

Pedro M Alzari

List of Publications by Year in descending order

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170
papers

10,714
citations

26630

56
h-index

36028

97
g-index

177
all docs

177
docs citations

177
times ranked

10543
citing authors

#	ARTICLE	IF	CITATIONS
1	Severe Spinal Cord Injury in Rats Induces Chronic Changes in the Spinal Cord and Cerebral Cortex Metabolism, Adjusted by Thiamine That Improves Locomotor Performance. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 620593.	2.9	16
2	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. <i>Communications Biology</i> , 2021, 4, 684.	4.4	3
3	SepF is the FtsZ anchor in archaea, with features of an ancestral cell division system. <i>Nature Communications</i> , 2021, 12, 3214.	12.8	35
4	Proteome remodeling in the <i>Mycobacterium tuberculosis</i> PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. <i>Journal of Proteomics</i> , 2021, 244, 104276.	2.4	6
5	Elimination of PknL and MSMEG_4242 in <i>Mycobacterium smegmatis</i> alters the character of the outer cell envelope and selects for mutations in Lsr2. <i>Cell Surface</i> , 2021, 7, 100060.	3.0	3
6	A Tetratricopeptide Repeat Scaffold Couples Signal Detection to OdhI Phosphorylation in Metabolic Control by the Protein Kinase PknG. <i>MBio</i> , 2021, 12, e0171721.	4.1	2
7	Actinobacteria challenge the paradigm: A unique protein architecture for a well-known, central metabolic complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
8	<i>Arabidopsis thaliana</i> Hcc1 is a ScoA-like metallochaperone for Cu A assembly in Cytochrome c Oxidase. <i>FEBS Journal</i> , 2020, 287, 749-762.	4.7	8
9	Unexpected electron spin density on the axial methionine ligand in Cu _A suggests its involvement in electron pathways. <i>Chemical Communications</i> , 2020, 56, 1223-1226.	4.1	3
10	Essential dynamic interdependence of FtsZ and SepF for Z-ring and septum formation in <i>Corynebacterium glutamicum</i> . <i>Nature Communications</i> , 2020, 11, 1641.	12.8	29
11	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. <i>Microbes and Infection</i> , 2019, 21, 222-229.	1.9	6
12	Conformational transitions in the active site of mycobacterial 2-oxoglutarate dehydrogenase upon binding phosphonate analogues of 2-oxoglutarate: From a Michaelis-like complex to ThDP adducts. <i>Journal of Structural Biology</i> , 2019, 208, 182-190.	2.8	11
13	Structural insights into the functional versatility of an FHA domain protein in mycobacterial signaling. <i>Science Signaling</i> , 2019, 12, .	3.6	22
14	A novel variant m.641A>T in the mitochondrial MT-TF gene is associated with epileptic encephalopathy in adolescent. <i>Mitochondrion</i> , 2019, 47, 10-17.	3.4	2
15	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. <i>Genes and Immunity</i> , 2019, 20, 383-393.	4.1	16
16	The crystal structure of Rv2991 from <i>Mycobacterium tuberculosis</i> : An F420 binding protein with unknown function. <i>Journal of Structural Biology</i> , 2019, 206, 216-224.	2.8	0
17	Overall Structures of <i>Mycobacterium tuberculosis</i> DNA Gyrase Reveal the Role of a <i>Corynebacteriales</i> CyrB-Specific Insert in ATPase Activity. <i>Structure</i> , 2019, 27, 579-589.e5.	3.3	24
18	Double autoinhibition mechanism of signal transduction ATPases with numerous domains (STAND) with a tetratricopeptide repeat sensor. <i>Nucleic Acids Research</i> , 2019, 47, 3795-3810.	14.5	11

