

# Esko Oksanen

## List of Publications by Year in descending order

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Version: 2024-02-01

44  
papers

1,032  
citations

430874

18  
h-index

434195

31  
g-index

47  
all docs

47  
docs citations

47  
times ranked

1753  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the actin-depolymerizing factor homology domain in complex with actin. <i>Journal of Cell Biology</i> , 2008, 182, 51-59.	5.2	143
2	The structure of the conserved neurotrophic factors MANF and CDFN explains why they are bifunctional. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 233-241.	2.1	106
3	Interplay between Conformational Entropy and Solvation Entropy in Protein-Ligand Binding. <i>Journal of the American Chemical Society</i> , 2019, 141, 2012-2026.	13.7	89
4	A Trimetal Site and Substrate Distortion in a Family II Inorganic Pyrophosphatase. <i>Journal of Biological Chemistry</i> , 2007, 282, 1422-1431.	3.4	45
5	A Complete Structural Description of the Catalytic Cycle of Yeast Pyrophosphatase. <i>Biochemistry</i> , 2007, 46, 1228-1239.	2.5	45
6	Mechanism of hydrogen peroxide formation by lytic polysaccharide monooxygenase. <i>Chemical Science</i> , 2019, 10, 576-586.	7.4	45
7	The 2.1 Å structure of <i>Aerococcus viridans</i> lactate oxidase (LOX). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1185-1190.	0.7	40
8	A combined quantum chemical and crystallographic study on the oxidized binuclear center of cytochrome c oxidase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2011, 1807, 769-778.	1.0	39
9	Neutron Crystallography for the Study of Hydrogen Bonds in Macromolecules. <i>Molecules</i> , 2017, 22, 596.	3.8	39
10	Crystal Structures of the CBS and DRTGG Domains of the Regulatory Region of <i>Clostridium perfringens</i> Pyrophosphatase Complexed with the Inhibitor, AMP, and Activator, Diadenosine Tetraphosphate. <i>Journal of Molecular Biology</i> , 2010, 398, 400-413.	4.2	35
11	Elucidation of Hydrogen Bonding Patterns in Ligand-Free, Lactose- and Glycerol-Bound Galectin-3C by Neutron Crystallography to Guide Drug Design. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4412-4420.	6.4	32
12	Crystal structure of the second PDZ domain of SAP97 in complex with a GluR-A C-terminal peptide. <i>FEBS Journal</i> , 2006, 273, 5219-5229.	4.7	31
13	First measurements with new high-resolution gadolinium-GEM neutron detectors. <i>Journal of Instrumentation</i> , 2016, 11, P05011-P05011.	1.2	28
14	The Neutron Structure of Urate Oxidase Resolves a Long-Standing Mechanistic Conundrum and Reveals Unexpected Changes in Protonation. <i>PLoS ONE</i> , 2014, 9, e86651.	2.5	27
15	The $\hat{1}/4$ TPC method: improving the position resolution of neutron detectors based on MPCDs. <i>Journal of Instrumentation</i> , 2015, 10, P04004-P04004.	1.2	25
16	Critical evaluation of a crystal structure of nitrogenase with bound N <sub>2</sub> ligands. <i>Journal of Biological Inorganic Chemistry</i> , 2021, 26, 341-353.	2.6	24
17	Reindeer $\hat{1}^2$ -lactoglobulin crystal structure with pseudo-body-centred noncrystallographic symmetry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1369-1374.	2.5	22
18	Large crystal growth by thermal control allows combined X-ray and neutron crystallographic studies to elucidate the protonation states in <i>Aspergillus flavus</i> urate oxidase. <i>Journal of the Royal Society Interface</i> , 2009, 6, S599-610.	3.4	19

