

# Albert M Berghuis

## List of Publications by Year in descending order

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108  
papers

6,024  
citations

87888

38  
h-index

76900

74  
g-index

109  
all docs

109  
docs citations

109  
times ranked

7799  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Structure of the first C2 domain of synaptotagmin I: A novel Ca <sup>2+</sup> /phospholipid-binding fold. <i>Cell</i> , 1995, 80, 929-938.  | 28.9 | 698       |
| 2  | <i>IRF8</i> Mutations and Human Dendritic-Cell Immunodeficiency. <i>New England Journal of Medicine</i> , 2011, 365, 127-138.   | 27.0 | 564       |
| 3  | Oxidation state-dependent conformational changes in cytochrome c. <i>Journal of Molecular Biology</i> , 1992, 223, 959-976.   | 4.2  | 391       |
| 4  | Structure of an Enzyme Required for Aminoglycoside Antibiotic Resistance Reveals Homology to Eukaryotic Protein Kinases. <i>Cell</i> , 1997, 89, 887-895.   | 28.9 | 236       |
| 5  | Lactose binding to heat-labile enterotoxin revealed by X-ray crystallography. <i>Nature</i> , 1992, 355, 561-564.   | 27.8 | 223       |
| 6  | Crystal Structures of Cyclohexanone Monooxygenase Reveal Complex Domain Movements and a Sliding Cofactor. <i>Journal of the American Chemical Society</i> , 2009, 131, 8848-8854.   | 13.7 | 151       |
| 7  | Germline and somatic <i>FGFR1</i> abnormalities in dysembryoplastic neuroepithelial tumors. <i>Acta Neuropathologica</i> , 2016, 131, 847-863.  | 7.7  | 143       |
| 8  | Crystal structure of an aminoglycoside 6- <i>N</i> -acetyltransferase: defining the GCN5-related <i>N</i> -acetyltransferase superfamily fold. <i>Structure</i> , 1999, 7, 497-507.   | 3.3  | 137       |
| 9  | A Recurrent <i>PDGFRB</i> Mutation Causes Familial Infantile Myofibromatosis. <i>American Journal of Human Genetics</i> , 2013, 92, 996-1000.   | 6.2  | 135       |
| 10 | Substrate promiscuity of an aminoglycoside antibiotic resistance enzyme via target mimicry. <i>EMBO Journal</i> , 2002, 21, 2323-2331.  | 7.8  | 132       |
| 11 | The Role of a Conserved Internal Water Molecule and Its Associated Hydrogen Bond Network in Cytochrome c. <i>Journal of Molecular Biology</i> , 1994, 236, 786-799.   | 4.2  | 119       |
| 12 | A Single Bifunctional UDP-GlcNAc/Glc 4-Epimerase Supports the Synthesis of Three Cell Surface Glycoconjugates in <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 4792-4802.                                       | 3.4  | 117       |
| 13 | Aminoglycoside Antibiotics. <i>Advances in Experimental Medicine and Biology</i> , 1998, , 27-69.   | 1.6  | 116       |
| 14 | Structural Basis for Ubiquitin-Mediated Dimerization and Activation of the Ubiquitin Protein Ligase Cbl-b. <i>Molecular Cell</i> , 2007, 27, 474-485.   | 9.7  | 107       |
| 15 | Overlapping and Distinct Roles of <i>Aspergillus fumigatus</i> UDP-glucose 4-Epimerases in Galactose Metabolism and the Synthesis of Galactose-containing Cell Wall Polysaccharides. <i>Journal of Biological Chemistry</i> , 2014, 289, 1243-1256. | 3.4  | 102       |
| 16 | Histone H3.3G34-Mutant Interneuron Progenitors Co-opt <i>PDGFRA</i> for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.  | 28.9 | 93        |
| 17 | Mutation of Tyrosine-67 to Phenylalanine in Cytochrome c Significantly Alters the Local Heme Environment. <i>Journal of Molecular Biology</i> , 1994, 235, 1326-1341.   | 4.2  | 91        |
| 18 | The Substrate-Bound Crystal Structure of a Baeyer-Villiger Monooxygenase Exhibits a Criegee-like Conformation. <i>Journal of the American Chemical Society</i> , 2012, 134, 7788-7795.  | 13.7 | 81        |

