ClaraÂ L Kielkopf

List of Publications by Year
in descending order

#	Article	IF	Citations
1	Pre-mRNA splicing factor U2AF2 recognizes distinct conformations of nucleotide variants at the center of the pre-mRNA splice site signal. Nucleic Acids Research, 2022, 50, 5299-5312.	14.5	8
2	A UHMâ€"ULM interface with unusual structural features contributes to U2AF2 and SF3B1 association for pre-mRNA splicing. Journal of Biological Chemistry, 2022, 298, 102224.	3.4	4
3	A synthetic small molecule stalls pre-mRNA splicing by promoting an early-stage U2AF2-RNA complex. Cell Chemical Biology, 2021, 28, 1145-1157.e6.	5.2	24
4	Representative cancer-associated U2AF2 mutations alter RNA interactions and splicing. Journal of Biological Chemistry, 2020, 295, 17148-17157.	3.4	29
5	A splice site-sensing conformational switch in U2AF2 is modulated by U2AF1 and its recurrent myelodysplasia-associated mutation. Nucleic Acids Research, 2020, 48, 5695-5709.	14.5	19
6	Structures of SF3b1 reveal a dynamic Achilles heel of spliceosome assembly: Implications for cancer-associated abnormalities and drug discovery. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 194440.	1.9	16
7	Cus2 enforces the first ATP-dependent step of splicing by binding to yeast SF3b1 through a UHMâ€"ULM interaction. Rna, 2019, 25, 1020-1037.	3.5	19
8	Dynamic stacking of an expected branch point adenosine in duplexes containing pseudouridine-modified or unmodified U2 snRNA sites. Biochemical and Biophysical Research Communications, 2019, 511, 416-421.	2.1	12
9	The pre-mRNA splicing and transcription factor Tat-SF1 is a functional partner of the spliceosome SF3b1 subunit via a U2AF homology motif interface. Journal of Biological Chemistry, 2019, 294, 2892-5793.	3.4	33
10	U2AF1 Driver Mutations in Hematopoietic Disorders Alter but Do Not Abrogate RNA Binding and Enlighten Structural Dependencies of the U2AF-RNA Complex. Blood, 2019, 134, 1230-1230.	1.4	0
11	Insights from structures of cancer-relevant pre-mRNA splicing factors. Current Opinion in Genetics and Development, 2018, 48, 57-66.	3.3	16
12	Splicing Factor Mutations in Myelodysplasias: Insights from Spliceosome Structures. Trends in Genetics, 2017, 33, 336-348.	6.7	56
13	Cancer-Associated Mutations Mapped on High-Resolution Structures of the U2AF2 RNA Recognition Motifs. Biochemistry, 2017, 56, 4757-4761.	2.5	28
14	Wild-Type U2AF1 Antagonizes the Splicing Program Characteristic of U2AF1-Mutant Tumors and Is Required for Cell Survival. PLoS Genetics, 2016, 12, e1006384.	3.5	72
15	SF1 Phosphorylation Enhances Specific Binding to U2AF 65 and Reduces Binding to 3â€²-Splice-Site RNA. Biophysical Journal, 2016, 111, 2570-2586.	0.5	28
16	An extended U2AF65â€"RNA-binding domain recognizes the 3â€² splice site signal. Nature Communications, 2016, 7, 10950.	12.8	58
17	Unmasking the U2AF homology motif family: a bona fide proteinâ€"protein interaction motif in disguise. Rna, 2016, 22, 1795-1807.	3.5	48
18	U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing. Leukemia, 2015, 29, 909-917.	7.2	107

