

# Karl Harlos

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

2,698  
citations

185998

28  
h-index

197535

49  
g-index

58  
all docs

58  
docs citations

58  
times ranked

4673  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mouse and human antibodies bind HLA-E-leader peptide complexes and enhance NK cell cytotoxicity. <i>Communications Biology</i> , 2022, 5, 271.	2.0	14
2	Contrasting Modes of New World Arenavirus Neutralization by Immunization-Elicited Monoclonal Antibodies. <i>MBio</i> , 2022, 13, e0265021.	1.8	7
3	Inhibition of <i>Plasmodium falciparum</i> phenylalanine tRNA synthetase provides opportunity for antimalarial drug development. <i>Structure</i> , 2022, 30, 962-972.e3.	1.6	4
4	Structural Analysis and Development of Notum Fragment Screening Hits. <i>ACS Chemical Neuroscience</i> , 2022, 13, 2060-2077.	1.7	3
5	Inhibition of <i>Plasmodium falciparum</i> Lysyl-tRNA Synthetase via a Piperidine Ring Scaffold Inspired Cladosporin Analogues. <i>ChemBioChem</i> , 2021, 22, 2468-2477.	1.3	7
6	Structural basis of malaria parasite phenylalanine tRNA-synthetase inhibition by bicyclic azetidines. <i>Nature Communications</i> , 2021, 12, 343.	5.8	19
7	Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains Unravels the Mannose 6-Phosphate Binding Site of Domain 9. <i>Structure</i> , 2020, 28, 1300-1312.e5.	1.6	8
8	Natural Killer Cell Activation Receptor NKp30 Oligomerization Depends on Its N-Glycosylation. <i>Cancers</i> , 2020, 12, 1998.	1.7	12
9	Structural basis of semaphorin-plexin cis interaction. <i>EMBO Journal</i> , 2020, 39, e102926.	3.5	17
10	Crystal structures of the two domains that constitute the <i>Plasmodium vivax</i> p43 protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 135-146.	1.1	8
11	Disruption of the dimerization interface of the sensing domain in the dimeric heme-based oxygen sensor AfCgHK abolishes bacterial signal transduction. <i>Journal of Biological Chemistry</i> , 2020, 295, 1587-1597.	1.6	11
12	A key region of molecular specificity orchestrates unique ephrin-B1 utilization by Cedar virus. <i>Life Science Alliance</i> , 2020, 3, e201900578.	1.3	22
13	Diversity of oligomerization in <i>Drosophila</i> semaphorins suggests a mechanism of functional fine-tuning. <i>Nature Communications</i> , 2019, 10, 3691.	5.8	10
14	Insights from the crystal structure of the chicken CREB3 bZIP suggest that members of the CREB3 subfamily transcription factors may be activated in response to oxidative stress. <i>Protein Science</i> , 2019, 28, 779-787.	3.1	5
15	The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. <i>Nature Communications</i> , 2019, 10, 846.	5.8	37
16	Shielding and activation of a viral membrane fusion protein. <i>Nature Communications</i> , 2018, 9, 349.	5.8	78
17	Structures of monomeric and oligomeric forms of the <i>Toxoplasma gondii</i> perforin-like protein 1. <i>Science Advances</i> , 2018, 4, eaq0762.	4.7	32
18	A Protective Monoclonal Antibody Targets a Site of Vulnerability on the Surface of Rift Valley Fever Virus. <i>Cell Reports</i> , 2018, 25, 3750-3758.e4.	2.9	41

