link modification events in CLIP-seq for motif discovery. <i>Nucleic Acids Research</i> , 2015, 43, 95-103.	6.5	40
121	Quantitative assessment of RNA-protein interactions with high-throughput sequencing-RNA affinity profiling. <i>Nature Protocols</i> , 2015, 10, 1212-1233.	5.5	19
122	One, Two, Three, Four! How Multiple RRMs Read the Genome Sequence. <i>Methods in Enzymology</i> , 2015, 558, 235-278.	0.4	72
123	The human RBPome: From genes and proteins to human disease. <i>Journal of Proteomics</i> , 2015, 127, 61-70.	1.2	106
124	RNA-binding proteins in neurodegeneration: Seq and you shall receive. <i>Trends in Neurosciences</i> , 2015, 38, 226-236.	4.2	97
125	Endogenous tRNA-Derived Fragments Suppress Breast Cancer Progression via YBX1 Displacement. <i>Cell</i> , 2015, 161, 790-802.	13.5	626
126	Computational approaches towards understanding human long non-coding RNA biology. <i>Bioinformatics</i> , 2015, 31, 2241-2251.	1.8	71
127	SRSF1-Regulated Alternative Splicing in Breast Cancer. <i>Molecular Cell</i> , 2015, 60, 105-117.	4.5	290
128	Post-Transcriptional Regulation of Endothelial Nitric Oxide Synthase Expression by Polypyrimidine Tract-Binding Protein 1. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2153-2160.	1.1	12
129	Specificity and nonspecificity in RNA-protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 533-544.	16.1	216

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130	Algorithms in Bioinformatics. Lecture Notes in Computer Science, 2015, , .	1.0	1
131	Affinity regression predicts the recognition code of nucleic acidâ€™binding proteins. Nature Biotechnology, 2015, 33, 1242-1249.	9.4	55
132	Computational challenges, tools, and resources for analyzing coâ€™and postâ€™transcriptional events in high throughput. Wiley Interdisciplinary Reviews RNA, 2015, 6, 291-310.	3.2	16
133	Competition between target sites of regulators shapes post-transcriptional gene regulation. Nature Reviews Genetics, 2015, 16, 113-126.	7.7	220
134	SNPllice: variants that modulate Intron retention from RNA-sequencing data. Bioinformatics, 2015, 31, 1191-1198.	1.8	18
135	Does conservation account for splicing patterns?. BMC Genomics, 2016, 17, 787.	1.2	15
136	Efficient Design of Compact Unstructured RNA Libraries Covering All <i>k</i>-mers. Journal of Computational Biology, 2016, 23, 67-79.	0.8	5
137	Succession of splicing regulatory elements determines cryptic 5â€™ss functionality. Nucleic Acids Research, 2017, 45, gkw1317.	6.5	16
138	IPMiner: hidden ncRNA-protein interaction sequential pattern mining with stacked autoencoder for accurate computational prediction. BMC Genomics, 2016, 17, 582.	1.2	117
139	Advances in the characterization of RNAâ€™binding proteins. Wiley Interdisciplinary Reviews RNA, 2016, 7, 793-810.	3.2	89
140	Position-dependent interactions of Y-box protein 2 (YBX2) with mRNA enable mRNA storage in round spermatids by repressing mRNA translation and blocking translation-dependent mRNA decay. Molecular Reproduction and Development, 2016, 83, 190-207.	1.0	17
141	NMR solution structure determination of large RNA-protein complexes. Progress in Nuclear Magnetic Resonance Spectroscopy, 2016, 97, 57-81.	3.9	25
142	RNA Structure Switches RBP Binding. Molecular Cell, 2016, 64, 219-220.	4.5	11
143	Regulation of Tissue-Specific Alternative Splicing: C. elegans as a Model System. Advances in Experimental Medicine and Biology, 2016, 907, 229-261.	0.8	11
144	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. , 2016, , .		6
146	PAR-CLIP: A Genomic Technique to Dissect RNA-Protein Interactions. , 2016, , 261-289.		0
147	BindUP: a web server for non-homology-based prediction of DNA and RNA binding proteins. Nucleic Acids Research, 2016, 44, W568-W574.	6.5	62
148	RCK: accurate and efficient inference of sequence- and structure-based proteinâ€™RNA binding models from RNAcompete data. Bioinformatics, 2016, 32, i351-i359.	1.8	67

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149	Revealing proteinâ€“lncRNA interaction. Briefings in Bioinformatics, 2016, 17, 106-116.	3.2	536
150	High-throughput analyses of hnRNP H1 dissects its multi-functional aspect. RNA Biology, 2016, 13, 400-411.	1.5	50
151	RNA binding proteins as regulators of immune cell biology. Clinical and Experimental Immunology, 2015, 183, 37-49.	1.1	50
