

Shabir Najmudin

List of Publications by Year in descending order

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57
papers

1,021
citations

394286

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454834

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58
all docs

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docs citations

58
times ranked

1382
citing authors

#	ARTICLE	IF	CITATIONS
1	Xyloglucan Is Recognized by Carbohydrate-binding Modules That Interact with Î²-Glucan Chains. Journal of Biological Chemistry, 2006, 281, 8815-8828.	1.6	102
2	Periplasmic nitrate reductase revisited: a sulfur atom completes the sixth coordination of the catalytic molybdenum. Journal of Biological Inorganic Chemistry, 2008, 13, 737-753.	1.1	94
3	Complexity of the <i>Ruminococcus flavefaciens</i> cellulosome reflects an expansion in glycan recognition. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7136-7141.	3.3	58
4	Putting an N-terminal end to the Clostridium thermocellum xylanase Xyn10B story: Crystal structure of the CBM22-GH10 modules complexed with xylohexaose. Journal of Structural Biology, 2010, 172, 353-362.	1.3	52
5	Crystal structures of an N-terminal fragment from moloney murine leukemia virus reverse transcriptase complexed with nucleic acid: functional implications for template-primer binding to the fingers domain 1 Edited by D. C. Rees. Journal of Molecular Biology, 2000, 296, 613-632.	2.0	48
6	Structure of the bovine eye lens protein Î³B(Î³II)-crystallin at 1.47 Å... Acta Crystallographica Section D: Biological Crystallography, 1993, 49, 223-233.	2.5	38
7	Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and Î²-1,3-1,4-Glucans through Distinct Mechanisms. Journal of Biological Chemistry, 2015, 290, 10572-10586.	1.6	36
8	The Mechanism by Which Arabinoxylanases Can Recognize Highly Decorated Xylans. Journal of Biological Chemistry, 2016, 291, 22149-22159.	1.6	34
9	Exploring the Effects of Axial Pseudohalide Ligands on the Photophysical and Cyclic Voltammetry Properties and Molecular Structures of Mg ^{II} Tetraphenylporphyrin Complexes. European Journal of Inorganic Chemistry, 2014, 2014, 5348-5361.	1.0	33
10	Understanding How Noncatalytic Carbohydrate Binding Modules Can Display Specificity for Xyloglucan. Journal of Biological Chemistry, 2013, 288, 4799-4809.	1.6	31
11	Complexity of the Ruminococcus flavefaciens FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. Scientific Reports, 2017, 7, 42355.	1.6	31
12	Serum HER2 levels are increased in cats with mammary carcinomas and predict tissue HER2 status. Oncotarget, 2016, 7, 17314-17326.	0.8	31
13	Novel Clostridium thermocellum Type I Cohesin-Dockerin Complexes Reveal a Single Binding Mode. Journal of Biological Chemistry, 2012, 287, 44394-44405.	1.6	27
14	Insights on the UV/Vis, Fluorescence, and Cyclic Voltammetry Properties and the Molecular Structures of Zn ^{II} Tetraphenylporphyrin Complexes with Pseudohalide Axial Azido, Cyanato ^N , Thiocyanato ^N , and Cyanido Ligands. European Journal of Inorganic Chemistry, 2015, 2015, 2596-2610.	1.0	27
15	Cloning, expression, and purification of a catalytic fragment of moloney murine leukemia virus reverse transcriptase: Crystallization of nucleic acid complexes. Protein Science, 1998, 7, 1575-1582.	3.1	26
16	Structure and Mechanism of Acetolactate Decarboxylase. ACS Chemical Biology, 2013, 8, 2339-2344.	1.6	26
17	Cell-surface Attachment of Bacterial Multienzyme Complexes Involves Highly Dynamic Protein-Protein Anchors. Journal of Biological Chemistry, 2015, 290, 13578-13590.	1.6	22
18	Diverse specificity of cellulosome attachment to the bacterial cell surface. Scientific Reports, 2016, 6, 38292.	1.6	20