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|----|--|------|-----------|
| 19 | Crystal Structure of WbpP, a Genuine UDP-N-acetylglucosamine 4-Epimerase from <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 22635-22642.   | 3.4  | 80        |
| 20 | X-ray structure of the AAC(6')-II antibiotic resistance enzyme at 1.8 Å resolution; examination of oligomeric arrangements in GNAT superfamily members. <i>Protein Science</i> , 2003, 12, 426-437.                                  | 7.6  | 78        |
| 21 | Competing allosteric mechanisms modulate substrate binding in a dimeric enzyme. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 288-294.  | 8.2  | 75        |
| 22 | Synthesis and Structure-Activity Relationships of Truncated Bisubstrate Inhibitors of Aminoglycoside 6'-N-Acetyltransferases. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5273-5281.   | 6.4  | 74        |
| 23 | Look and Outlook on Enzyme-Mediated Macrolide Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 1942.  | 3.5  | 69        |
| 24 | Structure of the GDP-Pi complex of Gly203Ala G1±1: a mimic of the ternary product complex of G1±-catalyzed GTP hydrolysis. <i>Structure</i> , 1996, 4, 1277-1290.  | 3.3  | 67        |
| 25 | Functional characterization of the human dendritic cell immunodeficiency associated with the IRF8K108E mutation. <i>Blood</i> , 2014, 124, 1894-1904.  | 1.4  | 65        |
| 26 | TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. <i>Nature Communications</i> , 2018, 9, 4572.   | 12.8 | 58        |
| 27 | Regio- and Chemoselective 6'-N-Derivatization of Aminoglycosides: Bisubstrate Inhibitors as Probes To Study Aminoglycoside 6'-N-Acetyltransferases. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 6859-6862.          | 13.8 | 54        |
| 28 | Prospects for circumventing aminoglycoside kinase mediated antibiotic resistance. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 22.   | 3.9  | 54        |
| 29 | Crystallization and Preliminary Crystallographic Studies of G1±1 and Mutants of G1±1 in the GTP and GDP-bound States. <i>Journal of Molecular Biology</i> , 1994, 238, 630-634.  | 4.2  | 50        |
| 30 | Crystal structures of homoserine dehydrogenase suggest a novel catalytic mechanism for oxidoreductases. <i>Nature Structural Biology</i> , 2000, 7, 238-244.   | 9.7  | 48        |
| 31 | Structural Studies of FlaA1 from <i>Helicobacter pylori</i> Reveal the Mechanism for Inverting 4,6-Dehydratase Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 24489-24495.  | 3.4  | 48        |
| 32 | Design and Synthesis of Active Site Inhibitors of the Human Farnesyl Pyrophosphate Synthase: Apoptosis and Inhibition of ERK Phosphorylation in Multiple Myeloma Cells. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 3201-3215. | 6.4  | 46        |
| 33 | The Role of a Conserved Water Molecule in the Redox-dependent Thermal Stability of Iso-1-cytochrome c. <i>Journal of Biological Chemistry</i> , 1996, 271, 29088-29093.  | 3.4  | 45        |
| 34 | Crystal Structure of Homoserine Transacetylase from <i>Haemophilus influenzae</i> Reveals a New Family of $\beta$ -Hydrolases. <i>Biochemistry</i> , 2005, 44, 15768-15773.  | 2.5  | 44        |
| 35 | Flagellin Glycosylation in <i>Pseudomonas aeruginosa</i> PAK Requires the O-antigen Biosynthesis Enzyme WbpO. <i>Journal of Biological Chemistry</i> , 2008, 283, 3507-3518.   | 3.4  | 44        |
| 36 | Thienopyrimidine Bisphosphonate (ThPBP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase: Optimization and Characterization of the Mode of Inhibition. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 7939-7950.           | 6.4  | 43        |

