

# Richard Stefl

## List of Publications by Year in descending order

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41  
papers

2,404  
citations

201674

27  
h-index

276875

41  
g-index

43  
all docs

43  
docs citations

43  
times ranked

2649  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cooperation between intrinsically disordered and ordered regions of Spt6 regulates nucleosome and Pol II CTD binding, and nucleosome assembly. <i>Nucleic Acids Research</i> , 2022, 50, 5961-5973.	14.5	2
2	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021, 12, 6078.	12.8	21
3	Yeast Spt6 Reads Multiple Phosphorylation Patterns of RNA Polymerase II C-Terminal Domain In Vitro. <i>Journal of Molecular Biology</i> , 2020, 432, 4092-4107.	4.2	6
4	Termination of non-coding transcription in yeast relies on both an RNA Pol II CTD interaction domain and a CTD-mimicking region in Sen1. <i>EMBO Journal</i> , 2020, 39, e101548.	7.8	23
5	Efficient and robust preparation of tyrosine phosphorylated intrinsically disordered proteins. <i>BioTechniques</i> , 2019, 67, 16-22.	1.8	2
6	Structural insight into recognition of phosphorylated threonine-4 of RNA polymerase II C-terminal domain by Rtt103p. <i>EMBO Reports</i> , 2017, 18, 906-913.	4.5	24
7	Structure and dynamics of the RNAPII CTDsomes with Rtt103. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11133-11138.	7.1	18
8	RBM7 subunit of the NEXT complex binds U-rich sequences and targets 3'-end extended forms of snRNAs. <i>Nucleic Acids Research</i> , 2015, 43, 4236-4248.	14.5	52
9	Structure and semi-sequence-specific RNA binding of Nrd1. <i>Nucleic Acids Research</i> , 2014, 42, 8024-8038.	14.5	14
10	Molecular Basis for Coordinating Transcription Termination with Noncoding RNA Degradation. <i>Molecular Cell</i> , 2014, 55, 467-481.	9.7	99
11	The CTD code of RNA polymerase II: a structural view. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 1-16.	6.4	61
12	Serine phosphorylation and proline isomerization in RNAP II CTD control recruitment of Nrd1. <i>Genes and Development</i> , 2012, 26, 1891-1896.	5.9	97
13	Recognition of asymmetrically dimethylated arginine by TDRD3. <i>Nucleic Acids Research</i> , 2012, 40, 11748-11755.	14.5	38
14	Air2p is critical for the assembly and RNA-binding of the TRAMP complex and the KOW domain of Mtr4p is crucial for exosome activation. <i>Nucleic Acids Research</i> , 2012, 40, 5679-5693.	14.5	41
15	<i>In vivo</i> SELEX reveals novel sequence and structural determinants of Nrd1-Nab3-Sen1-dependent transcription termination. <i>EMBO Journal</i> , 2012, 31, 3935-3948.	7.8	67
16	Recognition of Transcription Termination Signal by the Nuclear Polyadenylated RNA-binding (NAB) 3 Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 3645-3657.	3.4	42
17	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N chemical shift assignments of ZCCHC9. <i>Biomolecular NMR Assignments</i> , 2011, 5, 19-21.	0.8	6
18	<sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N resonance assignments for the CTD-interacting domain of Nrd1 bound to Ser5-phosphorylated CTD of RNA polymerase II. <i>Biomolecular NMR Assignments</i> , 2011, 5, 203-205.	0.8	4

