

# Juan A Hermoso

## List of Publications by Year in descending order

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171  
papers

6,732  
citations

57758

44  
h-index

85541

71  
g-index

179  
all docs

179  
docs citations

179  
times ranked

7156  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure and Pathophysiological Role of the Pneumococcal Nucleoside-binding Protein PnrA. <i>Journal of Molecular Biology</i> , 2021, 433, 166723.	4.2	2
2	Structural Cues for Understanding eEF1A2 Moonlighting. <i>ChemBioChem</i> , 2021, 22, 374-391.	2.6	8
3	Biochemical and Structural Characterization of a novel thermophilic esterase EstD11 provide catalytic insights for the HSL family. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1214-1232.	4.1	17
4	Unconventional Antibacterials and Adjuvants. <i>Accounts of Chemical Research</i> , 2021, 54, 917-929.	15.6	20
5	Binding of non-canonical peptidoglycan controls <i>Vibrio cholerae</i> broad spectrum racemase activity. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1119-1126.	4.1	5
6	First Lanthanide Complex for De Novo Phasing in Native Protein Crystallography at 1 Å... Radiation. <i>ACS Applied Bio Materials</i> , 2021, 4, 4575-4581.	4.6	1
7	Teaching an old dog new tricks: repurposing $\beta$ -lactams. <i>Trends in Pharmacological Sciences</i> , 2021, 42, 617-619.	8.7	1
8	Integrative structural biology of the penicillin-binding protein-1 from <i>Staphylococcus aureus</i> , an essential component of the divisome machinery. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5392-5405.	4.1	2
9	Catalytic Cycle of Glycoside Hydrolase BglX from <i>Pseudomonas aeruginosa</i> and Its Implications for Biofilm Formation. <i>ACS Chemical Biology</i> , 2020, 15, 189-196.	3.4	11
10	Structural Characterization of the Essential Cell Division Protein FtsE and Its Interaction with FtsX in <i>Streptococcus pneumoniae</i> . <i>MBio</i> , 2020, 11, .	4.1	11
11	Class A PBPs have a distinct and unique role in the construction of the pneumococcal cell wall. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6129-6138.	7.1	40
12	SEQUENCE SLIDER: expanding polyalanine fragments for phasing with multiple side-chain hypotheses. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 221-237.	2.3	10
13	Disulfide Engineered Lipase to Enhance the Catalytic Activity: A Structure-Based Approach on BTL2. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5245.	4.1	13
14	Structure of the Large Extracellular Loop of FtsX and Its Interaction with the Essential Peptidoglycan Hydrolase PcsB in <i>Streptococcus pneumoniae</i> . <i>MBio</i> , 2019, 10, .	4.1	35
15	Structure of full-length human phenylalanine hydroxylase in complex with tetrahydrobiopterin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11229-11234.	7.1	44
16	The Quinazolinone Allosteric Inhibitor of PBP 2a Synergizes with Piperacillin and Tazobactam against Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	40
17	Cold-induced aldimine bond cleavage by Tris in <i>Bacillus subtilis</i> alanine racemase. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 4350-4358.	2.8	2
18	Pyrrolopyrimidine vs Imidazole-Phenyl-Thiazole Scaffolds in Nonpeptidic Dimerization Inhibitors of <i>Leishmania infantum</i> Trypanothione Reductase. <i>ACS Infectious Diseases</i> , 2019, 5, 873-891.	3.8	26