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|----|--|------|-----------|
| 37 | Mechanism of Aminoglycoside Antibiotic Kinase APH(3 $\hat{\epsilon}$ )-IIIa: A Role of the Nucleotide Positioning Loop. <i>Biochemistry</i> , 2002, 41, 7001-7007.   | 2.5  | 42        |
| 38 | Structural basis for streptogramin B resistance in <i>Staphylococcus aureus</i> by virginiamycin B lyase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10388-10393. | 7.1  | 42        |
| 39 | Identification and Characterization of a Protein-tyrosine Phosphatase in <i>Leishmania</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 36257-36268.  | 3.4  | 39        |
| 40 | Lactone-Bound Structures of Cyclohexanone Monooxygenase Provide Insight into the Stereochemistry of Catalysis. <i>ACS Chemical Biology</i> , 2014, 9, 2843-2851.   | 3.4  | 39        |
| 41 | The COOH Terminus of Aminoglycoside Phosphotransferase (3 $\hat{\epsilon}$ )-IIIa Is Critical for Antibiotic Recognition and Resistance. <i>Journal of Biological Chemistry</i> , 1999, 274, 30697-30706.                  | 3.4  | 37        |
| 42 | Human isoprenoid synthase enzymes as therapeutic targets. <i>Frontiers in Chemistry</i> , 2014, 2, 50.   | 3.6  | 37        |
| 43 | Structure of the Antibiotic Resistance Factor Spectinomycin Phosphotransferase from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 9545-9555.   | 3.4  | 36        |
| 44 | Functionally Null <i>RAD51D</i> Missense Mutation Associates Strongly with Ovarian Carcinoma. <i>Cancer Research</i> , 2017, 77, 4517-4529.  | 0.9  | 34        |
| 45 | Multiple Conformers in Active Site of Human Dihydrofolate Reductase F31R/Q35E Double Mutant Suggest Structural Basis for Methotrexate Resistance. <i>Journal of Biological Chemistry</i> , 2009, 284, 20079-20089.         | 3.4  | 33        |
| 46 | Unraveling the Prenylation "Cancer Paradox in Multiple Myeloma with Novel Geranylgeranyl Pyrophosphate Synthase (GGPPS) Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 6904-6917.                           | 6.4  | 33        |
| 47 | Human farnesyl pyrophosphate synthase is allosterically inhibited by its own product. <i>Nature Communications</i> , 2017, 8, 14132.   | 12.8 | 32        |
| 48 | DGCR8 microprocessor defect characterizes familial multinodular goiter with schwannomatosis. <i>Journal of Clinical Investigation</i> , 2020, 130, 1479-1490.  | 8.2  | 31        |
| 49 | Magnesium and Phosphate Ions Enable NAD Binding to Methylenetetrahydrofolate Dehydrogenase-Methenyltetrahydrofolate Cyclohydrolase. <i>Journal of Biological Chemistry</i> , 2005, 280, 34316-34323.                       | 3.4  | 30        |
| 50 | Mechanistic and Structural Contributions of Critical Surface and Internal Residues to Cytochrome c Electron Transfer Reactivity. <i>Biochemistry</i> , 1996, 35, 10784-10792.  | 2.5  | 29        |
| 51 | Maintenance of Native-like Protein Dynamics May Not Be Required for Engineering Functional Proteins. <i>Chemistry and Biology</i> , 2014, 21, 1330-1340.   | 6.0  | 29        |
| 52 | Multistage Screening Reveals Chameleon Ligands of the Human Farnesyl Pyrophosphate Synthase: Implications to Drug Discovery for Neurodegenerative Diseases. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 5764-5776.   | 6.4  | 29        |
| 53 | Enzyme-Assisted Suicide. <i>Chemistry and Biology</i> , 2003, 10, 989-995.   | 6.0  | 28        |
| 54 | Protein Tyrosine Phosphatases Are Regulated by Mononuclear Iron Dicitrate. <i>Journal of Biological Chemistry</i> , 2010, 285, 24620-24628.  | 3.4  | 25        |

