

Sean M Cascarina

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3858103/publications.pdf>

Version: 2024-02-01

20
papers

419
citations

933447

10
h-index

940533

16
g-index

23
all docs

23
docs citations

23
times ranked

551
citing authors

#	ARTICLE	IF	CITATIONS
1	A proposed role for the SARS-CoV-2 nucleocapsid protein in the formation and regulation of biomolecular condensates. <i>FASEB Journal</i> , 2020, 34, 9832-9842.	0.5	100
2	Yeast prions and human prion-like proteins: sequence features and prediction methods. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 2047-2063.	5.4	50
3	Phase separation by the SARS-CoV-2 nucleocapsid protein: Consensus and open questions. <i>Journal of Biological Chemistry</i> , 2022, 298, 101677.	3.4	44
4	The prion-like protein kinase Sky1 is required for efficient stress granule disassembly. <i>Nature Communications</i> , 2019, 10, 3614.	12.8	36
5	Composition-based prediction and rational manipulation of prion-like domain recruitment to stress granules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5826-5835.	7.1	32
6	Effects of Mutations on the Aggregation Propensity of the Human Prion-Like Protein hnRNPA2B1. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	31
7	Atypical structural tendencies among low-complexity domains in the Protein Data Bank proteome. <i>PLoS Computational Biology</i> , 2020, 16, e1007487.	3.2	28
8	Proteome-scale relationships between local amino acid composition and protein fates and functions. <i>PLoS Computational Biology</i> , 2018, 14, e1006256.	3.2	26
9	Increasing Prion Propensity by Hydrophobic Insertion. <i>PLoS ONE</i> , 2014, 9, e89286.	2.5	23
10	Sequence features governing aggregation or degradation of prion-like proteins. <i>PLoS Genetics</i> , 2018, 14, e1007517.	3.5	16
11	LCD-Composer: an intuitive, composition-centric method enabling the identification and detailed functional mapping of low-complexity domains. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab048.	3.2	12
12	Manipulating the aggregation activity of human prion-like proteins. <i>Prion</i> , 2017, 11, 323-331.	1.8	9
13	Natural and pathogenic protein sequence variation affecting prion-like domains within and across human proteomes. <i>BMC Genomics</i> , 2020, 21, 23.	2.8	5
14	Aggregation and degradation scales for prion-like domains: sequence features and context weigh in. <i>Current Genetics</i> , 2019, 65, 387-392.	1.7	2
15	Sky1: at the intersection of prion-like proteins and stress granule regulation. <i>Current Genetics</i> , 2020, 66, 463-468.	1.7	2
16	Generalizable Compositional Features Influencing the Proteostatic Fates of Polar Low-Complexity Domains. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8944.	4.1	2
17	Atypical structural tendencies among low-complexity domains in the Protein Data Bank proteome. , 2020, 16, e1007487.		0
18	Atypical structural tendencies among low-complexity domains in the Protein Data Bank proteome. , 2020, 16, e1007487.		0

#	ARTICLE	IF	CITATIONS
19	Atypical structural tendencies among low-complexity domains in the Protein Data Bank proteome. , 2020, 16, e1007487.		0
20	Atypical structural tendencies among low-complexity domains in the Protein Data Bank proteome. , 2020, 16, e1007487.		0