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19	High-Throughput Crystallization Pipeline at the Crystallography Core Facility of the Institut Pasteur. <i>Molecules</i> , 2019, 24, 4451.	3.8	49
20	The Reaction Mechanism of Metallo- β -Lactamases Is Tuned by the Conformation of an Active-Site Mobile Loop. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	26
21	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. <i>Journal of Proteomics</i> , 2019, 192, 321-333.	2.4	30
22	The synthesis and kinetic evaluation of aryl β -aminophosphonates as novel inhibitors of T. <i>trans</i> -sialidase. <i>European Journal of Medicinal Chemistry</i> , 2018, 158, 25-33.	5.5	10
23	Conformational plasticity of the response regulator CpxR, a key player in Gammaproteobacteria virulence and drug-resistance. <i>Journal of Structural Biology</i> , 2018, 204, 165-171.	2.8	13
24	The crystal structure of PknI from <i>Mycobacterium tuberculosis</i> shows an inactive, pseudokinase-like conformation. <i>FEBS Journal</i> , 2017, 284, 602-614.	4.7	4
25	Structural Coupling between Autokinase and Phosphotransferase Reactions in a Bacterial Histidine Kinase. <i>Structure</i> , 2017, 25, 939-944.e3.	3.3	33
26	PknG senses amino acid availability to control metabolism and virulence of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006399.	4.7	81
27	Delayed Influence of Spinal Cord Injury on the Amino Acids of NO β Metabolism in Rat Cerebral Cortex Is Attenuated by Thiamine. <i>Frontiers in Medicine</i> , 2017, 4, 249.	2.6	17
28	Modification in hydrophobic packing of HAMP domain induces a destabilization of the auto-phosphorylation site in the histidine kinase CpxA. <i>Biopolymers</i> , 2016, 105, 670-682.	2.4	2
29	Molecular Basis of Membrane Association by the Phosphatidylinositol Mannosyltransferase PimA Enzyme from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 13955-13963.	3.4	16
30	Bidirectional Allosteric Communication between the ATP-Binding Site and the Regulatory PIF Pocket in PDK1 Protein Kinase. <i>Cell Chemical Biology</i> , 2016, 23, 1193-1205.	5.2	65
31	Ser/Thr Phosphorylation Regulates the Fatty Acyl-AMP Ligase Activity of FadD32, an Essential Enzyme in Mycolic Acid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2016, 291, 22793-22805.	3.4	14
32	Structural Basis of Pullulanase Membrane Binding and Secretion Revealed by X-Ray Crystallography, Molecular Dynamics and Biochemical Analysis. <i>Structure</i> , 2016, 24, 92-104.	3.3	26
33	Structure-based Virtual Screening to Get New Scaffold Inhibitors of the Ser/Thr Protein Kinase PknB from <i>Mycobacterium tuberculosis</i> . <i>Letters in Drug Design and Discovery</i> , 2016, 13, 1012-1018.	0.7	4
34	The crystal structure of the catalytic domain of the ser/thr kinase PknA from <i>M. tuberculosis</i> shows an Src-like autoinhibited conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 982-988.	2.6	11
35	Thiophenecarboxamide Derivatives Activated by EthA Kill <i>Mycobacterium tuberculosis</i> by Inhibiting the CTP Synthetase PyrG. <i>Chemistry and Biology</i> , 2015, 22, 917-927.	6.0	72
36	Molecular Basis of the Activity and the Regulation of the Eukaryotic-like S/T Protein Kinase PknG from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2015, 23, 1039-1048.	3.3	37

