

Giuseppe Zanotti

List of Publications by Year in descending order

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138
papers

5,059
citations

94433

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114465

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139
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139
docs citations

139
times ranked

6030
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the trigonal form of bovine beta-lactoglobulin and of its complex with retinol at 2.5 Å... resolution. <i>Journal of Molecular Biology</i> , 1987, 197, 695-706.	4.2	348
2	Bicyclic Peptide Inhibitor Reveals Large Contact Interface with a Protease Target. <i>ACS Chemical Biology</i> , 2012, 7, 817-821.	3.4	156
3	Biochemical and three-dimensional-structural study of the specific inhibition of protein kinase CK2 by [5-oxo-5,6-dihydroindolo-(1,2-a)quinazolin-7-yl]acetic acid (IQA). <i>Biochemical Journal</i> , 2003, 374, 639-646.	3.7	145
4	Toward the rational design of protein kinase casein kinase-2 inhibitors. , 2002, 93, 159-168.		139
5	The Replacement of ATP by the Competitive Inhibitor Emodin Induces Conformational Modifications in the Catalytic Site of Protein Kinase CK2. <i>Journal of Biological Chemistry</i> , 2000, 275, 29618-29622.	3.4	136
6	Structure of the Neutrophil-activating Protein from <i>Helicobacter pylori</i> . <i>Journal of Molecular Biology</i> , 2002, 323, 125-130.	4.2	133
7	Plasma Retinol-Binding Protein: Structure and Interactions with Retinol, Retinoids, and Transthyretin. <i>Vitamins and Hormones</i> , 2004, 69, 271-295.	1.7	130
8	Structural features underlying selective inhibition of protein kinase CK2 by ATP site-directed tetrabromo-2-benzotriazole. <i>Protein Science</i> , 2008, 10, 2200-2206.	7.6	130
9	Crystal Structure of Peach Pru p 3, the Prototypic Member of the Family of Plant Non-specific Lipid Transfer Protein Pan-allergens. <i>Journal of Molecular Biology</i> , 2006, 356, 684-694.	4.2	122
10	<i>Helicobacter pylori</i> secreted peptidyl prolyl cis, trans-isomerase drives Th17 inflammation in gastric adenocarcinoma. <i>Internal and Emergency Medicine</i> , 2014, 9, 303-309.	2.0	118
11	Structure of Two Iron-binding Proteins from <i>Bacillus anthracis</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 15093-15098.	3.4	111
12	Inspecting the Structure-Activity Relationship of Protein Kinase CK2 Inhibitors Derived from Tetrabromo-Benzimidazole. <i>Chemistry and Biology</i> , 2005, 12, 1211-1219.	6.0	108
13	The ATP Binding Site of Protein Kinase CK2 Holds a Positive Electrostatic Area and Conserved Water Molecules. <i>ChemBioChem</i> , 2007, 8, 1804-1809.	2.6	98
14	<i>Borrelia burgdorferi</i> -driven Th17 cell inflammation in lyme arthritis. <i>Arthritis and Rheumatism</i> , 2008, 58, 3609-3617.	6.7	93
15	Crystal Structure of the Trigonal Form of Human Plasma Retinol-binding Protein at 2.5 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 230, 613-624.	4.2	82
16	Ligand Binding and Structural Analysis of a Human Putative Cellular Retinol-binding Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 41970-41977.	3.4	80
17	Crystal Structure of Amine Oxidase from Bovine Serum. <i>Journal of Molecular Biology</i> , 2005, 346, 991-1004.	4.2	79
18	Crystal structure of the PsbQ protein of photosystem II from higher plants. <i>EMBO Reports</i> , 2003, 4, 900-905.	4.5	78

