

Ronny Helland

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5397071/publications.pdf>

Version: 2024-02-01

19
papers

641
citations

759233

12
h-index

839539

18
g-index

19
all docs

19
docs citations

19
times ranked

1136
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and functional characterization of a conserved pair of bacterial cellulose-oxidizing lytic polysaccharide monooxygenases. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 8446-8451.	7.1	241
2	Discovery of Novel Inhibitor Scaffolds against the Metallo- β -lactamase VIM-2 by Surface Plasmon Resonance (SPR) Based Fragment Screening. Journal of Medicinal Chemistry, 2015, 58, 8671-8682.	6.4	56
3	Crystal structures of g-type lysozyme from Atlantic cod shed new light on substrate binding and the catalytic mechanism. Cellular and Molecular Life Sciences, 2009, 66, 2585-2598.	5.4	48
4	The 1.4 Å crystal structure of the large and cold-active <i>Vibrio</i> sp. alkaline phosphatase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 297-308.	2.3	48
5	An Oxidized Tryptophan Facilitates Copper Binding in <i>Methylococcus capsulatus</i> -secreted Protein MopE. Journal of Biological Chemistry, 2008, 283, 13897-13904.	3.4	45
6	Electrostatics of mesophilic and psychrophilic trypsin isoenzymes: Qualitative evaluation of electrostatic differences at the substrate binding site. Proteins: Structure, Function and Bioinformatics, 2000, 40, 207-217.	2.6	40
7	The 1.8 Å crystal structure of a proteinase K-like enzyme from a psychrotroph <i>Serratia</i> species. FEBS Journal, 2006, 273, 61-71.	4.7	32
8	The crystal structure of anionic salmon trypsin in complex with bovine pancreatic trypsin inhibitor. FEBS Journal, 1998, 256, 317-324.	0.2	30
9	CorA Is a Copper Repressible Surface-Associated Copper(I)-Binding Protein Produced in <i>Methylobacterium album</i> BG8. PLoS ONE, 2014, 9, e87750.	2.5	18
10	Structural insight into a CE15 esterase from the marine bacterial metagenome. Scientific Reports, 2017, 7, 17278.	3.3	17
11	Structural Consequences of Accommodation of Four Non-cognate Amino Acid Residues in the S1 Pocket of Bovine Trypsin and Chymotrypsin. Journal of Molecular Biology, 2003, 333, 845-861.	4.2	15
12	Effects of salt on the kinetics and thermodynamic stability of endonuclease <i>fl</i> from <i>Vibrio salmonicida</i> and <i>Vibrio cholerae</i> . FEBS Journal, 2008, 275, 1593-1605.	4.7	14
13	Multiple specialised goose-type lysozymes potentially compensate for an exceptional lack of chicken-type lysozymes in Atlantic cod. Scientific Reports, 2016, 6, 28318.	3.3	12
14	Structural insights of the enzymes from the chitin utilization locus of <i>Flavobacterium johnsoniae</i> . Scientific Reports, 2020, 10, 13775.	3.3	9
15	Features and structure of a cold active N-acetylneuraminase lyase. PLoS ONE, 2019, 14, e0217713.	2.5	5
16	Psoriasis pathogenesis – Pso p27 constitutes a compact structure forming large aggregates. Biochemistry and Biophysics Reports, 2015, 2, 132-136.	1.3	4
17	X-ray crystal structure of <i>Vibrio</i> alkaline phosphatase with the non-competitive inhibitor cyclohexylamine. Biochemistry and Biophysics Reports, 2020, 24, 100830.	1.3	4
18	The high catalytic rate of the cold-active <i>Vibrio</i> alkaline phosphatase requires a hydrogen bonding network involving a large interface loop. FEBS Open Bio, 2021, 11, 173-184.	2.3	3

#	ARTICLE	IF	CITATIONS
19	The crystal structure of haemoglobin from Atlantic cod. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 537-542.	0.8	0