

Kaspar Locher

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

7,691
citations

159525

30
h-index

182361

51
g-index

71
all docs

71
docs citations

71
times ranked

5893
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Structure of a bacterial multidrug ABC transporter. <i>Nature</i> , 2006, 443, 180-185. | 13.7 | 1,200 |
| 2 | The <i>E. coli</i> BtuCD Structure: A Framework for ABC Transporter Architecture and Mechanism. <i>Science</i> , 2002, 296, 1091-1098. | 6.0 | 1,039 |
| 3 | Mechanistic diversity in ATP-binding cassette (ABC) transporters. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 487-493. | 3.6 | 612 |
| 4 | Structure of an ABC transporter in complex with its binding protein. <i>Nature</i> , 2007, 446, 213-216. | 13.7 | 441 |
| 5 | Structure and mechanism of ATP-binding cassette transporters. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 239-245. | 1.8 | 344 |
| 6 | Structure of the human multidrug transporter ABCG2. <i>Nature</i> , 2017, 546, 504-509. | 13.7 | 332 |
| 7 | Structural insight into substrate and inhibitor discrimination by human P-glycoprotein. <i>Science</i> , 2019, 363, 753-756. | 6.0 | 330 |
| 8 | X-ray structure of a bacterial oligosaccharyltransferase. <i>Nature</i> , 2011, 474, 350-355. | 13.7 | 323 |
| 9 | Asymmetry in the Structure of the ABC Transporter-Binding Protein Complex BtuCD-BtuF. <i>Science</i> , 2007, 317, 1387-1390. | 6.0 | 260 |
| 10 | Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 333-340. | 3.6 | 258 |
| 11 | The structure of <i>Escherichia coli</i> BtuF and binding to its cognate ATP binding cassette transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16642-16647. | 3.3 | 209 |
| 12 | Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. <i>Nature</i> , 2018, 563, 426-430. | 13.7 | 188 |
| 13 | Structure and mechanism of an active lipid-linked oligosaccharide flippase. <i>Nature</i> , 2015, 524, 433-438. | 13.7 | 184 |
| 14 | Structure of the yeast oligosaccharyltransferase complex gives insight into eukaryotic N-glycosylation. <i>Science</i> , 2018, 359, 545-550. | 6.0 | 157 |
| 15 | Structure of AMP-PNP-bound vitamin B12 transporter BtuCD-F. <i>Nature</i> , 2012, 490, 367-372. | 13.7 | 153 |
| 16 | Structure of a zosuquidar and UIC2-bound human-mouse chimeric ABCB1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1973-E1982. | 3.3 | 153 |
| 17 | In Vitro Functional Characterization of BtuCD-F, the <i>Escherichia coli</i> ABC Transporter for Vitamin B12 Uptake. <i>Biochemistry</i> , 2005, 44, 16301-16309. | 1.2 | 146 |
| 18 | Cryo-EM structures reveal distinct mechanisms of inhibition of the human multidrug transporter ABCB1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26245-26253. | 3.3 | 137 |

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|----|--|------|-----------|
| 19 | A distinct mechanism for the ABC transporter BtuCDâ€“BtuF revealed by the dynamics of complex formation. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 332-338. | 3.6 | 105 |
| 20 | Cryoâ€“electron microscopy structures of human oligosaccharyltransferase complexes OST-A and OST-B. <i>Science</i> , 2019, 366, 1372-1375. | 6.0 | 77 |
| 21 | Mechanism of Bacterial Oligosaccharyltransferase. <i>Journal of Biological Chemistry</i> , 2013, 288, 8849-8861. | 1.6 | 72 |
| 22 | Molecular basis of lipid-linked oligosaccharide recognition and processing by bacterial oligosaccharyltransferase. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1100-1106. | 3.6 | 68 |
| 23 | Structure of the human lipid exporter ABCB4 in a lipid environment. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 62-70. | 3.6 | 68 |
| 24 | Structure of AMP-PNPâ€“bound BtuCD and mechanism of ATP-powered vitamin B12 transport by BtuCDâ€“F. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1097-1099. | 3.6 | 65 |
| 25 | Unexpected reactivity and mechanism of carboxamide activation in bacterial N-linked protein glycosylation. <i>Nature Communications</i> , 2013, 4, 2627. | 5.8 | 53 |
| 26 | Structure and mechanism of the ER-based glucosyltransferase ALG6. <i>Nature</i> , 2020, 579, 443-447. | 13.7 | 52 |
| 27 | Structural Basis of Drug Recognition by the Multidrug Transporter ABCG2. <i>Journal of Molecular Biology</i> , 2021, 433, 166980. | 2.0 | 52 |
| 28 | Structures of ABCG2 under turnover conditions reveal a key step in the drug transport mechanism. <i>Nature Communications</i> , 2021, 12, 4376. | 5.8 | 46 |
| 29 | Development of a universal nanobody-binding Fab module for fiducial-assisted cryo-EM studies of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 40 |
| 30 | Structural basis of transcobalamin recognition by human CD320 receptor. <i>Nature Communications</i> , 2016, 7, 12100. | 5.8 | 39 |
| 31 | Role of Multidrug Resistance Protein 3 in Antifungal-Induced Cholestasis. <i>Molecular Pharmacology</i> , 2016, 90, 23-34. | 1.0 | 39 |
| 32 | Chemo-enzymatic synthesis of lipid-linked GlcNAc2Man5 oligosaccharides using recombinant Alg1, Alg2 and Alg11 proteins. <i>Glycobiology</i> , 2017, 27, 726-733. | 1.3 | 33 |
| 33 | Characterization of the single-subunit oligosaccharyltransferase STT3A from <i>Trypanosoma brucei</i> using synthetic peptides and lipid-linked oligosaccharide analogs. <i>Glycobiology</i> , 2017, 27, 525-535. | 1.3 | 31 |
| 34 | Structural basis of the molecular ruler mechanism of a bacterial glycosyltransferase. <i>Nature Communications</i> , 2018, 9, 445. | 5.8 | 31 |
| 35 | Membrane lipids and transporter function. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166079. | 1.8 | 31 |
| 36 | Asymmetric states of vitamin B ₁₂ transporter BtuCD are not discriminated by its cognate substrate binding protein BtuF. <i>FEBS Letters</i> , 2012, 586, 972-976. | 1.3 | 29 |

