

Jermaine L Jenkins

List of Publications by Year in descending order

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40
papers

1,067
citations

394421

19
h-index

434195

31
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46
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docs citations

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times ranked

1412
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of a PreQ1 Riboswitch Aptamer in Metabolite-bound and Free States with Implications for Gene Regulation. <i>Journal of Biological Chemistry</i> , 2011, 286, 24626-24637.	3.4	114
2	High-resolution structure of human D-glyceraldehyde-3-phosphate dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 290-301.	2.5	108
3	Structural Basis of the Transcriptional Regulation of the Proline Utilization Regulon by Multifunctional PutA. <i>Journal of Molecular Biology</i> , 2008, 381, 174-188.	4.2	62
4	An extended U2AF65 RNA-binding domain recognizes the 3' splice site signal. <i>Nature Communications</i> , 2016, 7, 10950.	12.8	58
5	Splicing Factor Mutations in Myelodysplasias: Insights from Spliceosome Structures. <i>Trends in Genetics</i> , 2017, 33, 336-348.	6.7	56
6	U2AF65 adapts to diverse pre-mRNA splice sites through conformational selection of specific and promiscuous RNA recognition motifs. <i>Nucleic Acids Research</i> , 2013, 41, 3859-3873.	14.5	43
7	Crystal structures of the DNA-binding domain of <i>Escherichia coli</i> proline utilization A flavoprotein and analysis of the role of Lys9 in DNA recognition. <i>Protein Science</i> , 2006, 15, 2630-2641.	7.6	38
8	Metalloriboswitches: RNA-based inorganic ion sensors that regulate genes. <i>Journal of Biological Chemistry</i> , 2017, 292, 9441-9450.	3.4	37
9	Three RNA Recognition Motifs Participate in RNA Recognition and Structural Organization by the Pro-Apoptotic Factor TIA-1. <i>Journal of Molecular Biology</i> , 2012, 415, 727-740.	4.2	35
10	Interaction of human biliverdin reductase with Akt/protein kinase B and phosphatidylinositol-dependent kinase 1 regulates glycogen synthase kinase 3 activity: a novel mechanism of Akt activation. <i>FASEB Journal</i> , 2016, 30, 2926-2944.	0.5	34
11	The pre-mRNA splicing and transcription factor Tat-SF1 is a functional partner of the spliceosome SF3b1 subunit via a U2AF homology motif interface. <i>Journal of Biological Chemistry</i> , 2019, 294, 2892-5793.	3.4	33
12	Solution Conformation and Thermodynamic Characteristics of RNA Binding by the Splicing Factor U2AF65. <i>Journal of Biological Chemistry</i> , 2008, 283, 33641-33649.	3.4	30
13	Representative cancer-associated U2AF2 mutations alter RNA interactions and splicing. <i>Journal of Biological Chemistry</i> , 2020, 295, 17148-17157.	3.4	29
14	Cancer-Associated Mutations Mapped on High-Resolution Structures of the U2AF2 RNA Recognition Motifs. <i>Biochemistry</i> , 2017, 56, 4757-4761.	2.5	28
15	Human CaaX protease <sc>ZMPSTE</sc>24 expressed in yeast: Structure and inhibition by <sc>HIV</sc> protease inhibitors. <i>Protein Science</i> , 2017, 26, 242-257.	7.6	25
16	Use of Surface Plasmon Resonance (SPR) to Determine Binding Affinities and Kinetic Parameters Between Components Important in Fusion Machinery. <i>Methods in Molecular Biology</i> , 2019, 1860, 199-210.	0.9	25
17	A Transition-State Interaction Shifts Nucleobase Ionization toward Neutrality To Facilitate Small Ribozyme Catalysis. <i>Journal of the American Chemical Society</i> , 2012, 134, 16933-16936.	13.7	24
18	Phosphatidic acid induces conformational changes in Sec18 protomers that prevent SNARE priming. <i>Journal of Biological Chemistry</i> , 2019, 294, 3100-3116.	3.4	24

