

# Kaspars Tars

## List of Publications by Year in descending order

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110  
papers

3,388  
citations

147801

31  
h-index

175258

52  
g-index

110  
all docs

110  
docs citations

110  
times ranked

3920  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	13.7	254
2	Structure of fully protonated proteins by proton-detected magic-angle spinning NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9187-9192.	7.1	224
3	Sulfocoumarins (1,2-Benzoxathiane-2,2-dioxides): A Class of Potent and Isoform-Selective Inhibitors of Tumor-Associated Carbonic Anhydrases. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 293-300.	6.4	199
4	Efficient Expression and Crystallization System of Cancer-Associated Carbonic Anhydrase Isoform IX. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 9004-9009.	6.4	141
5	NMR Spectroscopic Assignment of Backbone and Side-Chain Protons in Fully Protonated Proteins: Microcrystals, Sedimented Assemblies, and Amyloid Fibrils. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 15504-15509.	13.8	116
6	Asymmetric cryo-EM reconstruction of phage MS2 reveals genome structure in situ. <i>Nature Communications</i> , 2016, 7, 12524.	12.8	114
7	New anticancer drug candidates sulfonamides as selective hCA IX or hCA XII inhibitors. <i>Bioorganic Chemistry</i> , 2018, 77, 411-419.	4.1	99
8	Long-chain acylcarnitines determine ischaemia/reperfusion-induced damage in heart mitochondria. <i>Biochemical Journal</i> , 2016, 473, 1191-1202.	3.7	77
9	The crystal structure of bacteriophage GA and a comparison of bacteriophages belonging to the major groups of <i>Escherichia coli</i> leviviruses. <i>Journal of Molecular Biology</i> , 1997, 271, 759-773.	4.2	75
10	Structure and Function of CutC Choline Lyase from Human Microbiota Bacterium <i>Klebsiella pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 21732-21740.	3.4	70
11	X-ray crystallography-promoted drug design of carbonic anhydrase inhibitors. <i>Chemical Communications</i> , 2015, 51, 7108-7111.	4.1	61
12	Dynamic Nuclear Polarization-Enhanced Biomolecular NMR Spectroscopy at High Magnetic Field with Fast Magic-Angle Spinning. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7458-7462.	13.8	56
13	Fragment-Based Discovery of 2-Aminoquinazolin-4(3 <i>H</i> )-ones As Novel Class Nonpeptidomimetic Inhibitors of the Plasmepsins I, II, and IV. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 374-387.	6.4	55
14	Out-and-back <sup>13</sup> C- <sup>13</sup> C scalar transfers in protein resonance assignment by proton-detected solid-state NMR under ultra-fast MAS. <i>Journal of Biomolecular NMR</i> , 2013, 56, 379-386.	2.8	54
15	The True Story and Advantages of RNA Phage Capsids as Nanotools. <i>Intervirology</i> , 2016, 59, 74-110.	2.8	52
16	The Three-Dimensional Structure of Bacteriophage PP7 from <i>Pseudomonas aeruginosa</i> at 3.7-Å... Resolution. <i>Virology</i> , 2000, 272, 331-337.	2.4	49
17	Highly efficient production of phosphorylated hepatitis B core particles in yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2011, 75, 218-224.	1.3	48
18	Structural Basis of RNA Binding Discrimination between Bacteriophages Q $\beta$ and MS2. <i>Structure</i> , 2006, 14, 487-495.	3.3	47