152	De-coding and re-coding RNA recognition by PUF and PPR repeat proteins. Current Opinion in Structural Biology, 2016, 36, 116-121.	2.6	40
153	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. Proceedings of the IEEE, 2016, 104, 176-197.	16.4	186
154	Can we observe changes in mRNA â€œstateâ€? Overview of methods to study mRNA interactions with regulatory proteins relevant in cancer related processes. Analyst, The, 2016, 141, 548-562.	1.7	5
155	Transcriptomics and Gene Regulation. Translational Bioinformatics, 2016, , .	0.0	2
156	Introduction to Bioinformatics Resources for Post-transcriptional Regulation of Gene Expression. Methods in Molecular Biology, 2016, 1358, 3-28.	0.4	2
157	Post-Transcriptional Regulation of the Human Mu-Opioid Receptor (MOR) by Morphine-Induced RNA Binding Proteins hnRNP K and PCBP1. Journal of Cellular Physiology, 2017, 232, 576-584.	2.0	11
158	Emerging roles for RNA-binding proteins as effectors and regulators of cardiovascular disease. European Heart Journal, 2017, 38, ehw567.	1.0	94
159	Pathogenic variants that alter protein code often disrupt splicing. Nature Genetics, 2017, 49, 848-855.	9.4	176
160	An RRMâ€“ZnF RNA recognition module targets RBM10 to exonic sequences to promote exon exclusion. Nucleic Acids Research, 2017, 45, 6761-6774.	6.5	31
161	RNA localization: Making its way to the center stage. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2956-2970.	1.1	98
162	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. Nucleic Acids Research, 2017, 45, e129-e129.	6.5	19
163	LIN-41 and OMA Ribonucleoprotein Complexes Mediate a Translational Repression-to-Activation Switch Controlling Oocyte Meiotic Maturation and the Oocyte-to-Embryo Transition in <i>Caenorhabditis elegans</i> . Genetics, 2017, 206, 2007-2039.	1.2	52
164	Mapping specificity landscapes of RNA-protein interactions by high throughput sequencing. Methods, 2017, 118-119, 111-118.	1.9	11
165	A combined sequence and structure based method for discovering enriched motifs in RNA from in vivo binding data. Methods, 2017, 118-119, 73-81.	1.9	13
166	Cytosolic YB-1 and NSUN2 are the only proteins recognizing specific motifs present in mRNAs enriched in exosomes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 664-673.	1.1	84

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167	PRIMA: a gene-centered, RNA-to-protein method for mapping RNA-protein interactions. <i>Translation</i> , 2017, 5, e1295130.	2.9	2
168	Integrated structural biology to unravel molecular mechanisms of protein-RNA recognition. <i>Methods</i> , 2017, 118-119, 119-136.	1.9	49
169	Bioinformatic tools for analysis of <scp>CLIP</scp> ribonucleoprotein data. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1404.	3.2	9
170	RNAcompete methodology and application to determine sequence preferences of unconventional RNA-binding proteins. <i>Methods</i> , 2017, 118-119, 3-15.	1.9	46
171	Optimized Sequence Library Design for Efficient InÂVitro Interaction Mapping. <i>Cell Systems</i> , 2017, 5, 230-236.e5.	2.9	0
172	Associating transcription factors and conserved RNA structures with gene regulation in the human brain. <i>Scientific Reports</i> , 2017, 7, 5776.	1.6	12
173	Oncogenic Activation of the RNA Binding Protein NELFE and MYC Signaling in Hepatocellular Carcinoma. <i>Cancer Cell</i> , 2017, 32, 101-114.e8.	7.7	121
174	RNAcompete-S: Combined RNA sequence/structure preferences for RNA binding proteins derived from a single-step in vitro selection. <i>Methods</i> , 2017, 126, 18-28.	1.9	35
175	Structure alignment-based classification of RNA-binding pockets reveals regional RNA recognition motifs on protein surfaces. <i>BMC Bioinformatics</i> , 2017, 18, 27.	1.2	7
176	RNA-protein binding motifs mining with a new hybrid deep learning based cross-domain knowledge integration approach. <i>BMC Bioinformatics</i> , 2017, 18, 136.	1.2	173
177	Recognizing RNA structural motifs in HT-SELEX data for ribosomal protein S15. <i>BMC Bioinformatics</i> , 2017, 18, 298.	1.2	9
178	RNA Binding Protein Human Antigen R Is Translocated in Astrocytes following Spinal Cord Injury and Promotes the Inflammatory Response. <i>Journal of Neurotrauma</i> , 2017, 34, 1249-1259.	1.7	22
179	The Atypical Dual Specificity Phosphatase hYVH1 Associates with Multiple Ribonucleoprotein Particles. <i>Journal of Biological Chemistry</i> , 2017, 292, 539-550.	1.6	12
