

TomaÅ¾ Curk

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

7,471
citations

87723

38
h-index

91712

69
g-index

76
all docs

76
docs citations

76
times ranked

10799
citing authors

#	ARTICLE	IF	CITATIONS
1	iCLIP reveals the function of hnRNP particles in splicing at individual nucleotide resolution. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 909-915.	3.6	1,026
2	Characterizing the RNA targets and position-dependent splicing regulation by TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 452-458.	7.1	956
3	Comprehensive Identification of RNA-Binding Domains in Human Cells. <i>Molecular Cell</i> , 2016, 63, 696-710.	4.5	493
4	The RNA-binding proteomes from yeast to man harbour conserved enigmRBPs. <i>Nature Communications</i> , 2015, 6, 10127.	5.8	385
5	SR proteins are NXF1 adaptors that link alternative RNA processing to mRNA export. <i>Genes and Development</i> , 2016, 30, 553-566.	2.7	242
6	Widespread binding of FUS along nascent RNA regulates alternative splicing in the brain. <i>Scientific Reports</i> , 2012, 2, 603.	1.6	231
7	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
8	iCLIP Predicts the Dual Splicing Effects of TIA-RNA Interactions. <i>PLoS Biology</i> , 2010, 8, e1000530.	2.6	226
9	Polymorphic Members of the lag Gene Family Mediate Kin Discrimination in <i>Dictyostelium</i> . <i>Current Biology</i> , 2009, 19, 567-572.	1.8	204
10	Analysis of alternative splicing associated with aging and neurodegeneration in the human brain. <i>Genome Research</i> , 2011, 21, 1572-1582.	2.4	199
11	Analysis of CLIP and iCLIP methods for nucleotide-resolution studies of protein-RNA interactions. <i>Genome Biology</i> , 2012, 13, R67.	13.9	195
12	Orange: From Experimental Machine Learning to Interactive Data Mining. <i>Lecture Notes in Computer Science</i> , 2004, , 537-539.	1.0	174
13	iCLIP - Transcriptome-wide Mapping of Protein-RNA Interactions with Individual Nucleotide Resolution. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	168
14	Conserved developmental transcriptomes in evolutionarily divergent species. <i>Genome Biology</i> , 2010, 11, R35.	13.9	164
15	Microarray data mining with visual programming. <i>Bioinformatics</i> , 2005, 21, 396-398.	1.8	131
16	Recursive splicing in long vertebrate genes. <i>Nature</i> , 2015, 521, 371-375.	13.7	128
17	The RNA-binding protein HuR is essential for the B cell antibody response. <i>Nature Immunology</i> , 2015, 16, 415-425.	7.0	125
18	Aubergine iCLIP Reveals piRNA-Dependent Decay of mRNAs Involved in Germ Cell Development in the Early Embryo. <i>Cell Reports</i> , 2015, 12, 1205-1216.	2.9	113

