

Pedro M Alzari

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

170
papers

9,252
citations

52
h-index

92
g-index

177
ext. papers

10,029
ext. citations

6.8
avg, IF

5.43
L-index

#	Paper	IF	Citations
170	A Tetratricopeptide Repeat Scaffold Couples Signal Detection to OdhI Phosphorylation in Metabolic Control by the Protein Kinase PknG. <i>MBio</i> , 2021 , 12, e0171721	7.8	1
169	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	6.1	4
168	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. <i>Communications Biology</i> , 2021 , 4, 684	6.7	1
167	SepF is the FtsZ anchor in archaea, with features of an ancestral cell division system. <i>Nature Communications</i> , 2021 , 12, 3214	17.4	7
166	Proteome remodeling in the Mycobacterium tuberculosis 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	3.9	3
165	Elimination of PknL and MSMEG_4242 in alters the character of the outer cell envelope and selects for mutations in Lsr2. <i>Cell Surface</i> , 2021 , 7, 100060	4.8	0
164	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	17.4	11
163	Unexpected electron spin density on the axial methionine ligand in Cu suggests its involvement in electron pathways. <i>Chemical Communications</i> , 2020 , 56, 1223-1226	5.8	0
162	<i>Arabidopsis thaliana</i> Hcc1 is a Sco-like metallochaperone for Cu assembly in Cytochrome c Oxidase. <i>FEBS Journal</i> , 2020 , 287, 749-762	5.7	8
161	Structural insights into the functional versatility of an FHA domain protein in mycobacterial signaling. <i>Science Signaling</i> , 2019 , 12,	8.8	13
160	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	4.9	2
159	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. <i>Genes and Immunity</i> , 2019 , 20, 383-393	4.4	11
158	The crystal structure of Rv2991 from Mycobacterium tuberculosis: An F binding protein with unknown function. <i>Journal of Structural Biology</i> , 2019 , 206, 216-224	3.4	
157	Overall Structures of Mycobacterium tuberculosis DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. <i>Structure</i> , 2019 , 27, 579-589.e5	5.2	14
156	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	20.1	4
155	Novel mechanistic insights into physiological signaling pathways mediated by mycobacterial Ser/Thr protein kinases. <i>Microbes and Infection</i> , 2019 , 21, 222-229	9.3	4
154	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	3.4	7

153	High-Throughput Crystallization Pipeline at the Crystallography Core Facility of the Institut Pasteur. <i>Molecules</i> , 2019 , 24,	4.8	17
152	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,	5.9	18
151	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	3.9	10
150	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	3.4	7
149	The synthesis and kinetic evaluation of aryl β -aminophosphonates as novel inhibitors of T. β -cruxi trans-sialidase. <i>European Journal of Medicinal Chemistry</i> , 2018 , 158, 25-33	6.8	9
148	The crystal structure of PknI from Mycobacterium tuberculosis shows an inactive, pseudokinase-like conformation. <i>FEBS Journal</i> , 2017 , 284, 602-614	5.7	3
147	Structural Coupling between Autokinase and Phosphotransferase Reactions in a Bacterial Histidine Kinase. <i>Structure</i> , 2017 , 25, 939-944.e3	5.2	22
146	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2017 , 13, e1006399	7.6	58
145	Delayed Influence of Spinal Cord Injury on the Amino Acids of NO Metabolism in Rat Cerebral Cortex Is Attenuated by Thiamine. <i>Frontiers in Medicine</i> , 2017 , 4, 249	4.9	10
144	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	5.4	12
143	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	5.2	24
142	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, 670-82	2.2	2
141	Molecular Basis of Membrane Association by the Phosphatidylinositol Mannosyltransferase PimA Enzyme from Mycobacteria. <i>Journal of Biological Chemistry</i> , 2016 , 291, 13955-13963	5.4	11
140	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	8.2	44
139	Thiophenecarboxamide Derivatives Activated by EthA Kill Mycobacterium tuberculosis by Inhibiting the CTP Synthetase PyrG. <i>Chemistry and Biology</i> , 2015 , 22, 917-27		51
138	Molecular Basis of the Activity and the Regulation of the Eukaryotic-like S/T Protein Kinase PknG from Mycobacterium tuberculosis. <i>Structure</i> , 2015 , 23, 1039-48	5.2	26
137	Secondary structure reshuffling modulates glycosyltransferase function at the membrane. <i>Nature Chemical Biology</i> , 2015 , 11, 16-8	11.7	30
136	The crystal structure of the catalytic domain of the ser/thr kinase PknA from M. tuberculosis shows an Src-like autoinhibited conformation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 982-8	4.2	10