180	Quantifying RNA binding sites transcriptome-wide using DO-RIP-seq. <i>Rna</i> , 2017, 23, 32-46.	1.6	46
181	Crucial role of noncoding RNA in driving prostate cancer development and progression. <i>Epigenomics</i> , 2017, 9, 1-3.	1.0	4
182	An in vitro technique to identify the RNA binding-site sequences for RNA-binding proteins. <i>BioTechniques</i> , 2017, 63, 28-33.	0.8	9
183	ssHMM: extracting intuitive sequence-structure motifs from high-throughput RNA-binding protein data. <i>Nucleic Acids Research</i> , 2017, 45, 11004-11018.	6.5	39
184	Screening the Molecular Framework Underlying Local Dendritic mRNA Translation. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 45.	1.4	6

#	ARTICLE	IF	CITATIONS
185	The combinatorial control of alternative splicing in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2017, 13, e1007033.	1.5	10
186	Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. <i>Nature Communications</i> , 2018, 9, 1549.	5.8	35
187	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. <i>Genome Research</i> , 2018, 28, 699-713.	2.4	62
188	A Translational Repression Complex in Developing Mammalian Neural Stem Cells that Regulates Neuronal Specification. <i>Neuron</i> , 2018, 97, 520-537.e6.	3.8	124
189	Transacting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1465.	3.2	79
190	Transcriptome-wide Identification and Validation of Interactions between the miRNA Machinery and HuR on mRNA Targets. <i>Journal of Molecular Biology</i> , 2018, 430, 285-296.	2.0	17
191	Translational co-regulation of a ligand and inhibitor by a conserved RNA element. <i>Nucleic Acids Research</i> , 2018, 46, 104-119.	6.5	18
192	Finding RNA structure in the unstructured RBPome. <i>BMC Genomics</i> , 2018, 19, 154.	1.2	7
193	A General Small-Angle X-ray Scattering-Based Screening Protocol Validated for Protein-RNA Interactions. <i>ACS Combinatorial Science</i> , 2018, 20, 197-202.	3.8	18
194	RNA-mediated gene regulation is less evolvable than transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3481-E3490.	3.3	31
195	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 337-344.	2.3	116
196	CASH: a constructing comprehensive splice site method for detecting alternative splicing events. <i>Briefings in Bioinformatics</i> , 2018, 19, 905-917.	3.2	47
197	In silico approaches to RNA aptamer design. <i>Biochimie</i> , 2018, 145, 8-14.	1.3	38
198	Saturation mutagenesis reveals manifold determinants of exon definition. <i>Genome Research</i> , 2018, 28, 11-24.	2.4	55
199	Structural features of the interaction of the 3'-untranslated region of mRNA containing exosomal RNA-specific motifs with YB-1, a potential mediator of mRNA sorting. <i>Biochimie</i> , 2018, 144, 134-143.	1.3	37
200	The TRIM-NHL protein NHL-2 is a co-factor in the nuclear and somatic RNAi pathways in <i>C. elegans</i> . <i>ELife</i> , 2018, 7, .	2.8	13
201	CLIP-Seq in Bacteria: Global Recognition Patterns of Bacterial RNA-Binding Proteins. <i>Methods in Enzymology</i> , 2018, 612, 127-145.	0.4	6
202	Alternative splicing rewires Hippo signaling pathway in hepatocytes to promote liver regeneration. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 928-939.	3.6	58

#	ARTICLE	IF	CITATIONS
203	Non-coding RNAs in Complex Diseases. <i>Advances in Experimental Medicine and Biology</i> , 2018, , .	0.8	6
204	Methods for Identification of Protein-RNA Interaction. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1094, 117-126.	0.8	4
205	A deep neural network approach for learning intrinsic protein-RNA binding preferences. <i>Bioinformatics</i> , 2018, 34, i638-i646.	1.8	68
206	Biological functions, regulatory mechanisms, and disease relevance of RNA localization pathways. <i>FEBS Letters</i> , 2018, 592, 2948-2972.	1.3	32
207	Motif models for RNA-binding proteins. <i>Current Opinion in Structural Biology</i> , 2018, 53, 115-123.	2.6	19
208	SMARTIV: combined sequence and structure de-novo motif discovery for in-vivo RNA binding data. <i>Nucleic Acids Research</i> , 2018, 46, W221-W228.	6.5	7
209	Posttranscriptional regulation of cyclin D1 by ARE-binding proteins AUF1 and HuR in cycling myoblasts. <i>Journal of Biosciences</i> , 2018, 43, 685-691.	0.5	8
210	Mapping transcriptome-wide protein-RNA interactions to elucidate RNA regulatory programs. <i>Quantitative Biology</i> , 2018, 6, 228-238.	0.3	10
