

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 | X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. Quarterly Reviews of Biophysics, 2007, 40, 191-285. | 5.7 | 1,026 |
| 2 | Structural Insights into NEDD8 Activation of Cullin-RING Ligases: Conformational Control of Conjugation. Cell, 2008, 134, 995-1006. | 28.9 | 659 |
| 3 | Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). Nature Methods, 2009, 6, 606-612. | 19.0 | 610 |
| 4 | XPD Helicase Structures and Activities: Insights into the Cancer and Aging Phenotypes from XPD Mutations. Cell, 2008, 133, 789-800. | 28.9 | 593 |
| 5 | Accurate SAXS Profile Computation and its Assessment by Contrast Variation Experiments. Biophysical Journal, 2013, 105, 962-974. | 0.5 | 489 |
| 6 | FoXS: a web server for rapid computation and fitting of SAXS profiles. Nucleic Acids Research, 2010, 38, W540-W544. | 14.5 | 474 |
| 7 | FoXS, FoXSDock and MultiFoXS: Single-state and multi-state structural modeling of proteins and their complexes based on SAXS profiles. Nucleic Acids Research, 2016, 44, W424-W429. | 14.5 | 427 |
| 8 | Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases. Molecular Cell, 2009, 36, 39-50. | 9.7 | 403 |
| 9 | Structure and flexibility within proteins as identified through small angle X-ray scattering. General Physiology and Biophysics, 2009, 28, 174-189. | 0.9 | 374 |
| 10 | ModBase, a database of annotated comparative protein structure models and associated resources. Nucleic Acids Research, 2014, 42, D336-D346. | 14.5 | 275 |
| 11 | Implementation and performance of SIBYLS: a dual endstation small-angle X-ray scattering and macromolecular crystallography beamline at the Advanced Light Source. Journal of Applied Crystallography, 2013, 46, 1-13. | 4.5 | 208 |
| 12 | Ku and DNA-dependent Protein Kinase Dynamic Conformations and Assembly Regulate DNA Binding and the Initial Non-homologous End Joining Complex. Journal of Biological Chemistry, 2010, 285, 1414-1423. | 3.4 | 189 |
| 13 | High-Throughput SAXS for the Characterization of Biomolecules in Solution: A Practical Approach. Methods in Molecular Biology, 2014, 1091, 245-258. | 0.9 | 176 |
| 14 | Structural insights into the interaction of IL-33 with its receptors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14918-14923. | 7.1 | 155 |
| 15 | XRCC4 Protein Interactions with XRCC4-like Factor (XLF) Create an Extended Grooved Scaffold for DNA Ligation and Double Strand Break Repair. Journal of Biological Chemistry, 2011, 286, 32638-32650. | 3.4 | 151 |
| 16 | ABC ATPase signature helices in Rad50 link nucleotide state to Mre11 interface for DNA repair. Nature Structural and Molecular Biology, 2011, 18, 423-431. | 8.2 | 149 |
| 17 | A structural basis for complement inhibition by Staphylococcus aureus. Nature Immunology, 2007, 8, 430-437. | 14.5 | 148 |
| 18 | Enhancement of RAD51 recombinase activity by the tumor suppressor PALB2. Nature Structural and Molecular Biology, 2010, 17, 1255-1259. | 8.2 | 146 |

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|----|---|------|-----------|
| 19 | HU multimerization shift controls nucleoid compaction. <i>Science Advances</i> , 2016, 2, e1600650. | 10.3 | 144 |
| 20 | 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 |
| 21 | Mechanism of ubiquitin ligation and lysine prioritization by a HECT E3. <i>ELife</i> , 2013, 2, e00828. | 6.0 | 130 |
| 22 | Comprehensive macromolecular conformations mapped by quantitative SAXS analyses. <i>Nature Methods</i> , 2013, 10, 453-454. | 19.0 | 112 |
| 23 | Structural Basis for Marburg Virus Neutralization by a Cross-Reactive Human Antibody. <i>Cell</i> , 2015, 160, 904-912. | 28.9 | 110 |
| 24 | XLF Regulates Filament Architecture of the XRCC4-Ligase IV Complex. <i>Structure</i> , 2010, 18, 1431-1442. | 3.3 | 104 |
| 25 | 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 |
| 26 | 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 |
| 27 | Macromolecular docking restrained by a small angle X-ray scattering profile. <i>Journal of Structural Biology</i> , 2011, 173, 461-471. | 2.8 | 97 |
| 28 | 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 |
| 29 | 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 |
| 30 | Solution Structure of Human and Bovine β 2-Glycoprotein I Revealed by Small-angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2002, 321, 85-97. | 4.2 | 90 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | Modular Structure of Solubilized Human Apolipoprotein B-100. <i>Journal of Biological Chemistry</i> , 2006, 281, 19732-19739. | 3.4 | 67 |