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19	Specific Stereoisomeric Conformations Determine the Drug Potency of Cladosporin Scaffold against Malarial Parasite. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 5664-5678.	2.9	41
20	Structure of the Wnt signaling enhancer <scp>LYPD</scp>6 and its interactions with the Wnt coreceptor <scp>LRP</scp>6. <i>FEBS Letters</i> , 2018, 592, 3152-3162.	1.3	13
21	Structure of 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinaseâ€™ dihydropteroate synthase from <i>Plasmodium vivax</i> sheds light on drug resistance. <i>Journal of Biological Chemistry</i> , 2018, 293, 14962-14972.	1.6	18
22	Pathogen-derived HLA-E bound epitopes reveal broad primary anchor pocket tolerability and conformationally malleable peptide binding. <i>Nature Communications</i> , 2018, 9, 3137.	5.8	57
23	A Twoâ€™tailed Phosphopeptide Crystallizes to Form a Lamellar Structure. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 3252-3255.	7.2	10
24	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017, 14, 805-810.	9.0	106
25	A Twoâ€™tailed Phosphopeptide Crystallizes to Form a Lamellar Structure. <i>Angewandte Chemie</i> , 2017, 129, 3300-3303.	1.6	0
26	Ligand-Induced Conformational Change of Insulin-Regulated Aminopeptidase: Insights on Catalytic Mechanism and Active Site Plasticity. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 2963-2972.	2.9	33
27	Structural Transitions of the Conserved and Metastable Hantaviral Glycoprotein Envelope. <i>Journal of Virology</i> , 2017, 91, .	1.5	38
28	Targeting Prolyl-tRNA Synthetase to Accelerate Drug Discovery against Malaria, Leishmaniasis, Toxoplasmosis, Cryptosporidiosis, and Coccidiosis. <i>Structure</i> , 2017, 25, 1495-1505.e6.	1.6	68
29	Convergent immunological solutions to Argentine hemorrhagic fever virus neutralization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7031-7036.	3.3	31
30	The crystal structure of human dopamine Î²-hydroxylase at 2.9 Å... resolution. <i>Science Advances</i> , 2016, 2, e1500980.	4.7	80
31	Structure of astrotactin-2: a conserved vertebrate-specific and perforin-like membrane protein involved in neuronal development. <i>Open Biology</i> , 2016, 6, 160053.	1.5	28
32	Structure of glycosylated <scp>NPC</scp>1 luminal domain C reveals insights into <scp>NPC</scp>2 and Ebola virus interactions. <i>FEBS Letters</i> , 2016, 590, 605-612.	1.3	39
33	A Molecular-Level Account of the Antigenic Hantaviral Surface. <i>Cell Reports</i> , 2016, 15, 959-967.	2.9	57
34	Structure of a phleboviral envelope glycoprotein reveals a consolidated model of membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7154-7159.	3.3	87
35	Toremifene interacts with and destabilizes the Ebola virus glycoprotein. <i>Nature</i> , 2016, 535, 169-172.	13.7	210
36	Initiation of T cell signaling by CD45 segregation at 'close contacts'. <i>Nature Immunology</i> , 2016, 17, 574-582.	7.0	253

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37	Crystal Structure of the Herpesvirus Nuclear Egress Complex Provides Insights into Inner Nuclear Membrane Remodeling. <i>Cell Reports</i> , 2015, 13, 2645-2652.	2.9	80
38	Improved crystallization and diffraction of caffeine-induced death suppressor protein 1 (Cid1). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 346-353.	0.4	2
39	New insights into the enzymatic mechanism of human chitotriosidase (CHIT1) catalytic domain by atomic resolution X-ray diffraction and hybrid QM/MM. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1455-1470.	2.5	23
40	Four crystal structures of human LLT1, a ligand of human NKR-P1, in varied glycosylation and oligomerization states. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 578-591.	2.5	20
41	Structural plasticity of Cid1 provides a basis for its distributive RNA terminal uridylyl transferase activity. <i>Nucleic Acids Research</i> , 2015, 43, 2968-2979.	6.5	25
42	Crystal Structure of Insulin-Regulated Aminopeptidase with Bound Substrate Analogue Provides Insight on Antigenic Epitope Precursor Recognition and Processing. <i>Journal of Immunology</i> , 2015, 195, 2842-2851.	0.4	41
43	Structure and functional properties of Norrin mimic Wnt for signalling with Frizzled4, Lrp5/6, and proteoglycan. <i>ELife</i> , 2015, 4, .	2.8	90
44	FLRT Structure: Balancing Repulsion and Cell Adhesion in Cortical and Vascular Development. <i>Neuron</i> , 2014, 84, 370-385.	3.8	117
45	Pushing the limits of sulfur SAD phasing: <i>de novo</i> structure solution of the N-terminal domain of the ectodomain of HCV E1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2197-2203.	2.5	33
46	Structural Insights into the Inhibition of Wnt Signaling by Cancer Antigen 5T4/Wnt-Activated Inhibitory Factor 1. <i>Structure</i> , 2014, 22, 612-620.	1.6	42
47	Structure and Self-Assembly of the Calcium Binding Matrix Protein of Human Metapneumovirus. <i>Structure</i> , 2014, 22, 136-148.	1.6	44
48	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. <i>Nature Communications</i> , 2014, 5, 4874.	5.8	72
49	Drastic changes in conformational dynamics of the antiterminator M2-1 regulate transcription efficiency in Pneumovirinae. <i>ELife</i> , 2014, 3, e02674.	2.8	39
50	Structure of a Pestivirus Envelope Glycoprotein E2 Clarifies Its Role in Cell Entry. <i>Cell Reports</i> , 2013, 3, 30-35.	2.9	124
51	Structural basis for the activity of a cytoplasmic RNA terminal uridylyl transferase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 782-787.	3.6	47
52	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 651-657.	2.5	234
53	The ligand-binding face of the semaphorins revealed by the high-resolution crystal structure of SEMA4D. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 843-848.	3.6	143