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19	DJ-1 Is a Copper Chaperone Acting on SOD1 Activation. Journal of Biological Chemistry, 2014, 289, 10887-10899.	3.4	76
20	Inhibition of Protein Kinase CK2 by Anthraquinone-related Compounds. Journal of Biological Chemistry, 2003, 278, 1831-1836.	3.4	75
21	Features and potentials of ATP-site directed CK2 inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 263-270.	2.3	69
22	Crystal structure and refolding properties of the mutant F99S/M153T/V163A of the green fluorescent protein. Proteins: Structure, Function and Bioinformatics, 2000, 41, 429-437.	2.6	68
23	Crystal structure of chicken liver basic fatty acid-binding protein at 2.7 Å resolution. Molecular and Cellular Biochemistry, 1990, 98, 95-9.	3.1	64
24	Logical Identification of an Allantoinase Analog (puuE) Recruited from Polysaccharide Deacetylases. Journal of Biological Chemistry, 2008, 283, 23295-23304.	3.4	62
25	Nidogens are therapeutic targets for the prevention of tetanus. Science, 2014, 346, 1118-1123.	12.6	62
26	<i>Helicobacter pylori</i> , asthma and allergy. FEMS Immunology and Medical Microbiology, 2009, 56, 1-8.	2.7	53
27	Structure of Zebra fish HIUase: Insights into Evolution of an Enzyme to a Hormone Transporter. Journal of Molecular Biology, 2006, 363, 1-9.	4.2	52
28	Permeation Pathway of Homomeric Connexin 26 and Connexin 30 Channels Investigated by Molecular Dynamics. Journal of Biomolecular Structure and Dynamics, 2012, 29, 985-998.	3.5	50
29	Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence similarity. Biopolymers, 1992, 32, 457-465.	2.4	49
30	Active Site Structural Features for Chemically Modified Forms of Rhodanese. Journal of Biological Chemistry, 1996, 271, 21054-21061.	3.4	47
31	The Structure of 2-Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline Decarboxylase Provides Insights into the Mechanism of Uric Acid Degradation. Journal of Biological Chemistry, 2007, 282, 18182-18189.	3.4	46
32	The neutrophil-activating protein of <i>Helicobacter pylori</i> . International Journal of Medical Microbiology, 2001, 291, 545-550.	3.6	45
33	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	3.4	44
34	Crystal structure of the non-regulatory A 4 isoform of spinach chloroplast glyceraldehyde-3-phosphate dehydrogenase complexed with NADP ⁺ Edited by R. Huber. Journal of Molecular Biology, 2001, 314, 527-542.	4.2	42
35	Transthyretin Binding Heterogeneity and Anti-amyloidogenic Activity of Natural Polyphenols and Their Metabolites. Journal of Biological Chemistry, 2015, 290, 29769-29780.	3.4	42
36	Structure of the trigonal crystal form of bovine annexin IV. Biochemical Journal, 1998, 329, 101-106.	3.7	41