211	Regulation of Neuronal Differentiation, Function, and Plasticity by Alternative Splicing. <i>Annual Review of Cell and Developmental Biology</i> , 2018, 34, 451-469.	4.0	108
212	Inferring RNA sequence preferences for poorly studied RNA-binding proteins based on co-evolution. <i>BMC Bioinformatics</i> , 2018, 19, 96.	1.2	7
213	RBPvsMIR: A Computational Pipeline to Identify Competing miRNAs and RNA-Binding Protein Pairs Regulating the Shared Transcripts. <i>Genes</i> , 2018, 9, 426.	1.0	8
214	A Chemical Biology Approach to Model Pontocerebellar Hypoplasia Type 1B (PCH1B). <i>ACS Chemical Biology</i> , 2018, 13, 3000-3010.	1.6	9
215	SSMART: sequence-structure motif identification for RNA-binding proteins. <i>Bioinformatics</i> , 2018, 34, 3990-3998.	1.8	21
216	Prediction of the RBP binding sites on lncRNAs using the high-order nucleotide encoding convolutional neural network. <i>Analytical Biochemistry</i> , 2019, 583, 113364.	1.1	18
217	Modeling RNA-Binding Protein Specificity In Vivo by Precisely Registering Protein-RNA Crosslink Sites. <i>Molecular Cell</i> , 2019, 74, 1189-1204.e6.	4.5	75
218	Integration of CLIP experiments of RNA-binding proteins: a novel approach to predict context-dependent splicing factors from transcriptomic data. <i>BMC Genomics</i> , 2019, 20, 521.	1.2	4
219	A deep learning framework to predict binding preference of RNA constituents on protein surface. <i>Nature Communications</i> , 2019, 10, 4941.	5.8	69
220	Identifying Cancer-Specific circRNA-RBP Binding Sites Based on Deep Learning. <i>Molecules</i> , 2019, 24, 4035.	1.7	55

#	ARTICLE	IF	CITATIONS
221	Hypoxia-induced H19/YB-1 cascade modulates cardiac remodeling after infarction. <i>Theranostics</i> , 2019, 9, 6550-6567.	4.6	61
222	ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development. <i>Nucleic Acids Research</i> , 2019, 47, 2856-2870.	6.5	20
223	Emerging RNA-binding roles in the TRIM family of ubiquitin ligases. <i>Biological Chemistry</i> , 2019, 400, 1443-1464.	1.2	59
224	PTBP1 enhances exon11a skipping in Mena pre-mRNA to promote migration and invasion in lung carcinoma cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2019, 1862, 858-869.	0.9	17
225	Beyond CLIP: advances and opportunities to measure RBP-RNA and RNA-RNA interactions. <i>Nucleic Acids Research</i> , 2019, 47, 5490-5501.	6.5	48
226	Massively Parallel Assays and Quantitative Sequence-Function Relationships. <i>Annual Review of Genomics and Human Genetics</i> , 2019, 20, 99-127.	2.5	101
227	Deep learning in bioinformatics: Introduction, application, and perspective in the big data era. <i>Methods</i> , 2019, 166, 4-21.	1.9	247
228	BCFE: A Deep Learning Model for ncRNA-Protein Interaction Predictions Based on Improved Sequence Information. <i>International Journal of Molecular Sciences</i> , 2019, 20, 978.	1.8	17
229	Long Noncoding RNA and Protein Interactions: From Experimental Results to Computational Models Based on Network Methods. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1284.	1.8	29
230	Recent Advances of Deep Learning in Bioinformatics and Computational Biology. <i>Frontiers in Genetics</i> , 2019, 10, 214.	1.1	163
231	oRNAment: a database of putative RNA binding protein target sites in the transcriptomes of model species. <i>Nucleic Acids Research</i> , 2020, 48, D166-D173.	6.5	52
232	HuR biological function involves RRM3-mediated dimerization and RNA binding by all three RRMs. <i>Nucleic Acids Research</i> , 2019, 47, 1011-1029.	6.5	56
233	The contribution of NOS3 variants to coronary artery disease: A combined genetic epidemiology and computational biochemistry perspective. <i>International Journal of Biological Macromolecules</i> , 2019, 123, 494-499.	3.6	4
234	Computational approaches for the analysis of RNA-protein interactions: A primer for biologists. <i>Journal of Biological Chemistry</i> , 2019, 294, 1-9.	1.6	9
235	beRBP: binding estimation for human RNA-binding proteins. <i>Nucleic Acids Research</i> , 2019, 47, e26-e26.	6.5	35
236	Linking RNA Sequence, Structure, and Function on Massively Parallel High-Throughput Sequencers. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032300.	2.3	17
237	Upstream analysis of alternative splicing: a review of computational approaches to predict context-dependent splicing factors. <i>Briefings in Bioinformatics</i> , 2019, 20, 1358-1375.	3.2	53
