

# Michal Hammel

## List of Publications by Year in descending order

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96  
papers

9,967  
citations

57758

44  
h-index

39675

94  
g-index

103  
all docs

103  
docs citations

103  
times ranked

12794  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predictive high-throughput screening of PEGylated lipids in oligonucleotide-loaded lipid nanoparticles for neuronal gene silencing. <i>Nanoscale Advances</i> , 2022, 4, 2107-2123.	4.6	21
2	Structural arrangement of the VH and VL domains in the COBRA $\alpha$ , $\beta$ T-cell engaging single-chain diabody. <i>Antibody Therapeutics</i> , 2022, 5, 1-10.	1.9	0
3	Structural basis for SHOC2 modulation of RAS signalling. <i>Nature</i> , 2022, 609, 400-407.	27.8	14
4	A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. <i>Nature Communications</i> , 2022, 13, .	12.8	5
5	Uncovering DNA-PKcs ancient phylogeny, unique sequence motifs and insights for human disease. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 87-108.	2.9	45
6	Heparin-mediated dimerization of follistatin. <i>Experimental Biology and Medicine</i> , 2021, 246, 467-482.	2.4	3
7	Visualizing functional dynamicity in the DNA-dependent protein kinase holoenzyme DNA-PK complex by integrating SAXS with cryo-EM. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 74-86.	2.9	13
8	Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein. <i>MAbs</i> , 2021, 13, 1905978.	5.2	16
9	Albumin in patients with liver disease shows an altered conformation. <i>Communications Biology</i> , 2021, 4, 731.	4.4	14
10	X-ray scattering reveals disordered linkers and dynamic interfaces in complexes and mechanisms for $\lambda$ -DNA double-strand break repair impacting cell and cancer biology. <i>Protein Science</i> , 2021, 30, 1735-1756.	7.6	19
11	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. <i>Biophysical Journal</i> , 2021, 120, 3152-3165.	0.5	39
12	Direct interaction of DNA repair protein tyrosyl DNA phosphodiesterase 1 and the DNA ligase III catalytic domain is regulated by phosphorylation of its flexible N-terminus. <i>Journal of Biological Chemistry</i> , 2021, 297, 100921.	3.4	6
13	An atypical BRCT $\alpha$ -BRCT interaction with the XRCC1 scaffold protein compacts human DNA Ligase III $\beta$ within a flexible DNA repair complex. <i>Nucleic Acids Research</i> , 2021, 49, 306-321.	14.5	21
14	A Structural Basis for Inhibition of the Complement Initiator Protease C1r by Lyme Disease Spirochetes. <i>Journal of Immunology</i> , 2021, 207, 2856-2867.	0.8	11
15	A key interaction with RPA orients XPA in NER complexes. <i>Nucleic Acids Research</i> , 2020, 48, 2173-2188.	14.5	34
16	Mechanism of efficient double-strand break repair by a long non-coding RNA. <i>Nucleic Acids Research</i> , 2020, 48, 10953-10972.	14.5	43
17	Structural analysis of a new carotenoid-binding protein: the C-terminal domain homolog of the OCP. <i>Scientific Reports</i> , 2020, 10, 15564.	3.3	18
18	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	9.3	46

