Samuel E Butcher

List of Publications by Year in descending order

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67 papers 3,085 citations

147801 31 h-index 53 g-index

70 all docs

70 docs citations

times ranked

70

2885 citing authors

#	Article	IF	CITATIONS
1	Perturbing HIV-1 Ribosomal Frameshifting Frequency Reveals a <i>cis</i> Preference for Gag-Pol Incorporation into Assembling Virions. Journal of Virology, 2022, 96, JVI0134921.	3.4	5
2	Structural basis for the evolution of cyclic phosphodiesterase activity in the U6 snRNA exoribonuclease Usb1. Nucleic Acids Research, 2020, 48, 1423-1434.	14.5	1
3	Expanded DNA and RNA Trinucleotide Repeats in Myotonic Dystrophy Type 1 Select Their Own Multitarget, Sequence-Selective Inhibitors. Biochemistry, 2020, 59, 3463-3472.	2.5	8
4	Molecular basis for the distinct cellular functions of the Lsm1–7 and Lsm2–8 complexes. Rna, 2020, 26, 1400-1413.	3.5	22
5	Conformational flexibility in the enterovirus RNA replication platform. Rna, 2019, 25, 376-387.	3.5	9
6	Structure of an RNA helix with pyrimidine mismatches and cross-strand stacking. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 652-656.	0.8	4
7	RNA binding properties of the Lsm1–7 ring from Schizosaccharomyces pombe. FASEB Journal, 2019, 33, 460.12.	0.5	O
8	The life of U6 small nuclear RNA, from cradle to grave. Rna, 2018, 24, 437-460.	3. 5	92
9	Architecture of the U6 snRNP reveals specific recognition of 3′-end processed U6 snRNA. Nature Communications, 2018, 9, 1749.	12.8	17
10	Structural and mechanistic basis for preferential deadenylation of U6 snRNA by Usb1. Nucleic Acids Research, 2018, 46, 11488-11501.	14.5	16
11	Pathogenic TFG Mutations Underlying Hereditary Spastic Paraplegia Impair Secretory Protein Trafficking and Axon Fasciculation. Cell Reports, 2018, 24, 2248-2260.	6.4	24
12	Usb1 controls U6 snRNP assembly through evolutionarily divergent cyclic phosphodiesterase activities. Nature Communications, 2017, 8, 497.	12.8	20
13	Structure and conformational plasticity of the U6 small nuclear ribonucleoprotein core. Acta Crystallographica Section D: Structural Biology, 2017, 73, 1-8.	2.3	5
14	A multi-step model for facilitated unwinding of the yeast U4/U6 RNA duplex. Nucleic Acids Research, 2016, 44, 10912-10928.	14.5	14
15	Integrative NMR for biomolecular research. Journal of Biomolecular NMR, 2016, 64, 307-332.	2.8	47
16	tRNA-mimicry in IRES-mediated translation and recoding. RNA Biology, 2016, 13, 1068-1074.	3.1	16
17	Measuring the Kinetics of Molecular Association by Isothermal Titration Calorimetry. Methods in Enzymology, 2016, 567, 181-213.	1.0	10
18	Stability of HIV Frameshift Site RNA Correlates with Frameshift Efficiency and Decreased Virus Infectivity. Journal of Virology, 2016, 90, 6906-6917.	3.4	33