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37	Novel Pathogenic Mechanisms of Congenital Insensitivity to Pain with Anhidrosis Genetic Disorder Unveiled by Functional Analysis of Neurotrophic Tyrosine Receptor Kinase Type 1/Nerve Growth Factor Receptor Mutations. <i>Journal of Biological Chemistry</i> , 2002, 277, 6455-6462.	3.4	41
38	Multiple Binding Sites for Substrates and Modulators of Semicarbazide-Sensitive Amine Oxidases: Kinetic Consequences. <i>Molecular Pharmacology</i> , 2008, 73, 525-538.	2.3	40
39	Chicken liver basic fatty acid-binding protein (pI= 9.0) Purification, crystallization and preliminary X-ray data. <i>FEBS Letters</i> , 1988, 240, 196-200.	2.8	38
40	Acidic pH-induced Conformational Changes in Amyloidogenic Mutant Transthyretin. <i>Journal of Molecular Biology</i> , 2007, 366, 711-719.	4.2	38
41	Probing the Structure of Hirudin from <i>Hirudinaria manillensis</i> by Limited Proteolysis. Isolation, Characterization and Thrombin-Inhibitory Properties of N-Terminal Fragments. <i>FEBS Journal</i> , 1994, 226, 323-333.	0.2	37
42	The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray data. <i>FEBS Journal</i> , 1990, 192, 507-513.	0.2	35
43	Crystal Structure of the Transthyretin-Retinoic-Acid Complex. <i>FEBS Journal</i> , 1995, 234, 563-569.	0.2	35
44	Crystal structure of sarcoplasmic reticulum Ca ²⁺ -ATPase (SERCA) from bovine muscle. <i>Journal of Structural Biology</i> , 2012, 178, 38-44.	2.8	35
45	<sc>H</sc> <i>elicobacter pylori</i> periplasmic receptor <sc>Ceue</sc> (<sc>HP</sc> 1561) modulates its nickel affinity via organic metallophores. <i>Molecular Microbiology</i> , 2014, 91, 724-735.	2.5	35
46	The crystal structure of the complex of <i>Zea mays</i> Î± subunit with a fragment of human Î² subunit provides the clue to the architecture of protein kinase CK2 holoenzyme. <i>FEBS Journal</i> , 2000, 267, 5184-5190.	0.2	34
47	Distinctive binding and structural properties of piscine transthyretin. <i>FEBS Letters</i> , 2003, 555, 279-284.	2.8	34
48	Structural and mutational analyses of protein-protein interactions between transthyretin and retinol-binding protein. <i>FEBS Journal</i> , 2008, 275, 5841-5854.	4.7	34
49	Expression of <i>Helicobacter pylori</i> CagA domains by library-based construct screening. <i>FEBS Journal</i> , 2009, 276, 816-824.	4.7	33
50	The <i>Helicobacter pylori</i> CagD (HP0545, Cag24) Protein Is Essential for CagA Translocation and Maximal Induction of Interleukin-8 Secretion. <i>Journal of Molecular Biology</i> , 2009, 386, 204-217.	4.2	33
51	Structure of the uncomplexed <i>Neisseria meningitidis</i> factor H-binding protein fHbp (rLP2086). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 531-535.	0.7	33
52	Structural and functional aspects of the <i>Helicobacter pylori</i> secretome. <i>World Journal of Gastroenterology</i> , 2014, 20, 1402.	3.3	33
53	Is tensegrity a unifying concept of protein folds?. <i>FEBS Letters</i> , 2003, 534, 7-10.	2.8	32
54	Stop the killer: how to inhibit the anthrax lethal factor metalloprotease. <i>Trends in Biochemical Sciences</i> , 2004, 29, 282-285.	7.5	32

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55	Structural and functional aspects of unique type IV secretory components in the <i>Helicobacter pylori</i> cag pathogenicity island. FEBS Journal, 2011, 278, 1223-1231.	4.7	32
56	Crystal Structure of HydF Scaffold Protein Provides Insights into [FeFe]-Hydrogenase Maturation. Journal of Biological Chemistry, 2011, 286, 43944-43950.	3.4	32
57	High-resolution Structures of Retinol-binding Protein in Complex with Retinol: pH-induced Protein Structural Changes in the Crystal State. Journal of Molecular Biology, 2003, 329, 841-850.	4.2	30
58	Structural and enzymatic characterization of HP0496, a YbgC thioesterase from <i>Helicobacter pylori</i> . Proteins: Structure, Function and Bioinformatics, 2008, 72, 1212-1221.	2.6	30
59	Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap. Scientific Reports, 2017, 7, 10067.	3.3	30
60	Crystal structure of alkyl hydroperoxide-reductase (AhpC) from <i>Helicobacter pylori</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1753, 240-246.	2.3	29
61	Atomic structure of potato virus X, the prototype of the Alphaflexiviridae family. Nature Chemical Biology, 2020, 16, 564-569.	8.0	29
62	Muscle fatty acid-binding protein. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 1999, 1441, 94-105.	2.4	28
63	PROuST: A Comparison Method of Three-Dimensional Structures of Proteins Using Indexing Techniques. Journal of Computational Biology, 2004, 11, 1061-1072.	1.6	28
64	Three-dimensional atomic structure of a catalytic subunit mutant of human protein kinase CK2. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2133-2139.	2.5	27
65	The lipoprotein HP1454 of <i>Helicobacter pylori</i> regulates T cell response by shaping T cell receptor signalling. Cellular Microbiology, 2019, 21, e13006.	2.1	27
66	<i>Helicobacter pylori</i> acidic stress response factor HP1286 is a Ycel homolog with new binding specificity. FEBS Journal, 2010, 277, 1896-1905.	4.7	26
67	An aminotransferase branch point connects purine catabolism to amino acid recycling. Nature Chemical Biology, 2010, 6, 801-806.	8.0	26
68	Diphtheria toxin conformational switching at acidic pH. FEBS Journal, 2014, 281, 2115-2122.	4.7	26
69	NH2-terminal Sequence Truncation Decreases the Stability of Bovine Rhodanese, Minimally Perturbs Its Crystal Structure, and Enhances Interaction with GroEL under Native Conditions. Journal of Biological Chemistry, 1999, 274, 13938-13947.	3.4	25
70	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. International Journal of Molecular Sciences, 2020, 21, 4496.	4.1	25
71	The <i>Helicobacter cinaedi</i> antigen CAIP participates in atherosclerotic inflammation by promoting the differentiation of macrophages in foam cells. Scientific Reports, 2017, 7, 40515.	3.3	24
72	Conformational and binding properties of chicken liver basic fatty acid binding protein in solution. Biopolymers, 1994, 34, 879-887.	2.4	23

