Kevin L Weiss

List of Publications by Year
in descending order

31	960	394421	454955
papers	citations	19 h-index	30 g-index

33	33	33	1344
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Unusual zwitterionic catalytic site of SARSâ€“CoV-2 main protease revealed by neutron crystallography. Journal of Biological Chemistry, 2020, 295, 17365-17373.	3.4	97
2	The Bio-SANS instrument at the High Flux Isotope Reactor of Oak Ridge National Laboratory. Journal of Applied Crystallography, 2014, 47, 1238-1246.	4.5	83
3	Covalent narlaprevir- and boceprevir-derived hybrid inhibitors of SARS-CoV-2 main protease. Nature Communications, 2022, 13, 2268.	12.8	69
4	The Macromolecular Neutron Diffractometer MaNDi at the Spallation Neutron Source. Journal of Applied Crystallography, 2015, 48, 1302-1306.	4.5	64
5	Direct visualization of critical hydrogen atoms in a pyridoxal 5â€²-phosphate enzyme. Nature Communications, 2017, 8, 955.	12.8	55
6	New sources and instrumentation for neutrons in biology. Chemical Physics, 2008, 345, 133-151.	1.9	53
7	Neutron scattering in the biological sciences: progress and prospects. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1129-1168.	2.3	47
8	Exploring the Mechanism of Î²-Lactam Ring Protonation in the Class A Î²-lactamase Acylation Mechanism Using Neutron and X-ray Crystallography. Journal of Medicinal Chemistry, 2016, 59, 474-479.	6.4	43
9	Anomalous X-ray diffraction studies of ion transport in K+ channels. Nature Communications, 2018, 9, 4540.	12.8	42
10	Neutron and X-ray Crystal Structures of a Perdeuterated Enzyme Inhibitor Complex Reveal the Catalytic Proton Network of the Toho-1 Î²-Lactamase for the Acylation Reaction. Journal of Biological Chemistry, 2013, 288, 4715-4722.	3.4	41
11	Direct Observation of Protonation State Modulation in SARS-CoV-2 Main Protease upon Inhibitor Binding with Neutron Crystallography. Journal of Medicinal Chemistry, 2021, 64, 4991-5000.	6.4	36
12	X-ray crystallographic studies of family 11 xylanase Michaelis and product complexes: implications for the catalytic mechanism. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 11-23.	2.5	34
13	The active site protonation states of perdeuterated Toho-1 Î²-lactamase determined by neutron diffraction support a role for Glu166 as the general base in acylation. FEBS Letters, 2011, 585, 364-368.	2.8	32
14	Structural, Electronic, and Electrostatic Determinants for Inhibitor Binding to Subsites S1 and S2 in SARS-CoV-2 Main Protease. Journal of Medicinal Chemistry, 2021, 64, 17366-17383.	6.4	32
15	Cryogenic neutron protein crystallography: routine methods and potential benefits. Journal of Applied Crystallography, 2014, 47, 1431-1434.	4.5	30
16	Substrate Binding Induces Conformational Changes in a Class A Î²-lactamase That Prime It for Catalysis. ACS Catalysis, 2018, 8, 2428-2437.	11.2	27
17	Active-Site Protonation States in an Acyl-Enzyme Intermediate of a Class A Î²-Lactamase with a Monobactam Substrate. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	26
18	Zooming in on protons: Neutron structure of protein kinase A trapped in a product complex. Science Advances, 2019, 5, eaav0482.	10.3	26

#	Article	IF	Citations
19	Direct detection of coupled proton and electron transfers in human manganese superoxide dismutase. Nature Communications, 2021, 12, 2079.	12.8	23
20	Conformational Dynamics in the Interaction of SARS-CoV-2 Papain-like Protease with Human Interferon-Stimulated Gene 15 Protein. Journal of Physical Chemistry Letters, 2021, 12, 5608-5615.	4.6	14
21	Structural plasticity of the selectivity filter in a nonselective ion channel. IUCrJ, 2021, 8, 421-430.	2.2	13
22	Small-angle neutron scattering solution structures of NADPH-dependent sulfite reductase. Journal of Structural Biology, 2021, 213, 107724.	2.8	10
23	Redox manipulation of the manganese metal in human manganese superoxide dismutase for neutron diffraction. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 677-687.	0.8	10
24	Dynamic Behavior of Oligomeric Inorganic Pyrophosphatase Explored by Quasielastic Neutron Scattering. Journal of Physical Chemistry B, 2012, 116, 9917-9921.	2.6	9
25	The structure of a potassium-selective ion channel reveals a hydrophobic gate regulating ion permeation. IUCrJ, 2020, 7, 835-843.	2.2	8
26	Pressure and Temperature Effects on the Formation of Aminoacrylate Intermediates of Tyrosine Phenol-lyase Demonstrate Reaction Dynamics. ACS Catalysis, 2020, 10, 1692-1703.	11.2	6
27	Cryotrapping peroxide in the active site of human mitochondrial manganese superoxide dismutase crystals for neutron diffraction. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 8-16.	0.8	5
28	A nucleotide-dependent oligomerization of the Escherichia coli replication initiator DnaA requires residue His136 for remodeling of the chromosomal origin. Nucleic Acids Research, 2019, 48, 200-211.	14.5	4
29	Neutron diffraction analysis ofPseudomonas aeruginosapeptidyl-tRNA hydrolase 1. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 220-223.	0.8	3
30	Crystallization of a potassium ion channel and X-ray and neutron data collection. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 435-438.	0.8	3
31	Probing the role of the conserved residue Glu166 in a class A Î²-lactamase using neutron and X-ray protein crystallography. Acta Crystallographica Section D: Structural Biology, 2020, 76, 118-123.	2.3	2