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19	The Structure of the NTPase That Powers DNA Packaging into Sulfolobus Turreted Icosahedral Virus 2. <i>Journal of Virology</i> , 2013, 87, 8388-8398.	3.4	19
20	A crystallization apparatus for temperature-controlled flow-cell dialysis with real-time visualization. <i>Journal of Applied Crystallography</i> , 2016, 49, 806-813.	4.5	19
21	Entropy“Entropy Compensation between the Protein, Ligand, and Solvent Degrees of Freedom Fine-Tunes Affinity in Ligand Binding to Galectin-3C. <i>Jacs Au</i> , 2021, 1, 484-500.	7.9	17
22	Are crystallographic <i>B</i> -factors suitable for calculating protein conformational entropy?. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 18149-18160.	2.8	16
23	Perdeuteration, crystallization, data collection and comparison of five neutron diffraction data sets of complexes of human galectin-3C. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1194-1202.	2.3	15
24	Is the bovine lysosomal phospholipase B-like protein an amidase?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 300-311.	2.6	14
25	Refinement of protein structures using a combination of quantum-mechanical calculations with neutron and X-ray crystallographic data. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 368-380.	2.3	13
26	Water structure in solution and crystal molecular dynamics simulations compared to protein crystal structures. <i>RSC Advances</i> , 2020, 10, 8435-8443.	3.6	11
27	Biological Structures. <i>Experimental Methods in the Physical Sciences</i> , 2017, 49, 1-75.	0.1	10
28	fragHAR: towards <i>ab initio</i> quantum-crystallographic X-ray structure refinement for polypeptides and proteins. <i>IUCr</i> , 2020, 7, 158-165.	2.2	10
29	Perdeuteration, large crystal growth and neutron data collection of <i>Leishmania mexicana</i> triose-phosphate isomerase E65Q variant. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 260-269.	0.8	9
30	Combining crystallography with quantum mechanics. <i>Current Opinion in Structural Biology</i> , 2022, 72, 18-26.	5.7	8
31	Membrane-protein crystals for neutron diffraction. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1208-1218.	2.3	7
32	Quantum-refinement studies of the bidentate ligand of $\alpha$ -nitrogenase and the protonation state of CO-inhibited $\alpha$ -nitrogenase. <i>Journal of Inorganic Biochemistry</i> , 2021, 219, 111426.	3.5	7
33	Neutron structures of <i>Leishmania mexicana</i> triosephosphate isomerase in complex with reaction-intermediate mimics shed light on the proton-shuttling steps. <i>IUCr</i> , 2021, 8, 633-643.	2.2	6
34	Optimization of crystallization of biological macromolecules using dialysis combined with temperature control. <i>Journal of Applied Crystallography</i> , 2020, 53, 686-698.	4.5	5
35	Exploring ligand dynamics in protein crystal structures with ensemble refinement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1099-1115.	2.3	3
36	Neutron macromolecular crystallography at the European spallation source. <i>Methods in Enzymology</i> , 2020, 634, 125-151.	1.0	3

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37	Automated orientation of water molecules in neutron crystallographic structures of proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1025-1032.	2.3	3
38	Design of a novel Peltier-based cooling device and its use in neutron diffraction data collection of perdeuterated yeast pyrophosphatase. <i>Journal of Applied Crystallography</i> , 2010, 43, 1113-1120.	4.5	1
39	A protocol for production of perdeuterated OmpF porin for neutron crystallography. <i>Protein Expression and Purification</i> , 2021, 188, 105954.	1.3	1
40	Crystallization and preliminary crystallographic analysis of mouse peroxiredoxin II with significant pseudosymmetry. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 357-360.	0.7	0
41	Introduction to Macromolecular X-Ray Crystallography. , 2010, , 51-89.		0
42	Prospects for membrane protein crystals in NMX. <i>Methods in Enzymology</i> , 2020, 634, 47-68.	1.0	0
43	Introduction to Macromolecular X-Ray Crystallography. , 2010, , 312-343.		0
44	Can the results of quantum refinement be improved with a continuum-solvation model?. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2021, 77, 906-918.	1.1	0