

Oliver Weichenrieder

List of Publications by Year in descending order

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117625

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docs citations

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4903
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellular Traffic Jam and Disease Due to Mutations in SRP54. <i>Structure</i> , 2021, 29, 3-5.	3.3	2
2	Crystal structure and functional properties of the human CCR4-CAF1 deadenylase complex. <i>Nucleic Acids Research</i> , 2021, 49, 6489-6510.	14.5	16
3	A conserved CAF40-binding motif in metazoan NOT4 mediates association with the CCR4-NOT complex. <i>Genes and Development</i> , 2019, 33, 236-252.	5.9	30
4	<i>Drosophila</i> Bag-of-marbles directly interacts with the CAF40 subunit of the CCR4-NOT complex to elicit repression of mRNA targets. <i>Rna</i> , 2018, 24, 381-395.	3.5	35
5	Structural and biochemical analysis of a NOT1 MIF4G-like domain of the CCR4-NOT complex. <i>Journal of Structural Biology</i> , 2018, 204, 388-395.	2.8	14
6	Human LINE-1 retrotransposition requires a metastable coiled coil and a positively charged N-terminus in L1ORF1p. <i>ELife</i> , 2018, 7, .	6.0	31
7	A CAF40-binding motif facilitates recruitment of the CCR4-NOT complex to mRNAs targeted by <i>Drosophila</i> Roquin. <i>Nature Communications</i> , 2017, 8, 14307.	12.8	71
8	Mille viae in eukaryotic mRNA decapping. <i>Current Opinion in Structural Biology</i> , 2017, 47, 40-51.	5.7	24
9	Mobilization of LINE-1 retrotransposons is restricted by Tex19.1 in mouse embryonic stem cells. <i>ELife</i> , 2017, 6, .	6.0	43
10	Structure of the Dcp2-Dcp1 mRNA-decapping complex in the activated conformation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 574-579.	8.2	45
11	The Structures of eIF4E-eIF4G Complexes Reveal an Extended Interface to Regulate Translation Initiation. <i>Molecular Cell</i> , 2016, 64, 467-479.	9.7	91
12	Distinct modes of recruitment of the CCR4-NOT complex by <i>Drosophila</i> and vertebrate Nanos. <i>EMBO Journal</i> , 2016, 35, 974-990.	7.8	56
13	Retrotransposition and Crystal Structure of an Alu RNP in the Ribosome-Stalling Conformation. <i>Molecular Cell</i> , 2015, 60, 715-727.	9.7	54
14	Molecular Architecture of 4E-BP Translational Inhibitors Bound to eIF4E. <i>Molecular Cell</i> , 2015, 57, 1074-1087.	9.7	130
15	Mextli proteins use both canonical bipartite and novel tripartite binding modes to form eIF4E complexes that display differential sensitivity to 4E-BP regulation. <i>Genes and Development</i> , 2015, 29, 1835-1849.	5.9	19
16	Fast native-SAD phasing for routine macromolecular structure determination. <i>Nature Methods</i> , 2015, 12, 131-133.	19.0	120
17	RNA binding by Hfq and ring-forming (L)Sm proteins. <i>RNA Biology</i> , 2014, 11, 537-549.	3.1	39
18	Structural basis for the Nanos-mediated recruitment of the CCR4-NOT complex and translational repression. <i>Genes and Development</i> , 2014, 28, 888-901.	5.9	93