238	Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 972-980.	1.9	43

#	ARTICLE	IF	CITATIONS
239	RNA-centric approaches to study RNA-protein interactions in vitro and in silico. <i>Methods</i> , 2020, 178, 11-18.	1.9	14
240	rec-Y3H screening allows the detection of simultaneous RNA-protein interface mutations. <i>Methods</i> , 2020, 178, 19-32.	1.9	4
241	High throughput approaches to study RNA-protein interactions in vitro. <i>Methods</i> , 2020, 178, 3-10.	1.9	5
242	Approaches for measuring the dynamics of RNA-protein interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1565.	3.2	32
243	RDense: A Protein-RNA Binding Prediction Model Based on Bidirectional Recurrent Neural Network and Densely Connected Convolutional Networks. <i>IEEE Access</i> , 2020, 8, 14588-14605.	2.6	21
244	RNA: interactions drive functionalities. <i>Molecular Biology Reports</i> , 2020, 47, 1413-1434.	1.0	33
245	Integrative Structural Biology of Protein-RNA Complexes. <i>Structure</i> , 2020, 28, 6-28.	1.6	33
246	Clip for studying protein-RNA interactions that regulate virus replication. <i>Methods</i> , 2020, 183, 84-92.	1.9	8
247	Identifying Regulatory Elements via Deep Learning. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 315-338.	2.8	14
248	Evolution of a Human-Specific Tandem Repeat Associated with ALS. <i>American Journal of Human Genetics</i> , 2020, 107, 445-460.	2.6	39
249	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. <i>Genome Biology</i> , 2020, 21, 195.	3.8	55
250	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020, 30, 962-973.	2.4	55
251	Intrinsic Regulatory Role of RNA Structural Arrangement in Alternative Splicing Control. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5161.	1.8	18
252	A Review About RNA-Protein-Binding Sites Prediction Based on Deep Learning. <i>IEEE Access</i> , 2020, 8, 150929-150944.	2.6	9
253	RNA-Binding Protein Rbm24 as a Multifaceted Post-Transcriptional Regulator of Embryonic Lineage Differentiation and Cellular Homeostasis. <i>Cells</i> , 2020, 9, 1891.	1.8	25
254	Deep neural networks for inferring binding sites of RNA-binding proteins by using distributed representations of RNA primary sequence and secondary structure. <i>BMC Genomics</i> , 2020, 21, 866.	1.2	15
255	DeepA-RBPBS: A hybrid convolution and recurrent neural network combined with attention mechanism for predicting RBP binding site. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 4250-4258.	2.0	8
256	RNA structure-wide discovery of functional interactions with multiplexed RNA motif library. <i>Nature Communications</i> , 2020, 11, 6275.	5.8	12

#	ARTICLE	IF	CITATIONS
257	Transite: A Computational Motif-Based Analysis Platform That Identifies RNA-Binding Proteins Modulating Changes in Gene Expression. <i>Cell Reports</i> , 2020, 32, 108064.	2.9	30
258	Single nucleotide polymorphisms affect RNA-protein interactions at a distance through modulation of RNA secondary structures. <i>PLoS Computational Biology</i> , 2020, 16, e1007852.	1.5	20
259	ProbeRating: a recommender system to infer binding profiles for nucleic acid-binding proteins. <i>Bioinformatics</i> , 2020, 36, 4797-4804.	1.8	6
260	Transcriptome-wide organization of subcellular microenvironments revealed by ATLAS-Seq. <i>Nucleic Acids Research</i> , 2020, 48, 5859-5872.	6.5	9
261	YBX1 Indirectly Targets Heterochromatin-Repressed Inflammatory Response-Related Apoptosis Genes through Regulating CBX5 mRNA. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4453.	1.8	11
262	Predicting lncRNA-Protein Interactions With miRNAs as Mediators in a Heterogeneous Network Model. <i>Frontiers in Genetics</i> , 2019, 10, 1341.	1.1	27
263	Localization elements and zip codes in the intracellular transport and localization of messenger RNAs in <i>Saccharomyces cerevisiae</i> . <i>Wiley Interdisciplinary Reviews RNA</i> , 2020, 11, e1591.	3.2	11
264	Cold Shock Domain Proteins: Structure and Interaction with Nucleic Acids. <i>Biochemistry (Moscow)</i> , 2020, 85, 1-19.	0.7	33
265	Degenerate consensus sequences in the 3'-untranslated regions of cellular mRNAs as specific motifs potentially involved in the YB-1-mediated packaging of these mRNAs. <i>Biochimie</i> , 2020, 170, 152-162.	1.3	5
