

# 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	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989, 342, 877-883.	27.8	1,199
2	Mitochondrial Release of Caspase-2 and -9 during the Apoptotic Process. <i>Journal of Experimental Medicine</i> , 1999, 189, 381-394.	8.5	678
3	Missense mutations in the catalase-peroxidase gene, <i>katG</i> , are associated with isoniazid resistance in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 1995, 15, 235-245.	2.5	337
4	Three-dimensional structure of a thermostable bacterial cellulase. <i>Nature</i> , 1992, 357, 89-91.	27.8	245
5	Interleukin 2 and its receptors: recent advances and new immunological functions. <i>Trends in Immunology</i> , 1996, 17, 481-486.	7.5	220
6	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
7	Structural Insights into the Catalytic Mechanism of <i>Trypanosoma cruzi</i> trans-Sialidase. <i>Structure</i> , 2004, 12, 775-784.	3.3	197
8	<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
9	The crystal structure of endoglucanase CelA, a family 8 glycosyl hydrolase from <i>Clostridium thermocellum</i> . <i>Structure</i> , 1996, 4, 265-275.	3.3	172
10	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
11	The crystal structure of the mouse apoptosis-inducing factor AIF. <i>Nature Structural Biology</i> , 2002, 9, 442-446.	9.7	163
12	The Ser/Thr Protein Kinase PknB Is Essential for Sustaining Mycobacterial Growth. <i>Journal of Bacteriology</i> , 2006, 188, 7778-7784.	2.2	162
13	Crystal structure of glycogen synthase: homologous enzymes catalyze glycogen synthesis and degradation. <i>EMBO Journal</i> , 2004, 23, 3196-3205.	7.8	155
14	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
15	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
16	A common protein fold and similar active site in two distinct families of $\beta$ -2-glycanases. <i>Nature Structural Biology</i> , 1995, 2, 569-576.	9.7	149
17	Regulation of glutamate metabolism by protein kinases in mycobacteria. <i>Molecular Microbiology</i> , 2008, 70, 1408-1423.	2.5	147
18	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

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19	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
20	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
21	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
22	Use of site-directed mutagenesis to probe the structure, function and isoniazid activation of the catalase/peroxidase, KatG, from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 1999, 338, 753-760.	3.7	108
23	Structure of catalase-A from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1999, 286, 135-149.	4.2	106
24	Identification of the Critical Residues Involved in Peptidoglycan Detection by Nod1. <i>Journal of Biological Chemistry</i> , 2005, 280, 38648-38656.	3.4	106
25	Molecular Basis of Phosphatidyl-myo-inositol Mannoside Biosynthesis and Regulation in <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 33577-33583.	3.4	105
26	Structural basis of lipid biosynthesis regulation in Gram-positive bacteria. <i>EMBO Journal</i> , 2006, 25, 4074-4083.	7.8	104
27	Allosteric activation of the protein kinase PDK1 with low molecular weight compounds. <i>EMBO Journal</i> , 2006, 25, 5469-5480.	7.8	104
28	The structure of PknB in complex with mitoxantrone, an ATP-competitive inhibitor, suggests a mode of protein kinase regulation in <i>mycobacteria</i> . <i>FEBS Letters</i> , 2006, 580, 3018-3022.	2.8	100
29	Segmental Helical Motions and Dynamical Asymmetry Modulate Histidine Kinase Autophosphorylation. <i>PLoS Biology</i> , 2014, 12, e1001776.	5.6	100
30	The crystal structure of a type I cohesin domain at 1.7 Å... resolution 1 Edited by D. Rees. <i>Journal of Molecular Biology</i> , 1997, 273, 701-713.	4.2	92
31	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
32	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
33	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