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19	1H, 13C, and 15N chemical shift assignments for the RNA recognition motif of Nab3. <i>Biomolecular NMR Assignments</i> , 2010, 4, 119-121.	0.8	3
20	The Solution Structure of the ADAR2 dsRBM-RNA Complex Reveals a Sequence-Specific Readout of the Minor Groove. <i>Cell</i> , 2010, 143, 225-237.	28.9	212
21	The testis-specific human protein RBMY recognizes RNA through a novel mode of interaction. <i>EMBO Reports</i> , 2007, 8, 372-379.	4.5	84
22	The exosome and RNA quality control in the nucleus. <i>EMBO Reports</i> , 2007, 8, 651-657.	4.5	118
23	Shape-specific recognition in the structure of the Vts1p SAM domain with RNA. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 160-167.	8.2	102
24	Structure and Specific RNA Binding of ADAR2 Double-Stranded RNA Binding Motifs. <i>Structure</i> , 2006, 14, 345-355.	3.3	101
25	RNA sequence- and shape-dependent recognition by proteins in the ribonucleoprotein particle. <i>EMBO Reports</i> , 2005, 6, 33-38.	4.5	154
26	Letter to the Editor: Resonance assignments of the double-stranded RNA-binding of adenosine deaminase acting on RNA 2 (ADAR2). <i>Journal of Biomolecular NMR</i> , 2005, 31, 71-72.	2.8	5
27	A novel RNA pentaloop fold involved in targeting ADAR2. <i>Rna</i> , 2005, 11, 592-597.	3.5	26
28	DNA A-tract bending in three dimensions: Solving the dA4T4 vs. dT4A4 conundrum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1177-1182.	7.1	140
29	Molecular Dynamics Simulations of Guanine Quadruplex Loops: Advances and Force Field Limitations. <i>Biophysical Journal</i> , 2004, 87, 227-242.	0.5	116
30	Formation Pathways of a Guanine-Quadruplex DNA Revealed by Molecular Dynamics and Thermodynamic Analysis of the Substates. <i>Biophysical Journal</i> , 2003, 85, 1787-1804.	0.5	128
31	Non-Watson-Crick Basepairing and Hydration in RNA Motifs: Molecular Dynamics of 5S rRNA Loop E. <i>Biophysical Journal</i> , 2003, 84, 3564-3582.	0.5	108
32	Determination of the glycosidic torsion angles in uniformly 13C-labeled nucleic acids from vicinal coupling constants 3J(C2)/4-H1' and 3J(C6)/8-H1'. <i>Journal of Biomolecular NMR</i> , 2002, 23, 1-12.	2.8	27
33	Refinement of d(GCCAAGC) hairpin structure using one- and two-bond residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2002, 24, 1-14.	2.8	61
34	A-like guanine-guanine stacking in the aqueous DNA duplex of d(GGGGCCCC)11 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2001, 307, 513-524.	4.2	60
35	Molecular dynamics of the frame-shifting pseudoknot from beet western yellows virus: the role of non-Watson-Crick base-pairing, ordered hydration, cation binding and base mutations on stability and unfolding 1 Edited by J. Doudna. <i>Journal of Molecular Biology</i> , 2001, 313, 1073-1091.	4.2	70
36	Molecular Dynamics of DNA Quadruplex Molecules Containing Inosine, 6-Thioguanine and 6-Thiopurine. <i>Biophysical Journal</i> , 2001, 80, 455-468.	0.5	54

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37	NMR methodology for the study of nucleic acids. Current Opinion in Structural Biology, 2001, 11, 275-281.	5.7	71
38	An A -type double helix of DNA having B -type puckering of the deoxyribose rings 1 Edited by I. Tinoco. Journal of Molecular Biology, 2000, 297, 907-922.	4.2	91
39	Unrestrained Molecular Dynamics Simulations of [d(AT)5]2Duplex in Aqueous Solution: Å Hydration and Binding of Sodium Ions in the Minor Groove. Journal of the American Chemical Society, 2000, 122, 5025-5033.	13.7	27
40	A Method for Direct Determination of Helical Parameters in Nucleic Acids Using Residual Dipolar Couplings. Journal of the American Chemical Society, 2000, 122, 10454-10455.	13.7	27
41	Differences in Conformational Behavior of ATA and TAT Sequences in Single Strand DNA Trimer. Journal of Biomolecular Structure and Dynamics, 1999, 16, 1087-1095.	3.5	1