

# Bertrand SÃ©raphin

## List of Publications by Year in descending order

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61  
papers

10,499  
citations

87888

38  
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123424

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62  
docs citations

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times ranked

9757  
citing authors

#	ARTICLE	IF	CITATIONS
1	A generic protein purification method for protein complex characterization and proteome exploration. <i>Nature Biotechnology</i> , 1999, 17, 1030-1032.	17.5	2,543
2	The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification. <i>Methods</i> , 2001, 24, 218-229.	3.8	1,550
3	Cryptic Pol II Transcripts Are Degraded by a Nuclear Quality Control Pathway Involving a New Poly(A) Polymerase. <i>Cell</i> , 2005, 121, 725-737.	28.9	764
4	Cytoplasmic foci are sites of mRNA decay in human cells. <i>Journal of Cell Biology</i> , 2004, 165, 31-40.	5.2	553
5	Human Dcp2: a catalytically active mRNA decapping enzyme located in specific cytoplasmic structures. <i>EMBO Journal</i> , 2002, 21, 6915-6924.	7.8	398
6	Identification of functional U1 snRNA-pre-mRNA complexes committed to spliceosome assembly and splicing. <i>Cell</i> , 1989, 59, 349-358.	28.9	396
7	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 15-22.	8.2	381
8	REF, an evolutionarily conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export. <i>Rna</i> , 2000, 6, 638-650.	3.5	331
9	Endonucleolytic RNA cleavage by a eukaryotic exosome. <i>Nature</i> , 2008, 456, 993-996.	27.8	284
10	The Apoptosis-Promoting Factor TIA-1 Is a Regulator of Alternative Pre-mRNA Splicing. <i>Molecular Cell</i> , 2000, 6, 1089-1098.	9.7	252
11	Extensive Degradation of RNA Precursors by the Exosome in Wild-Type Cells. <i>Molecular Cell</i> , 2012, 48, 409-421.	9.7	218
12	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006, 7, 605-610.	4.5	168
13	Proteomic analysis identifies a new complex required for nuclear pre-mRNA retention and splicing. <i>EMBO Journal</i> , 2004, 23, 4847-4856.	7.8	139
14	Architecture of the Nuclease Module of the Yeast Ccr4-Not Complex: the Not1-Caf1-Ccr4 Interaction. <i>Molecular Cell</i> , 2012, 48, 207-218.	9.7	131
15	RNA channelling by the archaeal exosome. <i>EMBO Reports</i> , 2007, 8, 470-476.	4.5	108
16	X-ray structure and activity of the yeast Pop2 protein: a nuclease subunit of the mRNA deadenylase complex. <i>EMBO Reports</i> , 2003, 4, 1150-1155.	4.5	104
17	The BTG2 protein is a general activator of mRNA deadenylation. <i>EMBO Journal</i> , 2008, 27, 1039-1048.	7.8	100
18	Surveillance pathways rescuing eukaryotic ribosomes lost in translation. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 727-735.	37.0	99

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19	Small nuclear RNAs in messenger RNA and ribosomal RNA processing.. FASEB Journal, 1993, 7, 47-53.	0.5	98
20	â€ˆCap-tabolismâ€™™. Trends in Biochemical Sciences, 2004, 29, 436-444.	7.5	97
21	New constructs and strategies for efficient PCR-based gene manipulations in yeast. Yeast, 1998, 14, 1139-1146.	1.7	86
22	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. Nature Structural and Molecular Biology, 2012, 19, 314-320.	8.2	85
23	Conservation of the deadenylase activity of proteins of the Caf1 family in human. Rna, 2005, 11, 487-494.	3.5	84
24	The HIT protein family: a new family of proteins present in prokaryotes, yeast and mammals. DNA Sequence, 1992, 3, 177-179.	0.7	82
25	Transient interaction of BBP/ScSF1 and Mud2 with the splicing machinery affects the kinetics of spliceosome assembly. Rna, 1999, 5, 819-831.	3.5	79
26	DcpS can act in the 5'-3' mRNA decay pathway in addition to the 3'-5' pathway. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12081-12086.	7.1	75
27	Architecture of the yeast Elongator complex. EMBO Reports, 2017, 18, 264-279.	4.5	75
28	Dom34-Hbs1 mediated dissociation of inactive 80S ribosomes promotes restart of translation after stress. EMBO Journal, 2014, 33, n/a-n/a.	7.8	74
29	Structure of the yeast Pml1 splicing factor and its integration into the RES complex. Nucleic Acids Research, 2009, 37, 129-143.	14.5	69
30	BTG2 bridges PABPC1 RNA-binding domains and CAF1 deadenylase to control cell proliferation. Nature Communications, 2016, 7, 10811.	12.8	69
31	Exosome-mediated quality control: Substrate recruitment and molecular activity. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2008, 1779, 558-565.	1.9	67
32	C2ORF29/CNOT11 and CNOT10 form a new module of the CCR4-NOT complex. RNA Biology, 2013, 10, 267-276.	3.1	66
33	Genomic-scale quantitative analysis of yeast pre-mRNA splicing: Implications for splice-site recognition. Rna, 1999, 5, 1135-1137.	3.5	62
34	Dissection of Dom34â€™Hbs1 reveals independent functions in two RNA quality control pathways. Nature Structural and Molecular Biology, 2010, 17, 1446-1452.	8.2	60
35	Structural basis for tRNA modification by Elp3 from Dehalococcoides mccartyi. Nature Structural and Molecular Biology, 2016, 23, 794-802.	8.2	59
36	Intracellular ribonucleases involved in transcript processing and decay: Precision tools for RNA. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 491-513.	1.9	52