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73	Structure of Sulfur-Substituted Rhodanese at 1.36 Å... Resolution. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 481-486.	2.5	23
74	Crystal structure of antigen TpF1 from <i>Treponema pallidum</i> . Proteins: Structure, Function and Bioinformatics, 2005, 62, 827-830.	2.6	22
75	Structure of chicken plasma retinol-binding protein. BBA - Proteins and Proteomics, 2001, 1550, 64-69.	2.1	21
76	Crystal Structure of CagZ, a Protein from the <i>Helicobacter pylori</i> Pathogenicity Island that Encodes for a Type IV Secretion System. Journal of Molecular Biology, 2004, 340, 881-889.	4.2	21
77	Structural evidence for native state stabilization of a conformationally labile amyloidogenic transthyretin variant by fibrillogenesis inhibitors. FEBS Letters, 2013, 587, 2325-2331.	2.8	21
78	Structural evidence for asymmetric ligand binding to transthyretin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1582-1592.	2.5	21
79	Catalysis and Structure of Zebrafish Urate Oxidase Provide Insights into the Origin of Hyperuricemia in Hominoids. Scientific Reports, 2016, 6, 38302.	3.3	21
80	Crystal structure of bovine 3- α -hydroxyanthranilate 3,4-dioxygenase. Biopolymers, 2009, 91, 1189-1195.	2.4	20
81	Functional and structural aspects of <i>Helicobacter pylori</i> acidic stress response factors. IUBMB Life, 2010, 62, 715-723.	3.4	19
82	<i>Helicobacter pylori</i> antigenic Lpp20 is a structural homologue of Tip1 and promotes epithelial-mesenchymal transition. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3263-3271.	2.4	19
83	The Structure of <i>Helicobacter pylori</i> HP0310 Reveals an Atypical Peptidoglycan Deacetylase. PLoS ONE, 2011, 6, e19207.	2.5	19
84	The primary structure of piscine (<i>Oncorhynchus mykiss</i>) retinol-binding protein and a comparison with the three-dimensional structure of mammalian retinol-binding protein. FEBS Journal, 1992, 210, 937-943.	0.2	18
85	Structure at 1.44 Å... resolution of an N-terminally truncated form of the rat serum complement C3d fragment. BBA - Proteins and Proteomics, 2000, 1478, 232-238.	2.1	18
86	The crystal structure of the superoxide dismutase from <i>Helicobacter pylori</i> reveals a structured C-terminal extension. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1601-1606.	2.3	18
87	Differential Recognition of Old World and New World Arenavirus Envelope Glycoproteins by Subtilisin Kexin Isozyme 1 (SKI-1)/Site 1 Protease (S1P). Journal of Virology, 2013, 87, 6406-6414.	3.4	18
88	Identification and Structural Analysis of a Zebrafish Apo and Holo Cellular Retinol-binding Protein. Journal of Molecular Biology, 2002, 321, 527-535.	4.2	17
89	Specific interaction of lipoate at the active site of rhodanese. BBA - Proteins and Proteomics, 2000, 1481, 103-108.	2.1	16
90	Cloning of human 3-hydroxyanthranilic acid dioxygenase in <i>Escherichia coli</i> : characterisation of the purified enzyme and its in vitro inhibition by Zn ²⁺ . BBA - Proteins and Proteomics, 2002, 1596, 283-292.	2.1	16

