

Traci M Hall

List of Publications by Year in descending order

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56
papers

4,648
citations

147801

31
h-index

168389

53
g-index

73
all docs

73
docs citations

73
times ranked

4562
citing authors

#	ARTICLE	IF	CITATIONS
1	Size Selective Recognition of siRNA by an RNA Silencing Suppressor. <i>Cell</i> , 2003, 115, 799-811.	28.9	494
2	Modular Recognition of RNA by a Human Pumilio-Homology Domain. <i>Cell</i> , 2002, 110, 501-512.	28.9	450
3	Multiple modes of RNA recognition by zinc finger proteins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 367-373.	5.7	293
4	Crystal Structure of a Hedgehog Autoprocessing Domain: Homology between Hedgehog and Self-Splicing Proteins. <i>Cell</i> , 1997, 91, 85-97.	28.9	272
5	Crystal Structure of a Pumilio Homology Domain. <i>Molecular Cell</i> , 2001, 7, 855-865.	9.7	226
6	Structural basis for recognition of AU-rich element RNA by the HuD protein. , 2001, 8, 141-145.		220
7	Engineering RNA sequence specificity of Pumilio repeats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13635-13639.	7.1	209
8	A potential catalytic site revealed by the 1.7-Å... crystal structure of the amino-terminal signalling domain of Sonic hedgehog. <i>Nature</i> , 1995, 378, 212-216.	27.8	200
9	Sonic hedgehog protein signals not as a hydrolytic enzyme but as an apparent ligand for Patched. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10992-10999.	7.1	164
10	Engineering splicing factors with designed specificities. <i>Nature Methods</i> , 2009, 6, 825-830.	19.0	136
11	Post-transcriptional Regulatory Functions of Mammalian Pumilio Proteins. <i>Trends in Genetics</i> , 2018, 34, 972-990.	6.7	132
12	Phosphate and R2D2 Restrict the Substrate Specificity of Dicer-2, an ATP-Driven Ribonuclease. <i>Molecular Cell</i> , 2011, 42, 172-184.	9.7	124
13	Structural basis for an inositol pyrophosphate kinase surmounting phosphate crowding. <i>Nature Chemical Biology</i> , 2012, 8, 111-116.	8.0	123
14	Basis of altered RNA-binding specificity by PUF proteins revealed by crystal structures of yeast Puf4p. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 397-402.	8.2	116
15	Title is missing!. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1997, 62, 191-204.	1.1	111
16	Structural basis for specific recognition of multiple mRNA targets by a PUF regulatory protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20186-20191.	7.1	109
17	Structure and Function of Argonaute Proteins. <i>Structure</i> , 2005, 13, 1403-1408.	3.3	94
18	Specific and Modular Binding Code for Cytosine Recognition in Pumilio/FBF (PUF) RNA-binding Domains. <i>Journal of Biological Chemistry</i> , 2011, 286, 26732-26742.	3.4	94

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19	A 5â€² cytosine binding pocket in Puf3p specifies regulation of mitochondrial mRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20192-20197.	7.1	83
20	Alternate Modes of Cognate RNA Recognition by Human PUMILIO Proteins. Structure, 2011, 19, 361-367.	3.3	73
21	Understanding and engineering RNA sequence specificity of PUF proteins. Current Opinion in Structural Biology, 2009, 19, 110-115.	5.7	72
22	Drosophila Nanos acts as a molecular clamp that modulates the RNA-binding and repression activities of Pumilio. ELife, 2016, 5, .	6.0	66
23	RNA regulatory networks diversified through curvature of the PUF protein scaffold. Nature Communications, 2015, 6, 8213.	12.8	56
24	Engineered proteins with <sc>P</sc>umilio</i> femâ€³</i> m<sc>RNA</sc> binding factor scaffold to manipulate <sc>RNA</sc> metabolism. FEBS Journal, 2013, 280, 3755-3767.	4.7	55
25	Combinatorial control of messenger RNAs by Pumilio, Nanos and Brain Tumor Proteins. RNA Biology, 2017, 14, 1445-1456.	3.1	51
26	A divergent Pumilio repeat protein family for pre-rRNA processing and mRNA localization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18554-18559.	7.1	48
27	Stacking interactions in PUFâ€™RNA complexes. Rna, 2011, 17, 718-727.	3.5	43
28	Patterns and plasticity in RNA-protein interactions enable recruitment of multiple proteins through a single site. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6054-6059.	7.1	43
29	De-coding and re-coding RNA recognition by PUF and PPR repeat proteins. Current Opinion in Structural Biology, 2016, 36, 116-121.	5.7	40
30	Divergence of Pumilio/fem-3 mRNA Binding Factor (PUF) Protein Specificity through Variations in an RNA-binding Pocket. Journal of Biological Chemistry, 2012, 287, 6949-6957.	3.4	37
31	Nop9 is a PUF-like protein that prevents premature cleavage to correctly process pre-18S rRNA. Nature Communications, 2016, 7, 13085.	12.8	34
32	Selective release of a glycosylphosphatidylinositol-anchored antigen from the surface of Schistosoma mansoni. Molecular and Biochemical Parasitology, 1991, 46, 73-80.	1.1	32
33	Molecular mechanisms for the regulation of histone mRNA stem-loopâ€™binding protein by phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2937-46.	7.1	29
34	Schistosoma mansoni: Molecular Cloning and Sequencing of the 200-kDa Chemotherapeutic Target Antigen. Experimental Parasitology, 1995, 80, 242-249.	1.2	27
35	Solution structure of the Drosha double-stranded RNA-binding domain. Silence: A Journal of RNA Regulation, 2010, 1, 2.	8.1	26
36	U7 snRNP is recruited to histone pre-mRNA in a FLASH-dependent manner by two separate regions of the stemâ€™loop binding protein. Rna, 2017, 23, 938-951.	3.5	26

