

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 web server for mapping binding sites of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, W361-W367.	14.5	409
2	Evaluation of COVID-19 RT-qPCR Test in Multi sample Pools. <i>Clinical Infectious Diseases</i> , 2020, 71, 2073-2078.	5.8	350
3	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
4	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
5	Annotating Nucleic Acid-Binding Function Based on Protein Structure. <i>Journal of Molecular Biology</i> , 2003, 326, 1065-1079.	4.2	185
6	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
7	A role for CH \cdots O interactions in protein-DNA recognition. <i>Journal of Molecular Biology</i> , 1998, 277, 1129-1140.	4.2	171
8	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
9	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
10	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , 2007, 1, 492-501.	9.8	122
11	Exploring functional relationships between components of the gene expression machinery. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 175-182.	8.2	89
12	Detection and measurement of alternative splicing using splicing-sensitive microarrays. <i>Methods</i> , 2005, 37, 345-359.	3.8	89
13	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
14	Alternative splicing regulation at tandem 3' splice sites. <i>Nucleic Acids Research</i> , 2006, 34, 23-31.	14.5	68
15	Comparative metagenomic analyses reveal viral-induced shifts of host metabolism towards nucleotide biosynthesis. <i>Microbiome</i> , 2014, 2, 9.	11.1	66
16	Classifying RNA-Binding Proteins Based on Electrostatic Properties. <i>PLoS Computational Biology</i> , 2008, 4, e1000146.	3.2	65
17	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
18	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

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19	Characterization of Coding Synonymous and Non-Synonymous Variants in ADAMTS13 Using Ex Vivo and In Silico Approaches. PLoS ONE, 2012, 7, e38864.	2.5	61
20	Patch Finder Plus (PFplus): A web server for extracting and displaying positive electrostatic patches on protein surfaces. Nucleic Acids Research, 2007, 35, W526-W530.	14.5	54
21	A computational approach for genome-wide mapping of splicing factor binding sites. Genome Biology, 2009, 10, R30.	9.6	54
22	Covariation between homeodomain transcription factors and the shape of their DNA binding sites. Nucleic Acids Research, 2014, 42, 430-441.	14.5	54
23	DRIMust: a web server for discovering rank imbalanced motifs using suffix trees. Nucleic Acids Research, 2013, 41, W174-W179.	14.5	53
24	Contributions of residue pairing to β -sheet formation: conservation and covariation of amino acid residue pairs on antiparallel β -strands. Journal of Molecular Biology, 2001, 305, 1145-1159.	4.2	51
25	Cyanophage tRNAs may have a role in cross-infectivity of oceanic <i>Prochlorococcus</i> and <i>Synechococcus</i> hosts. ISME Journal, 2012, 6, 619-628.	9.8	50
26	A diverse epigenetic landscape at human exons with implication for expression. Nucleic Acids Research, 2015, 43, 3498-3508.	14.5	48
27	How motif environment influences transcription factor search dynamics: Finding a needle in a haystack. BioEssays, 2016, 38, 605-612.	2.5	48
28	Heterogeneous Nuclear Ribonucleoprotein H1/H2-dependent Unsplicing of Thymidine Phosphorylase Results in Anticancer Drug Resistance. Journal of Biological Chemistry, 2011, 286, 3741-3754.	3.4	45
29	Ancient diversity of splicing motifs and protein surfaces in the wild emmer wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Pathology, 2012, 13, 276-287.	4.2	45
30	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. Nucleic Acids Research, 2013, 41, 6577-6594.	14.5	44
31	Comparative analysis of fungal protein kinases and associated domains. BMC Genomics, 2010, 11, 133.	2.8	43
32	Adaptation to sub-optimal hosts is a driver of viral diversification in the ocean. Nature Communications, 2018, 9, 4698.	12.8	39
33	A novel <i>Plasmodium falciparum</i> SR protein is an alternative splicing factor required for the parasites' proliferation in human erythrocytes. Nucleic Acids Research, 2012, 40, 9903-9916.	14.5	32
34	The role of RNA conformation in RNA-protein recognition. RNA Biology, 2015, 12, 720-727.	3.1	31
35	Regulation of alternative splicing by p300-mediated acetylation of splicing factors. Rna, 2019, 25, 813-824.	3.5	31
36	The <i>Saccharomyces cerevisiae</i> GSK-3 homologs. Current Drug Targets, 2006, 7, 1455-1465.	2.1	31

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37	ARTS, the unusual septin: structural and functional aspects. <i>Biological Chemistry</i> , 2011, 392, 783-790.	2.5	29
38	Common Fragile Sites: G-Band Characteristics within an R-Band. <i>American Journal of Human Genetics</i> , 1999, 64, 908-910.	6.2	28
39	RNA-dependent chromatin localization of KDM4D lysine demethylase promotes H3K9me3 demethylation. <i>Nucleic Acids Research</i> , 2014, 42, 13026-13038.	14.5	28
40	Structural signatures of antibiotic binding sites on the ribosome. <i>Nucleic Acids Research</i> , 2010, 38, 5982-5994.	14.5	26
41	Divergent RNA binding specificity of yeast Puf2p. <i>Rna</i> , 2011, 17, 1479-1488.	3.5	25
42	Revealing unique properties of the ribosome using a network based analysis. <i>Nucleic Acids Research</i> , 2008, 36, 4641-4652.	14.5	24
43	A complex immunodeficiency is based on U1 snRNP-mediated poly(A) site suppression. <i>EMBO Journal</i> , 2012, 31, 4035-4044.	7.8	24
44	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
45	<i>Pf</i> SR1 controls alternative splicing and steady-state RNA levels in <i>Plasmodium falciparum</i> through preferential recognition of specific RNA motifs. <i>Molecular Microbiology</i> , 2015, 96, 1283-1297.	2.5	20
46	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
47	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
48	Does distance matter? Variations in alternative ϵ^2 splicing regulation. <i>Nucleic Acids Research</i> , 2007, 35, 5487-5498.	14.5	16
49	Conformational readout of RNA by small ligands. <i>RNA Biology</i> , 2013, 10, 981-989.	3.1	15
50	An Integrated Regulatory Network Reveals Pervasive Cross-Regulation among Transcription and Splicing Factors. <i>PLoS Computational Biology</i> , 2012, 8, e1002603.	3.2	14
51	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
52	Predicting nucleic acid binding interfaces from structural models of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 482-489.	2.6	12
53	Predicting and controlling the reactivity of immune cell populations against cancer. <i>Molecular Systems Biology</i> , 2009, 5, 265.	7.2	11
54	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

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55	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
56	Ribonucleoprotein particles: advances and challenges in computational methods. <i>Current Opinion in Structural Biology</i> , 2018, 53, 124-130.	5.7	8
57	A Novel Geometry-Based Approach to Infer Protein Interface Similarity. <i>Scientific Reports</i> , 2018, 8, 8192.	3.3	7
58	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
59	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
60	Mutual enrichment in aggregated ranked lists with applications to gene expression regulation. <i>Bioinformatics</i> , 2016, 32, i464-i472.	4.1	5
61	Searching for protein signatures using a multilevel alphabet. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1058-1068.	2.6	1