

Giuseppe Zanotti

List of Publications by Year in descending order

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papers

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docs citations

139
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citing authors

#	ARTICLE	IF	CITATIONS
1	Copper Binding and Oligomerization Studies of the Metal Resistance Determinant CrdA from <i>Helicobacter pylori</i> . <i>Molecules</i> , 2022, 27, 3387.	1.7	0
2	Structure of filamentous viruses. <i>Current Opinion in Virology</i> , 2021, 51, 25-33.	2.6	6
3	Exceptionally potent human monoclonal antibodies are effective for prophylaxis and treatment of tetanus in mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	8
4	Functional analysis and cryo-electron microscopy of <i>Campylobacter jejuni</i> serine protease HtrA. <i>Gut Microbes</i> , 2020, 12, 1810532.	4.3	12
5	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.	1.8	13
6	Atomic structure of potato virus X, the prototype of the Alphaflexiviridae family. <i>Nature Chemical Biology</i> , 2020, 16, 564-569.	3.9	29
7	Experimentally Determined Long Intrinsically Disordered Protein Regions Are Now Abundant in the Protein Data Bank. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4496.	1.8	25
8	Structure-activity relationships of flurbiprofen analogues as stabilizers of the amyloidogenic protein transthyretin. <i>Journal of Structural Biology</i> , 2019, 208, 165-173.	1.3	11
9	Structural Aspects of <i>Helicobacter pylori</i> Antibiotic Resistance. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1149, 227-241.	0.8	15
10	The lipoprotein HP1454 of <i>Helicobacter pylori</i> regulates T _H 1 cell response by shaping T _H 1 cell receptor signalling. <i>Cellular Microbiology</i> , 2019, 21, e13006.	1.1	27
11	Structural and molecular determinants affecting the interaction of retinol with human CRBP1. <i>Journal of Structural Biology</i> , 2017, 197, 330-339.	1.3	14
12	The <i>Helicobacter cinaedi</i> antigen CAIP participates in atherosclerotic inflammation by promoting the differentiation of macrophages in foam cells. <i>Scientific Reports</i> , 2017, 7, 40515.	1.6	24
13	<i>Helicobacter pylori</i> antigenic Lpp20 is a structural homologue of Tip1 and promotes epithelial-mesenchymal transition. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3263-3271.	1.1	19
14	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.	1.6	7
15	Pea PSII-LHCII supercomplexes form pairs by making connections across the stromal gap. <i>Scientific Reports</i> , 2017, 7, 10067.	1.6	30
16	Structural characterization of FlgE2 protein from <i>Helicobacter pylori</i> hook. <i>FEBS Journal</i> , 2017, 284, 4328-4342.	2.2	6
17	Evaluating the effect of mutations and ligand binding on transthyretin homotetramer dynamics. <i>PLoS ONE</i> , 2017, 12, e0181019.	1.1	9
18	Structural and dynamics evidence for scaffold asymmetric flexibility of the human transthyretin tetramer. <i>PLoS ONE</i> , 2017, 12, e0187716.	1.1	7

