Birte Hernandez Alvarez

List of Publications by Year in descending order

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933447 1058476 14 311 10 14 citations g-index h-index papers 15 15 15 381 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A topological refactoring design strategy yields highly stable granulopoietic proteins. Nature Communications, 2022, 13 , .	12.8	4
2	Sweet and Blind Spots in E3 Ligase Ligand Space Revealed by a Thermophoresis-Based Assay. ACS Medicinal Chemistry Letters, 2021, 12, 74-81.	2.8	14
3	Expanding the versatility of natural and de novo designed coiled coils and helical bundles. Current Opinion in Structural Biology, 2021, 68, 224-234.	5.7	8
4	Design of novel granulopoietic proteins by topological rescaffolding. PLoS Biology, 2020, 18, e3000919.	5.6	8
5	De-Novo Design of Cereblon (CRBN) Effectors Guided by Natural Hydrolysis Products of Thalidomide Derivatives. Journal of Medicinal Chemistry, 2019, 62, 6615-6629.	6.4	38
6	Structural diversity of coiled coils in protein fibers of the bacterial cell envelope. International Journal of Medical Microbiology, 2019, 309, 351-358.	3.6	5
7	Characterization of MCU-Binding Proteins MCUR1 and CCDC90B — Representatives of a Protein Family Conserved in Prokaryotes and Eukaryotic Organelles. Structure, 2019, 27, 464-475.e6.	3.3	19
8	Chemical Ligand Space of Cereblon. ACS Omega, 2018, 3, 11163-11171.	3.5	43
9	A FRET-Based Assay for the Identification and Characterization of Cereblon Ligands. Journal of Medicinal Chemistry, 2016, 59, 770-774.	6.4	18
10	$\hat{I}_{\pm}/\hat{I}^{2}$ coiled coils. ELife, 2016, 5, .	6.0	27
11	Structural Dynamics of the Cereblon Ligand Binding Domain. PLoS ONE, 2015, 10, e0128342.	2.5	22
12	Thalidomide mimics uridine binding to an aromatic cage in cereblon. Journal of Structural Biology, 2014, 188, 225-232.	2.8	54
13	Your personalized protein structure: Andrei N. Lupas fused to GCN4 adaptors. Journal of Structural Biology, 2014, 186, 380-385.	2.8	15
14	A new expression system for protein crystallization using trimeric coiled-coil adaptors. Protein Engineering, Design and Selection, 2007, 21, 11-18.	2.1	36