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37	The yeast U2Aâ€™/U2Bâ€™ complex is required for pre-spliceosome formation. <i>EMBO Journal</i> , 1998, 17, 6348-6358.	7.8	49
38	Structure of the active form of Dcp1â€™Dcp2 decapping enzyme bound to m7GDP and its Edc3 activator. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 982-986.	8.2	48
39	A unique surface on Pat1 C-terminal domain directly interacts with Dcp2 decapping enzyme and Xrn1 5â€™â€™3â€™ mRNA exonuclease in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9493-E9501.	7.1	45
40	The U1 snRNP-associated factor Luc7p affects 5' splice site selection in yeast and human. <i>Nucleic Acids Research</i> , 2007, 35, 5874-5885.	14.5	44
41	Elimination of cap structures generated by mRNA decay involves the new scavenger mRNA decapping enzyme Aph1/FHIT together with DcpS. <i>Nucleic Acids Research</i> , 2015, 43, 482-492.	14.5	43
42	Acetylation-Dependent Control of Global Poly(A) RNA Degradation by CBP/p300 and HDAC1/2. <i>Molecular Cell</i> , 2016, 63, 927-938.	9.7	35
43	In Vivo Targeting of the Yeast Pop2 Deadenylase Subunit to Reporter Transcripts Induces Their Rapid Degradation and Generates New Decay Intermediates. <i>Journal of Biological Chemistry</i> , 2006, 281, 25940-25947.	3.4	31
44	Loss of the scavenger mRNA decapping enzyme DCPS causes syndromic intellectual disability with neuromuscular defects. <i>Human Molecular Genetics</i> , 2015, 24, 3163-3171.	2.9	31
45	Cotranscriptional spliceosome assembly and splicing are independent of the Prp40p WW domain. <i>Rna</i> , 2011, 17, 2119-2129.	3.5	28
46	The highly conserved eukaryotic DRG factors are required for efficient translation in a manner redundant with the putative RNA helicase Slh1. <i>Nucleic Acids Research</i> , 2011, 39, 2221-2233.	14.5	28
47	Elongator. <i>Transcription</i> , 2012, 3, 273-276.	3.1	28
48	Catalytic Properties of the Eukaryotic Exosome. <i>Advances in Experimental Medicine and Biology</i> , 2010, 702, 63-78.	1.6	28
49	Gbp2 interacts with THO/TREX through a novel type of RRM domain. <i>Nucleic Acids Research</i> , 2016, 44, 437-448.	14.5	26
50	A role for U2/U6 helix Ib in 5â€™ splice site selection. <i>Rna</i> , 1998, 4, 915-927.	3.5	25
51	Rbg1â€™Tma46 dimer structure reveals new functional domains and their role in polysome recruitment. <i>Nucleic Acids Research</i> , 2012, 40, 11100-11114.	14.5	23
52	Structure of the Elongator cofactor complex Kti11/Kti13 provides insight into the role of Kti13 in Elongatorâ€™dependent <sc>tRNA</sc> modification. <i>FEBS Journal</i> , 2015, 282, 819-833.	4.7	20
53	Identification of the Rps28 binding motif from yeast Edc3 involved in the autoregulatory feedback loop controlling RPS28B mRNA decay. <i>Nucleic Acids Research</i> , 2013, 41, 9514-9523.	14.5	19
54	A Novel Protein-Protein Interaction in the RES (REtention and Splicing) Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 28640-28650.	3.4	19

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55	Mammalian Hbs1L deficiency causes congenital anomalies and developmental delay associated with Pelota depletion and 80S monosome accumulation. <i>PLoS Genetics</i> , 2019, 15, e1007917.	3.5	15
56	Structures and Activities of the Elongator Complex and Its Cofactors. <i>The Enzymes</i> , 2017, 41, 117-149.	1.7	14
57	The C-Terminal Domain from <i>S. cerevisiae</i> Pat1 Displays Two Conserved Regions Involved in Decapping Factor Recruitment. <i>PLoS ONE</i> , 2014, 9, e96828.	2.5	14
58	A conserved motif in human BTG1 and BTG2 proteins mediates interaction with the poly(A) binding protein PABPC1 to stimulate mRNA deadenylation. <i>RNA Biology</i> , 2021, 18, 2450-2465.	3.1	10
59	Rapid screening of yeast mutants with reporters identifies new splicing phenotypes. <i>FEBS Journal</i> , 2013, 280, 2712-2726.	4.7	6
60	Pby1 is a direct partner of the Dcp2 decapping enzyme. <i>Nucleic Acids Research</i> , 2020, 48, 6353-6366.	14.5	4
61	Twins take the job. <i>EMBO Journal</i> , 2010, 29, 2260-2261.	7.8	2