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37	Secondary structure reshuffling modulates glycosyltransferase function at the membrane. <i>Nature Chemical Biology</i> , 2015, 11, 16-18.	8.0	44
38	Segmental Helical Motions and Dynamical Asymmetry Modulate Histidine Kinase Autophosphorylation. <i>PLoS Biology</i> , 2014, 12, e1001776.	5.6	100
39	A dual conformation of the post-decarboxylation intermediate is associated with distinct enzyme states in mycobacterial KGD ($\hat{\Gamma}$ -ketoglutarate decarboxylase). <i>Biochemical Journal</i> , 2014, 457, 425-434.	3.7	27
40	Structural studies suggest a peptidoglycan hydrolase function for the <i>Mycobacterium tuberculosis</i> Tat-secreted protein Rv2525c. <i>Journal of Structural Biology</i> , 2014, 188, 156-164.	2.8	9
41	Structure-function relationships of membrane-associated GT-B glycosyltransferases. <i>Glycobiology</i> , 2014, 24, 108-124.	2.5	80
42	A novel <i>Plasmodium</i> -specific prodomain fold regulates the malaria drug target SUB1 subtilase. <i>Nature Communications</i> , 2014, 5, 4833.	12.8	20
43	Potent and Specific Inhibition of Glycosidases by Small Artificial Binding Proteins (Affitins). <i>PLoS ONE</i> , 2014, 9, e97438.	2.5	42
44	Generation of a vector suite for protein solubility screening. <i>Frontiers in Microbiology</i> , 2014, 5, 67.	3.5	27
45	Inhibition of <i>Mycobacterium tuberculosis</i> PknG by non-catalytic rubredoxin domain specific modification: reaction of an electrophilic nitro-fatty acid with the Fe $\hat{\Gamma}$ S center. <i>Free Radical Biology and Medicine</i> , 2013, 65, 150-161.	2.9	30
46	Tolerance of the archaeal Sac7d scaffold protein to alternative library designs: characterization of anti-immunoglobulin G Affitins. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 267-275.	2.1	38
47	<i>GarA</i> is an essential regulator of metabolism in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2013, 90, 356-366.	2.5	59
48	Structural Basis for Feed-Forward Transcriptional Regulation of Membrane Lipid Homeostasis in <i>Staphylococcus aureus</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003108.	4.7	37
49	Substrate-Selective Inhibition of Protein Kinase PDK1 by Small Compounds that Bind to the PIF-Pocket Allosteric Docking Site. <i>Chemistry and Biology</i> , 2012, 19, 1152-1163.	6.0	70
50	Mechanistic Insights into the Retaining Glucosyl-3-phosphoglycerate Synthase from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 24649-24661.	3.4	17
51	Conformational changes upon ligand binding in the essential class II fumarase Rv1098c from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2012, 586, 1606-1611.	2.8	20
52	Functional Plasticity and Allosteric Regulation of $\hat{\Gamma}$ -Ketoglutarate Decarboxylase in Central <i>Mycobacterial</i> Metabolism. <i>Chemistry and Biology</i> , 2011, 18, 1011-1020.	6.0	75
53	Allosteric Regulation of Protein Kinase PKC $\hat{\Gamma}$ by the N-Terminal C1 Domain and Small Compounds to the PIF-Pocket. <i>Chemistry and Biology</i> , 2011, 18, 1463-1473.	6.0	61
54	Crystal structure of an enzymatically inactive trans-sialidase-like lectin from <i>Trypanosoma cruzi</i> : The carbohydrate binding mechanism involves residual sialidase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1154-1161.	2.3	19

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55	3-Keto-5-aminohexanoate Cleavage Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 27399-27405.	3.4	20
56	Crystal structure of <i>Mycobacterium tuberculosis</i> LppA, a lipoprotein confined to pathogenic mycobacteria. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 769-772.	2.6	2
57	Biological and structural characterization of the <i>Mycobacterium smegmatis</i> nitroreductase NfnB, and its role in benzothiazinone resistance. <i>Molecular Microbiology</i> , 2010, 77, 1172-1185.	2.5	63
58	A Novel Role of Malonyl-ACP in Lipid Homeostasis,. <i>Biochemistry</i> , 2010, 49, 3161-3167.	2.5	28
59	Molecular Basis of Phosphatidyl-myo-inositol Mannoside Biosynthesis and Regulation in Mycobacteria. <i>Journal of Biological Chemistry</i> , 2010, 285, 33577-33583.	3.4	105
60	Structural plasticity and catalysis regulation of a thermosensor histidine kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16185-16190.	7.1	155
61	Structural Plasticity and Distinct Drug-Binding Modes of LfrR, a Mycobacterial Efflux Pump Regulator. <i>Journal of Bacteriology</i> , 2009, 191, 7531-7537.	2.2	34
62	Substrate-induced Conformational Changes in the Essential Peripheral Membrane-associated Mannosyltransferase PimA from Mycobacteria. <i>Journal of Biological Chemistry</i> , 2009, 284, 21613-21625.	3.4	35
63	Bacterial Metabolism under FHA Control. <i>Structure</i> , 2009, 17, 487-488.	3.3	1
64	The FHA-containing protein GarA acts as a phosphorylation-dependent molecular switch in mycobacterial signaling. <i>FEBS Letters</i> , 2009, 583, 301-307.	2.8	46
65	Mechanisms determining cell membrane expression of different TCR chain pairings. <i>European Journal of Immunology</i> , 2009, 39, 1937-1946.	2.9	6
66	Structure of <i>Mycobacterium tuberculosis</i> Rv2714, a representative of a duplicated gene family in Actinobacteria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 972-977.	0.7	6
67	Genome-wide regulon and crystal structure of Blal (Rv1846c) from <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2009, 71, 1102-1116.	2.5	61
68	Structure and allosteric effects of low-molecular-weight activators on the protein kinase PDK1. <i>Nature Chemical Biology</i> , 2009, 5, 758-764.	8.0	134
69	Discovery of novel inhibitors of <i>Trypanosoma cruzi</i> trans-sialidase from in silico screening. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009, 19, 589-596.	2.2	68
70	Functional in vitro assembly of the integral membrane bacterial thermosensor DesK. <i>Protein Expression and Purification</i> , 2009, 66, 39-45.	1.3	36
71	Crystal structure of a monoclonal antibody directed against an antigenic determinant common to Ogawa and Inaba serotypes of <i>Vibrio cholerae</i> O1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 284-288.	2.6	5
72	Mycobacterial Ser/Thr protein kinases and phosphatases: Physiological roles and therapeutic potential. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 193-202.	2.3	153

