

Peter J Simpson

List of Publications by Year in descending order

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38
papers

2,142
citations

186265

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315739

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38
docs citations

38
times ranked

2808
citing authors

#	ARTICLE	IF	CITATIONS
1	Solution structure of the Hop TPR2A domain and investigation of target druggability by NMR, biochemical and in silico approaches. <i>Scientific Reports</i> , 2020, 10, 16000.	3.3	8
2	Solution Structure of the SGT1 Dimerisation Domain and Investigation of Its Interactions with the Ubiquitin-Like Domains of BAG6 and UBL4A. <i>PLoS ONE</i> , 2014, 9, e113281.	2.5	18
3	Specific DNA recognition mediated by a type IV pilin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3065-3070.	7.1	141
4	Structure of the Sgt2/Get5 complex provides insights into GET-mediated targeting of tail-anchored membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1327-1332.	7.1	28
5	¹ H, ¹³ C and ¹⁵ N assignments of Sgt2 N-terminal dimerisation domain and its binding partner, Get5 Ubiquitin-like domain. <i>Biomolecular NMR Assignments</i> , 2013, 7, 271-274.	0.8	5
6	Structures of the Compact Helical Core Domains of Feline Calicivirus and Murine Norovirus VPg Proteins. <i>Journal of Virology</i> , 2013, 87, 5318-5330.	3.4	44
7	The actinobacterial transcription factor RbpA binds to the principal sigma subunit of RNA polymerase. <i>Nucleic Acids Research</i> , 2013, 41, 5679-5691.	14.5	42
8	Regulation of the Plasmodium Motor Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 36968-36977.	3.4	24
9	Structural insights into the biogenesis and biofilm formation by the <i>Escherichia coli</i> common pilus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3950-3955.	7.1	55
10	Structural insight into the role of <i>Streptococcus parasanguinis</i> Fap1 within oral biofilm formation. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 421-426.	2.1	32
11	¹ H, ¹³ C and ¹⁵ N resonance assignments of the kinetochore localisation domain of BUBR1, a central component of the spindle assembly checkpoint. <i>Biomolecular NMR Assignments</i> , 2012, 6, 115-118.	0.8	2
12	Enzymatic activities and functional interdependencies of <i>Bacillus subtilis</i> lipoteichoic acid synthesis enzymes. <i>Molecular Microbiology</i> , 2011, 79, 566-583.	2.5	64
13	Atomic Resolution Insights into Curli Fiber Biogenesis. <i>Structure</i> , 2011, 19, 1307-1316.	3.3	82
14	Crystallographic Analysis of Polypyrimidine Tract-Binding Protein-Raver1 Interactions Involved in Regulation of Alternative Splicing. <i>Structure</i> , 2011, 19, 1816-1825.	3.3	37
15	Complete ¹ H, ¹³ C and ¹⁵ N NMR assignments for donor-strand complemented AafA, the major pilin of aggregative adherence fimbriae (AAF/II) from enteroaggregative <i>E. coli</i> . <i>Biomolecular NMR Assignments</i> , 2011, 5, 1-5.	0.8	2
16	Structural basis for the broad specificity to host-cell ligands by the pathogenic fungus <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15775-15779.	7.1	78
17	Backbone ¹ H, ¹⁵ N, ¹³ C and Ile, Leu, Val methyl chemical shift assignments for the 33.5 kDa N-terminal domain of <i>Candida albicans</i> ALS1. <i>Biomolecular NMR Assignments</i> , 2010, 4, 187-190.	0.8	8
18	Structures of Get3, Get4, and Get5 Provide New Models for TA Membrane Protein Targeting. <i>Structure</i> , 2010, 18, 897-902.	3.3	34

