

Edwin Pozharski

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

1,882
citations

201674

27
h-index

276875

41
g-index

65
all docs

65
docs citations

65
times ranked

2631
citing authors

#	ARTICLE	IF	CITATIONS
1	Consolidation of glycosyl hydrolase family 30: A dual domain 4/7 hydrolase family consisting of two structurally distinct groups. FEBS Letters, 2010, 584, 4435-4441.	2.8	114
2	Cysteine p <i>K</i> _a Depression by a Protonated Glutamic Acid in Human DJ-1. Biochemistry, 2008, 47, 7430-7440.	2.5	110
3	Crystal structure of human thymine DNA glycosylase bound to DNA elucidates sequence-specific mismatch recognition. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8890-8895.	7.1	103
4	Techniques, tools and best practices for ligand electron-density analysis and results from their application to deposited crystal structures. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 150-167.	2.5	94
5	Physical correlates of the ultrasonic reflectivity of lipid dispersions suitable as diagnostic contrast agents. Ultrasound in Medicine and Biology, 2002, 28, 339-348.	1.5	82
6	A Fc-enhanced NTD-binding non-neutralizing antibody delays virus spread and synergizes with a nAb to protect mice from lethal SARS-CoV-2 infection. Cell Reports, 2022, 38, 110368.	6.4	82
7	Ligand Bound Structures of a Glycosyl Hydrolase Family 30 Glucuronoxylan Xylanohydrolase. Journal of Molecular Biology, 2011, 407, 92-109.	4.2	72
8	Visualizing ligand molecules in twilight electron density. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 195-200.	0.7	63
9	Thermodynamics of Cationic Lipid-DNA Complex Formation as Studied by Isothermal Titration Calorimetry. Biophysical Journal, 2002, 83, 556-565.	0.5	58
10	Divalent Metal Ion Complexes of S100B in the Absence and Presence of Pentamidine. Journal of Molecular Biology, 2008, 382, 56-73.	4.2	53
11	Lipoplex Thermodynamics: Determination of DNA-Cationic Lipid Interaction Energies. Biophysical Journal, 2003, 85, 3969-3978.	0.5	49
12	Detect, correct, retract: How to manage incorrect structural models. FEBS Journal, 2018, 285, 444-466.	4.7	49
13	Lesion processing by a repair enzyme is severely curtailed by residues needed to prevent aberrant activity on undamaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8091-8096.	7.1	48
14	The Effects of CapZ Peptide (TRTK-12) Binding to S100Bâ€Ca ²⁺ as Examined by NMR and X-ray Crystallography. Journal of Molecular Biology, 2010, 396, 1227-1243.	4.2	47
15	Structural basis of damage recognition by thymine DNA glycosylase: Key roles for N-terminal residues. Nucleic Acids Research, 2016, 44, gkw768.	14.5	44
16	Structural and Functional Analysis of the Pro-Domain of Human Cathelicidin, LL-37. Biochemistry, 2013, 52, 1547-1558.	2.5	42
17	Short Carboxylic Acidâ€Carboxylate Hydrogen Bonds Can Have Fully Localized Protons. Biochemistry, 2017, 56, 391-402.	2.5	41
18	Structure of human apurinic/aprimidinic endonuclease 1 with the essential Mg ²⁺ cofactor. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2555-2562.	2.5	39

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19	Diversity in Hapten Recognition: Structural Study of an Anti-cocaine Antibody M82G2. <i>Journal of Molecular Biology</i> , 2005, 349, 570-582.	4.2	37
20	Ni(II) coordination to mixed sites modulates DNA binding of <i>Hp</i> NikR via a long-range effect. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5633-5638.	7.1	37
21	Holo-Ni(II)HpNikR Is an Asymmetric Tetramer Containing Two Different Nickel-Binding Sites. <i>Journal of the American Chemical Society</i> , 2010, 132, 14447-14456.	13.7	36
22	Small-molecule inhibitors of ERK-mediated immediate early gene expression and proliferation of melanoma cells expressing mutated BRAf. <i>Biochemical Journal</i> , 2015, 467, 425-438.	3.7	35
23	Small Molecules Bound to Unique Sites in the Target Protein Binding Cleft of Calcium-Bound S100B As Characterized by Nuclear Magnetic Resonance and X-ray Crystallography. <i>Biochemistry</i> , 2009, 48, 6202-6212.	2.5	33
24	Structural Basis for Excision of 5-Formylcytosine by Thymine DNA Glycosylase. <i>Biochemistry</i> , 2016, 55, 6205-6208.	2.5	32
25	Anchoring a Cationic Ligand: The Structure of the Fab Fragment of the Anti-morphine Antibody 9B1 and its Complex with Morphine. <i>Journal of Molecular Biology</i> , 2004, 337, 691-697.	4.2	30
26	N-Acetylfarnesylcysteine Is a Novel Class of Peroxisome Proliferator-activated Receptor \hat{I}^3 Ligand with Partial and Full Agonist Activity in Vitro and in Vivo. <i>Journal of Biological Chemistry</i> , 2011, 286, 41626-41635.	3.4	30
27	In vitro screening and structural characterization of inhibitors of the S100B-p53 interaction. <i>International Journal of High Throughput Screening</i> , 2010, 2010, 109.	0.5	29
28	Thymine DNA glycosylase exhibits negligible affinity for nucleobases that it removes from DNA. <i>Nucleic Acids Research</i> , 2015, 43, 9541-9552.	14.5	28
29	A direct interaction between NQO1 and a chemotherapeutic dimeric naphthoquinone. <i>BMC Structural Biology</i> , 2016, 16, 1.	2.3	27
30	A novel member of glycoside hydrolase family 30 subfamily 8 with altered substrate specificity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2950-2958.	2.5	25
31	Structure of the cell-binding component of the <i>Clostridium difficile</i> binary toxin reveals a di-heptamer macromolecular assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1049-1058.	7.1	23
32	Excision of 5-Carboxylcytosine by Thymine DNA Glycosylase. <i>Journal of the American Chemical Society</i> , 2019, 141, 18851-18861.	13.7	21
33	A plasmid borne, functionally novel glycoside hydrolase family 30 subfamily 8 endoxylanase from solventogenic <i>Clostridium</i> . <i>Biochemical Journal</i> , 2018, 475, 1533-1551.	3.7	20
34	Percentile-based spread: a more accurate way to compare crystallographic models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 970-978.	2.5	18
35	Rapid Crystallization of α -Alanine on Engineered Surfaces by Use of Metal-Assisted and Microwave-Accelerated Evaporative Crystallization. <i>Crystal Growth and Design</i> , 2012, 12, 346-353.	3.0	18
36	Crystallization and crystallographic analysis of <i>Bacillus subtilis</i> xylanase C. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 499-503.	0.7	17

