

Yael Mandel-Gutfreund

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

3,972
citations

147801

31
h-index

128289

60
g-index

66
all docs

66
docs citations

66
times ranked

6535
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	0.9	11
2	Uncovering the RNA-binding protein landscape in the pluripotency network of human embryonic stem cells. <i>Cell Reports</i> , 2021, 35, 109198.	6.4	19
3	Evaluation of COVID-19 RT-qPCR Test in Multi sample Pools. <i>Clinical Infectious Diseases</i> , 2020, 71, 2073-2078.	5.8	350
4	Regulation of alternative splicing by p300-mediated acetylation of splicing factors. <i>Rna</i> , 2019, 25, 813-824.	3.5	31
5	Adaptation to sub-optimal hosts is a driver of viral diversification in the ocean. <i>Nature Communications</i> , 2018, 9, 4698.	12.8	39
6	Ribonucleoprotein particles: advances and challenges in computational methods. <i>Current Opinion in Structural Biology</i> , 2018, 53, 124-130.	5.7	8
7	A Novel Geometry-Based Approach to Infer Protein Interface Similarity. <i>Scientific Reports</i> , 2018, 8, 8192.	3.3	7
8	SMARTIV: combined sequence and structure de-novo motif discovery for in-vivo RNA binding data. <i>Nucleic Acids Research</i> , 2018, 46, W221-W228.	14.5	7
9	A combined sequence and structure based method for discovering enriched motifs in RNA from in vivo binding data. <i>Methods</i> , 2017, 118-119, 73-81.	3.8	13
10	OCT4 impedes cell fate redirection by the melanocyte lineage master regulator MITF in mouse ESCs. <i>Nature Communications</i> , 2017, 8, 1022.	12.8	6
11	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. <i>Bioinformatics</i> , 2016, 32, i464-i472.	4.1	5
12	How motif environment influences transcription factor search dynamics: Finding a needle in a haystack. <i>BioEssays</i> , 2016, 38, 605-612.	2.5	48
13	BindUP: a web server for non-homology-based prediction of DNA and RNA binding proteins. <i>Nucleic Acids Research</i> , 2016, 44, W568-W574.	14.5	62
14	<scp>P</scp>f<scp>SR</scp>1 controls alternative splicing and steady-state <scp>RNA</scp> levels in <scp><i>P</i></scp><i>lasmodium falciparum</i></scp> through preferential recognition of specific <scp>RNA</scp> motifs. <i>Molecular Microbiology</i> , 2015, 96, 1283-1297.	2.5	20
15	ORF57 Overcomes the Detrimental Sequence Bias of Kaposi's Sarcoma-Associated Herpesvirus Lytic Genes. <i>Journal of Virology</i> , 2015, 89, 5097-5109.	3.4	11
16	The role of RNA conformation in RNA-protein recognition. <i>RNA Biology</i> , 2015, 12, 720-727.	3.1	31
17	A diverse epigenetic landscape at human exons with implication for expression. <i>Nucleic Acids Research</i> , 2015, 43, 3498-3508.	14.5	48
18	A widespread role of the motif environment in transcription factor binding across diverse protein families. <i>Genome Research</i> , 2015, 25, 1268-1280.	5.5	134

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19	RNA-dependent chromatin localization of KDM4D lysine demethylase promotes H3K9me3 demethylation. <i>Nucleic Acids Research</i> , 2014, 42, 13026-13038.	14.5	28
20	Covariation between homeodomain transcription factors and the shape of their DNA binding sites. <i>Nucleic Acids Research</i> , 2014, 42, 430-441.	14.5	54
21	RBPmap: a web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, W361-W367.	14.5	409
22	Comparative metagenomic analyses reveal viral-induced shifts of host metabolism towards nucleotide biosynthesis. <i>Microbiome</i> , 2014, 2, 9.	11.1	66
23	Searching for protein signatures using a multilevel alphabet. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1058-1068.	2.6	1
24	The hnRNP F/H homologue of <i>Trypanosoma brucei</i> is differentially expressed in the two life cycle stages of the parasite and regulates splicing and mRNA stability. <i>Nucleic Acids Research</i> , 2013, 41, 6577-6594.	14.5	44
25	DRIMust: a web server for discovering rank imbalanced motifs using suffix trees. <i>Nucleic Acids Research</i> , 2013, 41, W174-W179.	14.5	53
26	Conformational readout of RNA by small ligands. <i>RNA Biology</i> , 2013, 10, 981-989.	3.1	15
27	A complex immunodeficiency is based on U1 snRNP-mediated poly(A) site suppression. <i>EMBO Journal</i> , 2012, 31, 4035-4044.	7.8	24
28	An Integrated Regulatory Network Reveals Pervasive Cross-Regulation among Transcription and Splicing Factors. <i>PLoS Computational Biology</i> , 2012, 8, e1002603.	3.2	14
29	Cyanophage tRNAs may have a role in cross-infectivity of oceanic <i>Prochlorococcus</i> and <i>Synechococcus</i> hosts. <i>ISME Journal</i> , 2012, 6, 619-628.	9.8	50
30	A novel <i>Plasmodium falciparum</i> SR protein is an alternative splicing factor required for the parasites' proliferation in human erythrocytes. <i>Nucleic Acids Research</i> , 2012, 40, 9903-9916.	14.5	32
31	Predicting nucleic acid binding interfaces from structural models of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 482-489.	2.6	12
32	Ancient diversity of splicing motifs and protein surfaces in the wild emmer wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22 Pathology, 2012, 13, 276-287.	4.2	45
33	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. <i>PLoS ONE</i> , 2012, 7, e38864.	2.5	61
34	Divergent RNA binding specificity of yeast Puf2p. <i>Rna</i> , 2011, 17, 1479-1488.	3.5	25
35	ARTS, the unusual septin: structural and functional aspects. <i>Biological Chemistry</i> , 2011, 392, 783-790.	2.5	29
36	Heterogeneous Nuclear Ribonucleoprotein H1/H2-dependent Unsplicing of Thymidine Phosphorylase Results in Anticancer Drug Resistance. <i>Journal of Biological Chemistry</i> , 2011, 286, 3741-3754.	3.4	45

