

Steven E Glynn

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/597143/publications.pdf>

Version: 2024-02-01

20
papers

966
citations

687363

13
h-index

752698

20
g-index

23
all docs

23
docs citations

23
times ranked

1247
citing authors

#	ARTICLE	IF	CITATIONS
1	Quality-control mechanisms targeting translationally stalled and C-terminally extended poly(GR) associated with ALS/FTD. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25104-25115.	7.1	39
2	Mitochondrial AAA proteases: A stairway to degradation. Mitochondrion, 2019, 49, 121-127.	3.4	11
3	Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. Molecular Cell, 2019, 75, 1073-1085.e6.	9.7	58
4	FABP1 controls hepatic transport and biotransformation of δ^9 -THC. Scientific Reports, 2019, 9, 7588.	3.3	15
5	Dissecting Substrate Specificities of the Mitochondrial AFG3L2 Protease. Biochemistry, 2018, 57, 4225-4235.	2.5	13
6	Identification of a Degradation Signal Sequence within Substrates of the Mitochondrial i-AAA Protease. Journal of Molecular Biology, 2017, 429, 873-885.	4.2	23
7	Covalently linked HslU hexamers support a probabilistic mechanism that links ATP hydrolysis to protein unfolding and translocation. Journal of Biological Chemistry, 2017, 292, 5695-5704.	3.4	13
8	Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing. Science, 2017, 358, .	12.6	179
9	Multifunctional Mitochondrial AAA Proteases. Frontiers in Molecular Biosciences, 2017, 4, 34.	3.5	56
10	Sending protein aggregates into a downward spiral. Nature Structural and Molecular Biology, 2016, 23, 769-770.	8.2	2
11	Engineered AAA+ proteases reveal principles of proteolysis at the mitochondrial inner membrane. Nature Communications, 2016, 7, 13301.	12.8	44
12	Defects in fatty acid amide hydrolase 2 in a male with neurologic and psychiatric symptoms. Orphanet Journal of Rare Diseases, 2015, 10, 38.	2.7	19
13	Reconstructing Membrane-Anchored Mitochondrial AAA+ Proteases For In Vitro Analysis. FASEB Journal, 2015, 29, LB165.	0.5	0
14	Nucleotide Binding and Conformational Switching in the Hexameric Ring of a AAA+ Machine. Cell, 2013, 153, 628-639.	28.9	97
15	Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. Nature Structural and Molecular Biology, 2012, 19, 616-622.	8.2	56
16	Structures of Asymmetric ClpX Hexamers Reveal Nucleotide-Dependent Motions in a AAA+ Protein-Unfolding Machine. Cell, 2009, 139, 744-756.	28.9	231
17	Structure and Mechanism of Imidazoleglycerol-Phosphate Dehydratase. Structure, 2005, 13, 1809-1817.	3.3	31
18	Purification, crystallization and preliminary crystallographic analysis of Arabidopsis thaliana imidazoleglycerol-phosphate dehydratase. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 776-778.	0.7	2

#	ARTICLE	IF	CITATIONS
19	Substrate Specificity and Mechanism from the Structure of <i>Pyrococcus furiosus</i> Galactokinase. <i>Journal of Molecular Biology</i> , 2004, 337, 387-398.	4.2	53
20	Cloning, purification, crystallization and preliminary crystallographic analysis of galactokinase from <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1819-1821.	2.5	4