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|----|--|------|-----------|
| 37 | Allosteric activation of the nitric oxide receptor soluble guanylate cyclase mapped by cryo-electron microscopy. <i>ELife</i> , 2019, 8, . | 6.0 | 66 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | Structural Flexibility of the N-terminal Î²-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 |
| 43 | Mechanism of the Interaction of Î²2-Glycoprotein I with Negatively Charged Phospholipid Membranes. <i>Biochemistry</i> , 2001, 40, 14173-14181. | 2.5 | 48 |
| 44 | 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 |
| 45 | 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 |
| 46 | Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166. | 9.3 | 46 |
| 47 | 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 |
| 48 | 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 |
| 49 | Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, . | 6.0 | 41 |
| 50 | Software for the high-throughput collection of SAXS data using an enhanced Blu-Ice/DCS control system. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 774-781. | 2.4 | 39 |
| 51 | 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 |
| 52 | Structural and functional characterization of the PNKP-XRCC4-LigIV DNA repair complex. <i>Nucleic Acids Research</i> , 2017, 45, 6238-6251. | 14.5 | 39 |
| 53 | Nucleoid remodeling during environmental adaptation is regulated by HU-dependent DNA bundling. <i>Nature Communications</i> , 2020, 11, 2905. | 12.8 | 39 |
| 54 | 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 |

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|----|---|------|-----------|
| 55 | Structural Insights into Yeast DNA Polymerase δ by Small Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2009, 394, 377-382. | 4.2 | 38 |
| 56 | 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 |
| 57 | A key interaction with RPA orients XPA in NER complexes. <i>Nucleic Acids Research</i> , 2020, 48, 2173-2188. | 14.5 | 34 |
| 58 | 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 |
| 59 | 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 |
| 60 | 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 |
| 61 | Modeling Structure and Dynamics of Protein Complexes with SAXS Profiles. <i>Methods in Molecular Biology</i> , 2018, 1764, 449-473. | 0.9 | 31 |
| 62 | 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 |
| 63 | Flexible Tethering of ASPP Proteins Facilitates PP-1c Catalysis. <i>Structure</i> , 2019, 27, 1485-1496.e4. | 3.3 | 23 |
| 64 | Kinetics of tryptophan oxidation in plasma lipoproteins by myeloperoxidase-generated HOCl. <i>FEBS Journal</i> , 2000, 267, 4137-4143. | 0.2 | 22 |
| 65 | An atypical BRCT-BRCT interaction with the XRCC1 scaffold protein compacts human DNA Ligase III β within a flexible DNA repair complex. <i>Nucleic Acids Research</i> , 2021, 49, 306-321. | 14.5 | 21 |
| 66 | 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 |
| 67 | 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 |
| 68 | Conformational Plasticity of the Immunoglobulin Fc Domain in Solution. <i>Structure</i> , 2018, 26, 1007-1014.e2. | 3.3 | 19 |
| 69 | X-ray scattering reveals disordered linkers and dynamic interfaces in complexes and mechanisms for λ -DNA double-strand break repair impacting cell and cancer biology. <i>Protein Science</i> , 2021, 30, 1735-1756. | 7.6 | 19 |
| 70 | 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 |
| 71 | Switchable resolution in soft x-ray tomography of single cells. <i>PLoS ONE</i> , 2020, 15, e0227601. | 2.5 | 18 |
| 72 | Hybrid Methods Reveal Multiple Flexibly Linked DNA Polymerases within the Bacteriophage T7 Replisome. <i>Structure</i> , 2017, 25, 157-166. | 3.3 | 17 |

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|----|--|------|-----------|
| 73 | Quantitative Protein Corona Composition and Dynamics on Carbon Nanotubes in Biological Environments. <i>Angewandte Chemie</i> , 2020, 132, 23876-23885. | 2.0 | 16 |
| 74 | Rigid monoclonal antibodies improve detection of SARS-CoV-2 nucleocapsid protein. <i>MAbs</i> , 2021, 13, 1905978. | 5.2 | 16 |
| 75 | 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 |
| 76 | Albumin in patients with liver disease shows an altered conformation. <i>Communications Biology</i> , 2021, 4, 731. | 4.4 | 14 |
| 77 | Structural basis for SHOC2 modulation of RAS signalling. <i>Nature</i> , 2022, 609, 400-407. | 27.8 | 14 |
| 78 | 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 |
| 79 | 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 |
| 80 | Interdomain Communication in the Mycobacterium tuberculosis Environmental Phosphatase Rv1364c. <i>Journal of Biological Chemistry</i> , 2009, 284, 29828-29835. | 3.4 | 11 |
| 81 | Atypical Response Regulator ChxR from Chlamydia trachomatis Is Structurally Poised for DNA Binding. <i>PLoS ONE</i> , 2014, 9, e91760. | 2.5 | 11 |
| 82 | 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 |
| 83 | 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 |
| 84 | 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 |
| 85 | 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 |
| 86 | 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 |
| 87 | A monomeric mycobacteriophage immunity repressor utilizes two domains to recognize an asymmetric DNA sequence. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 5 |
| 88 | 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 |
| 89 | 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 |
| 90 | 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 |

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|----|---|-----|-----------|
| 91 | Heparin-mediated dimerization of follistatin. <i>Experimental Biology and Medicine</i> , 2021, 246, 467-482. | 2.4 | 3 |
| 92 | 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 |
| 93 | 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 |
| 94 | Nucleoid Remodeling During Environmental Adaptation as Seen Through Soft X-ray Tomography. <i>Microscopy and Microanalysis</i> , 2020, 26, 2532-2533. | 0.4 | 0 |
| 95 | 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 |
| 96 | Structural arrangement of the VH and VL domains in the COBRA ^Δ T-cell engaging single-chain diabody. <i>Antibody Therapeutics</i> , 2022, 5, 1-10. | 1.9 | 0 |