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73	Structural insights into sialic acid enzymology. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 565-572.	6.1	70
74	Regulation of glutamate metabolism by protein kinases in mycobacteria. <i>Molecular Microbiology</i> , 2008, 70, 1408-1423.	2.5	147
75	Artificial Binding Proteins (Affitins) as Probes for Conformational Changes in Secretin PulD. <i>Journal of Molecular Biology</i> , 2008, 383, 1058-1068.	4.2	45
76	Rising standards for tuberculosis drug development. <i>Trends in Pharmacological Sciences</i> , 2008, 29, 576-581.	8.7	78
77	Kinetic and Mechanistic Analysis of <i>Trypanosoma cruzi</i> Trans-Sialidase Reveals a Classical Ping-Pong Mechanism with Acid/Base Catalysis. <i>Biochemistry</i> , 2008, 47, 3507-3512.	2.5	55
78	Genetic Basis for the Biosynthesis of Methylglucose Lipopolysaccharides in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 27270-27276.	3.4	54
79	Molecular Recognition and Interfacial Catalysis by the Essential Phosphatidylinositol Mannosyltransferase PimA from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 20705-20714.	3.4	121
80	Remodeling a DNA-binding protein as a specific <i>in vivo</i> inhibitor of bacterial secretin PulD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17983-17988.	7.1	78
81	The Crystal Structure of Rv0813c from <i>Mycobacterium tuberculosis</i> Reveals a New Family of Fatty Acid-Binding Protein-Like Proteins in Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 1899-1904.	2.2	14
82	Structural and Binding Studies of the Three-metal Center in Two <i>Mycobacterial</i> PPM Ser/Thr Protein Phosphatases. <i>Journal of Molecular Biology</i> , 2007, 374, 890-898.	4.2	66
83	Benzoic acid and pyridine derivatives as inhibitors of <i>Trypanosoma cruzi</i> trans-sialidase. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 2106-2119.	3.0	41
84	Insights into the inter-ring plasticity of caseinolytic proteases from the X-ray structure of <i>Mycobacterium tuberculosis</i> ClpP1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 249-259.	2.5	58
85	The crystal structure of <i>Trypanosoma cruzi</i> arginine kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 209-212.	2.6	28
86	Insights into the Catalytic Mechanism of PPM Ser/Thr Phosphatases from the Atomic Resolution Structures of a <i>Mycobacterial</i> Enzyme. <i>Structure</i> , 2007, 15, 863-872.	3.3	46
87	The crystal structure of <i>M. leprae</i> ML2640c defines a large family of putative S-adenosylmethionine-dependent methyltransferases in mycobacteria. <i>Protein Science</i> , 2007, 16, 1896-1904.	7.6	14
88	Structural and Kinetic Analysis of Two Covalent Sialosyl-Enzyme Intermediates on <i>Trypanosoma rangeli</i> Sialidase. <i>Journal of Biological Chemistry</i> , 2006, 281, 4149-4155.	3.4	75
89	Crystal structure, catalytic mechanism, and mitogenic properties of <i>Trypanosoma cruzi</i> proline racemase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1705-1710.	7.1	92
90	The structure of PknB in complex with mitoxantrone, an ATP-competitive inhibitor, suggests a mode of protein kinase regulation in mycobacteria. <i>FEBS Letters</i> , 2006, 580, 3018-3022.	2.8	100

