Tobias Krojer

List of Publications by Year
in descending order

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Version: 2024-02-01

61 papers	4,592 citations	117453 34 h-index	114278 63 g-index
72 all docs	72 docs citations	72 times ranked	6729 citing authors

#	Article	IF	Citations
1	Identification of fragments binding to SARS-CoV-2 nsp10 reveals ligand-binding sites in conserved interfaces between nsp10 and nsp14/nsp16. RSC Chemical Biology, 2022, 3, 44-55.	2.0	23
2	Experiences From Developing Software for Large X-Ray Crystallography-Driven Protein-Ligand Studies. Frontiers in Molecular Biosciences, 2022, 9, 861491.	1.6	1
3	Novel Starting Points for Human Glycolate Oxidase Inhibitors, Revealed by Crystallography-Based Fragment Screening. Frontiers in Chemistry, 2022, 10, .	1.8	1
4	Fragment Screening Reveals Starting Points for Rational Design of Galactokinase 1 Inhibitors to Treat Classic Galactosemia. ACS Chemical Biology, 2021, 16, 586-595.	1.6	6
5	Fragment binding to the Nsp3 macrodomain of SARS-CoV-2 identified through crystallographic screening and computational docking. Science Advances, 2021, 7, .	4.7	100
6	Achieving Efficient Fragment Screening at XChem Facility at Diamond Light Source. Journal of Visualized Experiments, 2021, , .	0.2	28
7	Structure and activation mechanism of the human liver-type glutaminase GLS2. Biochimie, 2021, 185, 96-104.	1.3	10
8	The low-cost Shifter microscope stage transforms the speed and robustness of protein crystal harvesting. Acta Crystallographica Section D: Structural Biology, 2021, 77, 62-74.	1.1	16
9	Discovery of Novel BRD4 Ligand Scaffolds by Automated Navigation of the Fragment Chemical Space. Journal of Medicinal Chemistry, 2021, 64, 17887-17900.	2.9	6
10	Synthesis and Biological Investigation of (+)-JD1, an Organometallic BET Bromodomain Inhibitor. Organometallics, 2020, 39, 408-416.	1.1	6
11	Crystallographic and electrophilic fragment screening of the SARS-CoV-2 main protease. Nature Communications, 2020, 11, 5047.	5.8	376
12	Discovery of allosteric binding sites by crystallographic fragment screening. Current Opinion in Structural Biology, 2020, 65, 209-216.	2.6	16
13	Deliberately Losing Control of Câ^'H Activation Processes in the Design of Smallâ€Moleculeâ€Fragment Arrays Targeting Peroxisomal Metabolism. ChemMedChem, 2020, 15, 2513-2520.	1.6	1
14	Rapid optimisation of fragments and hits to lead compounds from screening of crude reaction mixtures. Communications Chemistry, 2020, 3, .	2.0	11
15	Demonstration of the utility of DOS-derived fragment libraries for rapid hit derivatisation in a multidirectional fashion. Chemical Science, 2020, 11, 10792-10801.	3.7	11
16	Aspartate/asparagine-Î²-hydroxylase crystal structures reveal an unexpected epidermal growth factor-like domain substrate disulfide pattern. Nature Communications, 2019, 10, 4910.	5.8	34
17	Rapid Covalent-Probe Discovery by Electrophile-Fragment Screening. Journal of the American Chemical Society, 2019, 141, 8951-8968.	6.6	213
18	A Parsimonious Mechanism of Sugar Dehydration by Human GDP-Mannose-4,6-dehydratase. ACS Catalysis, 2019, 9, 2962-2968.	5.5	18

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19	Achieving a Good Crystal System for Crystallographic X-Ray Fragment Screening. Methods in Enzymology, 2018, 610, 251-264.	0.4	38
20	Structure and inhibitor specificity of the PCTAIRE-family kinase CDK16. Biochemical Journal, 2017, 474, 699-713.	1.7	26
21	A multi-crystal method for extracting obscured crystallographic states from conventionally uninterpretable electron density. Nature Communications, 2017, 8, 15123.	5.8	186
22	Partial-occupancy binders identified by the Pan-Dataset Density Analysis method offer new chemical opportunities and reveal cryptic binding sites. Structural Dynamics, 2017, 4, 032104.	0.9	25
23	Gentle, fast and effective crystal soaking by acoustic dispensing. Acta Crystallographica Section D: Structural Biology, 2017, 73, 246-255.	1.1	74
24	Proper modelling of ligand binding requires an ensemble of bound and unbound states. Acta Crystallographica Section D: Structural Biology, 2017, 73, 256-266.	1.1	42
25	TheXChemExplorergraphical workflow tool for routine or large-scale proteinâ€“ligand structure determination. Acta Crystallographica Section D: Structural Biology, 2017, 73, 267-278.	1.1	75
26	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. Cell Reports, 2016, 17, 2724-2737.	2.9	86
27	Mechanism of TAp73 inhibition by Î”Np63 and structural basis of p63/p73 hetero-tetramerization. Cell Death and Differentiation, 2016, 23, 1930-1940.	5.0	29
28	An overview of heavy-atom derivatization of protein crystals. Acta Crystallographica Section D: Structural Biology, 2016, 72, 303-318.	1.1	40
29	A generic protocol for protein crystal dehydration using the HC1b humidity controller. Acta Crystallographica Section D: Structural Biology, 2016, 72, 629-640.	1.1	14
30	A poised fragment library enables rapid synthetic expansion yielding the first reported inhibitors of PHIP(2), an atypical bromodomain. Chemical Science, 2016, 7, 2322-2330.	3.7	120
31	8-Substituted Pyrido[3,4-d]pyrimidin-4(3H)-one Derivatives As Potent, Cell Permeable, KDM4 (JMJD2) and KDM5 (JARID1) Histone Lysine Demethylase Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 1388-1409.	2.9	83
32	Docking and Linking of Fragments To Discover Jumonji Histone Demethylase Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 1580-1598.	2.9	43
33	Structural basis of glycogen branching enzyme deficiency and pharmacologic rescue by rational peptide design. Human Molecular Genetics, 2015, 24, 5667-5676.	1.4	58
34	Human ISPD Is a Cytidyltransferase Required for Dystroglycan O-Mannosylation. Chemistry and Biology, 2015, 22, 1643-1652.	6.2	67
35	Lysine methylation-dependent binding of 53BP1 to the pRb tumor suppressor. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11341-11346.	3.3	39
36	Optimisation of a triazolopyridine based histone demethylase inhibitor yields a potent and selective KDM2A (FBXL11) inhibitor. MedChemComm, 2014, 5, 1879-1886.	3.5	32