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19	A synthetic small molecule stalls pre-mRNA splicing by promoting an early-stage U2AF2-RNA complex. <i>Cell Chemical Biology</i> , 2021, 28, 1145-1157.e6.	5.2	24
20	Analysis of a preQ1-I riboswitch in effector-free and bound states reveals a metabolite-programmed nucleobase-stacking spine that controls gene regulation. <i>Nucleic Acids Research</i> , 2020, 48, 8146-8164.	14.5	21
21	Large Favorable Enthalpy Changes Drive Specific RNA Recognition by RNA Recognition Motif Proteins. <i>Biochemistry</i> , 2011, 50, 1429-1431.	2.5	20
22	ITC Analysis of Ligand Binding to PreQ1 Riboswitches. <i>Methods in Enzymology</i> , 2014, 549, 435-450.	1.0	20
23	Crystallographic Analysis of Small Ribozymes and Riboswitches. <i>Methods in Molecular Biology</i> , 2012, 848, 159-184.	0.9	20
24	Cus2 enforces the first ATP-dependent step of splicing by binding to yeast SF3b1 through a UHM $\hat{\epsilon}$ ULM interaction. <i>Rna</i> , 2019, 25, 1020-1037.	3.5	19
25	A small RNA that cooperatively senses two stacked metabolites in one pocket for gene control. <i>Nature Communications</i> , 2022, 13, 199.	12.8	19
26	A Broad Range of Conformations Contribute to the Solution Ensemble of the Essential Splicing Factor U2AF ⁶⁵ . <i>Biochemistry</i> , 2012, 51, 5223-5225.	2.5	17
27	Co-crystal structures of HIV TAR RNA bound to lab-evolved proteins show key roles for arginine relevant to the design of cyclic peptide TAR inhibitors. <i>Journal of Biological Chemistry</i> , 2020, 295, 16470-16486.	3.4	17
28	Structure-guided U2AF ⁶⁵ variant improves recognition and splicing of a defective pre-mRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17420-17425.	7.1	15
29	Sortilin facilitates VLDL-B100 secretion by insulin sensitive McArdle RH777 $\hat{\epsilon}$ cells. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 546-552.	2.1	14
30	RNA Induces Conformational Changes in the SF1/U2AF65 Splicing Factor Complex. <i>Journal of Molecular Biology</i> , 2011, 405, 1128-1138.	4.2	12
31	Phosphatidylinositol (3,4,5)-trisphosphate binds to sortilin and competes with neurotensin: Implications for very low density lipoprotein binding. <i>Biochemical and Biophysical Research Communications</i> , 2016, 479, 551-556.	2.1	10
32	An Allosteric Binding Site on Sortilin Regulates the Trafficking of VLDL, PCSK9, and LDLR in Hepatocytes. <i>Biochemistry</i> , 2020, 59, 4321-4335.	2.5	8
33	Pre-mRNA splicing factor U2AF2 recognizes distinct conformations of nucleotide variants at the center of the pre-mRNA splice site signal. <i>Nucleic Acids Research</i> , 2022, 50, 5299-5312.	14.5	8
34	A small-molecule competitive inhibitor of phosphatidic acid binding by the AAA+ protein NSF/Sec18 blocks the SNARE-priming stage of vacuole fusion. <i>Journal of Biological Chemistry</i> , 2019, 294, 17168-17185.	3.4	6
35	Affinity and Structural Analysis of the U1A RNA Recognition Motif with Engineered Methionines to Improve Experimental Phasing. <i>Crystals</i> , 2021, 11, 273.	2.2	4
36	A UHM $\hat{\epsilon}$ ULM interface with unusual structural features contributes to U2AF2 and SF3B1 association for pre-mRNA splicing. <i>Journal of Biological Chemistry</i> , 2022, 298, 102224.	3.4	4

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37	Structure of Sonic Hedgehog protein in complex with zinc(II) and magnesium(II) reveals ion-coordination plasticity relevant to peptide drug design. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 969-979.	2.3	3
38	The Quick and the Dead: A Guide to Fast Phasing of Small Ribozyme and Riboswitch Crystal Structures. <i>Methods in Molecular Biology</i> , 2016, 1490, 265-280.	0.9	1
39	Thermodynamic Characteristics of pre-mRNA Splice Site Recognition. <i>Biophysical Journal</i> , 2009, 96, 63a-64a.	0.5	0
40	Metal Dependence of Ligand Binding and Heavy-Atom Derivatization of Evolutionarily Distinct PreQ1 Riboswitches. , 2014, , 423-440.		0