34	The Crystal Structure of a Family 5 Endoglucanase Mutant in Complexed and Uncomplexed Forms Reveals an Induced Fit Activation Mechanism. <i>Journal of Molecular Biology</i> , 1996, 257, 1042-1051.	4.2	88
35	cDNA Cloning and Sequencing Reveal the Major Horse Allergen Equ c1 to Be a Glycoprotein Member of the Lipocalin Superfamily. <i>Journal of Biological Chemistry</i> , 1996, 271, 32951-32959.	3.4	84
36	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

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37	Crystal Structure of the Allergen Equ c 1. Journal of Biological Chemistry, 2000, 275, 21572-21577.	3.4	81
38	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2017, 13, e1006399.	4.7	81
39	Structure-function relationships of membrane-associated GT-B glycosyltransferases. Glycobiology, 2014, 24, 108-124.	2.5	80
40	Crystal Structure of a Cross-reaction Complex between Fab F9.13.7 and Guinea Fowl Lysozyme. Journal of Biological Chemistry, 1995, 270, 18067-18076.	3.4	79
41	Remodeling a DNA-binding protein as a specific <i>in vivo</i> inhibitor of bacterial secretin PulD. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17983-17988.	7.1	78
42	Rising standards for tuberculosis drug development. Trends in Pharmacological Sciences, 2008, 29, 576-581.	8.7	78
43	Induction of Protective Immunity by Synthetic Vibrio cholerae Hexasaccharide Derived from V. cholerae O1 Ogawa Lipopolysaccharide Bound to a Protein Carrier. Journal of Infectious Diseases, 2002, 185, 950-962.	4.0	77
44	Structural and Kinetic Analysis of Two Covalent Sialosyl-Enzyme Intermediates on Trypanosoma rangeli Sialidase. Journal of Biological Chemistry, 2006, 281, 4149-4155.	3.4	75
45	Functional Plasticity and Allosteric Regulation of $\alpha$ -Ketoglutarate Decarboxylase in Central Mycobacterial Metabolism. Chemistry and Biology, 2011, 18, 1011-1020.	6.0	75
46	A Sialidase Mutant Displaying trans-Sialidase Activity. Journal of Molecular Biology, 2005, 345, 923-934.	4.2	73
47	Thiophenecarboxamide Derivatives Activated by EthA Kill Mycobacterium tuberculosis by Inhibiting the CTP Synthetase PyrG. Chemistry and Biology, 2015, 22, 917-927.	6.0	72
48	Duplicated Dockerin Subdomains of Clostridium thermocellum Endoglucanase CelD Bind to a Cohesin Domain of the Scaffolding Protein CipA with Distinct Thermodynamic Parameters and a Negative Cooperativity. Biochemistry, 2002, 41, 2106-2114.	2.5	70
49	Structural insights into sialic acid enzymology. Current Opinion in Chemical Biology, 2008, 12, 565-572.	6.1	70
50	Substrate-Selective Inhibition of Protein Kinase PDK1 by Small Compounds that Bind to the PIF-Pocket Allosteric Docking Site. Chemistry and Biology, 2012, 19, 1152-1163.	6.0	70
51	Discovery of novel inhibitors of Trypanosoma cruzi trans-sialidase from in silico screening. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 589-596.	2.2	68
52	The High Resolution Structures of Free and Inhibitor-bound Trypanosoma rangeli Sialidase and its Comparison with T. cruzi Trans-sialidase. Journal of Molecular Biology, 2003, 325, 773-784.	4.2	67
53	Structural and Binding Studies of the Three-metal Center in Two Mycobacterial PPM Ser/Thr Protein Phosphatases. Journal of Molecular Biology, 2007, 374, 890-898.	4.2	66
54	Analysis of the fine specificity of Tn-binding proteins using synthetic glycopeptide epitopes and a biosensor based on surface plasmon resonance spectroscopy. FEBS Letters, 2000, 469, 24-28.	2.8	65

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55	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
56	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
57	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
58	Allosteric Regulation of Protein Kinase PKC $\zeta$ 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
59	GarA is an essential regulator of metabolism in <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2013, 90, 356-366.	2.5	59