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19	Quantitative Protein Corona Composition and Dynamics on Carbon Nanotubes in Biological Environments. <i>Angewandte Chemie</i> , 2020, 132, 23876-23885.	2.0	16
20	Quantitative Protein Corona Composition and Dynamics on Carbon Nanotubes in Biological Environments. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 23668-23677.	13.8	78
21	Nucleoid Remodeling During Environmental Adaptation as Seen Through Soft X-ray Tomography. <i>Microscopy and Microanalysis</i> , 2020, 26, 2532-2533.	0.4	0
22	Human XPG nuclease structure, assembly, and activities with insights for neurodegeneration and cancer from pathogenic mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14127-14138.	7.1	37
23	Nucleoid remodeling during environmental adaptation is regulated by HU-dependent DNA bundling. <i>Nature Communications</i> , 2020, 11, 2905.	12.8	39
24	Switchable resolution in soft x-ray tomography of single cells. <i>PLoS ONE</i> , 2020, 15, e0227601.	2.5	18
25	Functional Relevance of Interleukin-1 Receptor Inter-domain Flexibility for Cytokine Binding and Signaling. <i>Structure</i> , 2019, 27, 1296-1307.e5.	3.3	6
26	Flexible Tethering of ASPP Proteins Facilitates PP-1c Catalysis. <i>Structure</i> , 2019, 27, 1485-1496.e4.	3.3	23
27	Combined Solution and Crystal Methods Reveal the Electrostatic Tethers That Provide a Flexible Platform for Replication Activities in the Bacteriophage T7 Replisome. <i>Biochemistry</i> , 2019, 58, 4466-4479.	2.5	10
28	Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, .	6.0	41
29	Allosteric activation of the nitric oxide receptor soluble guanylate cyclase mapped by cryo-electron microscopy. <i>ELife</i> , 2019, 8, .	6.0	66
30	Scattering Methods and their Application in Colloid and Interface Science. By Otto Glatter. Elsevier, 2018. Paperback pp. 404. Price USD 225. Paperback (ISBN 9780128135808), ebook (ISBN 9780128135815).. <i>Journal of Applied Crystallography</i> , 2019, 52, 243-244.	4.5	0
31	Modeling Structure and Dynamics of Protein Complexes with SAXS Profiles. <i>Methods in Molecular Biology</i> , 2018, 1764, 449-473.	0.9	31
32	Structural Definition of a Unique Neutralization Epitope on the Receptor-Binding Domain of MERS-CoV Spike Glycoprotein. <i>Cell Reports</i> , 2018, 24, 441-452.	6.4	57
33	Conformational Plasticity of the Immunoglobulin Fc Domain in Solution. <i>Structure</i> , 2018, 26, 1007-1014.e2.	3.3	19
34	Hydrogen bonds are a primary driving force for <i>de novo</i> protein folding. Corrigendum. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 380-380.	2.3	1
35	The structural basis for the functional comparability of factor VIII and the long-acting variant recombinant factor VIII Fc fusion protein. <i>Journal of Thrombosis and Haemostasis</i> , 2017, 15, 1167-1179.	3.8	14
36	Structural and functional characterization of the PNKP-XRCC4-LigIV DNA repair complex. <i>Nucleic Acids Research</i> , 2017, 45, 6238-6251.	14.5	39

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37	Hybrid Methods Reveal Multiple Flexibly Linked DNA Polymerases within the Bacteriophage T7 Replisome. <i>Structure</i> , 2017, 25, 157-166.	3.3	17
38	Hydrogen bonds are a primary driving force for <i>de novo</i> protein folding. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 955-969.	2.3	9
39	FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. <i>Nucleic Acids Research</i> , 2016, 44, W424-W429.	14.5	427
40	Structural Basis for Interactions Between Contactin Family Members and Protein-tyrosine Phosphatase Receptor Type G in Neural Tissues. <i>Journal of Biological Chemistry</i> , 2016, 291, 21335-21349.	3.4	32
41	An Intrinsically Disordered APLF Links Ku, DNA-PKcs, and XRCC4-DNA Ligase IV in an Extended Flexible Non-homologous End Joining Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 26987-27006.	3.4	61
42	HU multimerization shift controls nucleoid compaction. <i>Science Advances</i> , 2016, 2, e1600650.	10.3	144
43	Structural Basis for Marburg Virus Neutralization by a Cross-Reactive Human Antibody. <i>Cell</i> , 2015, 160, 904-912.	28.9	110
44	Mechanistic insights into the role of Hop2-Mnd1 in meiotic homologous DNA pairing. <i>Nucleic Acids Research</i> , 2014, 42, 906-917.	14.5	52
45	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014, 42, D336-D346.	14.5	275
46	High-Throughput SAXS for the Characterization of Biomolecules in Solution: A Practical Approach. <i>Methods in Molecular Biology</i> , 2014, 1091, 245-258.	0.9	176
47	Structural insights into NHEJ: Building up an integrated picture of the dynamic DSB repair super complex, one component and interaction at a time. <i>DNA Repair</i> , 2014, 17, 110-120.	2.8	100
48	Distinct Structural Features of the Peroxide Response Regulator from Group A Streptococcus Drive DNA Binding. <i>PLoS ONE</i> , 2014, 9, e89027.	2.5	13
49	Atypical Response Regulator ChxR from <i>Chlamydia trachomatis</i> Is Structurally Poised for DNA Binding. <i>PLoS ONE</i> , 2014, 9, e91760.	2.5	11
50	Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. <i>Biophysical Journal</i> , 2013, 105, 962-974.	0.5	489
51	Implementation and performance of SIBYLS: a dual endstation small-angle X-ray scattering and macromolecular crystallography beamline at the Advanced Light Source. <i>Journal of Applied Crystallography</i> , 2013, 46, 1-13.	4.5	208
52	XRCC4 and XLF form long helical protein filaments suitable for DNA end protection and alignment to facilitate DNA double strand break repair. <i>Biochemistry and Cell Biology</i> , 2013, 91, 31-41.	2.0	91
53	Functional Intersection of ATM and DNA-Dependent Protein Kinase Catalytic Subunit in Coding End Joining during V(D)J Recombination. <i>Molecular and Cellular Biology</i> , 2013, 33, 3568-3579.	2.3	39
54	Structural insights into the interaction of IL-33 with its receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14918-14923.	7.1	155