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19	Assembly of <i>Ruminococcus flavefaciens</i> cellulosome revealed by structures of two cohesin-dockerin complexes. <i>Scientific Reports</i> , 2017, 7, 759.	1.6	20
20	Heterodimeric nitrate reductase (NapAB) from <i>Cupriavidus necator</i> H16: purification, crystallization and preliminary X-ray analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 516-519.	0.7	19
21	Single Binding Mode Integration of Hemicellulose-degrading Enzymes via Adaptor Scaffoldins in <i>Ruminococcus flavefaciens</i> Cellulosome. <i>Journal of Biological Chemistry</i> , 2016, 291, 26658-26669.	1.6	19
22	Stability and Ligand Promiscuity of Type A Carbohydrate-binding Modules Are Illustrated by the Structure of <i>Spirochaeta thermophila</i> StCBM64C. <i>Journal of Biological Chemistry</i> , 2017, 292, 4847-4860.	1.6	19
23	Zinc(II)-triazole-meso-arylsubstituted porphyrins for UV-visible chloride and bromide detection. Adsorption and catalytic degradation of malachite green dye. <i>RSC Advances</i> , 2020, 10, 22712-22725.	1.7	16
24	The 1.4 Å resolution structure of <i>Paracoccus pantotrophus</i> pseudoazurin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 627-635.	0.7	15
25	Structure-function analyses generate novel specificities to assemble the components of multi-enzyme bacterial cellulosome complexes. <i>Journal of Biological Chemistry</i> , 2018, 293, 4201-4212.	1.6	12
26	Structure of bovine β -crystallin at 150 K. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1993, 89, 2677-2682.	1.7	11
27	Purification, crystallization and preliminary X-ray crystallographic studies on acetolactate decarboxylase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1073-1075.	2.5	11
28	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
29	Overexpression, purification and crystallization of the two C-terminal domains of the bifunctional cellulase Cel9D-Cel44A from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 1043-1045.	0.7	10
30	Combined Crystal Structure of a Type I Cohesin. <i>Journal of Biological Chemistry</i> , 2015, 290, 16215-16225.	1.6	10
31	Crystallization and crystallographic analysis of the apo form of the orange protein (ORP) from <i>Desulfovibrio gigas</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 730-732.	0.7	9
32	Molecular determinants of substrate specificity revealed by the structure of <i>Clostridium thermocellum</i> arabinofuranosidase 43A from glycosyl hydrolase family 43 subfamily 16. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1281-1289.	1.1	9
33	Conservation in the mechanism of glucuronoxylan hydrolysis revealed by the structure of glucuronoxylan xylanohydrolase (Xyn30A) from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1162-1173.	1.1	9
34	A dual cohesin-dockerin complex binding mode in <i>Bacteroides cellulosolvens</i> contributes to the size and complexity of its cellulosome. <i>Journal of Biological Chemistry</i> , 2021, 296, 100552.	1.6	8
35	Synthesis, Mössbauer, cyclic voltammetry, magnetic properties and molecular structures of the low-spin iron(III) bis(pyrazine) complexes with the para-fluoro and para-chloro substituted meso-tetraphenylporphyrin. <i>Inorganica Chimica Acta</i> , 2018, 477, 114-121.	1.2	7
36	<i>Escherichia coli</i> Expression, Purification, Crystallization, and Structure Determination of Bacterial Cohesin-Dockerin Complexes. <i>Methods in Enzymology</i> , 2012, 510, 395-415.	0.4	6