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19	Structural basis of denuded glycan recognition by SPOR domains in bacterial cell division. <i>Nature Communications</i> , 2019, 10, 5567.	12.8	29
20	Exolytic and endolytic turnover of peptidoglycan by lytic transglycosylase Slt of <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4393-4398.	7.1	31
21	Structural insights into the binding and catalytic mechanisms of the <i>Listeria monocytogenes</i> bacteriophage glycosyl hydrolase PlyP40. <i>Molecular Microbiology</i> , 2018, 108, 128-142.	2.5	12
22	Allostery, Recognition of Nascent Peptidoglycan, and Cross-linking of the Cell Wall by the Essential Penicillin-Binding Protein 2x of <i>Streptococcus pneumoniae</i> . <i>ACS Chemical Biology</i> , 2018, 13, 694-702.	3.4	29
23	Mechanism of the <i>Escherichia coli</i> MltE lytic transglycosylase, the cell-wall-penetrating enzyme for Type VI secretion system assembly. <i>Scientific Reports</i> , 2018, 8, 4110.	3.3	27
24	Three-dimensional structures of Lipoproteins from <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 692-704.	3.6	11
25	A Structural Dissection of the Active Site of the Lytic Transglycosylase MltE from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2018, 57, 6090-6098.	2.5	2
26	Exploiting distant homologues for phasing through the generation of compact fragments, local fold refinement and partial solution combination. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 290-304.	2.3	30
27	Conformational Dynamics in Penicillin-Binding Protein 2a of Methicillin-Resistant <i>Staphylococcus aureus</i> , Allosteric Communication Network and Enablement of Catalysis. <i>Journal of the American Chemical Society</i> , 2017, 139, 2102-2110.	13.7	65
28	Carbohydrate recognition and lysis by bacterial peptidoglycan hydrolases. <i>Current Opinion in Structural Biology</i> , 2017, 44, 87-100.	5.7	45
29	Muropeptide Binding and the X-ray Structure of the Effector Domain of the Transcriptional Regulator AmpR of <i>Pseudomonas aeruginosa</i> . <i>Journal of the American Chemical Society</i> , 2017, 139, 1448-1451.	13.7	42
30	Catalytic Cycle of the N-Acetylglucosaminidase NagZ from <i>Pseudomonas aeruginosa</i> . <i>Journal of the American Chemical Society</i> , 2017, 139, 6795-6798.	13.7	28
31	A single amino acid polymorphism in the glycosyltransferase CpsK defines four <i>Streptococcus suis</i> serotypes. <i>Scientific Reports</i> , 2017, 7, 4066.	3.3	18
32	X-ray Structure of Catenated Lytic Transglycosylase SltB1. <i>Biochemistry</i> , 2017, 56, 6317-6320.	2.5	9
33	Deciphering how Cpl-7 cell wall-binding repeats recognize the bacterial peptidoglycan. <i>Scientific Reports</i> , 2017, 7, 16494.	3.3	23
34	Orthologous and Paralogous AmpD Peptidoglycan Amidases from Gram-Negative Bacteria. <i>Microbial Drug Resistance</i> , 2016, 22, 470-476.	2.0	23
35	Modular Architecture and Unique Teichoic Acid Recognition Features of Choline-Binding Protein L (Cbpl) Contributing to Pneumococcal Pathogenesis. <i>Scientific Reports</i> , 2016, 6, 38094.	3.3	32
36	Turnover of Bacterial Cell Wall by SltB3, a Multidomain Lytic Transglycosylase of <i>Pseudomonas aeruginosa</i> . <i>ACS Chemical Biology</i> , 2016, 11, 1525-1531.	3.4	16