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19	A DDX6-CNOT1 Complex and W-Binding Pockets in CNOT9 Reveal Direct Links between miRNA Target Recognition and Silencing. <i>Molecular Cell</i> , 2014, 54, 737-750.	9.7	242
20	An asymmetric PAN3 dimer recruits a single PAN2 exonuclease to mediate mRNA deadenylation and decay. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 599-608.	8.2	40
21	Structure of the PAN3 Pseudokinase Reveals the Basis for Interactions with the PAN2 Deadenylase and the GW182 Proteins. <i>Molecular Cell</i> , 2013, 51, 360-373.	9.7	93
22	Structure and assembly of the NOT module of the human CCR4â€“NOT complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1289-1297.	8.2	101
23	An unusual arrangement of two 14-3-3-like domains in the SMG5â€“SMG7 heterodimer is required for efficient nonsense-mediated mRNA decay. <i>Genes and Development</i> , 2013, 27, 211-225.	5.9	76
24	Structure and properties of the esterase from non-LTR retrotransposons suggest a role for lipids in retrotransposition. <i>Nucleic Acids Research</i> , 2013, 41, 10563-10572.	14.5	10
25	The structural basis for the interaction between the CAF1 nuclease and the NOT1 scaffold of the human CCR4â€“NOT deadenylase complex. <i>Nucleic Acids Research</i> , 2012, 40, 11058-11072.	14.5	110
26	Small RNA binding to the lateral surface of Hfq hexamers and structural rearrangements upon mRNA target recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9396-9401.	7.1	148
27	A direct interaction between DCP1 and XRN1 couples mRNA decapping to 5â€“2 exonucleolytic degradation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1324-1331.	8.2	144
28	Trimeric structure and flexibility of the L1ORF1 protein in human L1 retrotransposition. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1006-1014.	8.2	130
29	Crystal structure of the MID-PIWI lobe of a eukaryotic Argonaute protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10466-10471.	7.1	113
30	Structural basis for RNA 3â€“2-end recognition by Hfq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13065-13070.	7.1	185
31	The C-terminal Î±â€“Î± superhelix of Pat is required for mRNA decapping in metazoa. <i>EMBO Journal</i> , 2010, 29, 2368-2380.	7.8	50
32	Crystal structure and ligand binding of the MID domain of a eukaryotic Argonaute protein. <i>EMBO Reports</i> , 2010, 11, 522-527.	4.5	106
33	Non-LTR retrotransposons encode noncanonical RRM domains in their first open reading frame. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 731-736.	7.1	132
34	DCP1 forms asymmetric trimers to assemble into active mRNA decapping complexes in metazoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21591-21596.	7.1	60
35	Structural Basis for the Mutually Exclusive Anchoring of P Body Components EDC3 and Tral to the DEAD Box Protein DDX6/Me31B. <i>Molecular Cell</i> , 2009, 33, 661-668.	9.7	108
36	Active <i>Alu</i> retrotransposons in the human genome. <i>Genome Research</i> , 2008, 18, 1875-1883.	5.5	230

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37	Similar Modes of Interaction Enable Trailer Hitch and EDC3 To Associate with DCP1 and Me31B in Distinct Protein Complexes. <i>Molecular and Cellular Biology</i> , 2008, 28, 6695-6708.	2.3	72
38	Determinants for DNA target structure selectivity of the human LINE-1 retrotransposon endonuclease. <i>Nucleic Acids Research</i> , 2007, 35, 4914-4926.	14.5	35
39	A Divergent Sm Fold in EDC3 Proteins Mediates DCP1 Binding and P-Body Targeting. <i>Molecular and Cellular Biology</i> , 2007, 27, 8600-8611.	2.3	66
40	Structure and E3-ligase activity of the Ring complex of Polycomb proteins Bmi1 and Ring1b. <i>EMBO Journal</i> , 2006, 25, 2465-2474.	7.8	380
41	Thermodynamic characterization of an engineered tetracycline-binding riboswitch. <i>Nucleic Acids Research</i> , 2006, 34, 2607-2617.	14.5	139
42	Conserved tertiary base pairing ensures proper RNA folding and efficient assembly of the signal recognition particle Alu domain. <i>Nucleic Acids Research</i> , 2004, 32, 4915-4924.	14.5	22
43	Crystal Structure of the Targeting Endonuclease of the Human LINE-1 Retrotransposon. <i>Structure</i> , 2004, 12, 975-986.	3.3	74
44	Towards the structure of the mammalian signal recognition particle. <i>Current Opinion in Structural Biology</i> , 2002, 12, 72-81.	5.7	40
45	Hierarchical assembly of the Alu domain of the mammalian signal recognition particle. <i>Rna</i> , 2001, 7, 731-740.	3.5	31
46	Structure and assembly of the Alu domain of the mammalian signal recognition particle. <i>Nature</i> , 2000, 408, 167-173.	27.8	182