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37	Aqua(4-cyanopyridine- \hat{N})(5,10,15,20-tetraphenylporphyrinato- \hat{N})magnesium. Acta Crystallographica Section E: Structure Reports Online, 2013, 69, m17-m18.	0.2	6
38	Higher order scaffoldin assembly in Ruminococcus flavefaciens cellulosome is coordinated by a discrete cohesin-dockerin interaction. Scientific Reports, 2018, 8, 6987.	1.6	6
39	Flexibility and specificity of the cohesin-dockerin interaction: implications for cellulosome assembly and functionality. Biocatalysis and Biotransformation, 2012, 30, 309-315.	1.1	5
40	ArsC3 from Desulfovibrio alaskensis G20, a cation and sulfate-independent highly efficient arsenate reductase. Journal of Biological Inorganic Chemistry, 2014, 19, 1277-1285.	1.1	5
41	Molecular organization and protein stability of the Clostridium thermocellum glucuronoxylan endo- $\hat{1}$ -1,4-xylanase of family 30 glycoside hydrolase in solution. Journal of Structural Biology, 2019, 206, 335-344.	1.3	5
42	Substitutional disorder in bis[(cyanato- \hat{O})/hydroxido(0.5/0.5)](5,10,15,20-tetraphenylporphyrinato- \hat{N})tin(IV). Acta Crystallographica Section E: Structure Reports Online, 2011, 67, m903-m904.	0.2	4
43	Purification, crystallization and preliminary X-ray characterization of the pentamodular arabinoxylanase Ctxyl5A from Clostridium thermocellum. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 833-836.	0.7	4
44	Overexpression, purification, crystallization and preliminary X-ray characterization of the fourth scaffoldin A cohesin from Acetivibrio cellulolyticus in complex with a dockerin from a family 5 glycoside hydrolase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1065-1067.	0.4	4
45	Crystallization and preliminary X-ray diffraction analysis of a trimodular endo- $\hat{1}$ -1,4-glucanase (Cel5B) from Bacillus halodurans. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1628-1630.	0.4	4
46	Overproduction, purification, crystallization and preliminary X-ray characterization of the family 46 carbohydrate-binding module (CBM46) of endo- $\hat{1}$ -1,4-glucanase B (CelB) from Bacillus halodurans. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 754-757.	0.4	4
47	Purification, crystallization and crystallographic analysis of Clostridium thermocellum endo-1,4- \hat{D} -xylanase 10B in complex with xylohexaose. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 715-718.	0.7	3
48	Purification, crystallization and preliminary X-ray characterization of the Acetivibrio cellulolyticus type I cohesin ScaC in complex with the ScaB dockerin. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1030-1033.	0.7	3
49	Small angle X-ray scattering based structure, modeling and molecular dynamics analyses of family 43 glycoside hydrolase $\hat{1}$ -L-arabinofuranosidase from Clostridium thermocellum. Journal of Biomolecular Structure and Dynamics, 2021, 39, 209-218.	2.0	3
50	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A from Eubacterium cellulosolvens. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 491-493.	0.7	2
51	Overexpression, crystallization and preliminary X-ray characterization of Ruminococcus flavefaciens scaffoldin C cohesin in complex with a dockerin from an uncharacterized CBM-containing protein. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1061-1064.	0.4	2
52	Expression, purification, crystallization and preliminary X-ray analysis of CttA, a putative cellulose-binding protein from Ruminococcus flavefaciens. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 784-789.	0.4	2
53	Purification, crystallization and preliminary X-ray characterization of the third ScaB cohesin in complex with an ScaA X-dockerin from Acetivibrio cellulolyticus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 656-658.	0.4	1
54	Crystallization and preliminary crystallographic studies of a novel noncatalytic carbohydrate-binding module from the Ruminococcus flavefaciens cellulosome. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 45-48.	0.4	1

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55	Overproduction, purification, crystallization and preliminary X-ray characterization of the C-terminal family 65 carbohydrate-binding module (CBM65B) of endoglucanase Cel5A from <i>Eubacterium cellulosolvens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 191-194.	0.7	0
56	Expression, purification and crystallization of a novel carbohydrate-binding module from the <i>Ruminococcus flavefaciens</i> cellulosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1653-1656.	0.4	0
57	Purification and crystallographic studies of a putative carbohydrate-binding module from the <i>Ruminococcus flavefaciens</i> FD-1 endoglucanase Cel5A. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 958-961.	0.4	0