60	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
61	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
62	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
63	The trans-sialidase from the african trypanosome <i>Trypanosoma brucei</i> . <i>FEBS Journal</i> , 2002, 269, 2941-2950.	0.2	54
64	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
65	MICROBIOLOGY: Enhanced: TB-A New Target, a New Drug. <i>Science</i> , 2005, 307, 214-215.	12.6	52
66	High-Throughput Crystallization Pipeline at the Crystallography Core Facility of the Institut Pasteur. <i>Molecules</i> , 2019, 24, 4451.	3.8	49
67	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
68	Carbamate kinase: New structural machinery for making carbamoyl phosphate, the common precursor of pyrimidines and arginine. <i>Protein Science</i> , 1999, 8, 934-940.	7.6	46
69	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
70	Structural and Functional Analysis of the Metal-binding Sites of <i>Clostridium thermocellum</i> Endoglucanase CelD. <i>Journal of Biological Chemistry</i> , 1995, 270, 9757-9762.	3.4	45
71	The crystal structure of a plant lectin in complex with the Tn antigen. <i>FEBS Letters</i> , 2003, 536, 106-110.	2.8	45
72	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

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73	Secondary structure reshuffling modulates glycosyltransferase function at the membrane. <i>Nature Chemical Biology</i> , 2015, 11, 16-18.	8.0	44
74	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
75	Potent and Specific Inhibition of Glycosidases by Small Artificial Binding Proteins (Affitins). <i>PLoS ONE</i> , 2014, 9, e97438.	2.5	42
76	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
77	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
78	Use of site-directed mutagenesis to probe the structure, function and isoniazid activation of the catalase/peroxidase, KatG, from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 1999, 338, 753.	3.7	38
79	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
80	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
81	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
82	The crystal structure of <i>Mycobacterium tuberculosis</i> adenylate kinase in complex with two molecules of ADP and Mg <sup>2+</sup> supports an associative mechanism for phosphoryl transfer. <i>Protein Science</i> , 2006, 15, 1489-1493.	7.6	36
83	Functional in vitro assembly of the integral membrane bacterial thermosensor DesK. <i>Protein Expression and Purification</i> , 2009, 66, 39-45.	1.3	36
84	Epitope Mapping of trans-Sialidase from <i>Trypanosoma cruzi</i> Reveals the Presence of Several Cross-Reactive Determinants. <i>Infection and Immunity</i> , 2001, 69, 1869-1875.	2.2	35
85	Substrate-induced Conformational Changes in the Essential Peripheral Membrane-associated Mannosyltransferase PimA from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 21613-21625.	3.4	35
86	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
87	Structural Plasticity and Distinct Drug-Binding Modes of LfrR, a <i>Mycobacterial</i> Efflux Pump Regulator. <i>Journal of Bacteriology</i> , 2009, 191, 7531-7537.	2.2	34
88	Structural Coupling between Autokinase and Phosphotransferase Reactions in a Bacterial Histidine Kinase. <i>Structure</i> , 2017, 25, 939-944.e3.	3.3	33
89	Sub-families of $\beta$ -Barrel Enzymes: A New Adenine Deaminase Family. <i>Journal of Molecular Biology</i> , 2003, 334, 1117-1131.	4.2	32
90	Biochemical and functional characterization of the Tn-specific lectin from <i>Salvia sclarea</i> seeds. <i>FEBS Journal</i> , 2000, 267, 1434-1440.	0.2	30

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91	Inhibition of Mycobacterium tuberculosis PknG by non-catalytic rubredoxin domain specific modification: reaction of an electrophilic nitro-fatty acid with the Fe-S center. Free Radical Biology and Medicine, 2013, 65, 150-161.	2.9	30
