

Honghua Ge

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1041691/publications.pdf>

Version: 2024-02-01

38
papers

632
citations

623734

14
h-index

610901

24
g-index

39
all docs

39
docs citations

39
times ranked

1164
citing authors

#	ARTICLE	IF	CITATIONS
1	Neutralizing SARS-CoV-2 by dimeric side chain-to-side chain cross-linked ACE2 peptide mimetics. <i>Chemical Communications</i> , 2022, 58, 1804-1807.	4.1	3
2	Molecular basis for coordinating secondary metabolite production by bacterial and plant signaling molecules. <i>Journal of Biological Chemistry</i> , 2022, 298, 102027.	3.4	4
3	Structural insights into a new substrate binding mode of a histidine acid phosphatase from <i>Legionella pneumophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2021, 540, 90-94.	2.1	0
4	Genetic mapping identifies a rice naringenin O-glucosyltransferase that influences insect resistance. <i>Plant Journal</i> , 2021, 106, 1401-1413.	5.7	15
5	Epidemiological Characterization of Colistin and Carbapenem Resistant Enterobacteriaceae in a Tertiary: A Hospital from Anhui Province. <i>Infection and Drug Resistance</i> , 2021, Volume 14, 1325-1333.	2.7	10
6	Crystal structure of a hypothetical T2SS effector Lpg0189 from <i>Legionella pneumophila</i> reveals a novel protein fold. <i>Biochemical and Biophysical Research Communications</i> , 2020, 521, 799-805.	2.1	2
7	Intramolecular Annulation of Gossypol by Laccase to Produce Safe Cottonseed Protein. <i>Frontiers in Chemistry</i> , 2020, 8, 583176.	3.6	8
8	The phospholipase A effector PlaA from <i>Legionella pneumophila</i> : expression, purification and crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 138-144.	0.8	2
9	Identification of the Repressive Domain of the Negative Circadian Clock Component CHRONO. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2469.	4.1	15
10	Structural characterization of the hypothetical protein Lpg2622, a new member of the C1 family peptidases from <i>Legionella pneumophila</i> . <i>FEBS Letters</i> , 2018, 592, 2798-2810.	2.8	4
11	High-Resolution Crystal Structure of RpoS Fragment including a Partial Region 1.2 and Region 2 from the Intracellular Pathogen <i>Legionella pneumophila</i> . <i>Crystals</i> , 2018, 8, 54.	2.2	1
12	Crystal structure of lpg1832, a VirK family protein from <i>Legionella pneumophila</i> , reveals a novel fold for bacterial VirK proteins. <i>FEBS Letters</i> , 2017, 591, 2929-2935.	2.8	4
13	Crystal Structure and Biochemical Characterization of an Aminopeptidase LapB from <i>Legionella pneumophila</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 7569-7578.	5.2	11
14	Synergistic enhancement via plasmonic nanoplate-bacteria-nanorod supercrystals for highly efficient SERS sensing of food-borne bacteria. <i>Sensors and Actuators B: Chemical</i> , 2017, 239, 515-525.	7.8	36
15	A Versatile Anisometric Metallic Supercrystal with Controllable Orientation on a Chip as a Stable and Reliable Label-Free Biosensor. <i>Chemistry - an Asian Journal</i> , 2016, 11, 256-264.	3.3	5
16	Crystal structures of Apo and GMP bound hypoxanthine-guanine phosphoribosyltransferase from <i>Legionella pneumophila</i> and the implications in gouty arthritis. <i>Journal of Structural Biology</i> , 2016, 194, 311-316.	2.8	7
17	Core-Shell Nanorod Columnar Array Combined with Gold Nanoplate-Nanosphere Assemblies Enable Powerful In Situ SERS Detection of Bacteria. <i>ACS Applied Materials & Interfaces</i> , 2016, 8, 24394-24403.	8.0	36
18	Structure of lpg0406, a carboxymuconolactone decarboxylase family protein possibly involved in antioxidative response from <i>Legionella pneumophila</i> . <i>Protein Science</i> , 2015, 24, 2070-2075.	7.6	12

#	ARTICLE	IF	CITATIONS
19	Crystallization and preliminary crystallographic analysis of the major acid phosphatase from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 779-783.	0.8	2
20	Effects of <i>Fructus ligustri lucidi</i> on the growth, cell integrity, and metabolic activity of the <i>Microcystis aeruginosa</i> . <i>Environmental Science and Pollution Research</i> , 2015, 22, 8471-8479.	5.3	11
21	Fabricating a Long-Range Ordered 3D Bimetallic Nanoassembly with Edge-On Substrate for Highly Sensitive SERS Sensing of <i>Escherichia coli</i> Bacteria. <i>Plasmonics</i> , 2015, 10, 1889-1894.	3.4	7
22	Crystal structure of <i>Legionella pneumophila</i> dephospho-CoA kinase reveals a non-canonical conformation of P-loop. <i>Journal of Structural Biology</i> , 2014, 188, 233-239.	2.8	2
23	Crystallization and preliminary X-ray characterization of the dephospho-CoA kinase from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 608-610.	0.8	1
24	Crystal structure of wild-type and mutant human Ap4A hydrolase. <i>Biochemical and Biophysical Research Communications</i> , 2013, 432, 16-21.	2.1	12
25	Crystal structure of agkisacucetin, a GPI-binding snake C-type lectin that inhibits platelet adhesion and aggregation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1707-1711.	2.6	21
26	A bacterial laccase from marine microbial metagenome exhibiting chloride tolerance and dye decolorization ability. <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 1103-1110.	3.6	124
27	Purification, crystallization and preliminary crystallographic analysis of recombinant Lac15 from a marine microbial metagenome. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 956-958.	0.7	6
28	Crystal structure of isoamyl acetate-hydrolyzing esterase from <i>Saccharomyces cerevisiae</i> reveals a novel active site architecture and the basis of substrate specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 662-668.	2.6	16
29	Preparation of microporous starch by glucoamylase and ultrasound. <i>Starch/Staerke</i> , 2011, 63, 217-225.	2.1	76
30	Structural basis of pre-mRNA recognition by the human cleavage factor Im complex. <i>Cell Research</i> , 2011, 21, 1039-1051.	12.0	28
31	Crystal Structure of a <i>Legionella pneumophila</i> Ecto -Triphosphate Diphosphohydrolase, A Structural and Functional Homolog of the Eukaryotic NTPDases. <i>Structure</i> , 2010, 18, 228-238.	3.3	39
32	Crystallization and preliminary crystallographic analysis of recombinant VSP1 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 201-203.	0.7	1
33	Structure of native laccase B from <i>Trametes</i> sp. AH28-2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 254-258.	0.7	19
34	Crystal structure of Glutamate1-semialdehyde aminotransferase from <i>Bacillus subtilis</i> with bound pyridoxamine-5'-phosphate. <i>Biochemical and Biophysical Research Communications</i> , 2010, 402, 356-360.	2.1	18
35	Crystal structure and possible dimerization of the single RRM of human PABPN1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1539-1545.	2.6	18
36	Crystal structure of the C-terminal conserved domain of human GRP, a galectin-related protein, reveals a function mode different from those of galectins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1582-1588.	2.6	20

#	ARTICLE	IF	CITATIONS
37	Crystal structure of 3-hydroxyanthranilic acid 3,4-dioxygenase from <i>Saccharomyces cerevisiae</i> : A special subgroup of the type III extradiol dioxygenases. <i>Protein Science</i> , 2006, 15, 761-773.	7.6	34
38	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of the glutamate-1-semialdehyde aminotransferase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 483-485.	0.7	2