

Shankar Prasad Kanaujia

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

303
citations

1039406

9
h-index

1058022

14
g-index

41
all docs

41
docs citations

41
times ranked

360
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Structural and functional role of invariant water molecules in matrix metalloproteinases: a data-mining approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10074-10085. | 2.0 | 3 |
| 2 | Role of an orphan substrate-binding protein MhuP in transient heme transfer in <i>Mycobacterium tuberculosis</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 211, 342-356. | 3.6 | 3 |
| 3 | Exploiting the rationale behind substrate recognition by promiscuous thermophilic NDP-sugar pyrophosphorylase for expanding glycorandomization: an <i>in silico</i> study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 6099-6111. | 2.0 | 0 |
| 4 | Water-mediated structural rearrangement establishes active conformation of caspases for apoptosis and inflammation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-14. | 2.0 | 0 |
| 5 | Structural and thermodynamic insights into the novel dinucleotide-binding protein of ABC transporter unveils its moonlighting function. <i>FEBS Journal</i> , 2021, 288, 4614-4636. | 2.2 | 3 |
| 6 | Acyldepsipeptide activated ClpP1P2 macromolecule of <i>Leptospira</i> , an ideal Achilles' heel to hamper the cell survival and deregulate ClpP proteolytic activity. <i>Research in Microbiology</i> , 2021, 172, 103797. | 1.0 | 4 |
| 7 | Conserved features of the <i>scp</i> MlaD domain aid the trafficking of hydrophobic molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1473-1488. | 1.5 | 1 |
| 8 | Identification and characterization of metal uptake ABC transporters in <i>Mycobacterium tuberculosis</i> unveil their ligand specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 185, 324-337. | 3.6 | 4 |
| 9 | An updated classification and mechanistic insights into ligand binding of the substrate-binding proteins. <i>FEBS Letters</i> , 2021, 595, 2395-2409. | 1.3 | 15 |
| 10 | Structural and thermodynamic insights into a novel Mg ²⁺ citrate-binding protein from the ABC transporter superfamily. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1516-1534. | 1.1 | 1 |
| 11 | Structural and thermodynamic correlation illuminates the selective transport mechanism of disaccharide β -glucosides through ABC transporter. <i>FEBS Journal</i> , 2020, 287, 1576-1597. | 2.2 | 12 |
| 12 | Conformational Trapping of a β -Glucosides-Binding Protein Unveils the Selective Two-Step Ligand-Binding Mechanism of ABC Importers. <i>Journal of Molecular Biology</i> , 2020, 432, 5711-5734. | 2.0 | 8 |
| 13 | An insight into bacterial phospholipase C classification and their translocation through Tat and Sec pathways: A data mining study. <i>Meta Gene</i> , 2019, 20, 100547. | 0.3 | 4 |
| 14 | Designating ligand specificities to metal uptake ABC transporters in <i>Thermus thermophilus</i> HB8. <i>Metallomics</i> , 2019, 11, 597-612. | 1.0 | 15 |
| 15 | Design of novel PhMTNA inhibitors, targeting neurological disorder through homology modeling, molecular docking, and dynamics approaches. <i>Journal of Receptor and Signal Transduction Research</i> , 2019, 39, 28-38. | 1.3 | 7 |
| 16 | Role of Structural Features in Oligomerization, Active-Site Integrity and Ligand Binding of Ribose-1,5-Bisphosphate Isomerase. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 333-344. | 1.9 | 5 |
| 17 | Identification and characterization of ABC transporters for carbohydrate uptake in <i>Thermus thermophilus</i> HB8. <i>Gene</i> , 2019, 696, 135-148. | 1.0 | 15 |
| 18 | Structural insights into the catalytic mechanism of 5-methylthioribose 1-phosphate isomerase. <i>Journal of Structural Biology</i> , 2019, 205, 67-77. | 1.3 | 3 |