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|----|---|-----|-----------|
| 55 | Drug-target networks in aminoglycoside resistance: hierarchy of priority in structural drug design. <i>MedChemComm</i> , 2016, 7, 103-113.  | 3.4 | 25        |
| 56 | New phenolic inhibitors of yeast homoserine dehydrogenase. <i>Bioorganic and Medicinal Chemistry</i> , 2004, 12, 3825-3830.   | 3.0 | 24        |
| 57 | Structural Basis for Dual Nucleotide Selectivity of Aminoglycoside 2-Phosphotransferase IVa Provides Insight on Determinants of Nucleotide Specificity of Aminoglycoside Kinases. <i>Journal of Biological Chemistry</i> , 2012, 287, 13094-13102.                              | 3.4 | 24        |
| 58 | Protein kinase inhibitors and antibiotic resistance. , 2002, 93, 283-292.   |     | 23        |
| 59 | Structures of aminoglycoside acetyltransferase AAC(6)-II in a novel crystal form: structural and normal-mode analyses. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1273-1279.   | 2.5 | 23        |
| 60 | Structural Basis of APH(3)-IIIa-Mediated Resistance to N1-Substituted Aminoglycoside Antibiotics. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3049-3055.   | 3.2 | 23        |
| 61 | Small-Angle X-Ray Scattering Analysis of the Bifunctional Antibiotic Resistance Enzyme Aminoglycoside (6- Acetyltransferase-Ie/Aminoglycoside (2- Phosphotransferase-Ia Reveals a Rigid Solution Structure. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1899-1906. | 3.2 | 23        |
| 62 | Substrate-dependent switching of the allosteric binding mechanism of a dimeric enzyme. <i>Nature Chemical Biology</i> , 2014, 10, 937-942.  | 8.0 | 23        |
| 63 | Structural Analysis of the Tobramycin and Gentamicin Clinical Resistome Reveals Limitations for Next-generation Aminoglycoside Design. <i>ACS Chemical Biology</i> , 2016, 11, 1339-1346.   | 3.4 | 23        |
| 64 | Structural Basis for Kinase-Mediated Macrolide Antibiotic Resistance. <i>Structure</i> , 2017, 25, 750-761.e5.  | 3.3 | 23        |
| 65 | Crystal Structures of Two Aminoglycoside Kinases Bound with a Eukaryotic Protein Kinase Inhibitor. <i>PLoS ONE</i> , 2011, 6, e19589.   | 2.5 | 23        |
| 66 | Towards a better understanding of the substrate specificity of the UDP-N-acetylglucosamine C4 epimerase WbpP. <i>Biochemical Journal</i> , 2005, 389, 173-180.  | 3.7 | 22        |
| 67 | Structural Analysis of a Novel Cyclohexylamine Oxidase from <i>Brevibacterium oxydans</i> IH-35A. <i>PLoS ONE</i> , 2013, 8, e60072.  | 2.5 | 22        |
| 68 | Inhibition of Outer Membrane Proteases of the Omptin Family by Aprotinin. <i>Infection and Immunity</i> , 2015, 83, 2300-2311.  | 2.2 | 22        |
| 69 | Ternary complex structures of human farnesyl pyrophosphate synthase bound with a novel inhibitor and secondary ligands provide insights into the molecular details of the enzyme's active site closure. <i>BMC Structural Biology</i> , 2012, 12, 32.                           | 2.3 | 21        |
| 70 | The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1641-1648.  | 2.3 | 21        |
| 71 | Pharmacophore Mapping of Thienopyrimidine-Based Monophosphonate (ThP-MP) Inhibitors of the Human Farnesyl Pyrophosphate Synthase. <i>Journal of Medicinal Chemistry</i> , 2017, 60, 2119-2134.  | 6.4 | 21        |
| 72 | A potential gain-of-function variant of SLC9A6 leads to endosomal alkalinization and neuronal atrophy associated with Christianson Syndrome. <i>Neurobiology of Disease</i> , 2019, 121, 187-204.   | 4.4 | 21        |