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19	Structural Analysis of Multi-Helical RNAs by NMR–SAXS/WAXS: Application to the U4/U6 di-snRNA. Journal of Molecular Biology, 2016, 428, 777-789.	4.2	45
20	Structural requirements for protein-catalyzed annealing of U4 and U6 RNAs during di-snRNP assembly. Nucleic Acids Research, 2016, 44, 1398-1410.	14.5	22
21	$\langle i \rangle N \langle i \rangle$ -Methylation as a Strategy for Enhancing the Affinity and Selectivity of RNA-binding Peptides: Application to the HIV-1 Frameshift-Stimulating RNA. ACS Chemical Biology, 2016, 11, 88-94.	3.4	37
22	Dynamic Motions of the HIV-1 Frameshift Site RNA. Biophysical Journal, 2015, 108, 644-654.	0.5	4
23	Spliceosome assembly in the absence of stable U4/U6 RNA pairing. Rna, 2015, 21, 923-934.	3.5	9
24	Structural mechanisms of DNA binding and unwinding in bacterial RecQ helicases. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4292-4297.	7.1	58
25	8 The Spliceosome and Its Metal Ions. , 2015, , 235-252.		0
26	Global shape mimicry of tRNA within a viral internal ribosome entry site mediates translational reading frame selection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6446-55.	7.1	24
27	Core structure of the U6 small nuclear ribonucleoprotein at 1.7-Ã resolution. Nature Structural and Molecular Biology, 2014, 21, 544-551.	8.2	65
28	Structure and Dynamics of the HIV-1 Frameshift Element RNA. Biochemistry, 2014, 53, 4282-4291.	2.5	31
29	HIV-1 frameshift efficiency is primarily determined by the stability of base pairs positioned at the mRNA entrance channel of the ribosome. Nucleic Acids Research, 2013, 41, 1901-1913.	14.5	64
30	Characterization of the kinetic and thermodynamic landscape of RNA folding using a novel application of isothermal titration calorimetry. Nucleic Acids Research, 2012, 40, 2140-2151.	14.5	47
31	Structure of the yeast U2/U6 snRNA complex. Rna, 2012, 18, 673-683.	3.5	78
32	Targeting frameshifting in the human immunodeficiency virus. Expert Opinion on Therapeutic Targets, 2012, 16, 249-258.	3.4	49
33	Nucleic Acid Structure Characterization by Small Angle Xâ€Ray Scattering (SAXS). Current Protocols in Nucleic Acid Chemistry, 2012, 51, Unit7.18.	0.5	24
34	RNA-PAIRS: RNA probabilistic assignment of imino resonance shifts. Journal of Biomolecular NMR, 2012, 52, 289-302.	2.8	15
35	Investigating RNAs Involved in Translational Control by NMR and SAXS. , 2012, , 141-172.		0
36	Structure of the HIV-1 Frameshift Site RNA Bound to a Small Molecule Inhibitor of Viral Replication. ACS Chemical Biology, 2011, 6, 857-864.	3.4	55