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91	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1103-1113.	2.5	56
92	Structure of armadillo ACBP: a new member of the acyl-CoA-binding protein family. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 958-961.	0.7	12
93	Structural basis of lipid biosynthesis regulation in Gram-positive bacteria. <i>EMBO Journal</i> , 2006, 25, 4074-4083.	7.8	104
94	Allosteric activation of the protein kinase PDK1 with low molecular weight compounds. <i>EMBO Journal</i> , 2006, 25, 5469-5480.	7.8	104
95	Continuous fluorimetric assay for high-throughput screening of inhibitors of trans-sialidase from <i>Trypanosoma cruzi</i> . <i>Analytical Biochemistry</i> , 2006, 357, 302-304.	2.4	19
96	The crystal structure of <i>Mycobacterium tuberculosis</i> adenylate kinase in complex with two molecules of ADP and Mg ²⁺ supports an associative mechanism for phosphoryl transfer. <i>Protein Science</i> , 2006, 15, 1489-1493.	7.6	36
97	Peroxynitrite transforms nerve growth factor into an apoptotic factor for motor neurons. <i>Free Radical Biology and Medicine</i> , 2006, 41, 1632-1644.	2.9	41
98	The Ser/Thr Protein Kinase PknB Is Essential for Sustaining Mycobacterial Growth. <i>Journal of Bacteriology</i> , 2006, 188, 7778-7784.	2.2	162
99	Crystallization and preliminary crystallographic analysis of PimA, an essential mannosyltransferase from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 518-520.	0.7	12
100	Structure and Mechanism of the Alkyl Hydroperoxidase AhpC, a Key Element of the <i>Mycobacterium tuberculosis</i> Defense System against Oxidative Stress. <i>Journal of Biological Chemistry</i> , 2005, 280, 25735-25742.	3.4	92
101	Identification of the Critical Residues Involved in Peptidoglycan Detection by Nod1. <i>Journal of Biological Chemistry</i> , 2005, 280, 38648-38656.	3.4	106
102	A Sialidase Mutant Displaying trans-Sialidase Activity. <i>Journal of Molecular Biology</i> , 2005, 345, 923-934.	4.2	73
103	Conserved autophosphorylation pattern in activation loops and juxtamembrane regions of <i>Mycobacterium tuberculosis</i> Ser/Thr protein kinases. <i>Biochemical and Biophysical Research Communications</i> , 2005, 333, 858-867.	2.1	83
104	MICROBIOLOGY: Enhanced: TB-A New Target, a New Drug. <i>Science</i> , 2005, 307, 214-215.	12.6	52
105	Crystal structure of glycogen synthase: homologous enzymes catalyze glycogen synthesis and degradation. <i>EMBO Journal</i> , 2004, 23, 3196-3205.	7.8	155
106	Structural Insights into the Catalytic Mechanism of <i>Trypanosoma cruzi</i> trans-Sialidase. <i>Structure</i> , 2004, 12, 775-784.	3.3	197
107	First Structural Glimpse at a Bacterial Ser/Thr Protein Phosphatase. <i>Structure</i> , 2004, 12, 1923-1924.	3.3	7
108	Characterization of a UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase with an unusual lectin domain from the platyhelminth parasite <i>Echinococcus granulosus</i> . <i>Biochemical Journal</i> , 2004, 382, 501-510.	3.7	24