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19	Dividing and Conquering the Family of RNA Recognition Motifs: A Representative Case Based on hnRNP L. Journal of Molecular Biology, 2015, 427, 2997-3000.	4.2	10
20	Cancer-relevant Splicing Factor CAPERÎ± Engages the Essential Splicing Factor SF3b155 in a Specific Ternary Complex. Journal of Biological Chemistry, 2014, 289, 17325-17337.	3.4	49
21	Structure-guided U2AF ⁶⁵ variant improves recognition and splicing of a defective pre-mRNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17420-17425.	7.1	15
22	Structure of Phosphorylated SF1 Bound to U2AF65 in an Essential Splicing Factor Complex. Structure, 2013, 21, 197-208.	3.3	55
23	Staufen1 dimerizes through a conserved motif and a degenerate dsRNA-binding domain to promote mRNA decay. Nature Structural and Molecular Biology, 2013, 20, 515-524.	8.2	51
24	U2AF65 adapts to diverse pre-mRNA splice sites through conformational selection of specific and promiscuous RNA recognition motifs. Nucleic Acids Research, 2013, 41, 3859-3873.	14.5	43
25	A Broad Range of Conformations Contribute to the Solution Ensemble of the Essential Splicing Factor U2AF⁶⁵. Biochemistry, 2012, 51, 5223-5225.	2.5	17
26	Three RNA Recognition Motifs Participate in RNA Recognition and Structural Organization by the Pro-Apoptotic Factor TIA-1. Journal of Molecular Biology, 2012, 415, 727-740.	4.2	35
27	Large Favorable Enthalpy Changes Drive Specific RNA Recognition by RNA Recognition Motif Proteins. Biochemistry, 2011, 50, 1429-1431.	2.5	20
28	RNA Induces Conformational Changes in the SF1/U2AF65 Splicing Factor Complex. Journal of Molecular Biology, 2011, 405, 1128-1138.	4.2	12
29	Purification, crystallization and preliminary X-ray crystallographic analysis of a central domain of human splicing factor 1. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 486-490.	0.7	4
30	Structural Basis for NADH/NAD+ Redox Sensing by a Rex Family Repressor. Molecular Cell, 2010, 38, 563-575.	9.7	89
31	Thermodynamic Characteristics of pre-mRNA Splice Site Recognition. Biophysical Journal, 2009, 96, 63a-64a.	0.5	0
32	A Novel Domain Implicated in the Interactions between pre-mRNA Splicing Factors. Biophysical Journal, 2009, 96, 600a.	0.5	0
33	Structural and Thermodynamic Means for Adaptable 3â€² Splice Site Recognition. Biophysical Journal, 2009, 96, 366a.	0.5	0
34	Different Requirements of the Kinase and UHM Domains of KIS for Its Nuclear Localization and Binding to Splicing Factors. Journal of Molecular Biology, 2008, 381, 748-762.	4.2	33
35	Structure of the central RNA recognition motif of human TIA-1 at 1.95 Ã… resolution. Biochemical and Biophysical Research Communications, 2008, 367, 813-819.	2.1	20
36	X-ray Structures of U2 snRNAâ^'Branchpoint Duplexes Containing Conserved Pseudouridines. Biochemistry, 2008, 47, 5503-5514.	2.5	40

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37	Solution Conformation and Thermodynamic Characteristics of RNA Binding by the Splicing Factor U2AF65. Journal of Biological Chemistry, 2008, 283, 33641-33649.	3.4	30
38	Alternative Conformations at the RNA-binding Surface of the N-terminal U2AF65 RNA Recognition Motif. Journal of Molecular Biology, 2007, 366, 703-710.	4.2	20
39	Structure of a DNA Repair Substrate Containing an Alkyl Interstrand Cross-Link at 1.65 Ã… Resolution,. Biochemistry, 2007, 46, 4545-4553.	2.5	13
40	Multiple U2AF65 Binding Sites within SF3b155: Thermodynamic and Spectroscopic Characterization of Proteinâ€“Protein Interactions among pre-mRNA Splicing Factors. Journal of Molecular Biology, 2006, 356, 664-683.	4.2	63
41	Structural Basis for Polypyrimidine Tract Recognition by the Essential Pre-mRNA Splicing Factor U2AF65. Molecular Cell, 2006, 23, 49-59.	9.7	170
42	Crystallization and preliminary X-ray analysis of a U2AF65variant in complex with a polypyrimidine-tract analogue by use of protein engineering. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 457-459.	0.7	11
43	Major phosphorylation of SF1 on adjacent Ser-Pro motifs enhances interaction with U2AF65. FEBS Journal, 2006, 273, 577-587.	4.7	51
44	X-Ray Structure of a Rex-Family Repressor/NADH Complex Insights into the Mechanism of Redox Sensing. Structure, 2005, 13, 43-54.	3.3	78
45	U2AF homology motifs: protein recognition in the RRM world. Genes and Development, 2004, 18, 1513-1526.	5.9	203
46	X-ray Structures of Threonine Aldolase Complexes:Â Structural Basis of Substrate Recognitionâ€,â€¡. Biochemistry, 2002, 41, 11711-11720.	2.5	48
47	A Novel Peptide Recognition Mode Revealed by the X-Ray Structure of a Core U2AF35/U2AF65 Heterodimer. Cell, 2001, 106, 595-605.	28.9	192
48	Structure of a photoactive rhodium complex intercalated into DNA. Nature Structural Biology, 2000, 7, 117-121.	9.7	106
49	Structural effects of DNA sequence on TÂ·A recognition by hydroxypyrrole/pyrrole pairs in the minor groove 1 1Edited by I. Tinoco. Journal of Molecular Biology, 2000, 295, 557-567.	4.2	69
50	Conformational flexibility of B-DNA at 0.74 Ã¥ resolution: d(CCAGTACTGG)2. Journal of Molecular Biology, 2000, 296, 787-801.	4.2	106
51	Structural basis for Gâ€¢C recognition in the DNA minor groove. Nature Structural Biology, 1998, 5, 104-109.	9.7	226