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37	Ribosomal oxygenases are structurally conserved from prokaryotes to humans. Nature, 2014, 510, 422-426.	13.7	87
38	5-Carboxy-8-hydroxyquinoline is a broad spectrum 2-oxoglutarate oxygenase inhibitor which causes iron translocation. Chemical Science, 2013, 4, 3110.	3.7	142
39	Crystal Structures of Malonyl-Coenzyme A Decarboxylase Provide Insights into Its Catalytic Mechanism and Disease-Causing Mutations. Structure, 2013, 21, 1182-1192.	1.6	17
40	Structural Basis for Cul3 Protein Assembly with the BTB-Kelch Family of E3 Ubiquitin Ligases. Journal of Biological Chemistry, 2013, 288, 7803-7814.	1.6	227
41	Squeezing the most from every crystal: the fine details of data collection. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1303-1313.	2.5	14
42	Structural basis for Cul3 protein assembly with the BTB-Kelch family of E3 ubiquitin ligases.. Journal of Biological Chemistry, 2013, 288, 28304.	1.6	3
43	Plant Growth Regulator Daminozide Is a Selective Inhibitor of Human KDM2/7 Histone Demethylases. Journal of Medicinal Chemistry, 2012, 55, 6639-6643.	2.9	125
44	Structure of MMACHC Reveals an Arginine-Rich Pocket and a Domain-Swapped Dimer for Its B₁₂ Processing Function. Biochemistry, 2012, 51, 5083-5090.	1.2	45
45	Substrate-induced remodeling of the active site regulates human HTRA1 activity. Nature Structural and Molecular Biology, 2011, 18, 386-388.	3.6	116
46	Assessment of radiation damage behaviour in aÂlargeÂcollection of empirically optimized datasetsÂhighlights the importance of unmeasured complicatingÂeffects. Journal of Synchrotron Radiation, 2011, 18, 387-397.	1.0	17
47	Crystal structures of the endoplasmic reticulum aminopeptidase-1 (ERAP1) reveal the molecular basis for N-terminal peptide trimming. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7745-7750.	3.3	216
48	Molecular Adaptation of the DegQ Protease to Exert Protein Quality Control in the Bacterial Cell Envelope. Journal of Biological Chemistry, 2011, 286, 30680-30690.	1.6	55
49	Structural and Mechanistic Studies on Î³-Butyrobetaine Hydroxylase. Chemistry and Biology, 2010, 17, 1316-1324.	6.2	78
50	HtrA proteases have a conserved activation mechanism that can be triggered by distinct molecular cues. Nature Structural and Molecular Biology, 2010, 17, 844-852.	3.6	112
51	Crystal Structure of the 2-Oxoglutarate- and Fe(II)-Dependent Lysyl Hydroxylase JMJD6. Journal of Molecular Biology, 2010, 401, 211-222.	2.0	85
52	Crystal structure of the 2-oxoglutarate- and Fe(II)-dependent lysyl hydroxylase JMJD6. Journal of Molecular Biology, 2010, 401, 211-22.	2.0	46
53	Selectivity profiling of DegP substrates and inhibitors. Bioorganic and Medicinal Chemistry, 2009, 17, 2920-2924.	1.4	34
54	Structure, function and regulation of the conserved serine proteases DegP and DegS of Escherichia coli. Research in Microbiology, 2009, 160, 660-666.	1.0	56

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55	Allosteric Activation of HtrA Protease DegP by Stress Signals during Bacterial Protein Quality Control. Angewandte Chemie - International Edition, 2008, 47, 1332-1334.	7.2	54
56	Structural basis for the regulated protease and chaperone function of DegP. Nature, 2008, 453, 885-890.	13.7	327
57	Interplay of PDZ and protease domain of DegP ensures efficient elimination of misfolded proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7702-7707.	3.3	118
58	Regulation of the ÏƒE stress response by DegS: how the PDZ domain keeps the protease inactive in the resting state and allows integration of different OMP-derived stress signals upon folding stress. Genes and Development, 2007, 21, 2659-2670.	2.7	81
59	Biosynthesis of Riboflavin: Structure and Properties of 2,5-Diamino-6-ribosylamino-4(3H)-pyrimidinone 5â€²-phosphate Reductase of Methanocaldococcus jannaschii. Journal of Molecular Biology, 2006, 359, 1334-1351.	2.0	26
60	Crystal Structure of an Archaeal Pentameric Riboflavin Synthase in Complex with a Substrate Analog Inhibitor. Journal of Biological Chemistry, 2006, 281, 1224-1232.	1.6	31
61	Crystal structure of DegP (HtrA) reveals a new protease-chaperone machine. Nature, 2002, 416, 455-459.	13.7	374