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|----|---|------|-----------|
| 73 | Structural and functional insights into esterase-mediated macrolide resistance. <i>Nature Communications</i> , 2021, 12, 1732.  | 12.8 | 21        |
| 74 | Crystal Structures of Antibiotic-Bound Complexes of Aminoglycoside 2-Phosphotransferase IVa Highlight the Diversity in Substrate Binding Modes among Aminoglycoside Kinases. <i>Biochemistry</i> , 2011, 50, 6237-6244.                           | 2.5  | 19        |
| 75 | The Structural Dynamics of Engineered $\beta$ -Lactamases Vary Broadly on Three Timescales yet Sustain Native Function. <i>Scientific Reports</i> , 2019, 9, 6656.  | 3.3  | 19        |
| 76 | Phosphonate and Bisphosphonate Inhibitors of Farnesyl Pyrophosphate Synthases: A Structure-Guided Perspective. <i>Frontiers in Chemistry</i> , 2020, 8, 612728.   | 3.6  | 19        |
| 77 | Identification of the Adenovirus E4orf4 Protein Binding Site on the B55 $\alpha$ and Cdc55 Regulatory Subunits of PP2A: Implications for PP2A Function, Tumor Cell Killing and Viral Replication. <i>PLoS Pathogens</i> , 2013, 9, e1003742.      | 4.7  | 17        |
| 78 | Crystal structure of CTP:glycerol-3-phosphate cytidylyltransferase from <i>Staphylococcus aureus</i> : Examination of structural basis for kinetic mechanism. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 63-69. | 2.3  | 16        |
| 79 | Expression and purification of recombinant M-Pol I from <i>Saccharomyces cerevisiae</i> with $\beta$ -1,6 mannosylpolymerase activity. <i>Protein Expression and Purification</i> , 2009, 66, 1-6.  | 1.3  | 16        |
| 80 | Probing the molecular and structural elements of ligands binding to the active site versus an allosteric pocket of the human farnesyl pyrophosphate synthase. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 1117-1123.            | 2.2  | 15        |
| 81 | Derivatives of Mesoxalic Acid Block Translocation of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 2015, 290, 1474-1484.  | 3.4  | 14        |
| 82 | Genetic Analysis of B55 $\alpha$ /Cdc55 Protein Phosphatase 2A Subunits: Association with the Adenovirus E4orf4 Protein. <i>Journal of Virology</i> , 2011, 85, 286-295.  | 3.4  | 13        |
| 83 | Structural basis for plazomicin antibiotic action and resistance. <i>Communications Biology</i> , 2021, 4, 729.   | 4.4  | 13        |
| 84 | The type IA topoisomerase catalytic cycle: A normal mode analysis and molecular dynamics simulation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1984-1994.   | 2.6  | 12        |
| 85 | Antibiotic Binding Drives Catalytic Activation of Aminoglycoside Kinase APH(2 $\epsilon$ )-Ia. <i>Structure</i> , 2016, 24, 935-945.  | 3.3  | 10        |
| 86 | Chirality-Driven Mode of Binding of $\beta$ -Aminophosphonic Acid-Based Allosteric Inhibitors of the Human Farnesyl Pyrophosphate Synthase (hFPPS). <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9691-9702.                                  | 6.4  | 10        |
| 87 | Isolation, Crystallization and Preliminary Diffraction Analyses of Human Pancreatic $\beta$ -Amylase. <i>Journal of Molecular Biology</i> , 1993, 230, 1084-1085.   | 4.2  | 9         |
| 88 | Structure of human farnesyl pyrophosphate synthase in complex with an aminopyridine bisphosphonate and two molecules of inorganic phosphate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 299-304.      | 0.8  | 9         |
| 89 | Structural and phylogenetic analyses of resistance to next-generation aminoglycosides conferred by AAC(2 $\epsilon$ ) enzymes. <i>Scientific Reports</i> , 2021, 11, 11614.   | 3.3  | 9         |
| 90 | Novel crystallization conditions for tandem variant R67 DHFR yield a wild-type crystal structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1316-1322.   | 0.7  | 8         |