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37	Inactivation of <i>Escherichia coli</i> <i>scp</i> -Aspartate Aminotransferase by (<i>S</i>)-4-Amino-4,5-dihydro-2-thiophenecarboxylic Acid Reveals a Tale of Two Mechanisms. <i>Biochemistry</i> , 2007, 46, 10517-10527.	2.5	15
38	The role of bias in crystallization conditions in automated microseeding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1222-1227.	2.5	15
39	A Conserved Protein Interaction Interface on the Type 5 G Protein $\hat{1}^2$ Subunit Controls Proteolytic Stability and Activity of R7 Family Regulator of G Protein Signaling Proteins. <i>Journal of Biological Chemistry</i> , 2010, 285, 41100-41112.	3.4	15
40	Crystal structure of the human heterogeneous ribonucleoprotein A18 RNA-recognition motif. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 209-214.	0.8	14
41	Novel structural features of xylanase A1 from <i>Paenibacillus</i> sp. JDR-2. <i>Journal of Structural Biology</i> , 2012, 180, 303-311.	2.8	13
42	Structure of extracellular signal-regulated kinase 2 in complex with ATP and ADP. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1434-1439.	0.7	13
43	X-ray crystal structure of human calcium-bound S100A1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 215-221.	0.8	13
44	Structural Insights into the Mechanism of Base Excision by MBD4. <i>Journal of Molecular Biology</i> , 2021, 433, 167097.	4.2	13
45	Comment on Three X-ray Crystal Structure Papers. <i>Journal of Immunology</i> , 2016, 196, 521-524.	0.8	11
46	The Importance of Therapeutically Targeting the Binary Toxin from <i>Clostridioides difficile</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2926.	4.1	10
47	On the variability of experimental data in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1077-1087.	2.5	9
48	<i>Twilight</i> reloaded: the peptide experience. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 211-222.	2.3	9
49	Studies on ligand binding to histidine triad nucleotide binding protein 1. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 6756-6762.	3.0	7
50	Additional Comment on Three X-ray Crystal Structure Papers. <i>Journal of Immunology</i> , 2016, 196, 528-530.	0.8	7
51	Validation of Protein-Ligand Crystal Structure Models: Small Molecule and Peptide Ligands. <i>Methods in Molecular Biology</i> , 2017, 1607, 611-625.	0.9	7
52	Crystal structures of human 3-hydroxyanthranilate 3,4-dioxygenase with native and non-native metals bound in the active site. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 340-348.	2.3	7
53	Mechanism of Inactivation of <i>Escherichia coli</i> Aspartate Aminotransferase by (<i>S</i>)-4-Amino-4,5-dihydro-2-furancarboxylic Acid. <i>Biochemistry</i> , 2010, 49, 10507-10515.	2.5	5
54	Fluorescence Resonance Energy Transfer-Based Analysis of Lipoplexes. <i>Methods in Molecular Biology</i> , 2010, 606, 393-398.	0.9	4

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55	Apparent instability of crystallographic refinement in the presence of disordered model fragments and upon insufficiently restrained model geometry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 966-972.	2.5	2
56	How a mismatch repair enzyme balances the needs for efficient lesion processing and minimal action on undamaged DNA. <i>Cell Cycle</i> , 2012, 11, 3345-3346.	2.6	2
57	Crystal Structure of a Bivalent Antibody Fab Fragment. <i>Journal of Molecular Biology</i> , 2021, 433, 166714.	4.2	2
58	Fluorometric Analysis of Individual Cationic Lipid-DNA Complexes. <i>Methods in Molecular Biology</i> , 2010, 606, 385-391.	0.9	2
59	Fluorescence Resonance Energy Transfer (FRET)-Based Analysis of Lipoplexes. <i>Methods in Molecular Biology</i> , 2017, 1522, 251-256.	0.9	1
60	Structural Fine-Tuning of <i>Clostridioides difficile</i> Binary Toxin Components for Therapeutic Applications. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
61	Structural basis for excision of deaminated and oxidized 5-methylcytosine by thymine DNA glycosylase. <i>FASEB Journal</i> , 2012, 26, 539.10.	0.5	0
62	Evidence vs Expectations: How to validate your ligand in a protein structure. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1479-C1479.	0.1	0
63	Fluorometric Analysis of Individual Cationic Lipid-DNA Complexes. <i>Methods in Molecular Biology</i> , 2017, 1522, 237-243.	0.9	0
64	Enzymatic removal of epigenetic marks from DNA. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a325-a325.	0.1	0