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19	Orthogonal matrix factorization enables integrative analysis of multiple RNA binding proteins. <i>Bioinformatics</i> , 2016, 32, 1527-1535.	1.8	108
20	CELF4 Regulates Translation and Local Abundance of a Vast Set of mRNAs, Including Genes Associated with Regulation of Synaptic Function. <i>PLoS Genetics</i> , 2012, 8, e1003067.	1.5	106
21	Rbfox2-Coordinated Alternative Splicing of Mef2d and Rock2 Controls Myoblast Fusion during Myogenesis. <i>Molecular Cell</i> , 2014, 55, 592-603.	4.5	104
22	Yeast as a cell factory: current state and perspectives. <i>Microbial Cell Factories</i> , 2015, 14, 94.	1.9	87
23	Promiscuous RNA Binding Ensures Effective Encapsidation of APOBEC3 Proteins by HIV-1. <i>PLoS Pathogens</i> , 2015, 11, e1004609.	2.1	86
24	Deep Sequencing of Virus-Derived Small Interfering RNAs and RNA from Viral Particles Shows Highly Similar Mutational Landscapes of a Plant Virus Population. <i>Journal of Virology</i> , 2015, 89, 4760-4769.	1.5	84
25	Polygenic analysis and targeted improvement of the complex trait of high acetic acid tolerance in the yeast <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 5.	6.2	83
26	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. <i>Cell Reports</i> , 2017, 19, 1056-1067.	2.9	83
27	Crosslinking-immunoprecipitation (iCLIP) analysis reveals global regulatory roles of hnRNP L. <i>RNA Biology</i> , 2014, 11, 146-155.	1.5	82
28	FASTKD2 is an RNA-binding protein required for mitochondrial RNA processing and translation. <i>Rna</i> , 2015, 21, 1873-1884.	1.6	78
29	miR669a and miR669q prevent skeletal muscle differentiation in postnatal cardiac progenitors. <i>Journal of Cell Biology</i> , 2011, 193, 1197-1212.	2.3	77
30	Insights into the design and interpretation of iCLIP experiments. <i>Genome Biology</i> , 2017, 18, 7.	3.8	73
31	dictyBase—a Dictyostelium bioinformatics resource update. <i>Nucleic Acids Research</i> , 2009, 37, D515-D519.	6.5	71
32	Identification of Evolutionarily Conserved Exons as Regulated Targets for the Splicing Activator Tra2 ^{l2} in Development. <i>PLoS Genetics</i> , 2011, 7, e1002390.	1.5	65
33	Exon Junction Complexes Show a Distributional Bias toward Alternatively Spliced mRNAs and against mRNAs Coding for Ribosomal Proteins. <i>Cell Reports</i> , 2016, 16, 1588-1603.	2.9	65
34	Differential expression of microRNAs and other small RNAs in muscle tissue of patients with ALS and healthy age-matched controls. <i>Scientific Reports</i> , 2018, 8, 5609.	1.6	65
35	dictyExpress: a Dictyostelium discoideum gene expression database with an explorative data analysis web-based interface. <i>BMC Bioinformatics</i> , 2009, 10, 265.	1.2	63
36	Developmentally Regulated DNA Methylation in Dictyostelium discoideum. <i>Eukaryotic Cell</i> , 2006, 5, 18-25.	3.4	61

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37	VizRank: finding informative data projections in functional genomics by machine learning. <i>Bioinformatics</i> , 2005, 21, 413-414.	1.8	58
38	Tia1 dependent regulation of mRNA subcellular location and translation controls p53 expression in B cells. <i>Nature Communications</i> , 2017, 8, 530.	5.8	48
39	Human Tra2 proteins jointly control a CHEK1 splicing switch among alternative and constitutive target exons. <i>Nature Communications</i> , 2014, 5, 4760.	5.8	47
40	Polyketide synthase genes and the natural products potential of <i>Dictyostelium discoideum</i> . <i>Bioinformatics</i> , 2007, 23, 2543-2549.	1.8	39
41	The differential expression of alternatively polyadenylated transcripts is a common stress-induced response mechanism that modulates mammalian mRNA expression in a quantitative and qualitative fashion. <i>Rna</i> , 2016, 22, 1441-1453.	1.6	36
42	SNPsyn: detection and exploration of SNP-SNP interactions. <i>Nucleic Acids Research</i> , 2011, 39, W444-W449.	6.5	35
43	Control of a neuronal morphology program by an RNA-binding zinc finger protein, Unkempt. <i>Genes and Development</i> , 2015, 29, 501-512.	2.7	35
44	Improved binding site assignment by high-resolution mapping of RNA-protein interactions using iCLIP. <i>Nature Communications</i> , 2015, 6, 7921.	5.8	32
45	Identification of RNA-binding domains of RNA-binding proteins in cultured cells on a system-wide scale with RBDmap. <i>Nature Protocols</i> , 2017, 12, 2447-2464.	5.5	32
46	A systems view of spliceosomal assembly and branchpoints with iCLIP. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 930-940.	3.6	26
47	iCLIP identifies novel roles for SAFB1 in regulating RNA processing and neuronal function. <i>BMC Biology</i> , 2015, 13, 111.	1.7	23
48	Metabolomic profiling of CHO fed-batch growth phases at 10, 100, and 1,000‰. <i>Biotechnology and Bioengineering</i> , 2019, 116, 2720-2729.	1.7	23
49	TA-clustering: Cluster analysis of gene expression profiles through Temporal Abstractions. <i>International Journal of Medical Informatics</i> , 2005, 74, 505-517.	1.6	22
50	An ancient germ cell-specific RNA-binding protein protects the germline from cryptic splice site poisoning. <i>ELife</i> , 2019, 8, .	2.8	22
51	GenePath: a system for inference of genetic networks and proposal of genetic experiments. <i>Artificial Intelligence in Medicine</i> , 2003, 29, 107-130.	3.8	21
52	Bzpf is a CREB-like transcription factor that regulates spore maturation and stability in <i>Dictyostelium</i> . <i>Developmental Biology</i> , 2011, 358, 137-146.	0.9	19
53	Transcriptional Profiling of <i>Dictyostelium</i> with RNA Sequencing. <i>Methods in Molecular Biology</i> , 2013, 983, 139-171.	0.4	17
54	Heterogeneous computing architecture for fast detection of SNP-SNP interactions. <i>BMC Bioinformatics</i> , 2014, 15, 216.	1.2	17