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19	The SOCS-Box of HIV-1 Vif Interacts with ElonginBC by Induced-Folding to Recruit Its Cul5-Containing Ubiquitin Ligase Complex. <i>PLoS Pathogens</i> , 2010, 6, e1000925.	4.7	72
20	Automated Assignment in Selectively Methyl-Labeled Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 9480-9481.	13.7	30
21	A New Labeling Method for Methyl Transverse Relaxation-Optimized Spectroscopy NMR Spectra of Alanine Residues. <i>Journal of the American Chemical Society</i> , 2007, 129, 15428-15429.	13.7	108
22	A peptide motif in Raver1 mediates splicing repression by interaction with the PTB RRM2 domain. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 839-848.	8.2	92
23	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. <i>Structure</i> , 2004, 12, 1631-1643.	3.3	87
24	Calcium Binding and Thermostability of Carbohydrate Binding Module CBM4-2 of Xyn10A from <i>Rhodothermus marinus</i> . <i>Biochemistry</i> , 2002, 41, 5720-5729.	2.5	41
25	The Solution Structure of the CBM4-2 Carbohydrate Binding Module from a Thermostable <i>Rhodothermus marinus</i> Xylanase. <i>Biochemistry</i> , 2002, 41, 5712-5719.	2.5	68
26	Virtually complete ¹ H, ¹³ C and ¹⁵ N resonance assignments of the second family 4 xylan binding module of <i>Rhodothermus marinus</i> xylanase 10A. <i>Journal of Biomolecular NMR</i> , 2002, 22, 187-188.	2.8	4
27	Resonance assignment and topology of the ² H, ¹³ C, ¹⁵ N labelled 29 kDa N-terminal fragment of the polypyrimidine tract binding protein (PTB). <i>Journal of Biomolecular NMR</i> , 2002, 24, 79-80.	2.8	3
28	Evidence for Synergy between Family 2b Carbohydrate Binding Modules in <i>Cellulomonas fimi</i> Xylanase 11A. <i>Biochemistry</i> , 2001, 40, 2468-2477.	2.5	82
29	<i>Clostridium thermocellum</i> Xyn10B Carbohydrate-Binding Module 22-2: The Role of Conserved Amino Acids in Ligand Binding. <i>Biochemistry</i> , 2001, 40, 9167-9176.	2.5	80
30	Role of Hydrogen Bonding in the Interaction between a Xylan Binding Module and Xylan. <i>Biochemistry</i> , 2001, 40, 5700-5707.	2.5	57
31	Carbohydrate-binding modules from a thermostable <i>Rhodothermus marinus</i> xylanase: cloning, expression and binding studies. <i>Biochemical Journal</i> , 2000, 345, 53.	3.7	77
32	Carbohydrate-binding modules from a thermostable <i>Rhodothermus marinus</i> xylanase: cloning, expression and binding studies. <i>Biochemical Journal</i> , 2000, 345, 53-60.	3.7	89
33	The Structural Basis for the Ligand Specificity of Family 2 Carbohydrate-binding Modules. <i>Journal of Biological Chemistry</i> , 2000, 275, 41137-41142.	3.4	120
34	Solution Structure of the CBM10 Cellulose Binding Module from <i>Pseudomonas</i> Xylanase A. <i>Biochemistry</i> , 2000, 39, 978-984.	2.5	73
35	Trp22, Trp24, and Tyr8 Play a Pivotal Role in the Binding of the Family 10 Cellulose-Binding Module from <i>Pseudomonas</i> Xylanase A to Insoluble Ligands. <i>Biochemistry</i> , 2000, 39, 985-991.	2.5	52
36	A family IIb xylan-binding domain has a similar secondary structure to a homologous family IIa cellulose-binding domain but different ligand specificity. <i>Structure</i> , 1999, 7, 853-864.	3.3	90

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37	The starch-binding domain from glucoamylase disrupts the structure of starch. FEBS Letters, 1999, 447, 58-60.	2.8	140
38	The type II and X cellulose-binding domains of Pseudomonas xylanase A potentiate catalytic activity against complex substrates by a common mechanism. Biochemical Journal, 1999, 342, 473-480.	3.7	73