135	A dual conformation of the post-decarboxylation intermediate is associated with distinct enzyme states in mycobacterial KGD (Eketoglutarate decarboxylase). <i>Biochemical Journal</i> , 2014 , 457, 425-34	3.8	23
134	Structural studies suggest a peptidoglycan hydrolase function for the Mycobacterium tuberculosis Tat-secreted protein Rv2525c. <i>Journal of Structural Biology</i> , 2014 , 188, 156-64	3.4	6
133	Structure-function relationships of membrane-associated GT-B glycosyltransferases. <i>Glycobiology</i> , 2014 , 24, 108-24	5.8	63
132	A novel Plasmodium-specific prodomain fold regulates the malaria drug target SUB1 subtilase. <i>Nature Communications</i> , 2014 , 5, 4833	17.4	11
131	Segmental helical motions and dynamical asymmetry modulate histidine kinase autophosphorylation. <i>PLoS Biology</i> , 2014 , 12, e1001776	9.7	79
130	Potent and specific inhibition of glycosidases by small artificial binding proteins (affitins). <i>PLoS ONE</i> , 2014 , 9, e97438	3.7	33
129	Generation of a vector suite for protein solubility screening. <i>Frontiers in Microbiology</i> , 2014 , 5, 67	5.7	20
128	Inhibition of Mycobacterium tuberculosis PknG by non-catalytic rubredoxin domain specific modification: reaction of an electrophilic nitro-fatty acid with the Fe-S center. <i>Free Radical Biology and Medicine</i> , 2013 , 65, 150-161	7.8	24
127	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, 267-75	1.9	33
126	GarA is an essential regulator of metabolism in Mycobacterium tuberculosis. <i>Molecular Microbiology</i> , 2013 , 90, 356-66	4.1	43
125	Structural basis for feed-forward transcriptional regulation of membrane lipid homeostasis in Staphylococcus aureus. <i>PLoS Pathogens</i> , 2013 , 9, e1003108	7.6	31
124	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, 1152-63		52
123	Mechanistic insights into the retaining glucosyl-3-phosphoglycerate synthase from mycobacteria. <i>Journal of Biological Chemistry</i> , 2012 , 287, 24649-61	5.4	16
122	Conformational changes upon ligand binding in the essential class II fumarase Rv1098c from Mycobacterium tuberculosis. <i>FEBS Letters</i> , 2012 , 586, 1606-11	3.8	17
121	Functional plasticity and allosteric regulation of Eketoglutarate decarboxylase in central mycobacterial metabolism. <i>Chemistry and Biology</i> , 2011 , 18, 1011-20		60
120	Allosteric regulation of protein kinase PKC β by the N-terminal C1 domain and small compounds to the PIF-pocket. <i>Chemistry and Biology</i> , 2011 , 18, 1463-73		48
119	Crystal structure of an enzymatically inactive trans-sialidase-like lectin from Trypanosoma cruzi: the carbohydrate binding mechanism involves residual sialidase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 1154-61	4	18
118	3-Keto-5-aminohexanoate cleavage enzyme: a common fold for an uncommon Claisen-type condensation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 27399-405	5.4	14