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19	Plasmepsin Inhibitory Activity and Structure-Guided Optimization of a Potent Hydroxyethylamine-Based Antimalarial Hit. <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 373-377.	2.8	46
20	Structure of AP205 Coat Protein Reveals Circular Permutation in ssRNA Bacteriophages. <i>Journal of Molecular Biology</i> , 2016, 428, 4267-4279.	4.2	45
21	Is protein deuteration beneficial for proton detected solid-state NMR at and above 100 kHz magic-angle spinning?. <i>Solid State Nuclear Magnetic Resonance</i> , 2017, 87, 126-136.	2.3	45
22	Encapsulation mechanisms and structural studies of GRM2 bacterial microcompartment particles. <i>Nature Communications</i> , 2020, 11, 388.	12.8	44
23	Targeting Carnitine Biosynthesis: Discovery of New Inhibitors against $\hat{1}^3$ -Butyrobetaine Hydroxylase. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 2213-2236.	6.4	41
24	3 <i>H</i> -1,2-benzoxathiepine 2,2-dioxides: a new class of isoform-selective carbonic anhydrase inhibitors. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2017, 32, 767-775.	5.2	41
25	N-Substituted and ring opened saccharin derivatives selectively inhibit transmembrane, tumor-associated carbonic anhydrases IX and XII. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 3583-3589.	3.0	39
26	Structural Basis for Featuring of Steroid Isomerase Activity in Alpha Class Glutathione Transferases. <i>Journal of Molecular Biology</i> , 2010, 397, 332-340.	4.2	38
27	The three-dimensional structure of cocksfoot mottle virus at 2.7 Å resolution. <i>Virology</i> , 2003, 310, 287-297.	2.4	36
28	Structural Basis of the Suppressed Catalytic Activity of Wild-type Human Glutathione Transferase T1-1 Compared to its W234R Mutant. <i>Journal of Molecular Biology</i> , 2006, 355, 96-105.	4.2	36
29	Potent SARS-CoV-2 mRNA Cap Methyltransferase Inhibitors by Bioisosteric Replacement of Methionine in SAM Cosubstrate. <i>ACS Medicinal Chemistry Letters</i> , 2021, 12, 1102-1107.	2.8	36
30	Investigating the structural basis of purine specificity in the structures of MS2 coat protein RNA translational operator hairpins. <i>Nucleic Acids Research</i> , 2002, 30, 2678-2685.	14.5	34
31	New Substituted Piperazines as Ligands for Melanocortin Receptors. Correlation to the X-ray Structure of $\hat{\epsilon}$ THIQ. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 4613-4626.	6.4	32
32	Vaccination against IL-31 for the treatment of atopic dermatitis in dogs. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 279-281.e1.	2.9	32
33	Eliminating Factor H-Binding Activity of <i>Borrelia burgdorferi</i> CspZ Combined with Virus-Like Particle Conjugation Enhances Its Efficacy as a Lyme Disease Vaccine. <i>Frontiers in Immunology</i> , 2018, 9, 181.	4.8	32
34	5-Substituted-(1,2,3-triazol-4-yl)thiophene-2-sulfonamides strongly inhibit human carbonic anhydrases I, II, IX and XII: Solution and X-ray crystallographic studies. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 5130-5138.	3.0	31
35	Crystal structure of human gamma-butyrobetaine hydroxylase. <i>Biochemical and Biophysical Research Communications</i> , 2010, 398, 634-639.	2.1	30
36	Diversity of pili-specific bacteriophages: genome sequence of IncM plasmid-dependent RNA phage M. <i>BMC Microbiology</i> , 2012, 12, 277.	3.3	30