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19	Catalysis and Structure of Zebrafish Urate Oxidase Provide Insights into the Origin of Hyperuricemia in Hominoids. <i>Scientific Reports</i> , 2016, 6, 38302.	1.6	21
20	Roles of the cagPAI and CagA on Gastroduodenal Diseases. , 2016, , 89-111.		1
21	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.	1.2	7
22	Stability data of FlgD from <i>Helicobacter pylori</i> and structural comparison with other homologs. <i>Data in Brief</i> , 2016, 7, 493-501.	0.5	1
23	The Ca ²⁺ ATPase of the Sarco-/Endoplasmic Reticulum (SERCA): Structure and Control. , 2016, , 137-151.		0
24	Crystal structure of truncated FlgD from the human pathogen <i>Helicobacter pylori</i> . <i>Journal of Structural Biology</i> , 2016, 194, 147-155.	1.3	7
25	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.	1.2	5
26	The crystal structure of <i>Helicobacter pylori</i> HP1029 highlights the functional diversity of the sialic acid-related DUF386 family. <i>FEBS Journal</i> , 2015, 282, 3311-3322.	2.2	2
27	Structural evidence for asymmetric ligand binding to transthyretin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1582-1592.	2.5	21
28	Structure of β -carbonic anhydrase from the human pathogen <i>Helicobacter pylori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1005-1011.	0.4	8
29	Transthyretin Binding Heterogeneity and Anti-amyloidogenic Activity of Natural Polyphenols and Their Metabolites. <i>Journal of Biological Chemistry</i> , 2015, 290, 29769-29780.	1.6	42
30	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.	1.1	13
31	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.	0.1	4
32	Structural and functional aspects of the <i>Helicobacter pylori</i> secretome. <i>World Journal of Gastroenterology</i> , 2014, 20, 1402.	1.4	33
33	Nidogens are therapeutic targets for the prevention of tetanus. <i>Science</i> , 2014, 346, 1118-1123.	6.0	62
34	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.	1.5	2
35	<i>Helicobacter pylori</i> periplasmic receptor CeuE modulates its nickel affinity via organic metallophores. <i>Molecular Microbiology</i> , 2014, 91, 724-735.	1.2	35
36	<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.	1.0	118

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37	Diphtheria toxin conformational switching at acidic pH. FEBS Journal, 2014, 281, 2115-2122.	2.2	26
38	DJ-1 Is a Copper Chaperone Acting on SOD1 Activation. Journal of Biological Chemistry, 2014, 289, 10887-10899.	1.6	76
39	Characterization of the divalent metal binding site of bacterial polysaccharide deacetylase using crystallography and quantum chemical calculations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1311-1318.	1.5	2
40	The benefit of the European User Community from transnational access to national radiation facilities. Journal of Synchrotron Radiation, 2014, 21, 638-639.	1.0	2
41	Structural evidence for native state stabilization of a conformationally labile amyloidogenic transthyretin variant by fibrillogenesis inhibitors. FEBS Letters, 2013, 587, 2325-2331.	1.3	21
42	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.	1.5	18
43	Protein HP1028 from the human pathogen <i>Helicobacter pylori</i> belongs to the lipocalin family. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1387-1394.	2.5	3
44	Permeation Pathway of Homomeric Connexin 26 and Connexin 30 Channels Investigated by Molecular Dynamics. Journal of Biomolecular Structure and Dynamics, 2012, 29, 985-998.	2.0	50
45	Crystal structure of sarcoplasmic reticulum Ca ²⁺ -ATPase (SERCA) from bovine muscle. Journal of Structural Biology, 2012, 178, 38-44.	1.3	35
46	Bicyclic Peptide Inhibitor Reveals Large Contact Interface with a Protease Target. ACS Chemical Biology, 2012, 7, 817-821.	1.6	156
47	The crystal structure of ADP-L-glycero-D-manno-heptose-6-epimerase (HP0859) from <i>Helicobacter pylori</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1641-1647.	1.1	4
48	Probing the Evolution of Hydroxyisourate Hydrolase into Transthyretin through Active-Site Redesign. Journal of Molecular Biology, 2011, 409, 504-512.	2.0	15
49	Molecular aspects of <i>Helicobacter pylori</i> cag-pathogenicity island. FEBS Journal, 2011, 278, 1189-1189.	2.2	2
50	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.	2.2	32
51	Structure of the uncomplexed <i>Neisseria meningitidis</i> factor H-binding protein fHbp (rLP2086). Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 531-535.	0.7	33
52	Crystal Structure of HydF Scaffold Protein Provides Insights into [FeFe]-Hydrogenase Maturation. Journal of Biological Chemistry, 2011, 286, 43944-43950.	1.6	32
53	The Structure of <i>Helicobacter pylori</i> HP0310 Reveals an Atypical Peptidoglycan Deacetylase. PLoS ONE, 2011, 6, e19207.	1.1	19
54	Functional and structural aspects of <i>Helicobacter pylori</i> acidic stress response factors. IUBMB Life, 2010, 62, 715-723.	1.5	19