117	Biological and structural characterization of the Mycobacterium smegmatis nitroreductase NfnB, and its role in benzothiazinone resistance. <i>Molecular Microbiology</i> , 2010 , 77, 1172-85	4.1	53
116	A novel role of malonyl-ACP in lipid homeostasis. <i>Biochemistry</i> , 2010 , 49, 3161-7	3.2	26
115	Molecular basis of phosphatidyl-myo-inositol mannoside biosynthesis and regulation in mycobacteria. <i>Journal of Biological Chemistry</i> , 2010 , 285, 33577-83	5.4	78
114	Crystal structure of Mycobacterium tuberculosis LppA, a lipoprotein confined to pathogenic mycobacteria. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010 , 78, 769-72	4.2	2
113	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, 16185-90	11.5	135
112	Structural plasticity and distinct drug-binding modes of LfrR, a mycobacterial efflux pump regulator. <i>Journal of Bacteriology</i> , 2009 , 191, 7531-7	3.5	29
111	Substrate-induced conformational changes in the essential peripheral membrane-associated mannosyltransferase PimA from mycobacteria: implications for catalysis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 21613-25	5.4	30
110	Bacterial metabolism under FHA control. <i>Structure</i> , 2009 , 17, 487-8	5.2	
109	The FHA-containing protein GarA acts as a phosphorylation-dependent molecular switch in mycobacterial signaling. <i>FEBS Letters</i> , 2009 , 583, 301-7	3.8	40
108	Mechanisms determining cell membrane expression of different gammadelta TCR chain pairings. <i>European Journal of Immunology</i> , 2009 , 39, 1937-46	6.1	3
107	Structure of Mycobacterium tuberculosis Rv2714, a representative of a duplicated gene family in Actinobacteria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009 , 65, 972-7		6
106	Genome-wide regulon and crystal structure of Blal (Rv1846c) from Mycobacterium tuberculosis. <i>Molecular Microbiology</i> , 2009 , 71, 1102-16	4.1	51
105	Structure and allosteric effects of low-molecular-weight activators on the protein kinase PDK1. <i>Nature Chemical Biology</i> , 2009 , 5, 758-64	11.7	115
104	Discovery of novel inhibitors of Trypanosoma cruzi trans-sialidase from in silico screening. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009 , 19, 589-96	2.9	60
103	Functional in vitro assembly of the integral membrane bacterial thermosensor DesK. <i>Protein Expression and Purification</i> , 2009 , 66, 39-45	2	34
102	Regulation of glutamate metabolism by protein kinases in mycobacteria. <i>Molecular Microbiology</i> , 2008 , 70, 1408-23	4.1	130
101	Artificial binding proteins (Affitins) as probes for conformational changes in secretin PulD. <i>Journal of Molecular Biology</i> , 2008 , 383, 1058-68	6.5	40
100	Rising standards for tuberculosis drug development. <i>Trends in Pharmacological Sciences</i> , 2008 , 29, 576-81	3.2	67

99	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, 3507-12	3.2	51
98	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, 284-8	4.2	5
97	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	4	142
96	Structural insights into sialic acid enzymology. <i>Current Opinion in Chemical Biology</i> , 2008 , 12, 565-72	9.7	62
95	Benzoic acid and pyridine derivatives as inhibitors of <i>Trypanosoma cruzi</i> trans-sialidase. <i>Bioorganic and Medicinal Chemistry</i> , 2007 , 15, 2106-19	3.4	38
94	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, 249-59		51
93	The crystal structure of <i>Trypanosoma cruzi</i> arginine kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 209-12	4.2	22
92	Insights into the catalytic mechanism of PPM Ser/Thr phosphatases from the atomic resolution structures of a mycobacterial enzyme. <i>Structure</i> , 2007 , 15, 863-72	5.2	41
91	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, 1896-904	6.2	12
90	Genetic basis for the biosynthesis of methylglucose lipopolysaccharides in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2007 , 282, 27270-27276	5.4	47
89	Molecular recognition and interfacial catalysis by the essential phosphatidylinositol mannosyltransferase PimA from mycobacteria. <i>Journal of Biological Chemistry</i> , 2007 , 282, 20705-14	5.4	102
88	Remodeling a DNA-binding protein as a specific in vivo inhibitor of bacterial secretin PulD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 17983-8	11.5	68
87	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, 1899-904	3.5	12
86	Structural and binding studies of the three-metal center in two mycobacterial PPM Ser/Thr protein phosphatases. <i>Journal of Molecular Biology</i> , 2007 , 374, 890-8	6.5	52
85	Peroxynitrite transforms nerve growth factor into an apoptotic factor for motor neurons. <i>Free Radical Biology and Medicine</i> , 2006 , 41, 1632-44	7.8	34
84	The Ser/Thr protein kinase PknB is essential for sustaining mycobacterial growth. <i>Journal of Bacteriology</i> , 2006 , 188, 7778-84	3.5	150
83	Structural and kinetic analysis of two covalent sialosyl-enzyme intermediates on <i>Trypanosoma rangeli</i> sialidase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 4149-55	5.4	73
82	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, 1705-10	11.5	85

