Kaspar Locher

List of Publications by Year
in descending order

53	7,691	159525	182361
papers	citations	30 h-index	51 g-index

71	71	71	5893
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Generation of nanobodies targeting the human, transcobalaminâ€mediated vitamin B ₁₂ uptake route. FASEB Journal, 2022, 36, e22222.	0.2	0
2	Discovery and Characterization of Potent Dual P-Glycoprotein and CYP3A4 Inhibitors: Design, Synthesis, Cryo-EM Analysis, and Biological Evaluations. Journal of Medicinal Chemistry, 2022, 65, 191-216.	2.9	25
3	Structure of human NTCP reveals the basis of recognition and sodium-driven transport of bile salts into the liver. Cell Research, 2022, 32, 773-776.	5.7	21
4	Substrate specificities and reaction kinetics of the yeast oligosaccharyltransferase isoforms. Journal of Biological Chemistry, 2021, 296, 100809.	1.6	6
5	Membrane lipids and transporter function. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2021, 1867, 166079.	1.8	31
6	Structural Basis of Drug Recognition by the Multidrug Transporter ABCG2. Journal of Molecular Biology, 2021, 433, 166980.	2.0	52
7	Structures of ABCG2 under turnover conditions reveal a key step in the drug transport mechanism. Nature Communications, 2021, 12, 4376.	5.8	46
8	Structures of ABCB4 provide insight into phosphatidylcholine translocation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	24
9	Structure of the Human Cholesterol Transporter ABCG1. Journal of Molecular Biology, 2021, 433, 167218.	2.0	22
10	Development of a universal nanobody-binding Fab module for fiducial-assisted cryo-EM studies of membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	40
11	Functional analysis of Ost3p and Ost6p containing yeast oligosaccharyltransferases. Glycobiology, 2021, 31, 1604-1615.	1.3	4
12	Structure of the human lipid exporter ABCB4 in a lipid environment. Nature Structural and Molecular Biology, 2020, 27, 62-70.	3.6	68
13	Cryo-EM structures reveal distinct mechanisms of inhibition of the human multidrug transporter ABCB1. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26245-26253.	3.3	137
14	Structure and mechanism of the ER-based glucosyltransferase ALG6. Nature, 2020, 579, 443-447.	13.7	52
15	Tariquidar-related triazoles as potent, selective and stable inhibitors of ABCG2 (BCRP). European Journal of Medicinal Chemistry, 2020, 191, 112133.	2.6	22
16	Structure of Outward-Facing PglK and Molecular Dynamics of Lipid-Linked Oligosaccharide Recognition and Translocation. Structure, 2019, 27, 669-678.e5.	1.6	29
17	Structural insight into substrate and inhibitor discrimination by human P-glycoprotein. Science, 2019, 363, 753-756.	6.0	330
18	Cryoâ€“electron microscopy structures of human oligosaccharyltransferase complexes OST-A and OST-B. Science, 2019, 366, 1372-1375.	6.0	77