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37	Renew or die: The molecular mechanisms of peptidoglycan recycling and antibiotic resistance in Gram-negative pathogens. <i>Drug Resistance Updates</i> , 2016, 28, 91-104.	14.4	24
38	Activation by Allostery in Cell-Wall Remodeling by a Modular Membrane-Bound Lytic Transglycosylase from <i>Pseudomonas aeruginosa</i> . <i>Structure</i> , 2016, 24, 1729-1741.	3.3	27
39	Structural Bioinformatics in Broad-Spectrum Racemases: A New Path in Antimicrobial Research. <i>Current Organic Chemistry</i> , 2016, 20, 1222-1231.	1.6	4
40	Structural insights into the synthesis of FMN in prokaryotic organisms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2526-2542.	2.5	25
41	Discovery of Antibiotic (<i>E</i>)-3-(3-Carboxyphenyl)-2-(4-cyanostyryl)quinazolin-4(3<i>H</i>)-one. <i>Journal of the American Chemical Society</i> , 2015, 137, 1738-1741.	13.7	116
42	Structure and Function of Choline-Binding Proteins. , 2015, , 207-230.		31
43	Synthesis of a heterogeneous artificial metallolipase with chimeric catalytic activity. <i>Chemical Communications</i> , 2015, 51, 9324-9327.	4.1	39
44	The Allosteric Site for the Nascent Cell Wall in Penicillin-Binding Protein 2a: An Achillesâ€™ Heel of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>Current Medicinal Chemistry</i> , 2015, 22, 1678-1686.	2.4	32
45	Pneumococcal phosphoglycerate kinase interacts with plasminogen and its tissue activator. <i>Thrombosis and Haemostasis</i> , 2014, 112, 401-416.	3.4	37
46	Structural basis for the broad specificity of a new family of amino-acid racemases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 79-90.	2.5	61
47	Penicillinâ€™binding protein 2a of methicillinâ€™resistant <i>Staphylococcus aureus</i>. <i>IUBMB Life</i> , 2014, 66, 572-577.	3.4	176
48	Structure of the pneumococcal <sc>l</sc>, <sc>d</sc>â€™carboxypeptidase <sc>DacB</sc> and pathophysiological effects of disabled cell wall hydrolases <sc>DacA</sc> and <sc>DacB</sc>. <i>Molecular Microbiology</i> , 2014, 93, 1183-1206.	2.5	37
49	Structure solution with <sc>ARCIMBOLDO</sc> using fragments derived from distant homology models. <i>FEBS Journal</i> , 2014, 281, 4029-4045.	4.7	41
50	The C-terminal extension of bacterial flavodoxin-reductases: Involvement in the hydride transfer mechanism from the coenzyme. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 33-43.	1.0	8
51	A complement to the modern crystallographer's toolbox: caged gadolinium complexes with versatile binding modes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1506-1516.	2.5	7
52	Structural basis of PcsB-mediated cell separation in <i>Streptococcus pneumoniae</i> . <i>Nature Communications</i> , 2014, 5, 3842.	12.8	82
53	Comparative study of two <sc>GH</sc>19 chitinaseâ€™like proteins from <i>HeveaÂbrasiliensis</i>, one exhibiting a novel carbohydrateâ€™binding domain. <i>FEBS Journal</i> , 2014, 281, 4535-4554.	4.7	27
54	Peptidoglycan Remodeling by the Coordinated Action of Multispecific Enzymes. <i>Microbial Drug Resistance</i> , 2014, 20, 190-198.	2.0	33

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55	Structural Basis for Selective Recognition of Endogenous and Microbial Polysaccharides by Macrophage Receptor SIGN-R1. <i>Structure</i> , 2014, 22, 1595-1606.	3.3	31
56	Crystal structures of <i>Ophiostoma piceae</i> sterol esterase: Structural insights into activation mechanism and product release. <i>Journal of Structural Biology</i> , 2014, 187, 215-222.	2.8	32
57	Disruption of Allosteric Response as an Unprecedented Mechanism of Resistance to Antibiotics. <i>Journal of the American Chemical Society</i> , 2014, 136, 9814-9817.	13.7	93
58	Structure and Cell Wall Cleavage by Modular Lytic Transglycosylase MltC of <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2014, 9, 2058-2066.	3.4	41
59	Structural Insights into the Coenzyme Mediated Monomer→Dimer Transition of the Pro-Apoptotic Apoptosis Inducing Factor. <i>Biochemistry</i> , 2014, 53, 4204-4215.	2.5	52
60	Getting CAD in Shape: The Atomic Structure of Human Dihydroorotase Domain. <i>Structure</i> , 2014, 22, 179-181.	3.3	2
61	<i>Escherichia coli</i> LacZ $\beta$ -galactosidase inhibition by monohydroxy acetylated glycopyranosides: Role of the acetyl groups. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 107, 31-38.	1.8	3
62	Crystal structures of CbpF complexed with atropine and ipratropium reveal clues for the design of novel antimicrobials against <i>Streptococcus pneumoniae</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 129-135.	2.4	10
63	Cell-Wall Remodeling by the Zinc-Protease AmpDh3 from <i>Pseudomonas aeruginosa</i> . <i>Journal of the American Chemical Society</i> , 2013, 135, 12604-12607.	13.7	41
64	Molecular architecture of <i>Streptococcus pneumoniae</i> surface thioredoxin fold lipoproteins crucial for extracellular oxidative stress resistance and maintenance of virulence. <i>EMBO Molecular Medicine</i> , 2013, 5, 1852-1870.	6.9	99
65	Reaction Products and the X-ray Structure of AmpDh2, a Virulence Determinant of <i>Pseudomonas aeruginosa</i> . <i>Journal of the American Chemical Society</i> , 2013, 135, 10318-10321.	13.7	38
66	Structural and Phylogenetic Analysis of <i>Rhodobacter capsulatus</i> NifF: Uncovering General Features of Nitrogen-fixation (nif)-Flavodoxins. <i>International Journal of Molecular Sciences</i> , 2013, 14, 1152-1163.	4.1	13
67	Heteroresistance to Fosfomycin Is Predominant in <i>Streptococcus pneumoniae</i> and Depends on the <i>murA1</i> Gene. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 2801-2808.	3.2	28
68	How allosteric control of <i>Staphylococcus aureus</i> penicillin binding protein 2a enables methicillin resistance and physiological function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16808-16813.	7.1	235
69	Promiscuous enantioselective $\beta$ -lactamase activity in the <i>Pseudomonas fluorescens</i> esterase I. <i>Organic and Biomolecular Chemistry</i> , 2012, 10, 3388.	2.8	29
70	Semisynthetic peptide-lipase conjugates for improved biotransformations. <i>Chemical Communications</i> , 2012, 48, 9053.	4.1	31
71	Pneumococcal surface proteins: when the whole is greater than the sum of its parts. <i>Molecular Oral Microbiology</i> , 2012, 27, 221-245.	2.7	92
72	High-Resolution Crystal Structure of MltE, an Outer Membrane-Anchored Endolytic Peptidoglycan Lytic Transglycosylase from <i>Escherichia coli</i> . <i>Biochemistry</i> , 2011, 50, 2384-2386.	2.5	39

