

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 | 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. <i>Cell Reports</i> , 2022, 38, 110368. | 6.4 | 82 |
| 2 | Crystal Structure of a Bivalent Antibody Fab Fragment. <i>Journal of Molecular Biology</i> , 2021, 433, 166714. | 4.2 | 2 |
| 3 | 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 |
| 4 | Structural Fine-Tuning of <i>Clostridioides difficile</i> Binary Toxin Components for Therapeutic Applications. <i>FASEB Journal</i> , 2021, 35, . | 0.5 | 0 |
| 5 | Structural Insights into the Mechanism of Base Excision by MBD4. <i>Journal of Molecular Biology</i> , 2021, 433, 167097. | 4.2 | 13 |
| 6 | 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 |
| 7 | Excision of 5-Carboxylcytosine by Thymine DNA Glycosylase. <i>Journal of the American Chemical Society</i> , 2019, 141, 18851-18861. | 13.7 | 21 |
| 8 | 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 |
| 9 | Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466. | 4.7 | 49 |
| 10 | 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 |
| 11 | 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 |
| 12 | <i>Twilight</i> reloaded: the peptide experience. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 211-222. | 2.3 | 9 |
| 13 | Short Carboxylic Acid-Carboxylate Hydrogen Bonds Can Have Fully Localized Protons. <i>Biochemistry</i> , 2017, 56, 391-402. | 2.5 | 41 |
| 14 | Fluorescence Resonance Energy Transfer (FRET)-Based Analysis of Lipoplexes. <i>Methods in Molecular Biology</i> , 2017, 1522, 251-256. | 0.9 | 1 |
| 15 | 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 |
| 16 | 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 |
| 17 | Fluorometric Analysis of Individual Cationic Lipid-DNA Complexes. <i>Methods in Molecular Biology</i> , 2017, 1522, 237-243. | 0.9 | 0 |
| 18 | Enzymatic removal of epigenetic marks from DNA. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, a325-a325. | 0.1 | 0 |

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|----|---|------|-----------|
| 19 | A direct interaction between NQO1 and a chemotherapeutic dimeric naphthoquinone. <i>BMC Structural Biology</i> , 2016, 16, 1. | 2.3 | 27 |
| 20 | Structural basis of damage recognition by thymine DNA glycosylase: Key roles for N-terminal residues. <i>Nucleic Acids Research</i> , 2016, 44, gkw768. | 14.5 | 44 |
| 21 | Structural Basis for Excision of 5-Formylcytosine by Thymine DNA Glycosylase. <i>Biochemistry</i> , 2016, 55, 6205-6208. | 2.5 | 32 |
| 22 | Comment on Three X-ray Crystal Structure Papers. <i>Journal of Immunology</i> , 2016, 196, 521-524. | 0.8 | 11 |
| 23 | Additional Comment on Three X-ray Crystal Structure Papers. <i>Journal of Immunology</i> , 2016, 196, 528-530. | 0.8 | 7 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Structural and Functional Analysis of the Pro-Domain of Human Cathelicidin, LL-37. <i>Biochemistry</i> , 2013, 52, 1547-1558. | 2.5 | 42 |
| 29 | Techniques, tools and best practices for ligand electron-density analysis and results from their application to deposited crystal structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 150-167. | 2.5 | 94 |
| 30 | Structure of human apurinic/aprimidinic endonuclease 1 with the essential Mg ²⁺ cofactor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2555-2562. | 2.5 | 39 |
| 31 | Visualizing ligand molecules in twilight electron density. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 195-200. | 0.7 | 63 |
| 32 | 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 |
| 33 | 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 |
| 34 | Lesion processing by a repair enzyme is severely curtailed by residues needed to prevent aberrant activity on undamaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8091-8096. | 7.1 | 48 |
| 35 | On the variability of experimental data in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1077-1087. | 2.5 | 9 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | Ligand Bound Structures of a Glycosyl Hydrolase Family 30 Glucuronoxylan Xylanohydrolase. <i>Journal of Molecular Biology</i> , 2011, 407, 92-109. | 4.2 | 72 |
| 41 | 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 |
| 42 | N-Acetylfarnesylcysteine Is a Novel Class of Peroxisome Proliferator-activated Receptor β 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 |
| 43 | Consolidation of glycosyl hydrolase family 30: A dual domain 4/7 hydrolase family consisting of two structurally distinct groups. <i>FEBS Letters</i> , 2010, 584, 4435-4441. | 2.8 | 114 |
| 44 | Studies on ligand binding to histidine triad nucleotide binding protein 1. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 6756-6762. | 3.0 | 7 |
| 45 | 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 |
| 46 | 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 |
| 47 | A Conserved Protein Interaction Interface on the Type 5 G Protein β 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | The Effects of CapZ Peptide (TRTK-12) Binding to S100B-Ca ²⁺ as Examined by NMR and X-ray Crystallography. <i>Journal of Molecular Biology</i> , 2010, 396, 1227-1243. | 4.2 | 47 |
| 51 | Fluorescence Resonance Energy Transfer-Based Analysis of Lipoplexes. <i>Methods in Molecular Biology</i> , 2010, 606, 393-398. | 0.9 | 4 |
| 52 | Fluorometric Analysis of Individual Cationic Lipid-DNA Complexes. <i>Methods in Molecular Biology</i> , 2010, 606, 385-391. | 0.9 | 2 |
| 53 | Crystallization and crystallographic analysis of Bacillus subtilis xylanase C. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 499-503. | 0.7 | 17 |
| 54 | 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 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | Divalent Metal Ion Complexes of S100B in the Absence and Presence of Pentamidine. <i>Journal of Molecular Biology</i> , 2008, 382, 56-73. | 4.2 | 53 |
| 57 | Cysteine p <i>K</i> _a Depression by a Protonated Glutamic Acid in Human DJ-1. <i>Biochemistry</i> , 2008, 47, 7430-7440. | 2.5 | 110 |
| 58 | Crystal structure of human thymine DNA glycosylase bound to DNA elucidates sequence-specific mismatch recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8890-8895. | 7.1 | 103 |
| 59 | Inactivation of <i>Escherichia coli</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 |
| 60 | 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 |
| 61 | 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 |
| 62 | Lipoplex Thermodynamics: Determination of DNA-Cationic Lipid Interaction Energies. <i>Biophysical Journal</i> , 2003, 85, 3969-3978. | 0.5 | 49 |
| 63 | Thermodynamics of Cationic Lipid-DNA Complex Formation as Studied by Isothermal Titration Calorimetry. <i>Biophysical Journal</i> , 2002, 83, 556-565. | 0.5 | 58 |
| 64 | Physical correlates of the ultrasonic reflectivity of lipid dispersions suitable as diagnostic contrast agents. <i>Ultrasound in Medicine and Biology</i> , 2002, 28, 339-348. | 1.5 | 82 |