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19	Structure of a zosuquidar and UIC2-bound human-mouse chimeric ABCB1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1973-E1982.	3.3	153
20	Structural basis of the molecular ruler mechanism of a bacterial glycosyltransferase. Nature Communications, 2018, 9, 445.	5.8	31
21	Structure of the yeast oligosaccharyltransferase complex gives insight into eukaryotic N-glycosylation. Science, 2018, 359, 545-550.	6.0	157
22	Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. Nature Structural and Molecular Biology, 2018, 25, 333-340.	3.6	258
23	Binding Specificities of Nanobodyâ€¢Membrane Protein Complexes Obtained from Chemical Cross-Linking and High-Mass MALDI Mass Spectrometry. Analytical Chemistry, 2018, 90, 5306-5313.	3.2	15
24	Structure of bacterial oligosaccharyltransferase PglB bound to a reactive LLO and an inhibitory peptide. Scientific Reports, 2018, 8, 16297.	1.6	26
25	Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. Nature, 2018, 563, 426-430.	13.7	188
26	Conformational Change of a Tryptophan Residue in BtuF Facilitates Binding and Transport of Cobinamide by the Vitamin B12 Transporter BtuCD-F. Scientific Reports, 2017, 7, 41575.	1.6	18
27	Structural basis of inhibition of lipid-linked oligosaccharide flippase PglK by a conformational nanobody. Scientific Reports, 2017, 7, 46641.	1.6	23
28	Chemo-enzymatic synthesis of lipid-linked GlcNAc2Man5 oligosaccharides using recombinant Alg1, Alg2 and Alg11 proteins. Glycobiology, 2017, 27, 726-733.	1.3	33
29	Structure of the human multidrug transporter ABCG2. Nature, 2017, 546, 504-509.	13.7	332
30	Molecular basis of lipid-linked oligosaccharide recognition and processing by bacterial oligosaccharyltransferase. Nature Structural and Molecular Biology, 2017, 24, 1100-1106.	3.6	68
31	Structural basis of nanobody-mediated blocking of BtuF, the cognate substrate-binding protein of the Escherichia coli vitamin B12 transporter BtuCD. Scientific Reports, 2017, 7, 14296.	1.6	20
32	Characterization of the single-subunit oligosaccharyltransferase STT3A from Trypanosoma brucei using synthetic peptides and lipid-linked oligosaccharide analogs. Glycobiology, 2017, 27, 525-535.	1.3	31
33	Structure of the human transcobalamin beta domain in four distinct states. PLoS ONE, 2017, 12, e0184932.	1.1	5
34	Structural basis of transcobalamin recognition by human CD320 receptor. Nature Communications, 2016, 7, 12100.	5.8	39
35	Mechanistic diversity in ATP-binding cassette (ABC) transporters. Nature Structural and Molecular Biology, 2016, 23, 487-493.	3.6	612
36	Role of Multidrug Resistance Protein 3 in Antifungal-Induced Cholestasis. Molecular Pharmacology, 2016, 90, 23-34.	1.0	39

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37	Structure and mechanism of an active lipid-linked oligosaccharide flippase. Nature, 2015, 524, 433-438.	13.7	184
38	STRUCTURES AND REACTION MECHANISMS OF ABC TRANSPORTERS. , 2014, , .		0
39	Structure of AMP-PNPâ€“bound BtuCD and mechanism of ATP-powered vitamin B12 transport by BtuCDâ€“F. Nature Structural and Molecular Biology, 2014, 21, 1097-1099.	3.6	65
40	A Catalytically Essential Motif in External Loop 5 of the Bacterial Oligosaccharyltransferase PglB. Journal of Biological Chemistry, 2014, 289, 735-746.	1.6	26
41	Unexpected reactivity and mechanism of carboxamide activation in bacterial N-linked protein glycosylation. Nature Communications, 2013, 4, 2627.	5.8	53
42	Mechanism of Bacterial Oligosaccharyltransferase. Journal of Biological Chemistry, 2013, 288, 8849-8861.	1.6	72
43	Structure of AMP-PNP-bound vitamin B12 transporter BtuCDâ€“F. Nature, 2012, 490, 367-372.	13.7	153
44	Asymmetric states of vitamin B₁₂ transporter BtuCD are not discriminated by its cognate substrate binding protein BtuF. FEBS Letters, 2012, 586, 972-976.	1.3	29
45	X-ray structure of a bacterial oligosaccharyltransferase. Nature, 2011, 474, 350-355.	13.7	323
46	A distinct mechanism for the ABC transporter BtuCDâ€“BtuF revealed by the dynamics of complex formation. Nature Structural and Molecular Biology, 2010, 17, 332-338.	3.6	105
47	Structure and mechanism of ATP-binding cassette transporters. Philosophical Transactions of the Royal Society B: Biological Sciences, 2009, 364, 239-245.	1.8	344
48	Asymmetry in the Structure of the ABC Transporter-Binding Protein Complex BtuCD-BtuF. Science, 2007, 317, 1387-1390.	6.0	260
49	Structure of an ABC transporter in complex with its binding protein. Nature, 2007, 446, 213-216.	13.7	441
50	Structure of a bacterial multidrug ABC transporter. Nature, 2006, 443, 180-185.	13.7	1,200
51	In Vitro Functional Characterization of BtuCD-F, theEscherichia coliABC Transporter for Vitamin B12Uptakeâ€. Biochemistry, 2005, 44, 16301-16309.	1.2	146
52	The structure of Escherichia coli BtuF and binding to its cognate ATP binding cassette transporter. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16642-16647.	3.3	209
53	The E. coli BtuCD Structure: A Framework for ABC Transporter Architecture and Mechanism. Science, 2002, 296, 1091-1098.	6.0	1,039