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37	The Molecular Interactions That Stabilize RNA Tertiary Structure: RNA Motifs, Patterns, and Networks. Accounts of Chemical Research, 2011, 44, 1302-1311.	15.6	276
38	A novel occluded RNA recognition motif in Prp24 unwinds the U6 RNA internal stem loop. Nucleic Acids Research, 2011, 39, 7837-7847.	14.5	42
39	8. The Spliceosome and Its Metal Ions. Metal Ions in Life Sciences, 2011, 9, 235-251.	1.0	18
40	Structure and functional implications of a complex containing a segment of U6 RNA bound by a domain of Prp24. Rna, 2010, 16, 792-804.	3.5	22
41	Rapid global structure determination of large RNA and RNA complexes using NMR and small-angle X-ray scattering. Methods, 2010, 52, 180-191.	3.8	44
42	The spliceosome as ribozyme hypothesis takes a second step. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12211-12212.	7.1	20
43	1H, 13C and 15N resonance assignments of a ribonucleoprotein complex consisting of Prp24-RRM2 bound to a fragment of U6 RNA. Biomolecular NMR Assignments, 2009, 3, 227-230.	0.8	3
44	Selection and Characterization of Small Molecules That Bind the HIV-1 Frameshift Site RNA. ACS Chemical Biology, 2009, 4, 844-854.	3.4	35
45	Identification of the SSB Binding Site on E. coli RecQ Reveals a Conserved Surface for Binding SSB's C Terminus. Journal of Molecular Biology, 2009, 386, 612-625.	4.2	84
46	Minimum-Energy Path for a U6 RNA Conformational Change Involving Protonation, Base-Pair Rearrangement and Base Flipping. Journal of Molecular Biology, 2009, 391, 894-905.	4.2	31
47	Guanidinoneomycin B Recognition of an HIV‶ RNA Helix. ChemBioChem, 2008, 9, 93-102.	2.6	46
48	Thermodynamics and Folding Pathway of Tetraloop Receptor-Mediated RNA Helical Packing. Journal of Molecular Biology, 2008, 384, 702-717.	4.2	28
49	Global Molecular Structure and Interfaces:  Refining an RNA:RNA Complex Structure Using Solution X-ray Scattering Data. Journal of the American Chemical Society, 2008, 130, 3292-3293.	13.7	54
50	DNA mimicry by a high-affinity anti-NF-κB RNA aptamer. Nucleic Acids Research, 2008, 36, 1227-1236.	14.5	43
51	Measuring the dynamic surface accessibility of RNA with the small paramagnetic molecule TEMPOL. Nucleic Acids Research, 2008, 36, e20-e20.	14.5	25
52	A dynamic bulge in the U6 RNA internal stem–loop functions in spliceosome assembly and activation. Rna, 2007, 13, 2252-2265.	3.5	25
53	Structure and Interactions of the First Three RNA Recognition Motifs of Splicing Factor Prp24. Journal of Molecular Biology, 2007, 367, 1447-1458.	4.2	36
54	Resonance assignments for the two N-terminal RNA recognition motifs (RRM) of the S. cerevisiae Pre-mRNA Processing Protein Prp24. Journal of Biomolecular NMR, 2006, 36, 58-58.	2.8	5

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55	Solution Structure and Thermodynamic Investigation of the HIV-1 Frameshift Inducing Element. Journal of Molecular Biology, 2005, 349, 1011-1023.	4.2	92
56	RNA Helical Packing in Solution: NMR Structure of a 30kDa GAAA Tetraloop–Receptor Complex. Journal of Molecular Biology, 2005, 351, 371-382.	4.2	142
57	Dynamics and Metal Ion Binding in the U6 RNA Intramolecular Stem–Loop as Analyzed by NMR. Journal of Molecular Biology, 2005, 353, 540-555.	4.2	62
58	Pseudoknots: RNA Structures with Diverse Functions. PLoS Biology, 2005, 3, e213.	5 . 6	281
59	U2–U6 RNA folding reveals a group II intron-like domain and a four-helix junction. Nature Structural and Molecular Biology, 2004, 11, 1237-1242.	8.2	123
60	Dynamics in the U6 RNA Intramolecular Stemâ^'Loop: A Base Flipping Conformational Changeâ€,‡. Biochemistry, 2004, 43, 13739-13747.	2.5	64
61	Structural Basis for a Lethal Mutation in U6 RNAâ€,‡. Biochemistry, 2003, 42, 1470-1477.	2.5	30
62	Solution structure of the HIV-1 frameshift inducing stem-loop RNA. Nucleic Acids Research, 2003, 31, 4326-4331.	14.5	57
63	Structure of the U6 RNA intramolecular stem-loop harboring an SP-phosphorothioate modification. Rna, 2003, 9, 533-542.	3.5	31
64	Metal binding and base ionization in the U6 RNA intramolecular stem-loop structure. Nature Structural Biology, 2002, 9, 431-435.	9.7	135
65	Quantitative Analysis of the Isolated GAAA Tetraloop/Receptor Interaction in Solution: A Site-Directed Spin Labeling Studyâ€. Biochemistry, 2001, 40, 6929-6936.	2.5	125
66	Determination of Metal Ion Binding Sites within the Hairpin Ribozyme Domains by NMRâ€. Biochemistry, 2000, 39, 2174-2182.	2.5	74
67	Through-bond correlation of imino and aromatic resonances in 13C-,15N-labeled RNA via heteronuclear TOCSY. Journal of Biomolecular NMR, 1996, 7, 83-87.	2.8	59