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37	Alternative mutations of a positively selected residue elicit gain or loss of functionalities in enzyme evolution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4876-4881.	7.1	29
38	Crystal Structure of the Bacteriophage Q $\beta$ Coat Protein in Complex with the RNA Operator of the Replicase Gene. Journal of Molecular Biology, 2014, 426, 1039-1049.	4.2	29
39	The three-dimensional structure of ryegrass mottle virus at 2.9Å... resolution. Virology, 2007, 369, 364-374.	2.4	28
40	<i>N</i> -Acylbenzenesulfonamide Dihydro-1,3,4-oxadiazole Hybrids: Seeking Selectivity toward Carbonic Anhydrase Isoforms. ACS Medicinal Chemistry Letters, 2017, 8, 792-796.	2.8	27
41	The Structure of Bacteriophage $\phi$ Cb5 Reveals a Role of the RNA Genome and Metal Ions in Particle Stability and Assembly. Journal of Molecular Biology, 2009, 391, 635-647.	4.2	26
42	Production and purification of chimeric Hbc virus-like particles carrying influenza virus LAH domain as vaccine candidates. BMC Biotechnology, 2017, 17, 79.	3.3	26
43	Novel fluorinated carbonic anhydrase IX inhibitors reduce hypoxia-induced acidification and clonogenic survival of cancer cells. Oncotarget, 2018, 9, 26800-26816.	1.8	25
44	AP205 VLPs Based on Dimerized Capsid Proteins Accommodate RBM Domain of SARS-CoV-2 and Serve as an Attractive Vaccine Candidate. Vaccines, 2021, 9, 403.	4.4	25
45	Structural Analysis of a Glutathione Transferase A1-1 Mutant Tailored for High Catalytic Efficiency with Toxic Alkenals. Biochemistry, 2009, 48, 7698-7704.	2.5	24
46	Crystal structure of the read-through domain from bacteriophage Q $\beta$ A1 protein. Protein Science, 2011, 20, 1707-1712.	7.6	24
47	Crystal structures of the Erp protein family members ErpP and ErpC from <i>Borrelia burgdorferi</i> reveal the reason for different affinities for complement regulator factor H. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 349-355.	2.3	24
48	Crystal Structure of the Maturation Protein from Bacteriophage Q $\beta$ . Journal of Molecular Biology, 2017, 429, 688-696.	4.2	24
49	Genome Structure of Caulobacter Phage $\phi$ Cb5. Journal of Virology, 2011, 85, 4628-4631.	3.4	21
50	The Capsid of the Small RNA Phage PRR1 Is Stabilized by Metal Ions. Journal of Molecular Biology, 2008, 383, 914-922.	4.2	20
51	5-Substituted-benzylsulfanyl-thiophene-2-sulfonamides with effective carbonic anhydrase inhibitory activity: Solution and crystallographic investigations. Bioorganic and Medicinal Chemistry, 2017, 25, 857-863.	3.0	20
52	Structural characterization of CspZ, a complement regulator factor <i>H</i> and <i>FHL-1</i> binding protein from <i>Borrelia burgdorferi</i> . FEBS Journal, 2014, 281, 2613-2622.	4.7	19
53	Structure of Phage $\phi$ r Capsids with a Deletion in the FG Loop: Implications for Viral Assembly. Virology, 1998, 249, 80-88.	2.4	18
54	Structure and stability of icosahedral particles of a covalent coat protein dimer of bacteriophage MS2. Protein Science, 2009, 18, 1653-1661.	7.6	18

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55	Complete Genome Sequence of the Enterobacter cancerogenus Bacteriophage Enc34. <i>Journal of Virology</i> , 2012, 86, 11403-11404.	3.4	18
56	Zuordnung der Rückgrat- und Seitenkettenprotonen in vollständig protonierten Proteinen durch Festkörpers-NMR-Spektroskopie: Mikrokristalle, Sedimente und Amyloidfibrillen. <i>Angewandte Chemie</i> , 2016, 128, 15730-15735.	2.0	18
57	Molecular basis for regulation of Src by the docking protein p130Cas. <i>Journal of Molecular Recognition</i> , 2006, 19, 30-38.	2.1	17
58	Crystal packing of a bacteriophage MS2 coat protein mutant corresponds to octahedral particles. <i>Protein Science</i> , 2008, 17, 1731-1739.	7.6	17
59	Structure-Based Redesign of GST A2-2 for Enhanced Catalytic Efficiency with Azathioprine. <i>Chemistry and Biology</i> , 2012, 19, 414-421.	6.0	17
60	Synthesis of novel dipeptide sulfonamide conjugates with effective carbonic anhydrase I, II, IX, and XII inhibitory properties. <i>Bioorganic Chemistry</i> , 2018, 81, 311-318.	4.1	17
61	Structural and functional analysis of BB0689 from <i>Borrelia burgdorferi</i> , a member of the bacterial CAP superfamily. <i>Journal of Structural Biology</i> , 2015, 192, 320-330.	2.8	16
62	Modulating Catalytic Activity by Unnatural Amino Acid Residues in a GSH-Binding Loop of GST P1-1. <i>Journal of Molecular Biology</i> , 2008, 376, 811-826.	4.2	15
63	Structural Basis for DNA Recognition of a Single-stranded DNA-binding Protein from Enterobacter Phage Enc34. <i>Scientific Reports</i> , 2017, 7, 15529.	3.3	15
64	Structure determination of bacteriophage PP7 from <i>Pseudomonas aeruginosa</i> : from poor data to a good map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 398-405.	2.5	14
65	Expression and purification of active, stabilized trimethyllysine hydroxylase. <i>Protein Expression and Purification</i> , 2014, 104, 1-6.	1.3	14
66	Structures of plasmepsin II from <i>Plasmodium falciparum</i> in complex with two hydroxyethylamine-based inhibitors. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1531-1539.	0.8	14
67	Structure of an outer surface lipoprotein BBA64 from the Lyme disease agent <i>Borrelia burgdorferi</i> which is critical to ensure infection after a tick bite. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1099-1107.	2.5	13
68	The Factor H-Binding Site of CspZ as a Protective Target against Multistrain, Tick-Transmitted Lyme Disease. <i>Infection and Immunity</i> , 2020, 88, .	2.2	13
69	Different Binding Modes of Free and Carrier-Protein-Coupled Nicotine in a Human Monoclonal Antibody. <i>Journal of Molecular Biology</i> , 2012, 415, 118-127.	4.2	12
70	PRR1 coat protein binding to its RNA translational operator. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 367-372.	2.5	12
71	Production and characterization of novel ssRNA bacteriophage virus-like particles from metagenomic sequencing data. <i>Journal of Nanobiotechnology</i> , 2019, 17, 61.	9.1	12
72	Human carnitine biosynthesis proceeds via (2S,3S)-3-hydroxy-N <sup>μ</sup> -trimethyllysine. <i>Chemical Communications</i> , 2017, 53, 440-442.	4.1	11