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37	From face to interface recognition: a differential geometric approach to distinguish DNA from RNA binding surfaces. <i>Nucleic Acids Research</i> , 2011, 39, 7390-7399.	14.5	23
38	Comparative analysis of fungal protein kinases and associated domains. <i>BMC Genomics</i> , 2010, 11, 133.	2.8	43
39	Structural signatures of antibiotic binding sites on the ribosome. <i>Nucleic Acids Research</i> , 2010, 38, 5982-5994.	14.5	26
40	SFmap: a web server for motif analysis and prediction of splicing factor binding sites. <i>Nucleic Acids Research</i> , 2010, 38, W281-W285.	14.5	89
41	Predicting and controlling the reactivity of immune cell populations against cancer. <i>Molecular Systems Biology</i> , 2009, 5, 265.	7.2	11
42	A supervised learning approach for taxonomic classification of core-photosystem-II genes and transcripts in the marine environment. <i>BMC Genomics</i> , 2009, 10, 229.	2.8	17
43	A computational approach for genome-wide mapping of splicing factor binding sites. <i>Genome Biology</i> , 2009, 10, R30.	9.6	54
44	Classifying RNA-Binding Proteins Based on Electrostatic Properties. <i>PLoS Computational Biology</i> , 2008, 4, e1000146.	3.2	65
45	Revealing unique properties of the ribosome using a network based analysis. <i>Nucleic Acids Research</i> , 2008, 36, 4641-4652.	14.5	24
46	Does distance matter? Variations in alternative splicing regulation. <i>Nucleic Acids Research</i> , 2007, 35, 5487-5498.	14.5	16
47	Patch Finder Plus (PFplus): A web server for extracting and displaying positive electrostatic patches on protein surfaces. <i>Nucleic Acids Research</i> , 2007, 35, W526-W530.	14.5	54
48	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , 2007, 1, 492-501.	9.8	122
49	Alternative splicing regulation at tandem 3' splice sites. <i>Nucleic Acids Research</i> , 2006, 34, 23-31.	14.5	68
50	The <i>Saccharomyces cerevisiae</i> GSK-3 homologs. <i>Current Drug Targets</i> , 2006, 7, 1455-1465.	2.1	31
51	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 175-182.	8.2	89
52	Detection and measurement of alternative splicing using splicing-sensitive microarrays. <i>Methods</i> , 2005, 37, 345-359.	3.8	89
53	Hidden Markov models that use predicted local structure for fold recognition: Alphabets of backbone geometry. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 504-514.	2.6	178
54	Combining local-structure, fold-recognition, and new fold methods for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 491-496.	2.6	269

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55	Annotating Nucleic Acid-Binding Function Based on Protein Structure. <i>Journal of Molecular Biology</i> , 2003, 326, 1065-1079.	4.2	185
56	On the Significance of Alternating Patterns of Polar and Non-polar Residues in Beta-strands. <i>Journal of Molecular Biology</i> , 2002, 323, 453-461.	4.2	63
57	Contributions of residue pairing to β^2 -sheet formation: conservation and covariation of amino acid residue pairs on antiparallel β^2 -strands. <i>Journal of Molecular Biology</i> , 2001, 305, 1145-1159.	4.2	51
58	Common Fragile Sites: G-Band Characteristics within an R-Band. <i>American Journal of Human Genetics</i> , 1999, 64, 908-910.	6.2	28
59	A role for CH \cdots O interactions in protein-DNA recognition. <i>Journal of Molecular Biology</i> , 1998, 277, 1129-1140.	4.2	171
60	Quantitative parameters for amino acid-base interaction: Implications for prediction of protein-DNA binding sites. <i>Nucleic Acids Research</i> , 1998, 26, 2306-2312.	14.5	142
61	Comprehensive Analysis of Hydrogen Bonds in Regulatory Protein DNA-Complexes: In Search of Common Principles. <i>Journal of Molecular Biology</i> , 1995, 253, 370-382.	4.2	205