

Oliver Weichenrieder

List of Publications by Year in descending order

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46
papers

4,033
citations

117625

34
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223800

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all docs

79
docs citations

79
times ranked

4903
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and E3-ligase activity of the Ring complex of Polycomb proteins Bmi1 and Ring1b. EMBO Journal, 2006, 25, 2465-2474.	7.8	380
2	A DDX6-CNOT1 Complex and W-Binding Pockets in CNOT9 Reveal Direct Links between miRNA Target Recognition and Silencing. Molecular Cell, 2014, 54, 737-750.	9.7	242
3	Active <i>Alu</i> retrotransposons in the human genome. Genome Research, 2008, 18, 1875-1883.	5.5	230
4	Structural basis for RNA 3'-end recognition by Hfq. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13065-13070.	7.1	185
5	Structure and assembly of the Alu domain of the mammalian signal recognition particle. Nature, 2000, 408, 167-173.	27.8	182
6	Small RNA binding to the lateral surface of Hfq hexamers and structural rearrangements upon mRNA target recognition. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9396-9401.	7.1	148
7	A direct interaction between DCP1 and XRN1 couples mRNA decapping to 5' exonucleolytic degradation. Nature Structural and Molecular Biology, 2012, 19, 1324-1331.	8.2	144
8	Thermodynamic characterization of an engineered tetracycline-binding riboswitch. Nucleic Acids Research, 2006, 34, 2607-2617.	14.5	139
9	Non-LTR retrotransposons encode noncanonical RRM domains in their first open reading frame. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 731-736.	7.1	132
10	Trimeric structure and flexibility of the L1ORF1 protein in human L1 retrotransposition. Nature Structural and Molecular Biology, 2011, 18, 1006-1014.	8.2	130
11	Molecular Architecture of 4E-BP Translational Inhibitors Bound to eIF4E. Molecular Cell, 2015, 57, 1074-1087.	9.7	130
12	Fast native-SAD phasing for routine macromolecular structure determination. Nature Methods, 2015, 12, 131-133.	19.0	120
13	Crystal structure of the MID-PIWI lobe of a eukaryotic Argonaute protein. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10466-10471.	7.1	113
14	The structural basis for the interaction between the CAF1 nuclease and the NOT1 scaffold of the human CCR4-NOT deadenylase complex. Nucleic Acids Research, 2012, 40, 11058-11072.	14.5	110
15	Structural Basis for the Mutually Exclusive Anchoring of P Body Components EDC3 and Tral to the DEAD Box Protein DDX6/Me31B. Molecular Cell, 2009, 33, 661-668.	9.7	108
16	Crystal structure and ligand binding of the MID domain of a eukaryotic Argonaute protein. EMBO Reports, 2010, 11, 522-527.	4.5	106
17	Structure and assembly of the NOT module of the human CCR4-NOT complex. Nature Structural and Molecular Biology, 2013, 20, 1289-1297.	8.2	101
18	Structure of the PAN3 Pseudokinase Reveals the Basis for Interactions with the PAN2 Deadenylase and the GW182 Proteins. Molecular Cell, 2013, 51, 360-373.	9.7	93

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19	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
20	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
21	An unusual arrangement of two 14-3-3-like domains in the SMG5-SMG7 heterodimer is required for efficient nonsense-mediated mRNA decay. <i>Genes and Development</i> , 2013, 27, 211-225.	5.9	76
22	Crystal Structure of the Targeting Endonuclease of the Human LINE-1 Retrotransposon. <i>Structure</i> , 2004, 12, 975-986.	3.3	74
23	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
24	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
25	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
26	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
27	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
28	Retrotransposition and Crystal Structure of an Alu RNP in the Ribosome-Stalling Conformation. <i>Molecular Cell</i> , 2015, 60, 715-727.	9.7	54
29	The C-terminal α superhelix of Pat is required for mRNA decapping in metazoa. <i>EMBO Journal</i> , 2010, 29, 2368-2380.	7.8	50
30	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
31	Mobilization of LINE-1 retrotransposons is restricted by Tex19.1 in mouse embryonic stem cells. <i>ELife</i> , 2017, 6, .	6.0	43
32	Towards the structure of the mammalian signal recognition particle. <i>Current Opinion in Structural Biology</i> , 2002, 12, 72-81.	5.7	40
33	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
34	RNA binding by Hfq and ring-forming (L)Sm proteins. <i>RNA Biology</i> , 2014, 11, 537-549.	3.1	39
35	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
36	<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

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37	Hierarchical assembly of the Alu domain of the mammalian signal recognition particle. <i>Rna</i> , 2001, 7, 731-740.	3.5	31
38	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
39	A conserved CAF40-binding motif in metazoan NOT4 mediates association with the CCR4â€“NOT complex. <i>Genes and Development</i> , 2019, 33, 236-252.	5.9	30
40	Mille viae in eukaryotic mRNA decapping. <i>Current Opinion in Structural Biology</i> , 2017, 47, 40-51.	5.7	24
41	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
42	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
43	Crystal structure and functional properties of the human CCR4-CAF1 deadenylase complex. <i>Nucleic Acids Research</i> , 2021, 49, 6489-6510.	14.5	16
44	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
45	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
46	Cellular Traffic Jam and Disease Due to Mutations in SRP54. <i>Structure</i> , 2021, 29, 3-5.	3.3	2