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|-----|--|-----|-----------|
| 91  | Structure-Based Design of Dimeric Bisbenzimidazole Inhibitors to an Emergent Trimethoprim-Resistant Type II Dihydrofolate Reductase Guides the Design of Monomeric Analogues. <i>ACS Omega</i> , 2019, 4, 10056-10069.                                 | 3.5 | 7         |
| 92  | Bisphosphoglycerate Mutase Deficiency Protects against Cerebral Malaria and Severe Malaria-Induced Anemia. <i>Cell Reports</i> , 2020, 32, 108170.   | 6.4 | 7         |
| 93  | Sustained Development in Baeyer-Villiger Biooxidation Technology. <i>ACS Symposium Series</i> , 2010, , 343-372.   | 0.5 | 6         |
| 94  | ZBTB7B (ThPOK) Is Required for Pathogenesis of Cerebral Malaria and Protection against Pulmonary Tuberculosis. <i>Infection and Immunity</i> , 2020, 88, .   | 2.2 | 6         |
| 95  | De novo <i>TRPV4</i> Leu619Pro variant causes a new channelopathy characterised by giant cell lesions of the jaws and skull, skeletal abnormalities and polyneuropathy. <i>Journal of Medical Genetics</i> , 2022, 59, 305-312.                        | 3.2 | 6         |
| 96  | Crystallization and preliminary crystallographic analysis of 3-aminoglycoside kinase type IIIa complexed with a eukaryotic protein kinase inhibitor, CKI-7. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1897-1899. | 2.5 | 5         |
| 97  | Crystallographic and thermodynamic characterization of phenylaminopyridine bisphosphonates binding to human farnesyl pyrophosphate synthase. <i>PLoS ONE</i> , 2017, 12, e0186447.   | 2.5 | 5         |
| 98  | Plasticity of Aminoglycoside Binding to Antibiotic Kinase APH(2A)-Ia. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .   | 3.2 | 5         |
| 99  | Structural Aspects of Aminoglycoside-Modifying Enzymes. , 0, , 21-33.  |     | 5         |
| 100 | Crystallization and preliminary crystallographic analysis of an aminoglycoside kinase from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 606-608.                             | 0.7 | 4         |
| 101 | Preparation and Characterization of Bacterial Protein Complexes for Structural Analysis. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 76, 1-42.   | 2.3 | 4         |
| 102 | Comprehensive characterization of ligand-induced plasticity changes in a dimeric enzyme. <i>FEBS Journal</i> , 2016, 283, 3029-3038.   | 4.7 | 4         |
| 103 | Crystallization and preliminary X-ray diffraction studies of homoserine dehydrogenase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 413-415.                                  | 2.5 | 3         |
| 104 | Crystallization and preliminary X-ray diffraction studies of glycerol 3-phosphate cytidyltransferase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 918-920.                      | 2.5 | 3         |
| 105 | Effect of solvent and protein dynamics in ligand recognition and inhibition of aminoglycoside adenylyltransferase 2A. <i>Protein Science</i> , 2017, 26, 1852-1863.  | 7.6 | 2         |
| 106 | An <i>Entamoeba histolytica</i> ADP-ribosyl transferase from the diphtheria toxin family modifies the bacterial elongation factor Tu. <i>Molecular and Biochemical Parasitology</i> , 2016, 207, 68-74.  | 1.1 | 1         |
| 107 | Revisiting the Catalytic Cycle and Kinetic Mechanism of Aminoglycoside <i>O</i> -Nucleotidyltransferase(2A): A Structural and Kinetic Study. <i>ACS Chemical Biology</i> , 2020, 15, 686-694.  | 3.4 | 0         |
| 108 | Resistance to aminoglycoside Antibiotics: Function meets structure. <i>Focus on Biotechnology</i> , 2001, , 85-98.   | 0.4 | 0         |