92	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. Journal of Proteomics, 2019, 192, 321-333.	2.4	30
93	Molecular Recognition of Artificial Single-Electron Acceptor Cosubstrates by Glucose Oxidase?. Journal of the American Chemical Society, 1996, 118, 6788-6789.	13.7	29
94	Essential dynamic interdependence of FtsZ and SepF for Z-ring and septum formation in Corynebacterium glutamicum. Nature Communications, 2020, 11, 1641.	12.8	29
95	The crystal structure of <i>Trypanosoma cruzi</i> arginine kinase. Proteins: Structure, Function and Bioinformatics, 2007, 69, 209-212.	2.6	28
96	A Novel Role of Malonyl-ACP in Lipid Homeostasis,. Biochemistry, 2010, 49, 3161-3167.	2.5	28
97	A dual conformation of the post-decarboxylation intermediate is associated with distinct enzyme states in mycobacterial KGD (Î±-ketoglutarate decarboxylase). Biochemical Journal, 2014, 457, 425-434.	3.7	27
98	Generation of a vector suite for protein solubility screening. Frontiers in Microbiology, 2014, 5, 67.	3.5	27
99	Structural Basis of Pullulanase Membrane Binding and Secretion Revealed by X-Ray Crystallography, Molecular Dynamics and Biochemical Analysis. Structure, 2016, 24, 92-104.	3.3	26
100	The Reaction Mechanism of Metallo-Î²-Lactamases Is Tuned by the Conformation of an Active-Site Mobile Loop. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	26
101	Amino acid sequence and three-dimensional structure of the Tn-specific isolectin B4 from Vicia villosa. FEBS Letters, 1997, 412, 190-196.	2.8	25
102	Characterization of a UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase with an unusual lectin domain from the platyhelminth parasite Echinococcus granulosus. Biochemical Journal, 2004, 382, 501-510.	3.7	24
103	Overall Structures of Mycobacterium tuberculosis DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. Structure, 2019, 27, 579-589.e5.	3.3	24
104	The First Î± Helix of Interleukin (IL)-2 Folds as a Homotetramer, Acts as an Agonist of the IL-2 Receptor Î² Chain, and Induces Lymphokine-Activated Killer Cells. Journal of Experimental Medicine, 2000, 191, 529-540.	8.5	23
105	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
106	Crystallization and preliminary X-ray diffraction study of an endoglucanase from Clostridium thermocellum. Journal of Molecular Biology, 1986, 189, 249-250.	4.2	22
107	Structural insights into the functional versatility of an FHA domain protein in mycobacterial signaling. Science Signaling, 2019, 12, .	3.6	22
108	3-Keto-5-aminohexanoate Cleavage Enzyme. Journal of Biological Chemistry, 2011, 286, 27399-27405.	3.4	20



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109	Conformational changes upon ligand binding in the essential class II fumarase Rv1098c from <i>Mycobacterium tuberculosis</i> . FEBS Letters, 2012, 586, 1606-1611.	2.8	20
110	A novel Plasmodium-specific prodomain fold regulates the malaria drug target SUB1 subtilase. Nature Communications, 2014, 5, 4833.	12.8	20
111	Continuous fluorimetric assay for high-throughput screening of inhibitors of trans-sialidase from <i>Trypanosoma cruzi</i> . Analytical Biochemistry, 2006, 357, 302-304.	2.4	19
112	Crystal structure of an enzymatically inactive trans-sialidase-like lectin from <i>Trypanosoma cruzi</i> : The carbohydrate binding mechanism involves residual sialidase activity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1154-1161.	2.3	19
113	Crystallization and preliminary structural analysis of catalase A from <i>Saccharomyces cerevisiae</i> . Protein Science, 1997, 6, 481-483.	7.6	17
114	Crystallization and preliminary crystallographic analysis of the major horse allergen Equ c 1. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 880-882.	2.5	17
115	Mechanistic Insights into the Retaining Glucosyl-3-phosphoglycerate Synthase from Mycobacteria. Journal of Biological Chemistry, 2012, 287, 24649-24661.	3.4	17
