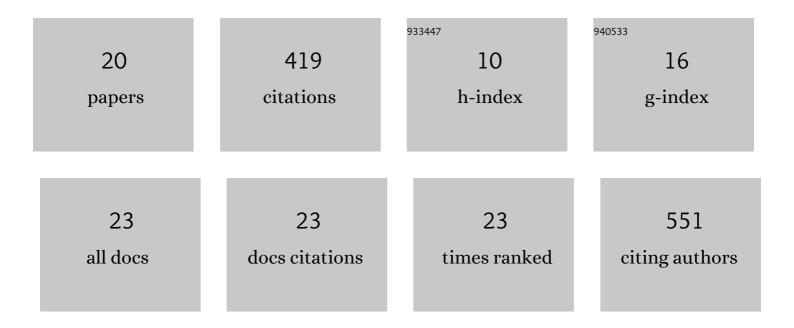
## Sean M Cascarina

List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
19	Increasing Prion Propensity by Hydrophobic Insertion. PLoS ONE, 2014, 9, e89286.	2.5	23
20	Yeast prions and human prion-like proteins: sequence features and prediction methods. Cellular and Molecular Life Sciences, 2014, 71, 2047-2063.	5.4	50