SÃ©bastien Fribourg

List of Publications by Year
in descending order

48 papers	3,199 citations	201674 27 h-index	197818 49 g-index
52 all docs	52 docs citations	52 times ranked	4062 citing authors

#	Article	IF	Citations
1	Crystal structure of SFPQ-NONO heterodimer. Biochimie, 2022, 198, 1-7.	2.6	5
2	De novo variants in POLR3B cause ataxia, spasticity, and demyelinating neuropathy. American Journal of Human Genetics, 2021, 108, 186-193.	6.2	19
3	In vitro dimerization of human RIO2 kinase. RNA Biology, 2019, 16, 1633-1642.	3.1	7
4	The hRPC62 subunit of human RNA polymerase III displays helicase activity. Nucleic Acids Research, 2019, 47, 10313-10326.	14.5	9
5	Structural insights into the 3â€²-end mRNA maturation machinery: Snapshot on polyadenylation signal recognition. Biochimie, 2019, 164, 105-110.	2.6	17
6	Clinical spectrum of POLR3-related leukodystrophy caused by biallelic POLR1C pathogenic variants. Neurology: Genetics, 2019, 5, e369.	1.9	38
7	The Npa1p complex chaperones the assembly of the earliest eukaryotic large ribosomal subunit precursor. PLoS Genetics, 2018, 14, e1007597.	3.5	23
8	Structural and interaction analysis of the Rrp5 Câ€terminal region. FEBS Open Bio, 2018, 8, 1605-1614.	2.3	1
9	Domain definition and interaction mapping for the endonuclease complex hNob1/hPno1. RNA Biology, 2018, 15, 1174-1180.	3.1	8
10	Varicella-zoster virus CNS vasculitis and RNA polymerase III gene mutation in identical twins. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e500.	6.0	49
11	Pwp2 mediates UTP-B assembly via two structurally independent domains. Scientific Reports, 2017, 7, 3169.	3.3	9
12	Structural characterization of the yeast CF IA complex through a combination of mass spectrometry approaches. International Journal of Mass Spectrometry, 2017, 420, 57-66.	1.5	5
13	Distinct roles of Pcf11 zinc-binding domains in pre-mRNA 3â€²-end processing. Nucleic Acids Research, 2017, 45, 10115-10131.	14.5	11
14	Inborn errors in RNA polymerase III underlie severe varicella zoster virus infections. Journal of Clinical Investigation, 2017, 127, 3543-3556.	8.2	125
15	Sqt1p is an eight-bladed WD40 protein. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 59-64.	0.8	2
16	Structural analysis of human RPC32Î²â€“RPC62 complex. Journal of Structural Biology, 2015, 192, 313-319.	2.8	11
17	Chemical shift assignments of a new folded domain from yeast Pcf11. Biomolecular NMR Assignments, 2015, 9, 421-425.	0.8	4
18	Recessive mutations in POLR1C cause a leukodystrophy by impairing biogenesis of RNA polymerase III. Nature Communications, 2015, 6, 7623.	12.8	127