266	Discovering protein-binding RNA motifs with a generative model of RNA sequences. <i>Computational Biology and Chemistry</i> , 2020, 84, 107171.	1.1	6
267	Molecular entrapment by RNA: an emerging tool for disrupting protein-RNA interactions in vivo. <i>RNA Biology</i> , 2020, 17, 417-424.	1.5	4
268	Mechanisms and consequences of subcellular RNA localization across diverse cell types. <i>Traffic</i> , 2020, 21, 404-418.	1.3	52
269	RNA-binding proteins in human genetic disease. <i>Nature Reviews Genetics</i> , 2021, 22, 185-198.	7.7	720
270	Identification of SRSF10 as a regulator of SMN2 ISSN1. <i>Human Mutation</i> , 2021, 42, 246-260.	1.1	15
271	Recent Progresses of Computational Analysis of RNA-Protein Interactions. , 2021, , 170-181.		0
272	DeepLPI: a multimodal deep learning method for predicting the interactions between lncRNAs and protein isoforms. <i>BMC Bioinformatics</i> , 2021, 22, 24.	1.2	13
273	A non-radioactive, improved PAR-CLIP and small RNA cDNA library preparation protocol. <i>Nucleic Acids Research</i> , 2021, 49, e45-e45.	6.5	16
274	Online Genomic Resources and Bioinformatics Tools Available for Epigenetics and Non-coding RNA. , 2021, , 306-328.		0

#	ARTICLE	IF	CITATIONS
275	Integrative analyses of transcriptome data reveal the mechanisms of post-transcriptional regulation. <i>Briefings in Functional Genomics</i> , 2021, 20, 207-212.	1.3	5
276	Structural basis for RNA recognition by the N-terminal tandem RRM domains of human RBM45. <i>Nucleic Acids Research</i> , 2021, 49, 2946-2958.	6.5	10
277	Predicting dynamic cellular protein-RNA interactions by deep learning using in vivo RNA structures. <i>Cell Research</i> , 2021, 31, 495-516.	5.7	64
278	EDLMFC: an ensemble deep learning framework with multi-scale features combination for ncRNA-protein interaction prediction. <i>BMC Bioinformatics</i> , 2021, 22, 133.	1.2	18
279	Huntington's disease-specific mis-splicing unveils key effector genes and altered splicing factors. <i>Brain</i> , 2021, 144, 2009-2023.	3.7	32
280	CLIP and complementary methods. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	152
282	NPI-GNN: Predicting ncRNA-protein interactions with deep graph neural networks. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	42
283	Convolutional neural networks (CNNs): concepts and applications in pharmacogenomics. <i>Molecular Diversity</i> , 2021, 25, 1569-1584.	2.1	14
284	Global importance analysis: An interpretability method to quantify importance of genomic features in deep neural networks. <i>PLoS Computational Biology</i> , 2021, 17, e1008925.	1.5	52
285	Matrix-screening reveals a vast potential for direct protein-protein interactions among RNA binding proteins. <i>Nucleic Acids Research</i> , 2021, 49, 6702-6721.	6.5	10
286	Recent Advances in Predicting Protein-lncRNA Interactions Using Machine Learning Methods. <i>Current Gene Therapy</i> , 2022, 22, 228-244.	0.9	12
287	SRSF10: an atypical splicing regulator with critical roles in stress response, organ development, and viral replication. <i>Rna</i> , 2021, 27, 1302-1317.	1.6	11
288	MultiRBP., 2021, , .		3
289	HCG18 Participates in Vascular Invasion of Hepatocellular Carcinoma by Regulating Macrophages and Tumor Stem Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 707073.	1.8	8
291	rBPDLPredicting RNA-Binding Proteins Using Deep Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 3668-3676.	3.9	10
294	Structure of SRSF1 RRM1 bound to RNA reveals an unexpected bimodal mode of interaction and explains its involvement in SMN1 exon7 splicing. <i>Nature Communications</i> , 2021, 12, 428.	5.8	37
295	RNA-Protein Interactions: An Overview. <i>Methods in Molecular Biology</i> , 2014, 1097, 491-521.	0.4	102
296	Predicting Alternative Splicing. <i>Methods in Molecular Biology</i> , 2014, 1126, 411-423.	0.4	4

#	ARTICLE	IF	CITATIONS
297	Regulation of Alternative Pre-mRNA Splicing. <i>Methods in Molecular Biology</i> , 2014, 1126, 55-82.	0.4	19
298	Global Approaches to Alternative Splicing and Its Regulation—Recent Advances and Open Questions. <i>Translational Bioinformatics</i> , 2016, , 37-71.	0.0	2
299	LPI-CNNCP: Prediction of lncRNA-protein interactions by using convolutional neural network with the copy-padding trick. <i>Analytical Biochemistry</i> , 2020, 601, 113767.	1.1	28
300	Structural basis for mRNA recognition by human RBM38. <i>Biochemical Journal</i> , 2020, 477, 161-172.	1.7	8
