

M Elizabeth Stroupe

List of Publications by Year in descending order

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32
papers

1,202
citations

430874

18
h-index

454955

30
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37
all docs

37
docs citations

37
times ranked

1607
citing authors

#	ARTICLE	IF	CITATIONS
1	Neutron scattering maps the higher-order assembly of NADPH-dependent assimilatory sulfite reductase. <i>Biophysical Journal</i> , 2022, 121, 1799-1812.	0.5	3
2	Small-angle neutron scattering solution structures of NADPH-dependent sulfite reductase. <i>Journal of Structural Biology</i> , 2021, 213, 107724.	2.8	10
3	An open interface in the pre-80S ribosome coordinated by ribosome assembly factors Tsr1 and Dim1 enables temporal regulation of Fap7. <i>Rna</i> , 2021, 27, 221-233.	3.5	20
4	10. The Siroheme-[4Fe-4S] Coupled Center. , 2020, 20, 343-380.		2
5	Siroheme synthase orients substrates for dehydrogenase and chelatase activities in a common active site. <i>Nature Communications</i> , 2020, 11, 864.	12.8	13
6	Bulged and Canonical G-Quadruplex Conformations Determine NDPK Binding Specificity. <i>Molecules</i> , 2019, 24, 1988.	3.8	4
7	NADPH-dependent sulfite reductase flavoprotein adopts an extended conformation unique to this diflavin reductase. <i>Journal of Structural Biology</i> , 2019, 205, 170-179.	2.8	12
8	Structure-Function Relationships in the Oligomeric NADPH-Dependent Assimilatory Sulfite Reductase. <i>Biochemistry</i> , 2018, 57, 3764-3772.	2.5	11
9	The role of extended Fe4S4 cluster ligands in mediating sulfite reductase hemoprotein activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 933-940.	2.3	3
10	Structural Heterogeneity in Pre-40S Ribosomes. <i>Structure</i> , 2017, 25, 329-340.	3.3	60
11	Structure, proteome and genome of <i>Sinorhizobium meliloti</i> phage $\hat{\imath}$ M5: A virus with LUZ24-like morphology and a highly mosaic genome. <i>Journal of Structural Biology</i> , 2017, 200, 343-359.	2.8	17
12	The DEAD-box Protein Rok1 Orchestrates 40S and 60S Ribosome Assembly by Promoting the Release of Rrp5 from Pre-40S Ribosomes to Allow for 60S Maturation. <i>PLoS Biology</i> , 2016, 14, e1002480.	5.6	40
13	Heterogeneity in the pre-40S ribosomal subunit reveals two distinct regions of variation at functionally important structural elements. <i>Microscopy and Microanalysis</i> , 2015, 21, 53-54.	0.4	0
14	The N-terminal Domain of <i>Escherichia coli</i> Assimilatory NADPH-Sulfite Reductase Hemoprotein Is an Oligomerization Domain That Mediates Holoenzyme Assembly. <i>Journal of Biological Chemistry</i> , 2015, 290, 19319-19333.	3.4	14
15	The Maize (<i>Zea mays</i> L.) Nucleoside Diphosphate Kinase1 (ZmNDPK1) Gene Encodes a Human NM23-H2 Homologue That Binds and Stabilizes G-Quadruplex DNA. <i>Biochemistry</i> , 2015, 54, 1743-1757.	2.5	19
16	Hrr25/CK1 $\hat{\imath}$ -directed release of Ltv1 from pre-40S ribosomes is necessary for ribosome assembly and cell growth. <i>Journal of Cell Biology</i> , 2015, 208, 745-759.	5.2	71
17	<i>Sinorhizobium meliloti</i> Phage $\hat{\imath}$ M9 Defines a New Group of T4 Superfamily Phages with Unusual Genomic Features but a Common T=16 Capsid. <i>Journal of Virology</i> , 2015, 89, 10945-10958.	3.4	29
18	G-Quadruplex (G4) Motifs in the Maize (<i>Zea mays</i> L.) Genome Are Enriched at Specific Locations in Thousands of Genes Coupled to Energy Status, Hypoxia, Low Sugar, and Nutrient Deprivation. <i>Journal of Genetics and Genomics</i> , 2014, 41, 627-647.	3.9	49

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19	The structure of Sinorhizobium meliloti phage $\hat{\Gamma}$ M12, which has a novel T=19I triangulation number and is the founder of a new group of T4-superfamily phages. <i>Virology</i> , 2014, 450-451, 205-212.	2.4	18
20	The genome, proteome and phylogenetic analysis of Sinorhizobium meliloti phage $\hat{\Gamma}$ M12, the founder of a new group of T4-superfamily phages. <i>Virology</i> , 2014, 450-451, 84-97.	2.4	34
21	Cryo-EM Structures of the Actin:Tropomyosin Filament Reveal the Mechanism for the Transition from C- to M-State. <i>Journal of Molecular Biology</i> , 2013, 425, 4544-4555.	4.2	27
22	Mutational Analysis of Sulfite Reductase Hemoprotein Reveals the Mechanism for Coordinated Electron and Proton Transfer. <i>Biochemistry</i> , 2012, 51, 9857-9868.	2.5	32
23	Actin filament labels for localizing protein components in large complexes viewed by electron microscopy. <i>Rna</i> , 2009, 15, 244-248.	3.5	13
24	High-resolution Electron Microscopy of Helical Specimens: A Fresh Look at Tobacco Mosaic Virus. <i>Journal of Molecular Biology</i> , 2007, 371, 812-835.	4.2	231
25	The Three-dimensional Arcitecture of the EJC Core. <i>Journal of Molecular Biology</i> , 2006, 360, 743-749.	4.2	32
26	Mutational analysis of human eIF4AIII identifies regions necessary for exon junction complex formation and nonsense-mediated mRNA decay. <i>Rna</i> , 2006, 12, 360-374.	3.5	65
27	Role of Hydrogen Bonding in the Active Site of Human Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2004, 43, 7038-7045.	2.5	38
28	Structure/Function Studies on a S-Adenosyl-L-methionine-dependent Uroporphyrinogen III C Methyltransferase (SUMT), a Key Regulatory Enzyme of Tetrapyrrole Biosynthesis. <i>Journal of Molecular Biology</i> , 2004, 344, 419-433.	4.2	56
29	CysG structure reveals tetrapyrrole-binding features and novel regulation of siroheme biosynthesis. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1064-1073.	8.2	78
30	Catalytic and Structural Effects of Amino Acid Substitution at Histidine 30 in Human Manganese Superoxide Dismutase: Insertion of Valine C ³ into the Substrate Access Channel. <i>Biochemistry</i> , 2003, 42, 2781-2789.	2.5	57
31	Kinetic Analysis of Product Inhibition in Human Manganese Superoxide Dismutase. <i>Biochemistry</i> , 2001, 40, 12051-12058.	2.5	75
32	Multiple Replacements of Glutamine 143 in Human Manganese Superoxide Dismutase: Effects on Structure, Stability, and Catalysis. <i>Biochemistry</i> , 2000, 39, 7131-7137.	2.5	65