

Clement Angkawidjaja

List of Publications by Year in descending order

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Version: 2024-02-01

22

papers

390

citations

840776

11

h-index

752698

20

g-index

22

all docs

22

docs citations

22

times ranked

565

citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Crystal structure of a family I.3 lipase from <i>Pseudomonas</i> sp. MIS38 in a closed conformation. FEBS Letters, 2007, 581, 5060-5064. | 2.8 | 71 |
| 2 | Structure and stability of a thermostable carboxylesterase from the thermoacidophilic archaeon <i>Sulfolobus tokodaii</i> . FEBS Journal, 2012, 279, 3071-3084. | 4.7 | 41 |
| 3 | Rational design of a glycosynthase by the crystal structure of β -galactosidase from <i>Bacillus circulans</i> (BgaC) and its use for the synthesis of N-acetyllactosamine type 1 glycan structures. Journal of Biotechnology, 2014, 191, 78-85. | 3.8 | 31 |
| 4 | X-ray Crystallographic and MD Simulation Studies on the Mechanism of Interfacial Activation of a Family I.3 Lipase with Two Lids. Journal of Molecular Biology, 2010, 400, 82-95. | 4.2 | 28 |
| 5 | Importance of a repetitive nine-residue sequence motif for intracellular stability and functional structure of a family I.3 lipase. FEBS Letters, 2005, 579, 4707-4712. | 2.8 | 26 |
| 6 | Engineering of monomeric FK506-binding protein 22 with peptidyl prolyl <i>cis</i> - <i>trans</i> isomerase. FEBS Journal, 2009, 276, 4091-4101. | 4.7 | 25 |
| 7 | Structure and stability of metagenome-derived glycoside hydrolase family 12 cellulase (LC-CelA) a homolog of Cel12A from <i>Rhodothermus marinus</i> . FEBS Open Bio, 2014, 4, 936-946. | 2.3 | 23 |
| 8 | Structure, activity, and stability of metagenome-derived glycoside hydrolase family 9 endoglucanase with an N-terminal Ig-like domain. Protein Science, 2015, 24, 408-419. | 7.6 | 17 |
| 9 | Requirement of lid2 for interfacial activation of a family I.3 lipase with unique two lid structures. FEBS Journal, 2012, 279, 3727-3737. | 4.7 | 16 |
| 10 | Stabilization by Fusion to the C-terminus of Hyperthermophile <i>Sulfolobus tokodaii</i> RNase H1: A Possibility of Protein Stabilization Tag. PLoS ONE, 2011, 6, e16226. | 2.5 | 15 |
| 11 | Role of polar and nonpolar residues at the active site for PPase activity of FKBP22 from <i>Shewanella</i> sp. SIB1. FEBS Journal, 2012, 279, 976-986. | 4.7 | 14 |
| 12 | Structural and biochemical characterization of a metagenome-derived esterase with a long N-terminal extension. Protein Science, 2015, 24, 93-104. | 7.6 | 14 |
| 13 | Crystal structure of N-domain of FKBP22 from <i>Shewanella</i> sp. SIB1: Dimer dissociation by disruption of Val-Leu knot. Protein Science, 2011, 20, 1755-1764. | 7.6 | 13 |
| 14 | Identification of the substrate binding site in the N-terminal TBP-like domain of RNase H3. FEBS Letters, 2011, 585, 2313-2317. | 2.8 | 10 |
| 15 | Activity, stability, and structure of metagenome-derived LC11-RNase H1, a homolog of <i>Sulfolobus tokodaii</i> RNase H1. Protein Science, 2012, 21, 553-561. | 7.6 | 10 |
| 16 | Structure and characterization of RNase-fH3 from <i>Aquifex aeolicus</i> . FEBS Journal, 2012, 279, 2737-2753. | 4.7 | 10 |
| 17 | Structural Basis for the <i>Serratia marcescens</i> Lipase Secretion System: Crystal Structures of the Membrane Fusion Protein and Nucleotide-Binding Domain. Biochemistry, 2017, 56, 6281-6291. | 2.5 | 9 |
| 18 | Extracellular overproduction and preliminary crystallographic analysis of a family I.3 lipase. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 187-189. | 0.7 | 6 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Structural and mechanistic insights into the kynurenone aminotransferase-mediated excretion of kynurenic acid. <i>Journal of Structural Biology</i> , 2014, 185, 257-266. | 2.8 | 5 |
| 20 | Role of <i>N</i> -terminal extension of <i>i>B</i> acillus <i>A</i> stearothermophilus <i>RNaseH</i> 2 and <i>C</i> -terminal extension of <i>i>T</i> hermotoga <i>A</i> maritima <i>RNaseH</i> 2. <i>FEBS Journal</i> , 2013, 280, 5065-5079. | 4.7 | 3 |
| 21 | Structural basis for salt-dependent folding of ribonuclease H1 from halophilic archaeon <i>Halobacterium</i> sp. NRC-1. <i>Journal of Structural Biology</i> , 2014, 187, 119-128. | 2.8 | 2 |
| 22 | Affinity shift of ATP upon glycerol binding to a glycerol kinase from the hyperthermophilic archaeon <i>Thermococcus kodakarensis</i> KOD1. <i>Journal of Bioscience and Bioengineering</i> , 2020, 129, 657-663. | 2.2 | 1 |