81	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, 3018-22	3.8	87
80	Implementation of semi-automated cloning and prokaryotic expression screening: the impact of SPINE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1103-13		49
79	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, 958-61		10
78	Structural basis of lipid biosynthesis regulation in Gram-positive bacteria. <i>EMBO Journal</i> , 2006 , 25, 4074-83		95
77	Allosteric activation of the protein kinase PDK1 with low molecular weight compounds. <i>EMBO Journal</i> , 2006 , 25, 5469-80	13	88
76	Continuous fluorimetric assay for high-throughput screening of inhibitors of trans-sialidase from <i>Trypanosoma cruzi</i> . <i>Analytical Biochemistry</i> , 2006 , 357, 302-4	3.1	17
75	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, 1489-93	6.3	31
74	A sialidase mutant displaying trans-sialidase activity. <i>Journal of Molecular Biology</i> , 2005 , 345, 923-34	6.5	71
73	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, 858-67	3.4	75
72	Microbiology. TB--a new target, a new drug. <i>Science</i> , 2005 , 307, 214-5	33.3	44
71	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, 518-20		11
70	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, 25735-42	5.4	81
69	Identification of the critical residues involved in peptidoglycan detection by Nod1. <i>Journal of Biological Chemistry</i> , 2005 , 280, 38648-56	5.4	91
68	Crystal structure of glycogen synthase: homologous enzymes catalyze glycogen synthesis and degradation. <i>EMBO Journal</i> , 2004 , 23, 3196-205	13	132
67	Structural insights into the catalytic mechanism of <i>Trypanosoma cruzi</i> trans-sialidase. <i>Structure</i> , 2004 , 12, 775-84	5.2	177
66	First structural glimpse at a bacterial Ser/Thr protein phosphatase. <i>Structure</i> , 2004 , 12, 1923-4	5.2	7
65	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, 501-10	3.8	24
64	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, 13094-100	5.4	124

63	PknB kinase activity is regulated by phosphorylation in two Thr residues and dephosphorylation by PstP, the cognate phospho-Ser/Thr phosphatase, in Mycobacterium tuberculosis. <i>Molecular Microbiology</i> , 2003 , 49, 1493-508	4.1	143
62	Preliminary crystallographic studies of glycogen synthase from Agrobacterium tumefaciens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 526-8		5
61	Trypanosoma cruzi trans-sialidase operates through a covalent sialyl-enzyme intermediate: tyrosine is the catalytic nucleophile. <i>Journal of the American Chemical Society</i> , 2003 , 125, 7532-3	16.4	171
60	Sub-families of alpha/beta barrel enzymes: a new adenine deaminase family. <i>Journal of Molecular Biology</i> , 2003 , 334, 1117-31	6.5	29
59	The high resolution structures of free and inhibitor-bound Trypanosoma rangeli sialidase and its comparison with T. cruzi trans-sialidase. <i>Journal of Molecular Biology</i> , 2003 , 325, 773-84	6.5	61
58	The crystal structure of a plant lectin in complex with the Tn antigen. <i>FEBS Letters</i> , 2003 , 536, 106-10	3.8	42
57	Crystallization and preliminary crystallographic analysis of a novel cytochrome P450 from Mycobacterium tuberculosis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 704-5		5
56	Crystallization and preliminary X-ray analysis of the hydroperoxidase I C-terminal domain from Escherichia coli. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 853-5		4
55	Advantages of high-resolution phasing: MAD to atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1433-41		13
54	The trans-sialidase from the african trypanosome Trypanosoma brucei. <i>FEBS Journal</i> , 2002 , 269, 2941-50		48
53	The crystal structure of the mouse apoptosis-inducing factor AIF. <i>Nature Structural Biology</i> , 2002 , 9, 442-6		136
52	¹ H, ¹³ C, ¹⁵ N NMR sequence-specific resonance assignment of a Clostridium thermocellum type II cohesin module. <i>Journal of Biomolecular NMR</i> , 2002 , 23, 73-4	3	10
51	Induction of protective immunity by synthetic Vibrio cholerae hexasaccharide derived from V. cholerae O1 Ogawa lipopolysaccharide bound to a protein carrier. <i>Journal of Infectious Diseases</i> , 2002 , 185, 950-62	7	73
50	Mapping by site-directed mutagenesis of the region responsible for cohesin-dockerin interaction on the surface of the seventh cohesin domain of Clostridium thermocellum CipA. <i>Biochemistry</i> , 2002 , 41, 2115-9	3.2	40
49	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. <i>Biochemistry</i> , 2002 , 41, 2106-14	3.2	66
48	Atomic (0.94 Å) resolution structure of an inverting glycosidase in complex with substrate. <i>Journal of Molecular Biology</i> , 2002 , 316, 1061-9	6.5	125
47	The crystal structure and catalytic mechanism of cellobiohydrolase CelS, the major enzymatic component of the Clostridium thermocellum Cellulosome. <i>Journal of Molecular Biology</i> , 2002 , 320, 587-96	6.5	79
46	The crystal structure and mode of action of trans-sialidase, a key enzyme in Trypanosoma cruzi pathogenesis. <i>Molecular Cell</i> , 2002 , 10, 757-68	17.6	198