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73	An esterase from <i>Thermus thermophilus</i> HB27 with hyper-thermoalkalophilic properties: Purification, characterisation and structural modelling. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2011, 70, 127-137.	1.8	21
74	Crystallization and preliminary X-ray diffraction analysis of the lytic transglycosylase MltE from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 161-163.	0.7	8
75	Crystallization and preliminary X-ray diffraction studies of the transcriptional repressor PaaX, the main regulator of the phenylacetic acid degradation pathway in <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1278-1280.	0.7	5
76	Crystallization and preliminary X-ray diffraction analysis of phosphoglycerate kinase from <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1285-1289.	0.7	8
77	Crystal Structures of Bacterial Peptidoglycan Amidase AmpD and an Unprecedented Activation Mechanism. <i>Journal of Biological Chemistry</i> , 2011, 286, 31714-31722.	3.4	49
78	New Alkaloid Antibiotics That Target the DNA Topoisomerase I of <i>Streptococcus pneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 6402-6413.	3.4	51
79	Promotion of multipoint covalent immobilization through different regions of genetically modified penicillin G acylase from <i>E. coli</i> . <i>Process Biochemistry</i> , 2010, 45, 390-398.	3.7	55
80	Crystallization of the pneumococcal autolysin LytC: in-house phasing using novel lanthanide complexes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 448-451.	0.7	3
81	Crystallization and preliminary crystallographic analysis of the catalytic module of endolysin from Cp-7, a phage infecting <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 670-673.	0.7	7
82	Pneumococcal CbpD is a murein hydrolase that requires a dual cell envelope binding specificity to kill target cells during fratricide. <i>Molecular Microbiology</i> , 2010, 76, 905-917.	2.5	74
83	Insights into pneumococcal fratricide from the crystal structures of the modular killing factor LytC. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 576-581.	8.2	57
84	Oligomeric State in the Crystal Structure of Modular FAD Synthetase Provides Insights into Its Sequential Catalysis in Prokaryotes. <i>Journal of Molecular Biology</i> , 2010, 400, 218-230.	4.2	40
85	Activation of Bacterial Thermoalkalophilic Lipases Is Spurred by Dramatic Structural Rearrangements. <i>Journal of Biological Chemistry</i> , 2009, 284, 4365-4372.	3.4	196
86	Flavodoxin: A compromise between efficiency and versatility in the electron transfer from Photosystem I to Ferredoxin-NADP+ reductase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 144-154.	1.0	37
87	Characterization of gadolinium complexes for SAD phasing in macromolecular crystallography: application to CbpF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 823-831.	2.5	8
88	Crystallization and preliminary X-ray diffraction studies of the carbohydrate-recognition domain of SIGN-R1, a receptor for microbial polysaccharides and sialylated antibody on splenic marginal zone macrophages. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1264-1266.	0.7	4
89	Crystallization and preliminary X-ray diffraction studies of FAD synthetase from <i>Corynebacterium ammoniagenes</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1285-1288.	0.7	10
90	Crystal structure of CbpF, a bifunctional choline-binding protein and autolysis regulator from <i>Streptococcus pneumoniae</i> . <i>EMBO Reports</i> , 2009, 10, 246-251.	4.5	56