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55	Comprehensive macromolecular conformations mapped by quantitative SAXS analyses. <i>Nature Methods</i> , 2013, 10, 453-454.	19.0	112
56	Mechanism of ubiquitin ligation and lysine prioritization by a HECT E3. <i>ELife</i> , 2013, 2, e00828.	6.0	130
57	Structure of a Glomulin-RBX1-CUL1 Complex: Inhibition of a RING E3 Ligase through Masking of Its E2-Binding Surface. <i>Molecular Cell</i> , 2012, 47, 371-382.	9.7	71
58	Binding to retinoblastoma pocket domain does not alter the inter-domain flexibility of the J domain of SV40 large T antigen. <i>Archives of Biochemistry and Biophysics</i> , 2012, 518, 111-118.	3.0	4
59	Validation of macromolecular flexibility in solution by small-angle X-ray scattering (SAXS). <i>European Biophysics Journal</i> , 2012, 41, 789-799.	2.2	100
60	Atg8 Transfer from Atg7 to Atg3: A Distinctive E1-E2 Architecture and Mechanism in the Autophagy Pathway. <i>Molecular Cell</i> , 2011, 44, 451-461.	9.7	135
61	Macromolecular docking restrained by a small angle X-ray scattering profile. <i>Journal of Structural Biology</i> , 2011, 173, 461-471.	2.8	97
62	The Immunoglobulin-like Domains 1 and 2 of the Protein Tyrosine Phosphatase LAR Adopt an Unusual Horseshoe-like Conformation. <i>Journal of Molecular Biology</i> , 2011, 408, 616-627.	4.2	19
63	ABC ATPase signature helices in Rad50 link nucleotide state to Mre11 interface for DNA repair. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 423-431.	8.2	149
64	XRCC4 Protein Interactions with XRCC4-like Factor (XLF) Create an Extended Grooved Scaffold for DNA Ligation and Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2011, 286, 32638-32650.	3.4	151
65	XLF Regulates Filament Architecture of the XRCC4-XLF-Ligase IV Complex. <i>Structure</i> , 2010, 18, 1431-1442.	3.3	104
66	Software for the high-throughput collection of SAXS data using an enhanced <i>BlueICE</i> control system. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 774-781.	2.4	39
67	Enhancement of RAD51 recombinase activity by the tumor suppressor PALB2. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1255-1259.	8.2	146
68	FoXS: a web server for rapid computation and fitting of SAXS profiles. <i>Nucleic Acids Research</i> , 2010, 38, W540-W544.	14.5	474
69	Ku and DNA-dependent Protein Kinase Dynamic Conformations and Assembly Regulate DNA Binding and the Initial Non-homologous End Joining Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 1414-1423.	3.4	189
70	Allosteric inhibition of complement function by a staphylococcal immune evasion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17621-17626.	7.1	77
71	Human DNA Ligase III Recognizes DNA Ends by Dynamic Switching between Two DNA-Bound States. <i>Biochemistry</i> , 2010, 49, 6165-6176.	2.5	90
72	Structure and flexibility within proteins as identified through small angle X-ray scattering. <i>General Physiology and Biophysics</i> , 2009, 28, 174-189.	0.9	374