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73	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
74	Construction and Immunogenicity of a Novel Multivalent Vaccine Prototype Based on Conserved Influenza Virus Antigens. <i>Vaccines</i> , 2020, 8, 197.	4.4	11
75	Structural Analysis of an Antigen Chemically Coupled on Virus-Like Particles in Vaccine Formulation. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 12847-12851.	13.8	11
76	Structural characterization of the <i>Borrelia burgdorferi</i> outer surface protein BBA73 implicates dimerization as a functional mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2013, 434, 848-853.	2.1	10
77	Yeast-Expressed Bacteriophage-Like Particles for the Packaging of Nanomaterials. <i>Molecular Biotechnology</i> , 2014, 56, 102-110.	2.4	10
78	2-Aminoquinazolin-4(3H)-one based plasmepsin inhibitors with improved hydrophilicity and selectivity. <i>Bioorganic and Medicinal Chemistry</i> , 2018, 26, 2488-2500.	3.0	10
79	CntA oxygenase substrate profile comparison and oxygen dependency of TMA production in <i>Providencia rettgeri</i> . <i>Journal of Basic Microbiology</i> , 2018, 58, 52-59.	3.3	10
80	Structure and applications of novel influenza HA tri-stalk protein for evaluation of HA stem-specific immunity. <i>PLoS ONE</i> , 2018, 13, e0204776.	2.5	10
81	Protein-RNA Interactions in the Single-Stranded RNA Bacteriophages. <i>Sub-Cellular Biochemistry</i> , 2018, 88, 281-303.	2.4	10
82	Halogenated and di-substituted benzenesulfonamides as selective inhibitors of carbonic anhydrase isoforms. <i>European Journal of Medicinal Chemistry</i> , 2020, 185, 111825.	5.5	10
83	Assembly of mixed rod-like and spherical particles from group I and II RNA bacteriophage coat proteins. <i>Virology</i> , 2009, 391, 187-194.	2.4	9
84	Crystal structure of the infectious phenotype-associated outer surface protein BBA66 from the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>Ticks and Tick-borne Diseases</i> , 2014, 5, 63-68.	2.7	9
85	Dynamic Nuclear Polarization-Enhanced Biomolecular NMR Spectroscopy at High Magnetic Field with Fast Magic-Angle Spinning. <i>Angewandte Chemie</i> , 2018, 130, 7580-7584.	2.0	8
86	Structural analysis of the outer surface proteins from <i>Borrelia burgdorferi</i> paralogous gene family 54 that are thought to be the key players in the pathogenesis of Lyme disease. <i>Journal of Structural Biology</i> , 2020, 210, 107490.	2.8	8
87	Crystal structure of <i>Borrelia burgdorferi</i> outer surface protein BBA69 in comparison to the paralogous protein CspA. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 1135-1141.	2.7	7
88	BBE31 from the Lyme disease agent <i>Borrelia burgdorferi</i> , known to play an important role in successful colonization of the mammalian host, shows the ability to bind glutathione. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129499.	2.4	7
89	Diversity of the lysozyme fold: structure of the catalytic domain from an unusual endolysin encoded by phage Enc34. <i>Scientific Reports</i> , 2022, 12, 5005.	3.3	7
90	QSAR of multiple mutated antibodies. <i>Journal of Molecular Recognition</i> , 2007, 20, 97-102.	2.1	6