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91	Crystal structure of CbpF, a bifunctional choline-binding protein and autolysis regulator from <i>Streptococcus pneumoniae</i> . <i>EMBO Reports</i> , 2009, 10, 413-413.	4.5	2
92	Coenzyme binding and hydride transfer in <i>Rhodobacter capsulatus</i> ferredoxin/ferredoxin NADP(H) oxidoreductase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 199-210.	2.3	18
93	Protein Motifs Involved in Coenzyme Interaction and Enzymatic Efficiency in <i>Anabaena</i> Ferredoxin-NADP <sup>+</sup> Reductase. <i>Biochemistry</i> , 2009, 48, 3109-3119.	2.5	15
94	Discovery of Specific Flavodoxin Inhibitors as Potential Therapeutic Agents against <i>Helicobacter pylori</i> Infection. <i>ACS Chemical Biology</i> , 2009, 4, 928-938.	3.4	48
95	Crystallization of a flavodoxin involved in nitrogen fixation in <i>Rhodobacter capsulatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 375-377.	0.7	3
96	Crystallization and preliminary X-ray diffraction studies of the BTL2 lipase from the extremophilic microorganism <i>Bacillus thermocatenulatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 1043-1045.	0.7	7
97	Solid-Phase Chemical Amination of a Lipase from <i>Bacillus thermocatenulatus</i> To Improve Its Stabilization via Covalent Immobilization on Highly Activated Glyoxyl-Agarose. <i>Biomacromolecules</i> , 2008, 9, 2553-2561.	5.4	98
98	A one-pot, simple methodology for cassette randomisation and recombination for focused directed evolution. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 567-576.	2.1	34
99	Elucidation of the Molecular Recognition of Bacterial Cell Wall by Modular Pneumococcal Phage Endolysin CPL-1. <i>Journal of Biological Chemistry</i> , 2007, 282, 24990-24999.	3.4	61
100	Enhancement of the Stability of a Prolipase from <i>Rhizopus oryzae</i> toward Aldehydes by Saturation Mutagenesis. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7291-7299.	3.1	28
101	Genetic Modification of the Penicillin G Acylase Surface To Improve Its Reversible Immobilization on Ionic Exchangers. <i>Applied and Environmental Microbiology</i> , 2007, 73, 312-319.	3.1	41
102	Tuning of the FMN binding and oxido-reduction properties by neighboring side chains in <i>Anabaena</i> flavodoxin. <i>Archives of Biochemistry and Biophysics</i> , 2007, 467, 206-217.	3.0	24
103	Insights into Molecular Plasticity of Choline Binding Proteins (Pneumococcal Surface Proteins) by SAXS. <i>Journal of Molecular Biology</i> , 2007, 365, 411-424.	4.2	23
104	Taking aim on bacterial pathogens: from phage therapy to enzybiotics. <i>Current Opinion in Microbiology</i> , 2007, 10, 461-472.	5.1	238
105	Mixed Ion Exchange Supports as Useful Ion Exchangers for Protein Purification: Purification of Penicillin G Acylase from <i>Escherichia coli</i> . <i>Biomacromolecules</i> , 2007, 8, 703-707.	5.4	40
106	Improved Stabilization of Genetically Modified Penicillin G Acylase in the Presence of Organic Cosolvents by Co-Immobilization of the Enzyme with Polyethyleneimine. <i>Advanced Synthesis and Catalysis</i> , 2007, 349, 459-464.	4.3	38
107	Crystallization and preliminary X-ray diffraction studies of choline-binding protein F from <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 742-745.	0.7	8
108	Common conformational changes in flavodoxins induced by FMN and anion binding: The structure of <i>Helicobacter pylori</i> apoflavodoxin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 581-594.	2.6	24