116	Delayed Influence of Spinal Cord Injury on the Amino Acids of NO $\alpha$ Metabolism in Rat Cerebral Cortex Is Attenuated by Thiamine. Frontiers in Medicine, 2017, 4, 249.	2.6	17
117	ANALYSIS OF HUMAN IL-2/IL-2 RECEPTOR $\beta$ CHAIN INTERACTIONS: MONOCLONAL ANTIBODY H2-8 AND NEW IL-2 MUTANTS DEFINE THE CRITICAL ROLE OF $\beta$ HELIX-A OF IL-2. Cytokine, 1997, 9, 488-498.	3.2	16
118	Advantages of high-resolution phasing: MAD to atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1433-1441.	2.5	16
119	Molecular Basis of Membrane Association by the Phosphatidylinositol Mannosyltransferase PimA Enzyme from Mycobacteria. Journal of Biological Chemistry, 2016, 291, 13955-13963.	3.4	16
120	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. Genes and Immunity, 2019, 20, 383-393.	4.1	16
121	Severe Spinal Cord Injury in Rats Induces Chronic Changes in the Spinal Cord and Cerebral Cortex Metabolism, Adjusted by Thiamine That Improves Locomotor Performance. Frontiers in Molecular Neuroscience, 2021, 14, 620593.	2.9	16
122	Crystal structures of pheasant and guinea fowl egg-white lysozymes. Protein Science, 1994, 3, 788-798.	7.6	15
123	Molecular Cloning of a Monoclonal Anti-Tumor Antibody Specific for the Tn Antigen and Expression of an Active Single-Chain Fv Fragment. Hybridoma, 1997, 16, 317-324.	0.6	14
124	The Crystal Structure of Rv0813c from <i>Mycobacterium tuberculosis</i> Reveals a New Family of Fatty Acid-Binding Protein-Like Proteins in Bacteria. Journal of Bacteriology, 2007, 189, 1899-1904.	2.2	14
125	The crystal structure of <i>M. leprae</i> ML2640c defines a large family of putative S-adenosylmethionine-dependent methyltransferases in mycobacteria. Protein Science, 2007, 16, 1896-1904.	7.6	14
126	Ser/Thr Phosphorylation Regulates the Fatty Acyl-AMP Ligase Activity of FadD32, an Essential Enzyme in Mycolic Acid Biosynthesis. Journal of Biological Chemistry, 2016, 291, 22793-22805.	3.4	14



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127	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
128	Crystallization, preliminary X-ray diffraction study, and crystal packing of a complex between anti-Hen lysozyme antibody F9.13.7 and Guinea-fowl lysozyme. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 209-212.	2.6	12
129	Conservative substitutions in the hydrophobic core of <i>Rhodobacter sphaeroides</i> thioredoxin produce distinct functional effects. <i>Protein Science</i> , 1995, 4, 2510-2516.	7.6	12
130	The MBP fusion protein restores the activity of the first phosphatase domain of CD45. <i>FEBS Letters</i> , 1997, 411, 231-235.	2.8	12
131	<sup>1</sup> H, <sup>13</sup> C, <sup>15</sup> N NMR sequence-specific resonance assignment of a <i>Clostridium thermocellum</i> type II cohesin module. <i>Journal of Biomolecular NMR</i> , 2002, 23, 73-74.	2.8	12
132	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
133	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
134	Characterization of two crystal forms of <i>Clostridium thermocellum</i> endoglucanase CelC. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 158-160.	2.6	11
135	Crystallization and Preliminary Diffraction Analysis of the Catalytic Domain of Xylanase Z from <i>Clostridium thermocellum</i> . <i>Journal of Molecular Biology</i> , 1994, 235, 1348-1350.	4.2	11
136	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
137	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
138	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
139	Preliminary crystallographic study of a complex between an heteroclitic anti-hen egg-white lysozyme antibody and the heterologous antigen pheasant egg-white lysozyme. <i>Journal of Molecular Biology</i> , 1987, 197, 375-376.	4.2	10
140	Structural Features Involved in the Formation of a Complex between the Monomeric or the Dimeric Form of the Rev-erb1 <sup>2</sup> DNA-Binding Domain and Its DNA Reactive Sites. <i>Biochemistry</i> , 1998, 37, 11488-11495.	2.5	10
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