

# Marcus D Hartmann

## List of Publications by Year in descending order

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58  
papers

1,947  
citations

257450

24  
h-index

289244

40  
g-index

68  
all docs

68  
docs citations

68  
times ranked

2489  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription regulation of iron carrier transport genes by ECF sigma factors through signaling from the cell surface into the cytoplasm. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	8.6	4
2	A complex struggle for direction. <i>Nature Chemical Biology</i> , 2022, 18, 119-120.	8.0	3
3	Replacing the phthalimide core in thalidomide with benzotriazole. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2022, 37, 527-530.	5.2	9
4	High-resolution structures of the bound effectors avadomide (CC-122) and iberdomide (CC-220) highlight advantages and limitations of the MsCl4 soaking system. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 290-298.	2.3	11
5	PotN represents a novel energy state sensing PII subfamily, occurring in firmicutes. <i>FEBS Journal</i> , 2022, 289, 5305-5321.	4.7	2
6	Functional and structural characterization of PII-like protein CutA does not support involvement in heavy metal tolerance and hints at a small molecule carrying/signaling role. <i>FEBS Journal</i> , 2021, 288, 1142-1162.	4.7	14
7	Sweet and Blind Spots in E3 Ligase Ligand Space Revealed by a Thermophoresis-Based Assay. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 74-81.	2.8	14
8	On the correlation of cereblon binding, fluorination and antiangiogenic properties of immunomodulatory drugs. <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 67-72.	2.1	11
9	Refolding and characterization of two G protein-coupled receptors purified from E. coli inclusion bodies. <i>PLoS ONE</i> , 2021, 16, e0247689.	2.5	2
10	Archaeal Connectase is a specific and efficient protein ligase related to proteasome $\beta^2$ subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	7
11	The breakthrough in protein structure prediction. <i>Biochemical Journal</i> , 2021, 478, 1885-1890.	3.7	39
12	High accuracy protein structure prediction in <code>CASP14</code> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1687-1699.	2.6	220
13	Assessing the utility of <code>CASP14</code> models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	2.6	47
14	Computational models in the service of X-ray and cryo-electron microscopy structure determination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1633-1646.	2.6	37
15	Target highlights in <code>CASP14</code> : Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	2.6	27
16	Diurnal metabolic control in cyanobacteria requires perception of second messenger signaling molecule c-di-AMP by the carbon control protein SbtB. <i>Science Advances</i> , 2021, 7, eabk0568.	10.3	26
17	Architecture and functional dynamics of the pentafunctional AROM complex. <i>Nature Chemical Biology</i> , 2020, 16, 973-978.	8.0	8
18	A secreted fungal histidine and alanine rich protein regulates metal ion homeostasis and oxidative stress. <i>New Phytologist</i> , 2020, 227, 1174-1188.	7.3	35

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19	LMO2 activation by deacetylation is indispensable for hematopoiesis and T-ALL leukemogenesis. <i>Blood</i> , 2019, 134, 1159-1175.	1.4	20
20	De-Novo Design of Cereblon (CRBN) Effectors Guided by Natural Hydrolysis Products of Thalidomide Derivatives. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 6615-6629.	6.4	38
21	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	2.6	12
22	On the Origins of Symmetry and Modularity in the Proteasome Family. <i>BioEssays</i> , 2019, 41, 1800237.	2.5	4
23	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
24	Characterization of MCU-Binding Proteins MCUR1 and CCDC90B – Representatives of a Protein Family Conserved in Prokaryotes and Eukaryotic Organelles. <i>Structure</i> , 2019, 27, 464-475.e6.	3.3	19
25	Structural diversity of oligomeric $\beta^2$ -propellers with different numbers of identical blades. <i>ELife</i> , 2019, 8, .	6.0	21
26	Target highlights from the first post-PSI CASP experiment (CASP12, May–August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	2.6	11
27	Structural characterization of the bacterial proteasome homolog BPH reveals a tetradecameric double-ring complex with unique inner cavity properties. <i>Journal of Biological Chemistry</i> , 2018, 293, 920-930.	3.4	6
28	Chemical Ligand Space of Cereblon. <i>ACS Omega</i> , 2018, 3, 11163-11171.	3.5	43
29	P <sub>II</sub> -like signaling protein SbtB links cAMP sensing with cyanobacterial inorganic carbon response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4861-E4869.	7.1	65
30	Rpn11-mediated ubiquitin processing in an ancestral archaeal ubiquitination system. <i>Nature Communications</i> , 2018, 9, 2696.	12.8	19
31	An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. <i>ACS Synthetic Biology</i> , 2018, 7, 2226-2235.	3.8	11
32	Functional and Structural Roles of Coiled Coils. <i>Sub-Cellular Biochemistry</i> , 2017, 82, 63-93.	2.4	26
33	The Architecture of the Anbu Complex Reflects an Evolutionary Intermediate at the Origin of the Proteasome System. <i>Structure</i> , 2017, 25, 834-845.e5.	3.3	11
34	Lactoferrin Is an Allosteric Enhancer of the Proteolytic Activity of Cathepsin G. <i>PLoS ONE</i> , 2016, 11, e0151509.	2.5	22
35	Some of the most interesting CASP11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	2.6	16
36	Structural Basis for Toughness and Flexibility in the C-terminal Passenger Domain of an Acinetobacter Trimeric Autotransporter Adhesin. <i>Journal of Biological Chemistry</i> , 2016, 291, 3705-3724.	3.4	41