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19	Crucial role of the Rcl1pâ€“Bms1p interaction for yeast pre-ribosomal RNA processing. Nucleic Acids Research, 2014, 42, 10161-10172.	14.5	26
20	Structural basis for ATP loss by Clp1p in a G135R mutant protein. Biochimie, 2014, 101, 203-207.	2.6	5
21	Clinical spectrum of 4H leukodystrophy caused by POLR3A and POLR3B mutations. Neurology, 2014, 83, 1898-1905.	1.1	170
22	An essential role for Clp1 in assembly of polyadenylation complex CF IA and Pol II transcription termination. Nucleic Acids Research, 2012, 40, 1226-1239.	14.5	31
23	Structural and functional aspects of winged-helix domains at the core of transcription initiation complexes. Transcription, 2012, 3, 2-7.	3.1	42
24	Mutations of POLR3A Encoding a Catalytic Subunit of RNA Polymerase Pol III Cause a Recessive Hypomyelinating Leukodystrophy p415. American Journal of Human Genetics, 2012, 91, 972.	6.2	1
25	Deciphering correct strategies for multiprotein complex assembly by co-expression: Application to complexes as large as the histone octamer. Journal of Structural Biology, 2011, 175, 178-188.	2.8	116
26	Hexameric architecture of CstF supported by CstF-50 homodimerization domain structure. Rna, 2011, 17, 412-418.	3.5	17
27	Structure-function analysis of hRPC62 provides insights into RNA polymerase III transcription initiation. Nature Structural and Molecular Biology, 2011, 18, 352-358.	8.2	43
28	Locked Tether Formation by Cooperative Folding of Rna14p Monkeytail and Rna15p Hinge Domains in the Yeast CF IA Complex. Structure, 2011, 19, 534-545.	3.3	29
29	Mutations of POLR3A Encoding a Catalytic Subunit of RNA Polymerase Pol III Cause a Recessive Hypomyelinating Leukodystrophy. American Journal of Human Genetics, 2011, 89, 415-423.	6.2	219
30	Recessive Mutations in POLR3B, Encoding the Second Largest Subunit of Pol III, Cause a Rare Hypomyelinating Leukodystrophy. American Journal of Human Genetics, 2011, 89, 652-655.	6.2	139
31	Peptides derived from the bifunctional kinase/RNase enzyme IRE1Î± modulate IRE1Î± activity and protect cells from endoplasmic reticulum stress. FASEB Journal, 2011, 25, 3115-3129.	0.5	71
32	RPS19 mutations in patients with Diamond-Blackfan anemia. Human Mutation, 2008, 29, 911-920.	2.5	94
33	Exploring TARâ€“RNA aptamer loopâ€“loop interaction by X-ray crystallography, UV spectroscopy and surface plasmon resonance. Nucleic Acids Research, 2008, 36, 7146-7156.	14.5	54
34	Mutation of ribosomal protein RPS24 in Diamond-Blackfan anemia results in a ribosome biogenesis disorder. Human Molecular Genetics, 2008, 17, 1253-1263.	2.9	100
35	Molecular basis of Diamond Blackfan anemia: structure and function analysis of RPS19. Nucleic Acids Research, 2007, 35, 5913-5921.	14.5	56
36	Impaired ribosome biogenesis in Diamond-Blackfan anemia. Blood, 2007, 109, 1275-1283.	1.4	202

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37	The structure of the CstF-77 homodimer provides insights into CstF assembly. Nucleic Acids Research, 2007, 35, 4515-4522.	14.5	42
38	The archaeal exosome core is a hexameric ring structure with three catalytic subunits. Nature Structural and Molecular Biology, 2005, 12, 575-581.	8.2	198
39	Solution Structure of the C-terminal Domain of TFIIH P44 Subunit Reveals a Novel Type of C4C4 Ring Domain Involved in Protein-Protein Interactions. Journal of Biological Chemistry, 2005, 280, 20785-20792.	3.4	28
40	A novel mode of RBD-protein recognition in the Y14â€“Mago complex. Nature Structural and Molecular Biology, 2003, 10, 433-439.	8.2	150
41	Structural similarity in the absence of sequence homology of the messenger RNA export factors Mtr2 and p15. EMBO Reports, 2003, 4, 699-703.	4.5	48
42	Expression of FLAG Fusion Proteins in Insect Cells: Application to the Multi-subunit Transcription/DNA Repair Factor TFIIH. Protein Expression and Purification, 2002, 24, 513-523.	1.3	15
43	Dissecting the interaction network of multiprotein complexes by pairwise coexpression of subunits in E. coli11Edited by K. Nagai. Journal of Molecular Biology, 2001, 306, 363-373.	4.2	64
44	Structural Basis for the Recognition of a Nucleoporin FG Repeat by the NTF2-like Domain of the TAP/p15 mRNA Nuclear Export Factor. Molecular Cell, 2001, 8, 645-656.	9.7	211
45	Structural Characterization of the Cysteine-rich Domain of TFIIH p44 Subunit. Journal of Biological Chemistry, 2000, 275, 31963-31971.	3.4	28
46	Molecular Structure of Human TFIIH. Cell, 2000, 102, 599-607.	28.9	175
47	Mutations in the XPD helicase gene result in XP and TTD phenotypes, preventing interaction between XPD and the p44 subunit of TFIIH. Nature Genetics, 1998, 20, 184-188.	21.4	320
48	Mutations in the amino-terminal domain of the human poly(ADP-ribose) polymerase that affect its catalytic activity but not its DNA binding capacity. FEBS Letters, 1996, 399, 313-316.	2.8	25