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55	Functional and structural aspects of helicobacter pylori acidic stress response factors. IUBMB Life, 2010, 62, spcone-spcone.	1.5	0
56	Structure and immunomodulatory property relationship in NapA of Borrelia burgdorferi. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 2191-2197.	1.1	12
57	<i>Helicobacter pylori</i> acidic stress response factor HP1286 is a Ycel homolog with new binding specificity. FEBS Journal, 2010, 277, 1896-1905.	2.2	26
58	An aminotransferase branch point connects purine catabolism to amino acid recycling. Nature Chemical Biology, 2010, 6, 801-806.	3.9	26
59	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	1.6	44
60	Crystal structure of bovine 3-hydroxyanthranilate 3,4-dioxygenase. Biopolymers, 2009, 91, 1189-1195.	1.2	20
61	Expression of <i>Helicobacter pylori</i> CagA domains by library-based construct screening. FEBS Journal, 2009, 276, 816-824.	2.2	33
62	Structural and mutational analysis of TenA protein (HP1287) from the <i>Helicobacter pylori</i> thiamin salvage pathway – evidence of a different substrate specificity. FEBS Journal, 2009, 276, 6227-6235.	2.2	12
63	<i>Helicobacter pylori</i> , asthma and allergy. FEMS Immunology and Medical Microbiology, 2009, 56, 1-8.	2.7	53
64	The Helicobacter pylori CagD (HP0545, Cag24) Protein Is Essential for CagA Translocation and Maximal Induction of Interleukin-8 Secretion. Journal of Molecular Biology, 2009, 386, 204-217.	2.0	33
65	Vertebrate 5-Hydroxyisourate Hydrolase Identification, Function, Structure, and Evolutionary Relationship with Transthyretin. , 2009, , 95-108.		2
66	Structural and enzymatic characterization of HP0496, a YbgC thioesterase from <i>Helicobacter pylori</i> . Proteins: Structure, Function and Bioinformatics, 2008, 72, 1212-1221.	1.5	30
67	<i>Borrelia burgdorferi</i> NapA-driven Th17 cell inflammation in lyme arthritis. Arthritis and Rheumatism, 2008, 58, 3609-3617.	6.7	93
68	The crystal structure of the superoxide dismutase from Helicobacter pylori reveals a structured C-terminal extension. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1601-1606.	1.1	18
69	Structural features underlying selective inhibition of protein kinase CK2 by ATP site-directed tetrabromo-2-benzotriazole. Protein Science, 2008, 10, 2200-2206.	3.1	130
70	Structural and mutational analyses of protein-protein interactions between transthyretin and retinol-binding protein. FEBS Journal, 2008, 275, 5841-5854.	2.2	34
71	MINING OVERREPRESENTED 3D PATTERNS OF SECONDARY STRUCTURES IN PROTEINS. Journal of Bioinformatics and Computational Biology, 2008, 06, 1067-1087.	0.3	1
72	Logical Identification of an Allantoinase Analog (puuE) Recruited from Polysaccharide Deacetylases. Journal of Biological Chemistry, 2008, 283, 23295-23304.	1.6	62