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109	PknB kinase activity is regulated by phosphorylation in two Thr residues and dephosphorylation by PstP, the cognate phospho-Ser/Thr phosphatase, in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2003, 49, 1493-1508.	2.5	166
110	Preliminary crystallographic studies of glycogen synthase from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 526-528.	2.5	5
111	<i>Trypanosoma cruzi</i> Trans-sialidase Operates through a Covalent Sialyl-Enzyme Intermediate: A Tyrosine Is the Catalytic Nucleophile. <i>Journal of the American Chemical Society</i> , 2003, 125, 7532-7533.	13.7	188
112	Sub-families of β/β^2 Barrel Enzymes: A New Adenine Deaminase Family. <i>Journal of Molecular Biology</i> , 2003, 334, 1117-1131.	4.2	32
113	The High Resolution Structures of Free and Inhibitor-bound <i>Trypanosoma rangeli</i> Sialidase and its Comparison with <i>T. cruzi</i> Trans-sialidase. <i>Journal of Molecular Biology</i> , 2003, 325, 773-784.	4.2	67
114	The crystal structure of a plant lectin in complex with the Tn antigen. <i>FEBS Letters</i> , 2003, 536, 106-110.	2.8	45
115	Crystal Structure of the Catalytic Domain of the PknB Serine/Threonine Kinase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 13094-13100.	3.4	146
116	Induction of Protective Immunity by Synthetic <i>Vibrio cholerae</i> Hexasaccharide Derived from <i>V. cholerae</i> O1 Ogawa Lipopolysaccharide Bound to a Protein Carrier. <i>Journal of Infectious Diseases</i> , 2002, 185, 950-962.	4.0	77
117	Mapping by Site-Directed Mutagenesis of the Region Responsible for Cohesin-Dockerin Interaction on the Surface of the Seventh Cohesin Domain of <i>Clostridium thermocellum</i> CipA. <i>Biochemistry</i> , 2002, 41, 2115-2119.	2.5	42
118	Duplicated Dockerin Subdomains of <i>Clostridium thermocellum</i> Endoglucanase CelD Bind to a Cohesin Domain of the Scaffolding Protein CipA with Distinct Thermodynamic Parameters and a Negative Cooperativity. <i>Biochemistry</i> , 2002, 41, 2106-2114.	2.5	70
119	Atomic (0.94 Å...) resolution structure of an inverting glycosidase in complex with substrate. <i>Journal of Molecular Biology</i> , 2002, 316, 1061-1069.	4.2	132
120	The Crystal Structure and Catalytic Mechanism of Cellobiohydrolase CelS, the Major Enzymatic Component of the <i>Clostridium thermocellum</i> Cellulosome. <i>Journal of Molecular Biology</i> , 2002, 320, 587-596.	4.2	89
121	The Crystal Structure and Mode of Action of Trans-Sialidase, a Key Enzyme in <i>Trypanosoma cruzi</i> Pathogenesis. <i>Molecular Cell</i> , 2002, 10, 757-768.	9.7	214
122	Crystallization and preliminary crystallographic analysis of a novel cytochrome P450 from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 704-705.	2.5	5
123	Crystallization and preliminary X-ray analysis of the hydroperoxidase I C-terminal domain from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 853-855.	2.5	5
124	Advantages of high-resolution phasing: MAD to atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 1433-1441.	2.5	16
125	The trans-sialidase from the african trypanosome <i>Trypanosoma brucei</i> . <i>FEBS Journal</i> , 2002, 269, 2941-2950.	0.2	54
126	The crystal structure of the mouse apoptosis-inducing factor AIF. <i>Nature Structural Biology</i> , 2002, 9, 442-446.	9.7	163

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127	1H, 13C, 15N NMR sequence-specific resonance assignment of a Clostridium thermocellum type II cohesin module. Journal of Biomolecular NMR, 2002, 23, 73-74.	2.8	12
128	Epitope Mapping of trans-Sialidase from Trypanosoma cruzi Reveals the Presence of Several Cross-Reactive Determinants. Infection and Immunity, 2001, 69, 1869-1875.	2.2	35
129	Biochemical and functional characterization of the Tn-specific lectin from Salvia sclarea seeds. FEBS Journal, 2000, 267, 1434-1440.	0.2	30
130	The First α Helix of Interleukin (IL)-2 Folds as a Homotetramer, Acts as an Agonist of the IL-2 Receptor β Chain, and Induces Lymphokine-Activated Killer Cells. Journal of Experimental Medicine, 2000, 191, 529-540.	8.5	23
131	Production and Functional Characterization of Two Mouse/Human Chimeric Antibodies With Specificity for the Tumor-Associated Tn-Antigen. Hybridoma, 2000, 19, 229-239.	0.6	23
132	Crystal Structure of the Allergen Equ c 1. Journal of Biological Chemistry, 2000, 275, 21572-21577.	3.4	81
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