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55	Simultaneous incremental matrix factorization for streaming recommender systems. Expert Systems With Applications, 2020, 160, 113685.	4.4	17
56	Genome Sequence of a Lethal Strain of Xylem-Invading <i>Verticillium nonalfalfae</i> . Genome Announcements, 2018, 6, .	0.8	13
57	Generating inter-dependent data streams for recommender systems. Simulation Modelling Practice and Theory, 2018, 88, 1-16.	2.2	13
58	Unravelling the RNA-Binding Properties of SAFB Proteins in Breast Cancer Cells. BioMed Research International, 2015, 2015, 1-9.	0.9	8
59	Yeast <i>Saccharomyces cerevisiae</i> adiponectin receptor homolog <i>Izh2</i> is involved in the regulation of zinc, phospholipid and pH homeostasis. Metallomics, 2015, 7, 1338-1351.	1.0	8
60	Approximate multiple kernel learning with least-angle regression. Neurocomputing, 2019, 340, 245-258.	3.5	5
61	Does replication groups scoring reduce false positive rate in SNP interaction discovery?. BMC Genomics, 2010, 11, 58.	1.2	4
62	Sparse data embedding and prediction by tropical matrix factorization. BMC Bioinformatics, 2021, 22, 89.	1.2	4
63	Inference of the Molecular Mechanism of Action from Genetic Interaction and Gene Expression Data. OMICS A Journal of Integrative Biology, 2010, 14, 357-367.	1.0	3
64	Identification of novel genes involved in neutral lipid storage by quantitative trait loci analysis of <i>Saccharomyces cerevisiae</i> . BMC Genomics, 2021, 22, 110.	1.2	3
65	On Quality of Different Annotation Sources for Gene Expression Analysis. Lecture Notes in Computer Science, 2009, , 421-425.	1.0	3
66	Combinations of Susceptibility Genes Are Associated with Higher Risk for Multiple Sclerosis and Imply Disease Course Specificity. PLoS ONE, 2015, 10, e0127632.	1.1	3
67	Rule-based Clustering for Gene Promoter Structure Discovery. Methods of Information in Medicine, 2009, 48, 229-235.	0.7	3
68	Relation chaining in binary positive-only recommender systems. Expert Systems With Applications, 2020, 150, 113296.	4.4	0
69	Analiza podatkov o prometnih tokovih in mobilnosti. , 0, , .		0
70	Text Mining Tourism Literature. , 0, , .		0
71	Similarity of Transcription Profiles for Genes in Gene Sets. Lecture Notes in Computer Science, 2011, , 393-399.	1.0	0