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73	Multiple Binding Sites for Substrates and Modulators of Semicarbazide-Sensitive Amine Oxidases: Kinetic Consequences. <i>Molecular Pharmacology</i> , 2008, 73, 525-538.	1.0	40
74	The Structure of 2-Oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline Decarboxylase Provides Insights into the Mechanism of Uric Acid Degradation. <i>Journal of Biological Chemistry</i> , 2007, 282, 18182-18189.	1.6	46
75	Acidic pH-induced Conformational Changes in Amyloidogenic Mutant Transthyretin. <i>Journal of Molecular Biology</i> , 2007, 366, 711-719.	2.0	38
76	The ATP-binding Site of Protein Kinase CK2 Holds a Positive Electrostatic Area and Conserved Water Molecules. <i>ChemBioChem</i> , 2007, 8, 1804-1809.	1.3	98
77	The crystal structure of CagS from the <i>Helicobacter pylori</i> pathogenicity island. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 440-443.	1.5	10
78	Structural biology of <i>Helicobacter pylori</i> type IV secretion system. <i>Microbial Cell Factories</i> , 2006, 5, P45.	1.9	1
79	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.	2.0	122
80	Structure of Zebra fish HIIase: Insights into Evolution of an Enzyme to a Hormone Transporter. <i>Journal of Molecular Biology</i> , 2006, 363, 1-9.	2.0	52
81	Inspecting the Structure-Activity Relationship of Protein Kinase CK2 Inhibitors Derived from Tetrabromo-Benzimidazole. <i>Chemistry and Biology</i> , 2005, 12, 1211-1219.	6.2	108
82	Features and potentials of ATP-site directed CK2 inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1754, 263-270.	1.1	69
83	Crystal structure of alkyl hydroperoxide-reductase (AhpC) from <i>Helicobacter pylori</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1753, 240-246.	1.1	29
84	Crystal structure of antigen TpF1 from <i>Treponema pallidum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 827-830.	1.5	22
85	Crystal Structure of Amine Oxidase from Bovine Serum. <i>Journal of Molecular Biology</i> , 2005, 346, 991-1004.	2.0	79
86	PROuST: A Comparison Method of Three-Dimensional Structures of Proteins Using Indexing Techniques. <i>Journal of Computational Biology</i> , 2004, 11, 1061-1072.	0.8	28
87	Stop the killer: how to inhibit the anthrax lethal factor metalloprotease. <i>Trends in Biochemical Sciences</i> , 2004, 29, 282-285.	3.7	32
88	Plasma Retinol-Binding Protein: Structure and Interactions with Retinol, Retinoids, and Transthyretin. <i>Vitamins and Hormones</i> , 2004, 69, 271-295.	0.7	130
89	Crystal Structure of CagZ, a Protein from the <i>Helicobacter pylori</i> Pathogenicity Island that Encodes for a Type IV Secretion System. <i>Journal of Molecular Biology</i> , 2004, 340, 881-889.	2.0	21
90	A grid-aware approach to protein structure comparison. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 728-737.	2.7	9

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91	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
92	Three-dimensional atomic structure of a catalytic subunit mutant of human protein kinase CK2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2133-2139.	2.5	27
93	Global secondary structure packing angle bias in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 252-261.	1.5	8
94	Crystal structure of the PsbQ protein of photosystem II from higher plants. <i>EMBO Reports</i> , 2003, 4, 900-905.	2.0	78
95	High-resolution Structures of Retinol-binding Protein in Complex with Retinol: pH-induced Protein Structural Changes in the Crystal State. <i>Journal of Molecular Biology</i> , 2003, 329, 841-850.	2.0	30
96	Is tensegrity a unifying concept of protein folds?. <i>FEBS Letters</i> , 2003, 534, 7-10.	1.3	32
97	Distinctive binding and structural properties of piscine transthyretin. <i>FEBS Letters</i> , 2003, 555, 279-284.	1.3	34
98	Functional and structural characterization of ovine ornithine transcarbamoylase Electronic 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.	1.5	8
99	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.	1.7	145
100	Inhibition of Protein Kinase CK2 by Anthraquinone-related Compounds. <i>Journal of Biological Chemistry</i> , 2003, 278, 1831-1836.	1.6	75
101	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.	1.6	41
102	Ligand Binding and Structural Analysis of a Human Putative Cellular Retinol-binding Protein. <i>Journal of Biological Chemistry</i> , 2002, 277, 41970-41977.	1.6	80
103	Structure of Two Iron-binding Proteins from <i>Bacillus anthracis</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 15093-15098.	1.6	111
104	Identification and Structural Analysis of a Zebrafish Apo and Holo Cellular Retinol-binding Protein. <i>Journal of Molecular Biology</i> , 2002, 321, 527-535.	2.0	17
105	Structure of the Neutrophil-activating Protein from <i>Helicobacter pylori</i> . <i>Journal of Molecular Biology</i> , 2002, 323, 125-130.	2.0	133
106	Toward the rational design of protein kinase casein kinase-2 inhibitors. , 2002, 93, 159-168.		139
107	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⁺ . <i>BBA - Proteins and Proteomics</i> , 2002, 1596, 283-292.	2.1	16
108	Gain of function mutations of RTK conserved residues display differential effects on NTRK1 kinase activity. <i>Oncogene</i> , 2002, 21, 8334-8339.	2.6	10