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109	Chemical Modification of Protein Surfaces To Improve Their Reversible Enzyme Immobilization on Ionic Exchangers. <i>Biomacromolecules</i> , 2006, 7, 3052-3058.	5.4	46
110	X-ray and Neutron Diffraction Approaches to the Structural Analysis of Protein-Lipid Interactions. , 2006, , 63-110.		1
111	Pneumococcal phosphorylcholine esterase, Pce, contains a metal binuclear center that is essential for substrate binding and catalysis. <i>Protein Science</i> , 2005, 14, 3013-3024.	7.6	10
112	Insights into pneumococcal pathogenesis from the crystal structure of the modular teichoic acid phosphorylcholine esterase Pce. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 533-538.	8.2	89
113	Probing the determinants of substrate specificity of a feruloyl esterase, AnFaeA, from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 2005, 272, 4362-4371.	4.7	59
114	Activation in the family of <i>Candida rugosa</i> islipases by polyethylene glycol. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2005, 32, 225-229.	1.8	13
115	Crystallization and preliminary X-ray diffraction studies of the pneumococcal teichoic acid phosphorylcholine esterase Pce. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 221-224.	0.7	11
116	Structural analysis of interactions for complex formation between Ferredoxin-NADP+ reductase and its protein partners. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 592-602.	2.6	24
117	Structural Basis for Membrane Anchorage of Viral $\Psi$ 29 DNA during Replication*. <i>Journal of Biological Chemistry</i> , 2005, 280, 42486-42488.	3.4	9
118	Structure of the Functional Domain of $\Psi$ 29 Replication Organizer. <i>Journal of Biological Chemistry</i> , 2005, 280, 20730-20739.	3.4	8
119	Structural Analysis of the <i>Laetiporus sulphureus</i> Hemolytic Pore-forming Lectin in Complex with Sugars. <i>Journal of Biological Chemistry</i> , 2005, 280, 17251-17259.	3.4	109
120	The Ferredoxin-NADP(H) Reductase from <i>Rhodobacter capsulatus</i> : Molecular Structure and Catalytic Mechanism,. <i>Biochemistry</i> , 2005, 44, 11730-11740.	2.5	36
121	The 1.49Å... Resolution Crystal Structure of PsbQ from Photosystem II of <i>Spinacia oleracea</i> Reveals a PPII Structure in the N-terminal Region. <i>Journal of Molecular Biology</i> , 2005, 350, 1051-1060.	4.2	60
122	C-Terminal Tyrosine of Ferredoxin $\rightarrow$ NADP+ Reductase in Hydride Transfer Processes with NAD(P)+/H. <i>Biochemistry</i> , 2005, 44, 13477-13490.	2.5	51
123	Stabilization of Penicillin G Acylase from <i>Escherichia coli</i> : Site-Directed Mutagenesis of the Protein Surface To Increase Multipoint Covalent Attachment. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1249-1251.	3.1	111
124	Crystallization and preliminary crystallographic analysis of a novel haemolytic lectin from the mushroom <i>Laetiporus sulphureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1139-1141.	2.5	15
125	Crystallization of a proteolyzed form of the horse pancreatic lipase-related protein 2: structural basis for the specific detergent requirement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2107-2109.	2.5	6
126	Crystallization and preliminary X-ray diffraction analysis of ferredoxin-NADP(H) reductase from <i>Rhodobacter capsulatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2332-2335.	2.5	2



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127	The Crystal Structure of Feruloyl Esterase A from <i>Aspergillus niger</i> Suggests Evolutive Functional Convergence in Feruloyl Esterase Family. <i>Journal of Molecular Biology</i> , 2004, 338, 495-506.	4.2	110
128	Structural Basis for Selective Recognition of Pneumococcal Cell Wall by Modular Endolysin from Phage Cp-1. <i>Structure</i> , 2003, 11, 1239-1249.	3.3	149
129	Crystal and Electron Microscopy Structures of Sticholysin II Actinoporin Reveal Insights into the Mechanism of Membrane Pore Formation. <i>Structure</i> , 2003, 11, 1319-1328.	3.3	218
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