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|----|---|-----|-----------|
| 19 | Archaeal and eukaryal translation initiation factor 1 differ in their RNA interacting loops. <i>FEBS Letters</i> , 2018, 592, 1602-1610. | 1.3 | 2 |
| 20 | A presumed homologue of the regulatory subunits of eIF2B functions as ribose-1,5-bisphosphate isomerase in <i>Pyrococcus horikoshii</i> OT3. <i>Scientific Reports</i> , 2018, 8, 1891. | 1.6 | 5 |
| 21 | In silico characterization of TTHA0596: A potential Zn ²⁺ binding protein of ATP-binding cassette transporter. <i>Gene Reports</i> , 2017, 6, 132-141. | 0.4 | 2 |
| 22 | UgpB, a periplasmic component of the UgpABCE ATP-binding cassette transporter, predominantly follows the Sec translocation pathway. <i>Meta Gene</i> , 2017, 13, 129-139. | 0.3 | 3 |
| 23 | Computational characterization of TTHA0379: A potential glycerophosphocholine binding protein of Ugp ATP-binding cassette transporter. <i>Gene</i> , 2016, 592, 260-268. | 1.0 | 10 |
| 24 | In silico analysis of 5' UTRs highlights the prevalence of Shine-Dalgarno and leaderless-dependent mechanisms of translation initiation in bacteria and archaea, respectively. <i>Journal of Theoretical Biology</i> , 2016, 402, 54-61. | 0.8 | 15 |
| 25 | Direct inhibition of matrix metalloproteinase-2 (MMP-2) by (âˆ”)-epigallocatechin-3-gallate: A possible role for the fibronectin type II repeats. <i>Gene</i> , 2016, 593, 126-130. | 1.0 | 12 |
| 26 | In silico analysis suggests that PH0702 and PH0208 encode for methylthioribose-1-phosphate isomerase and ribose-1,5-bisphosphate isomerase, respectively, rather than aIF2B ^{Î²} and aIF2B ^{Î³} . <i>Gene</i> , 2016, 575, 118-126. | 1.0 | 7 |
| 27 | Heterogeneous behavior of metalloproteins toward metal ion binding and selectivity: insights from molecular dynamics studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1470-1485. | 2.0 | 7 |
| 28 | Role of invariant water molecules and water-mediated ionic interactions in D-xylose isomerase from <i>Streptomyces rubiginosus</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 376-384. | 2.0 | 2 |
| 29 | Crystal structures and binding studies of atovaquone and its derivatives with cytochrome bc1: a molecular basis for drug design. <i>CrystEngComm</i> , 2013, 15, 4871. | 1.3 | 10 |
| 30 | Structure of SAICAR synthetase from <i>Pyrococcus horikoshii</i> OT3: Insights into thermal stability. <i>International Journal of Biological Macromolecules</i> , 2013, 53, 7-19. | 3.6 | 6 |
| 31 | Crystal structures, dynamics and functional implications of molybdenum-cofactor biosynthesis protein MogA from two thermophilic organisms. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 2-16. | 0.7 | 4 |
| 32 | Free and ATP-bound structures of Ap ₄ A hydrolase from <i>Aquifex aeolicus</i> V5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 116-124. | 2.5 | 7 |
| 33 | Structures of apo and GTP-bound molybdenum cofactor biosynthesis protein MoaC from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 821-833. | 2.5 | 22 |
| 34 | Structural and functional role of water molecules in bovine pancreatic phospholipase A ₂ : a data-mining approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 74-84. | 2.5 | 21 |
| 35 | Structures and molecular-dynamics studies of three active-site mutants of bovine pancreatic phospholipase A ₂ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1003-1011. | 2.5 | 3 |
| 36 | Observation of a calcium-binding site in the Î³-class carbonic anhydrase from <i>Pyrococcus horikoshii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1012-1019. | 2.5 | 48 |

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|----|---|-----|-----------|
| 37 | Crystallization and preliminary crystallographic analysis of molybdenum-cofactor biosynthesis protein C from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 27-29. | 0.7 | 4 |
| 38 | Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of DHNA synthetase from <i>Geobacillus kaustophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 103-105. | 0.7 | 4 |
| 39 | Cloning, expression, purification, crystallization and preliminary X-ray crystallographic study of molybdopterin synthase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 324-326. | 0.7 | 2 |
| 40 | Preliminary X-ray crystallographic study of glucose dehydrogenase from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 446-448. | 0.7 | 1 |
| 41 | Suggestive evidence for the involvement of the second calcium and surface loop in interfacial binding: monoclinic and trigonal crystal structures of a quadruple mutant of phospholipase A2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 717-724. | 2.5 | 3 |