311	Control of Gene Expression by RNA Binding Protein Action on Alternative Translation Initiation Sites. <i>PLoS Computational Biology</i> , 2016, 12, e1005198.	1.5	7
312	Probing instructions for expression regulation in gene nucleotide compositions. <i>PLoS Computational Biology</i> , 2018, 14, e1005921.	1.5	11
313	Drosophila TDP-43 RNA-Binding Protein Facilitates Association of Sister Chromatid Cohesion Proteins with Genes, Enhancers and Polycomb Response Elements. <i>PLoS Genetics</i> , 2016, 12, e1006331.	1.5	27
314	Paralogs hnRNP L and hnRNP LL Exhibit Overlapping but Distinct RNA Binding Constraints. <i>PLoS ONE</i> , 2013, 8, e80701.	1.1	36
315	Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. <i>PLoS ONE</i> , 2017, 12, e0174052.	1.1	15
316	The long noncoding RNA lncR492 inhibits neural differentiation of murine embryonic stem cells. <i>PLoS ONE</i> , 2018, 13, e0191682.	1.1	16
317	The 5' untranslated region of p16INK4a melanoma tumor suppressor acts as a cellular IRES, controlling mRNA translation under hypoxia through YBX1 binding. <i>Oncotarget</i> , 2015, 6, 39980-39994.	0.8	17
318	Deep Learning in the Study of Protein-Related Interactions. <i>Protein and Peptide Letters</i> , 2020, 27, 359-369.	0.4	4
319	Prediction and Dissection of Protein-RNA Interactions by Molecular Descriptors. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 604-615.	1.0	4
320	Computational Tools for Investigating RNA-Protein Interaction Partners. <i>Journal of Computer Science and Systems Biology</i> , 2013, 06, .	0.0	18
321	Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. <i>ELife</i> , 2016, 5, .	2.8	48
322	NPI-RGCNAE: Fast Predicting ncRNA-Protein Interactions Using the Relational Graph Convolutional Network Auto-Encoder. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 1861-1871.	3.9	7
323	Introduction to Bioinformatics Resources for Post-transcriptional Regulation of Gene Expression. <i>Methods in Molecular Biology</i> , 2022, 2404, 3-41.	0.4	0
324	RBPmap: A Tool for Mapping and Predicting the Binding Sites of RNA-Binding Proteins Considering the Motif Environment. <i>Methods in Molecular Biology</i> , 2022, 2404, 53-65.	0.4	11

#	ARTICLE	IF	CITATIONS
325	Transcriptome-Wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. Springer Theses, 2014, , 35-54.	0.0	0
326	Revealing Cell-Type Specific Differences in Protein Occupancy on RNA. Springer Theses, 2015, , 73-88.	0.0	0
328	Efficient Design of Compact Unstructured RNA Libraries Covering All k-mers. Lecture Notes in Computer Science, 2015, , 308-325.	1.0	0
342	Bioinformatic-Eggs: An Educational Primer for Use with "LIN-41 and OMA Ribonucleoprotein Complexes Mediate a Translational Repression-to-Activation Switch Controlling Oocyte Meiotic Maturation and the Oocyte-to-Embryo Transition in ". Genetics, 2018, 209, 675-683.	1.2	0
343	Roles of Emerging RNA-Binding Activity of cGAS in Innate Antiviral Response. Frontiers in Immunology, 2021, 12, 741599.	2.2	14
345	Multi-resBind: a residual network-based multi-label classifier for in vivo RNA binding prediction and preference visualization. BMC Bioinformatics, 2021, 22, 554.	1.2	4
346	Predicting NPI Based on Graph Convolutional Neural Networks. , 2021, , .		0
347	YB-1 Structure/Function Relationship in the Packaging of mRNPs and Consequences for Translation Regulation and Stress Granule Assembly in Cells. Biochemistry (Moscow), 2022, 87, S20-S31.	0.7	4
348	Advanced computational tools for quantitative analysis of proteinâ€“nucleic acid interfaces. , 2022, , 163-180.		0
349	Proteinâ€“RNA interaction prediction with deep learning: structure matters. Briefings in Bioinformatics, 2022, 23, .	3.2	37
350	Posttranscriptional regulation of cyclin D1 by ARE-binding proteins AUF1 and HuR in cycling myoblasts. Journal of Biosciences, 2018, 43, 685-691.	0.5	4
351	CHERP Regulates the Alternative Splicing of pre-mRNAs in the Nucleus. International Journal of Molecular Sciences, 2022, 23, 2555.	1.8	2
352	SAWRPI: A Stacking Ensemble Framework With Adaptive Weight for Predicting ncRNA-Protein Interactions Using Sequence Information. Frontiers in Genetics, 2022, 13, 839540.	1.1	3
353	RNAâ€“binding protein YBX1 promotes brown adipogenesis and thermogenesis via PINK1/PRKNâ€“mediated mitophagy. FASEB Journal, 2022, 36, e22219.	0.2	13
