

# Clement Angkawidjaja

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10531783/publications.pdf>

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	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
2	Structural Basis for the <i>Serratia marcescens</i> Lipase Secretion System: Crystal Structures of the Membrane Fusion Protein and Nucleotide-Binding Domain. <i>Biochemistry</i> , 2017, 56, 6281-6291.	2.5	9
3	Structure, activity, and stability of metagenome-derived glycoside hydrolase family 9 endoglucanase with an N-terminal Ig-like domain. <i>Protein Science</i> , 2015, 24, 408-419.	7.6	17
4	Structural and biochemical characterization of a metagenome-derived esterase with a long N-terminal extension. <i>Protein Science</i> , 2015, 24, 93-104.	7.6	14
5	Structure and stability of metagenome-derived glycoside hydrolase family 12 cellulase (LC-CelA) a homolog of Cel12A from <i>Rhodothermus marinus</i> . <i>FEBS Open Bio</i> , 2014, 4, 936-946.	2.3	23
6	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
7	Rational design of a glycosynthase by the crystal structure of $\beta$ -galactosidase from <i>Bacillus circulans</i> (BgaC) and its use for the synthesis of N-acetyllactosamine type 1 glycan structures. <i>Journal of Biotechnology</i> , 2014, 191, 78-85.	3.8	31
8	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
9	Role of $\text{N}$ -terminal extension of <i>Bacillus stearothermophilus</i> <i>Bse</i> and <i>C</i> -terminal extension of <i>hermotogaamaritima</i> <i>Hse</i> . <i>FEBS Journal</i> , 2013, 280, 5065-5079.	4.7	3
10	Requirement of lid2 for interfacial activation of a family I.3 lipase with unique two lid structures. <i>FEBS Journal</i> , 2012, 279, 3727-3737.	4.7	16
11	Activity, stability, and structure of metagenome-derived LC11-RNase H1, a homolog of <i>Sulfolobus tokodaii</i> RNase H1. <i>Protein Science</i> , 2012, 21, 553-561.	7.6	10
12	Structure and characterization of RNase-fH3 from <i>Aquifex aeolicus</i> . <i>FEBS Journal</i> , 2012, 279, 2737-2753.	4.7	10
13	Role of polar and nonpolar residues at the active site for PPIase activity of FKBP22 from <i>Shewanella</i> sp. SIB1. <i>FEBS Journal</i> , 2012, 279, 976-986.	4.7	14
14	Structure and stability of a thermostable carboxylesterase from the thermoacidophilic archaeon <i>Sulfolobus tokodaii</i> . <i>FEBS Journal</i> , 2012, 279, 3071-3084.	4.7	41
15	Stabilization by Fusion to the C-terminus of Hyperthermophile <i>Sulfolobus tokodaii</i> RNase H1: A Possibility of Protein Stabilization Tag. <i>PLoS ONE</i> , 2011, 6, e16226.	2.5	15
16	Identification of the substrate binding site in the N-terminal TBP-like domain of RNase H3. <i>FEBS Letters</i> , 2011, 585, 2313-2317.	2.8	10
17	Crystal structure of N-domain of FKBP22 from <i>Shewanella</i> sp. SIB1: Dimer dissociation by disruption of Val-Leu knot. <i>Protein Science</i> , 2011, 20, 1755-1764.	7.6	13
18	X-ray Crystallographic and MD Simulation Studies on the Mechanism of Interfacial Activation of a Family I.3 Lipase with Two Lids. <i>Journal of Molecular Biology</i> , 2010, 400, 82-95.	4.2	28

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19	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
20	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
21	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
22	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