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37	Pentatricopeptide repeats of protein-only RNase P use a distinct mode to recognize conserved bases and structural elements of pre-tRNA. <i>Nucleic Acids Research</i> , 2020, 48, 11815-11826.	14.5	26
38	Integrated analysis of RNA-binding protein complexes using in vitro selection and high-throughput sequencing and sequence specificity landscapes (SEQRS). <i>Methods</i> , 2017, 118-119, 171-181.	3.8	24
39	Evolution from DNA to RNA recognition by the b13 LAGLIDADG maturase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 779-787.	8.2	22
40	H/ACA snoRNA levels are regulated during stem cell differentiation. <i>Nucleic Acids Research</i> , 2020, 48, 8686-8703.	14.5	22
41	Poly(A) tail synthesis and regulation: recent structural insights. <i>Current Opinion in Structural Biology</i> , 2002, 12, 82-88.	5.7	21
42	A crystal structure of a collaborative RNA regulatory complex reveals mechanisms to refine target specificity. <i>ELife</i> , 2019, 8, .	6.0	21
43	The Drosophila hnRNP F/H Homolog Glorund Uses Two Distinct RNA-Binding Modes to Diversify Target Recognition. <i>Cell Reports</i> , 2017, 19, 150-161.	6.4	15
44	Expanding the RNA-recognition code of PUF proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 653-655.	8.2	14
45	Engineering a conserved RNA regulatory protein repurposes its biological function in vivo. <i>ELife</i> , 2019, 8, .	6.0	13
46	The molecular basis for ANE syndrome revealed by the large ribosomal subunit processome interactome. <i>ELife</i> , 2016, 5, .	6.0	11
47	SAM breaks its stereotype. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 677-679.	8.2	10
48	Effects of hemorrhagic serum on interleukin-2 generation and utilization. <i>Critical Care Medicine</i> , 1988, 16, 307-311.	0.9	9
49	Distinct RNA-binding modules in a single PUF protein cooperate to determine RNA specificity. <i>Nucleic Acids Research</i> , 2019, 47, 8770-8784.	14.5	9
50	Schistosoma: A 200-kDa Chemotherapeutic Target Antigen Is Differentially Localized in African vs Oriental Species. <i>Experimental Parasitology</i> , 1993, 76, 293-301.	1.2	6
51	Mass spectrometric identification of candidate RNA-binding proteins associated with Transition Nuclear Protein mRNA in the mouse testis. <i>Scientific Reports</i> , 2019, 9, 13618.	3.3	5
52	Bipartite interaction sites differentially modulate RNA-binding affinity of a protein complex essential for germline stem cell self-renewal. <i>Nucleic Acids Research</i> , 2022, 50, 536-548.	14.5	5
53	Structural analysis reveals the flexible C-terminus of Nop15 undergoes rearrangement to recognize a pre-ribosomal RNA folding intermediate. <i>Nucleic Acids Research</i> , 2016, 45, gkw961.	14.5	4
54	Nop9 recognizes structured and single-stranded RNA elements of preribosomal RNA. <i>Rna</i> , 2020, 26, 1049-1059.	3.5	3

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55	Preparation of cooperative RNA recognition complexes for crystallographic structural studies. <i>Methods in Enzymology</i> , 2019, 623, 1-22.	1.0	0
56	Probing RNA sequence specificity and function of PUF proteins. <i>FASEB Journal</i> , 2009, 23, .	0.5	0