45	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, 1869-75	3.7	32
44	Biochemical and functional characterization of the Tn-specific lectin from <i>Salvia sclarea</i> seeds. <i>FEBS Journal</i> , 2000 , 267, 1434-40		26
43	The first alpha helix of interleukin (IL)-2 folds as a homotetramer, acts as an agonist of the IL-2 receptor beta chain, and induces lymphokine-activated killer cells. <i>Journal of Experimental Medicine</i> , 2000 , 191, 529-40	16.6	21
42	Production and functional characterization of two mouse/human chimeric antibodies with specificity for the tumor-associated Tn-antigen. <i>Hybridoma</i> , 2000 , 19, 229-39		20
41	Crystal structure of the allergen Equ c 1. A dimeric lipocalin with restricted IgE-reactive epitopes. <i>Journal of Biological Chemistry</i> , 2000 , 275, 21572-7	5.4	66
40	Analysis of the fine specificity of Tn-binding proteins using synthetic glycopeptide epitopes and a biosensor based on surface plasmon resonance spectroscopy. <i>FEBS Letters</i> , 2000 , 469, 24-8	3.8	54
39	Carbamate kinase: New structural machinery for making carbamoyl phosphate, the common precursor of pyrimidines and arginine. <i>Protein Science</i> , 1999 , 8, 934-40	6.3	40
38	Mitochondrial release of caspase-2 and -9 during the apoptotic process. <i>Journal of Experimental Medicine</i> , 1999 , 189, 381-94	16.6	633
37	Crystallization and preliminary crystallographic analysis of the major horse allergen Equ c 1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 880-2		15
36	Structure of catalase-A from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1999 , 286, 135-49	6.5	93
35	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	3.8	103
34	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	3.8	34
33	Structural features involved in the formation of a complex between the monomeric or the dimeric form of the rev-erb beta DNA-binding domain and its DNA reactive sites. <i>Biochemistry</i> , 1998 , 37, 11488-95	3.2	10
32	Molecular cloning of a monoclonal anti-tumor antibody specific for the Tn antigen and expression of an active single-chain Fv fragment. <i>Hybridoma</i> , 1997 , 16, 317-24		12
31	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 alpha helix-A of IL-2. <i>Cytokine</i> , 1997 , 9, 488-98	4	16
30	The crystal structure of a type I cohesin domain at 1.7 Å resolution. <i>Journal of Molecular Biology</i> , 1997 , 273, 701-13	6.5	81
29	Amino acid sequence and three-dimensional structure of the Tn-specific isolectin B4 from <i>Vicia villosa</i> . <i>FEBS Letters</i> , 1997 , 412, 190-6	3.8	21
28	The MBP fusion protein restores the activity of the first phosphatase domain of CD45. <i>FEBS Letters</i> , 1997 , 411, 231-5	3.8	12

27	Crystallization and preliminary structural analysis of catalase A from <i>Saccharomyces cerevisiae</i> . <i>Protein Science</i> , 1997 , 6, 481-3	6.3	14
26	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, 32951-9	5.4	75
25	Molecular Recognition of Artificial Single-Electron Acceptor Cosubstrates by Glucose Oxidase?. <i>Journal of the American Chemical Society</i> , 1996 , 118, 6788-6789	16.4	22
24	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, 1042-51	6.5	75
23	The crystal structure of endoglucanase CelA, a family 8 glycosyl hydrolase from <i>Clostridium thermocellum</i> . <i>Structure</i> , 1996 , 4, 265-75	5.2	153
22	Crystallization of a family 8 cellulase from <i>Clostridium thermocellum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 134-6	4.2	
21	Interleukin 2 and its receptors: recent advances and new immunological functions. <i>Trends in Immunology</i> , 1996 , 17, 481-6		208
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16	A common protein fold and similar active site in two distinct families of beta-glycanases. <i>Nature Structural Biology</i> , 1995 , 2, 569-76		136
15	Structural and functional analysis of the metal-binding sites of <i>Clostridium thermocellum</i> endoglucanase CelD. <i>Journal of Biological Chemistry</i> , 1995 , 270, 9757-62	5.4	39
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6	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989 , 342, 877-83	50.4	1091
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2	Actinobacteria challenge the paradigm: a unique protein architecture for a well-known central metabolic complex		1
1	SepF is the FtsZ-anchor in Archaea: implications for cell division in the Last Universal Common Ancestor		2