## Yanxiang Zhao

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Quantitative multiplexed proteomics analysis reveals reshaping of the lysine 2-hydroxyisobutyrylome in Fusarium graminearum by tebuconazole. BMC Genomics, 2022, 23, 145.	2.8	7
2	The Transcription Factor FgAtrR Regulates Asexual and Sexual Development, Virulence, and DON Production and Contributes to Intrinsic Resistance to Azole Fungicides in Fusarium graminearum. Biology, 2022, 11, 326.	2.8	2
3	The FgCYP51B Y123H Mutation Confers Reduced Sensitivity to Prochloraz and Is Important for Conidiation and Ascospore Development in <i>Fusarium graminearum</i> . Phytopathology, 2021, 111, 1420-1427.	2.2	6
4	First Report of an <i>Alternaria alternata</i> Isolate That Causes Leaf Spot Disease on <i>Ilex crenata</i> var. <i>convexa</i> in China. Plant Disease, 2020, 104, 979-979.	1.4	1
5	First Report of <i>Colletotrichum gloeosporioides</i> Causing Leaf Spot Disease on <i>Hymenocallis littoralis</i> in China. Plant Disease, 2019, 103, 3286.	1.4	3
6	Crystal structures of <i>Magnaporthe oryzae</i> trehalose-6-phosphate synthase (MoTps1) suggest a model for catalytic process of Tps1. Biochemical Journal, 2019, 476, 3227-3240.	3.7	8
7	Crystal Structure of a Putative Modulator of Gyrase (TldE) from Thermococcus kodakarensis. Crystals, 2019, 9, 107.	2.2	2
8	Structural basis of dimerization and dual W-box DNA recognition by rice WRKY domain. Nucleic Acids Research, 2019, 47, 4308-4318.	14.5	56
9	The effect of phosphate ion on the ssDNA binding mode of MoSub1, a Sub1/PC4 homolog from rice blast fungus. Proteins: Structure, Function and Bioinformatics, 2019, 87, 257-264.	2.6	5
10	A positiveâ€charged patch and stabilized hydrophobic core are essential for avirulence function of AvrPib in the rice blast fungus. Plant Journal, 2018, 96, 133-146.	5.7	49
11	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the effector-interaction domain of the resistance protein RGA5-A from (i>Oryza sativa (i>L (i>japonica (i>. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 171-174.	0.8	6
12	Structural basis of DNA recognition by PCG2 reveals a novel DNA binding mode for winged helix-turn-helix domains. Nucleic Acids Research, 2015, 43, 1231-1240.	14.5	18
13	Substitution of tryptophan 89 with tyrosine switches the DNA binding mode of PC4. Scientific Reports, 2015, 5, 8789.	3.3	17
14	Structural features of the single-stranded DNA-binding protein MoSub1 from <i>Magnaporthe oryzae </i> . Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1071-1076.	2.5	10