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91	Extending the Inhibition Profiles of Coumarin-Based Compounds Against Human Carbonic Anhydrases: Synthesis, Biological, and In Silico Evaluation. <i>Molecules</i> , 2019, 24, 3580.	3.8	6
92	Novel ssRNA phage VLP platform for displaying foreign epitopes by genetic fusion. <i>Vaccine</i> , 2020, 38, 6019-6026.	3.8	6
93	Three-dimensional structure of 22 uncultured ssRNA bacteriophages: Flexibility of the coat protein fold and variations in particle shapes. <i>Science Advances</i> , 2020, 6, .	10.3	6
94	Variety of size and form of GRM2 bacterial microcompartment particles. <i>Protein Science</i> , 2021, 30, 1035-1043.	7.6	6
95	N-terminus Modification of Glycyl-Histidine-Tagged Proteins with Azidogluconolactone. <i>ChemBioChem</i> , 2021, 22, 3199-3207.	2.6	6
96	Isoform-Selective Enzyme Inhibitors by Exploring Pocket Size According to the Lock-and-Key Principle. <i>Biophysical Journal</i> , 2020, 119, 1513-1524.	0.5	6
97	Methyl 2-Halo-4-Substituted-5-Sulfamoyl-Benzoates as High Affinity and Selective Inhibitors of Carbonic Anhydrase IX. <i>International Journal of Molecular Sciences</i> , 2022, 23, 130.	4.1	6
98	Crystal structure of the membrane attack complex assembly inhibitor BGA71 from the Lyme disease agent <i>Borrelia bavariensis</i> . <i>Scientific Reports</i> , 2018, 8, 11286.	3.3	5
99	Aryl-4,5-dihydro-1H-pyrazole-1-carboxamide Derivatives Bearing a Sulfonamide Moiety Show Single-digit Nanomolar-to-Subnanomolar Inhibition Constants against the Tumor-associated Human Carbonic Anhydrases IX and XII. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2621.	4.1	5
100	Crystal structure of <i>Plasmodium falciparum</i> proplasmepsin IV: the plasticity of proplasmepsins. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 659-666.	0.8	4
101	Structural analysis of <i>Borrelia burgdorferi</i> periplasmic lipoprotein BB 0365 involved in Lyme disease infection. <i>FEBS Letters</i> , 2020, 594, 317-326.	2.8	4
102	Crystal structure of the N-terminal domain of the major virulence factor BB0323 from the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 825-830.	2.3	3
103	ssRNA Phages: Life Cycle, Structure and Applications. , 2020, , 261-292.		3
104	Solution NMR structure of <i>Borrelia burgdorferi</i> outer surface lipoprotein BBP28, a member of the mlp protein family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 588-594.	2.6	3
105	Sample Preparation Induced Artifacts in Cryo-Electron Tomographs. <i>Microscopy and Microanalysis</i> , 2012, 18, 1043-1048.	0.4	2
106	Plasmid dimerization increases the production of hepatitis B core particles in <i>E. coli</i> . <i>Biotechnology and Bioprocess Engineering</i> , 2013, 18, 850-857.	2.6	2
107	X-Ray Crystallographic Structures of High-Affinity and High-Selectivity Inhibitor Complexes with CA IX That Plays a Special Role in Cancer. , 2019, , 203-213.		0
108	Structural and Functional Analysis of BBA03, <i>Borrelia burgdorferi</i> Competitive Advantage Promoting Outer Surface Lipoprotein. <i>Pathogens</i> , 2020, 9, 826.	2.8	0

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109	Struktur eines an virusÄhnliche Partikel gekoppelten Antigens: Analyse einer Impfstoffâ€Formulierung. Angewandte Chemie, 2021, 133, 12957-12961.	2.0	0
110	A Positively Selected Residue Influences Enzyme Functionalities. FASEB Journal, 2006, 20, A474.	0.5	0