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73	A Molecular Insight into Complement Evasion by the Staphylococcal Complement Inhibitor Protein Family. <i>Journal of Immunology</i> , 2009, 183, 2565-2574.	0.8	63
74	Interdomain Communication in the Mycobacterium tuberculosis Environmental Phosphatase Rv1364c. <i>Journal of Biological Chemistry</i> , 2009, 284, 29828-29835.	3.4	11
75	Mechanism of DNA substrate recognition by the mammalian DNA repair enzyme, Polynucleotide Kinase. <i>Nucleic Acids Research</i> , 2009, 37, 6161-6173.	14.5	48
76	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). <i>Nature Methods</i> , 2009, 6, 606-612.	19.0	610
77	Structural Insights into Yeast DNA Polymerase $\hat{\nu}$ by Small Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2009, 394, 377-382.	4.2	38
78	Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases. <i>Molecular Cell</i> , 2009, 36, 39-50.	9.7	403
79	XPD Helicase Structures and Activities: Insights into the Cancer and Aging Phenotypes from XPD Mutations. <i>Cell</i> , 2008, 133, 789-800.	28.9	593
80	Structural Insights into NEDD8 Activation of Cullin-RING Ligases: Conformational Control of Conjugation. <i>Cell</i> , 2008, 134, 995-1006.	28.9	659
81	Characterization of Ehp, a Secreted Complement Inhibitory Protein from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 30051-30061.	3.4	84
82	A structural basis for complement inhibition by <i>Staphylococcus aureus</i> . <i>Nature Immunology</i> , 2007, 8, 430-437.	14.5	148
83	X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. <i>Quarterly Reviews of Biophysics</i> , 2007, 40, 191-285.	5.7	1,026
84	The <i>Staphylococcus aureus</i> extracellular adherence protein (Eap) adopts an elongated but structured conformation in solution. <i>Protein Science</i> , 2007, 16, 2605-2617.	7.6	32
85	Crystallization and X-ray diffraction analysis of the complement component-3 (C3) inhibitory domain of Efb from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 285-288.	0.7	3
86	Modular Structure of Solubilized Human Apolipoprotein B-100. <i>Journal of Biological Chemistry</i> , 2006, 281, 19732-19739.	3.4	67
87	Structural Basis of Cellulosome Efficiency Explored by Small Angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2005, 280, 38562-38568.	3.4	95
88	Structural Insights into the Mechanism of Formation of Cellulosomes Probed by Small Angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2004, 279, 55985-55994.	3.4	48
89	Structural Flexibility of the N-terminal $\hat{\nu}$ -Barrel Domain of 15-Lipoxygenase-1 Probed by Small Angle X-ray Scattering. Functional Consequences for Activity Regulation and Membrane Binding. <i>Journal of Molecular Biology</i> , 2004, 343, 917-929.	4.2	51
90	Structural characterisation of nucleoside loaded low density lipoprotein as a main criterion for the applicability as drug delivery system. <i>Chemistry and Physics of Lipids</i> , 2003, 123, 193-207.	3.2	23

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91	Solution Structure of Human and Bovine $\beta$ 2-Glycoprotein I Revealed by Small-angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2002, 321, 85-97.	4.2	90
92	Partition of local anesthetic heptacaine homologs between phosphatidylcholine bilayers in unilamellar liposomes and aqueous phase: UV-VIS spectrophotometry study. <i>Die Pharmazie</i> , 2002, 57, 499.	0.5	4
93	Mechanism of the Interaction of $\beta$ 2-Glycoprotein I with Negatively Charged Phospholipid Membranes. <i>Biochemistry</i> , 2001, 40, 14173-14181.	2.5	48
94	An improved method for the sensitive monitoring of low density lipoprotein modification by myeloperoxidase. <i>Redox Report</i> , 2001, 6, 257-264.	4.5	1
95	Kinetics of tryptophan oxidation in plasma lipoproteins by myeloperoxidase-generated HOCl. <i>FEBS Journal</i> , 2000, 267, 4137-4143.	0.2	22
96	Comparison of HOCl traps with myeloperoxidase inhibitors in prevention of low density lipoprotein oxidation. <i>BBA - Proteins and Proteomics</i> , 2000, 1481, 109-118.	2.1	33