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37	A FRET-Based Assay for the Identification and Characterization of Cereblon Ligands. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 770-774.	6.4	18
38	Î±/Î² coiled coils. <i>ELife</i> , 2016, 5, .	6.0	27
39	Origin of a folded repeat protein from an intrinsically disordered ancestor. <i>ELife</i> , 2016, 5, .	6.0	43
40	A domain dictionary of trimeric autotransporter adhesins. <i>International Journal of Medical Microbiology</i> , 2015, 305, 265-275.	3.6	50
41	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	4.2	23
42	STACâ€™A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339.	4.2	17
43	Structural Dynamics of the Cereblon Ligand Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0128342.	2.5	22
44	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	3.4	28
45	Thalidomide mimics uridine binding to an aromatic cage in cereblon. <i>Journal of Structural Biology</i> , 2014, 188, 225-232.	2.8	54
46	Crystallographic snapshot of the Escherichia coli EnvZ histidine kinase in an active conformation. <i>Journal of Structural Biology</i> , 2014, 186, 376-379.	2.8	46
47	A soluble mutant of the transmembrane receptor Af1503 features strong changes in coiled-coil periodicity. <i>Journal of Structural Biology</i> , 2014, 186, 357-366.	2.8	15
48	A Widespread Glutamine-Sensing Mechanism in the Plant Kingdom. <i>Cell</i> , 2014, 159, 1188-1199.	28.9	127
49	Your personalized protein structure: Andrei N. Lupas fused to GCN4 adaptors. <i>Journal of Structural Biology</i> , 2014, 186, 380-385.	2.8	15
50	Complete fiber structures of complex trimeric autotransporter adhesins conserved in enterobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20907-20912.	7.1	57
51	Crystal structure of a dimeric archaeal Cleavage and Polyadenylation Specificity Factor. <i>Journal of Structural Biology</i> , 2011, 173, 191-195.	2.8	31
52	The Structure of E.Âcoli IgG-Binding Protein D Suggests a General Model for Bending and Binding in Trimeric Autotransporter Adhesins. <i>Structure</i> , 2011, 19, 1021-1030.	3.3	66
53	A coiled-coil motif that sequesters ions to the hydrophobic core. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16950-16955.	7.1	77
54	Structure and Activity of the N-Terminal Substrate Recognition Domains in Proteasomal ATPases. <i>Molecular Cell</i> , 2009, 34, 580-590.	9.7	116

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55	A new expression system for protein crystallization using trimeric coiled-coil adaptors. <i>Protein Engineering, Design and Selection</i> , 2007, 21, 11-18.	2.1	36
56	A Divergent Sm Fold in EDC3 Proteins Mediates DCP1 Binding and P-Body Targeting. <i>Molecular and Cellular Biology</i> , 2007, 27, 8600-8611.	2.3	66
57	A CTP-Dependent Archaeal Riboflavin Kinase Forms a Bridge in the Evolution of Cradle-Loop Barrels. <i>Structure</i> , 2007, 15, 1577-1590.	3.3	29
58	Mechanism of Phosphoryl Transfer Catalyzed by Shikimate Kinase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2006, 364, 411-423.	4.2	63