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91	Crystallization of hen eggwhite riboflavin-binding protein. <i>Journal of Molecular Biology</i> , 1984, 180, 1185-1187.	4.2	15
92	Probing the Evolution of Hydroxyisourate Hydrolase into Transthyretin through Active-Site Redesign. <i>Journal of Molecular Biology</i> , 2011, 409, 504-512.	4.2	15
93	Structural Aspects of <i>Helicobacter pylori</i> Antibiotic Resistance. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1149, 227-241.	1.6	15
94	Structural and molecular determinants affecting the interaction of retinol with human CRBP1. <i>Journal of Structural Biology</i> , 2017, 197, 330-339.	2.8	14
95	Structural Insights into Complexes of Glucose-Regulated Protein94 (Grp94) with Human Immunoglobulin G. Relevance for Grp94-IgG Complexes that Form In Vivo in Pathological Conditions. <i>PLoS ONE</i> , 2014, 9, e86198.	2.5	13
96	High-Light versus Low-Light: Effects on Paired Photosystem II Supercomplex Structural Rearrangement in Pea Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8643.	4.1	13
97	Structural and mutational analysis of TenA protein (HP1287) from the <i>Helicobacter pylori</i> thiamin salvage pathway – evidence of a different substrate specificity. <i>FEBS Journal</i> , 2009, 276, 6227-6235.	4.7	12
98	Structure and immunomodulatory property relationship in NapA of <i>Borrelia burgdorferi</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010, 1804, 2191-2197.	2.3	12
99	Functional analysis and cryo-electron microscopy of <i>Campylobacter jejuni</i> serine protease HtrA. <i>Gut Microbes</i> , 2020, 12, 1810532.	9.8	12
100	Crystallization and preliminary X-ray data of human plasma retinol-binding protein. <i>Journal of Molecular Biology</i> , 1983, 163, 679-681.	4.2	11
101	Structure-activity relationships of flurbiprofen analogues as stabilizers of the amyloidogenic protein transthyretin. <i>Journal of Structural Biology</i> , 2019, 208, 165-173.	2.8	11
102	Gain of function mutations of RTK conserved residues display differential effects on NTRK1 kinase activity. <i>Oncogene</i> , 2002, 21, 8334-8339.	5.9	10
103	The crystal structure of CagS from the <i>Helicobacter pylori</i> pathogenicity island. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 440-443.	2.6	10
104	Crystallization of human plasma apo-retinol-binding protein. <i>Journal of Molecular Biology</i> , 1984, 178, 477-479.	4.2	9
105	A grid-aware approach to protein structure comparison. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 728-737.	4.1	9
106	Evaluating the effect of mutations and ligand binding on transthyretin homotetramer dynamics. <i>PLoS ONE</i> , 2017, 12, e0181019.	2.5	9
107	Crystallization and preliminary X-ray data of amine oxidase from bovine serum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 727-729.	2.5	8
108	Global secondary structure packing angle bias in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 252-261.	2.6	8