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|----|---|-----|-----------|
| 37 | Structure of Outward-Facing PglK and Molecular Dynamics of Lipid-Linked Oligosaccharide Recognition and Translocation. <i>Structure</i> , 2019, 27, 669-678.e5. | 1.6 | 29 |
| 38 | A Catalytically Essential Motif in External Loop 5 of the Bacterial Oligosaccharyltransferase PglB. <i>Journal of Biological Chemistry</i> , 2014, 289, 735-746. | 1.6 | 26 |
| 39 | Structure of bacterial oligosaccharyltransferase PglB bound to a reactive LLO and an inhibitory peptide. <i>Scientific Reports</i> , 2018, 8, 16297. | 1.6 | 26 |
| 40 | Discovery and Characterization of Potent Dual P-Glycoprotein and CYP3A4 Inhibitors: Design, Synthesis, Cryo-EM Analysis, and Biological Evaluations. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 191-216. | 2.9 | 25 |
| 41 | Structures of ABCB4 provide insight into phosphatidylcholine translocation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 3.3 | 24 |
| 42 | Structural basis of inhibition of lipid-linked oligosaccharide flippase PglK by a conformational nanobody. <i>Scientific Reports</i> , 2017, 7, 46641. | 1.6 | 23 |
| 43 | Tariquidar-related triazoles as potent, selective and stable inhibitors of ABCG2 (BCRP). <i>European Journal of Medicinal Chemistry</i> , 2020, 191, 112133. | 2.6 | 22 |
| 44 | Structure of the Human Cholesterol Transporter ABCG1. <i>Journal of Molecular Biology</i> , 2021, 433, 167218. | 2.0 | 22 |
| 45 | Structure of human NTCP reveals the basis of recognition and sodium-driven transport of bile salts into the liver. <i>Cell Research</i> , 2022, 32, 773-776. | 5.7 | 21 |
| 46 | Structural basis of nanobody-mediated blocking of BtuF, the cognate substrate-binding protein of the <i>Escherichia coli</i> vitamin B12 transporter BtuCD. <i>Scientific Reports</i> , 2017, 7, 14296. | 1.6 | 20 |
| 47 | Conformational Change of a Tryptophan Residue in BtuF Facilitates Binding and Transport of Cobinamide by the Vitamin B12 Transporter BtuCD-F. <i>Scientific Reports</i> , 2017, 7, 41575. | 1.6 | 18 |
| 48 | Binding Specificities of Nanobody-Membrane Protein Complexes Obtained from Chemical Cross-Linking and High-Mass MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 5306-5313. | 3.2 | 15 |
| 49 | Substrate specificities and reaction kinetics of the yeast oligosaccharyltransferase isoforms. <i>Journal of Biological Chemistry</i> , 2021, 296, 100809. | 1.6 | 6 |
| 50 | Structure of the human transcobalamin beta domain in four distinct states. <i>PLoS ONE</i> , 2017, 12, e0184932. | 1.1 | 5 |
| 51 | Functional analysis of Ost3p and Ost6p containing yeast oligosaccharyltransferases. <i>Glycobiology</i> , 2021, 31, 1604-1615. | 1.3 | 4 |
| 52 | STRUCTURES AND REACTION MECHANISMS OF ABC TRANSPORTERS. , 2014, , . | | 0 |
| 53 | Generation of nanobodies targeting the human, transcobalamin-mediated vitamin B ₁₂ uptake route. <i>FASEB Journal</i> , 2022, 36, e22222. | 0.2 | 0 |