354	RBPBind: Quantitative Prediction of Protein-RNA Interactions. Journal of Molecular Biology, 2022, 434, 167515.	2.0	2
355	Non-Darwinian Molecular Biology. Frontiers in Genetics, 2022, 13, 831068.	1.1	4
356	RBM24 in the Post-Transcriptional Regulation of Cancer Progression: Anti-Tumor or Pro-Tumor Activity?. Cancers, 2022, 14, 1843.	1.7	5
363	The X-linked splicing regulator MBNL3 has been co-opted to restrict placental growth in eutherians. PLoS Biology, 2022, 20, e3001615.	2.6	4

#	ARTICLE	IF	CITATIONS
364	Context-specific effects of sequence elements on subcellular localization of linear and circular RNAs. <i>Nature Communications</i> , 2022, 13, 2481.	5.8	13
366	Large-Scale Analysis of RNA-Protein Interactions for Functional RNA Motif Discovery Using FOREST. <i>Methods in Molecular Biology</i> , 2022, , 279-290.	0.4	2
367	Simple synthesis of massively parallel RNA microarrays via enzymatic conversion from DNA microarrays. <i>Nature Communications</i> , 2022, 13, .	5.8	4
368	RNA _{Net} Motif: Identifying sequence-structure RNA network motifs in RNA-protein binding sites. <i>PLoS Computational Biology</i> , 2022, 18, e1010293.	1.5	9
370	Regulation of alternative polyadenylation by the C2H2-zinc-finger protein Sp1. <i>Molecular Cell</i> , 2022, 82, 3135-3150.e9.	4.5	14
371	RNA nucleoprotein complexes in biological systems. <i>Proceedings of the Indian National Science Academy</i> , 0, , .	0.5	0
372	A model for predicting ncRNA-protein interactions based on graph neural networks and community detection. <i>Methods</i> , 2022, 207, 74-80.	1.9	2
374	Widespread autogenous mRNA-protein interactions detected by CLIP-seq. <i>Nucleic Acids Research</i> , 2022, 50, 9984-9999.	6.5	8
375	Predicting ncRNA-protein interactions based on dual graph convolutional network and pairwise learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	5
376	Positional motif analysis reveals the extent of specificity of protein-RNA interactions observed by CLIP. <i>Genome Biology</i> , 2022, 23, .	3.8	14
377	Computational tools to study RNA-protein complexes. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	2
378	Prediction of Dynamic RBP-RNA Interactions Using PrismNet. <i>Methods in Molecular Biology</i> , 2023, , 123-132.	0.4	0
381	The RNA-Binding Protein HuR Is Integral to the Function of Nociceptors in Mice and Humans. <i>Journal of Neuroscience</i> , 2022, 42, 9129-9141.	1.7	4
382	<scp>RNA</scp> regulation of inflammatory responses in glia and its potential as a therapeutic target in central nervous system disorders. <i>Glia</i> , 0, , .	2.5	3
384	Predicting potential interactions between lncRNAs and proteins via combined graph auto-encoder methods. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	12
385	The role of RNA-binding proteins in orchestrating germline development in <i>Caenorhabditis elegans</i> . <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
386	Applications of deep learning in understanding gene regulation. <i>Cell Reports Methods</i> , 2023, 3, 100384.	1.4	13
387	Current Technical Approaches to Study RNA-Protein Interactions in mRNAs and Long Non-Coding RNAs. <i>Biochem</i> , 2023, 3, 1-14.	0.5	0

#	ARTICLE	IF	CITATIONS
388	Deciphering the RRM-RNA recognition code: A computational analysis. PLoS Computational Biology, 2023, 19, e1010859.	1.5	4
389	HeadTailTransfer: An efficient sampling method to improve the performance of graph neural network method in predicting sparse ncRNA-protein interactions. Computers in Biology and Medicine, 2023, 157, 106783.	3.9	5
390	YBX1/lncRNA SBF2-AS1 interaction regulates proliferation and tamoxifen sensitivity via PI3K/AKT/MTOR signaling in breast cancer cells. Molecular Biology Reports, 2023, 50, 3413-3428.	1.0	5
392	ncRPI-LGAT: Prediction of ncRNA-protein interactions with line graph attention network framework. Computational and Structural Biotechnology Journal, 2023, 21, 2286-2295.	1.9	1
393	RNA-binding proteins that lack canonical RNA-binding domains are rarely sequence-specific. Scientific Reports, 2023, 13, .	1.6	6
394	Known sequence features explain half of all human gene ends. NAR Genomics and Bioinformatics, 2023, 5, .	1.5	1
395	Improved analysis of (e)CLIP data with RCRUNCH yields a compendium of RNA-binding protein binding sites and motifs. Genome Biology, 2023, 24, .	3.8	3
397	RNA-Protein Interactions. , 2022, , 572-626.		0