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109	Functional and structural characterization of ovine ornithine transcarbamoylaseElectronic supplementary information (ESI) available: a Ramachandran plot, and two figures illustrating statistics on the geometrical parameters of the structure. See http://www.rsc.org/suppdata/ob/b3/b304901a . <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 3178.	2.8	8
110	Structure of Î±-carbonic anhydrase from the human pathogen <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1005-1011.	0.8	8
111	Exceptionally potent human monoclonal antibodies are effective for prophylaxis and treatment of tetanus in mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	8
112	The Structure and Function of a Microbial Allantoin Racemase Reveal the Origin and Conservation of a Catalytic Mechanism. <i>Biochemistry</i> , 2016, 55, 6421-6432.	2.5	7
113	Crystal structure of truncated FlgD from the human pathogen <i>Helicobacter pylori</i> . <i>Journal of Structural Biology</i> , 2016, 194, 147-155.	2.8	7
114	A family of archaea-like carboxylesterases preferentially expressed in the symbiotic phase of the mycorrhizal fungus <i>Tuber melanosporum</i> . <i>Scientific Reports</i> , 2017, 7, 7628.	3.3	7
115	Structural and dynamics evidence for scaffold asymmetric flexibility of the human transthyretin tetramer. <i>PLoS ONE</i> , 2017, 12, e0187716.	2.5	7
116	Structural characterization of FlgE2 protein from <i>Helicobacter pylori</i> hook. <i>FEBS Journal</i> , 2017, 284, 4328-4342.	4.7	6
117	Structure of filamentous viruses. <i>Current Opinion in Virology</i> , 2021, 51, 25-33.	5.4	6
118	The p.R1819_C1948delinsS mutation makes von Willebrand factor ADAMTS13-resistant and reduces its collagen-binding capacity. <i>British Journal of Haematology</i> , 2015, 170, 564-573.	2.5	5
119	The crystal structure of ADP-L-glycero-D-manno-heptose-6-epimerase (HP0859) from <i>Helicobacter pylori</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1641-1647.	2.3	4
120	Structural Characterization at the Atomic Level of a Molecular Nano-Machine: The State of the Art of <i>Helicobacter Pylori</i> Flagellum Organization. <i>American Journal of Biochemistry and Biotechnology</i> , 2014, 10, 143-161.	0.4	4
121	Crystallization and preliminary X-ray data for the human transthyretin-retinol-binding protein (RBP) complex bound to an anti-RBP Fab. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 276-278.	2.5	3
122	Protein HP1028 from the human pathogen <i>Helicobacter pylori</i> belongs to the lipocalin family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1387-1394.	2.5	3
123	Linear and cyclic peptides as substrates for Lyn tyrosine kinase. , 1998, 4, 33-45.		2
124	Molecular aspects of <i>Helicobacter pylori</i> cag-pathogenicity island. <i>FEBS Journal</i> , 2011, 278, 1189-1189.	4.7	2
125	Crystal structure of the secreted protein HP1454 from the human pathogen <i>Helicobacter pylori</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2868-2873.	2.6	2
126	Characterization of the divalent metal binding site of bacterial polysaccharide deacetylase using crystallography and quantum chemical calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1311-1318.	2.6	2

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127	The crystal structure of <i>Helicobacter pylori</i> HP1029 highlights the functional diversity of the sialic acid-related DUF386 family. FEBS Journal, 2015, 282, 3311-3322.	4.7	2
128	Vertebrate 5-Hydroxyisourate Hydrolase Identification, Function, Structure, and Evolutionary Relationship with Transthyretin. , 2009, , 95-108.		2
129	The benefit of the European User Community from transnational access to national radiation facilities. Journal of Synchrotron Radiation, 2014, 21, 638-639.	2.4	2
130	Structural biology of <i>Helicobacter pylori</i> type IV secretion system. Microbial Cell Factories, 2006, 5, P45.	4.0	1
131	MINING OVERREPRESENTED 3D PATTERNS OF SECONDARY STRUCTURES IN PROTEINS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1067-1087.	0.8	1
132	Roles of the cagPAI and CagA on Gastrointestinal Diseases. , 2016, , 89-111.		1
133	Stability data of FlgD from <i>Helicobacter pylori</i> and structural comparison with other homologs. Data in Brief, 2016, 7, 493-501.	1.0	1
134	Crystal structure of chicken liver basic fatty acid-binding protein at 2.7 Å resolution. , 1990, , 95-99.		1
135	Functional and structural aspects of <i>Helicobacter pylori</i> acidic stress response factors. IUBMB Life, 2010, 62, spcone-spcone.	3.4	0
136	The Ca ²⁺ ATPase of the Sarco-/Endoplasmic Reticulum (SERCA): Structure and Control. , 2016, , 137-151.		0
137	Crystallographic Studies on Retinol-Binding Protein and Beta Lactoglobulin. , 1987, , 69-79.		0
138	Copper Binding and Oligomerization Studies of the Metal Resistance Determinant CrdA from <i>Helicobacter pylori</i> . Molecules, 2022, 27, 3387.	3.8	0