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109	Crystal structure of the non-regulatory A 4 isoform of spinach chloroplast glyceraldehyde-3-phosphate dehydrogenase complexed with NADP 1 Edited by R. Huber. Journal of Molecular Biology, 2001, 314, 527-542.	2.0	42
110	The neutrophil-activating protein of Helicobacter pylori. International Journal of Medical Microbiology, 2001, 291, 545-550.	1.5	45
111	Structure of chicken plasma retinol-binding protein. BBA - Proteins and Proteomics, 2001, 1550, 64-69.	2.1	21
112	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.	1.5	68
113	The crystal structure of the complex of Zea mays β subunit with a fragment of human β subunit provides the clue to the architecture of protein kinase CK2 holoenzyme. FEBS Journal, 2000, 267, 5184-5190.	0.2	34
114	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
115	Specific interaction of lipoate at the active site of rhodanese. BBA - Proteins and Proteomics, 2000, 1481, 103-108.	2.1	16
116	The Replacement of ATP by the Competitive Inhibitor Emodin Induces Conformational Modifications in the Catalytic Site of Protein Kinase CK2. Journal of Biological Chemistry, 2000, 275, 29618-29622.	1.6	136
117	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.	1.6	25
118	Crystallization and preliminary X-ray data for the human transthyretin-retinol-binding protein (RBP) complex bound to an anti-RBP Fab. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 276-278.	2.5	3
119	Muscle fatty acid-binding protein. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 1999, 1441, 94-105.	1.2	28
120	Linear and cyclic peptides as substrates for Lyn tyrosine kinase. , 1998, 4, 33-45.		2
121	Structure of Sulfur-Substituted Rhodanese at 1.36 Å... Resolution. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 481-486.	2.5	23
122	Structure of the trigonal crystal form of bovine annexin IV. Biochemical Journal, 1998, 329, 101-106.	1.7	41
123	Active Site Structural Features for Chemically Modified Forms of Rhodanese. Journal of Biological Chemistry, 1996, 271, 21054-21061.	1.6	47
124	Crystal Structure of the Transthyretin-Retinoic-Acid Complex. FEBS Journal, 1995, 234, 563-569.	0.2	35
125	Conformational and binding properties of chicken liver basic fatty acid binding protein in solution. Biopolymers, 1994, 34, 879-887.	1.2	23
126	Probing the Structure of Hirudin from Hirudinaria manillensis by Limited Proteolysis. Isolation, Characterization and Thrombin-Inhibitory Properties of N-Terminal Fragments. FEBS Journal, 1994, 226, 323-333.	0.2	37

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127	Crystal Structure of the Trigonal Form of Human Plasma Retinol-binding Protein at 2.5 Å... Resolution. Journal of Molecular Biology, 1993, 230, 613-624.	2.0	82
128	The primary structure of piscine (Oncorhynchus mykiss) 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
129	Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence similarity. Biopolymers, 1992, 32, 457-465.	1.2	49
130	The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray data. FEBS Journal, 1990, 192, 507-513.	0.2	35
131	Crystal structure of chicken liver basic fatty acid-binding protein at 2.7 Å resolution. Molecular and Cellular Biochemistry, 1990, 98, 95-9.	1.4	64
132	Crystal structure of chicken liver basic fatty acid-binding protein at 2.7 Å... resolution. , 1990, , 95-99.		1
133	Chicken liver basic fatty acid-binding protein (pI= 9.0) Purification, crystallization and preliminary X-ray data. FEBS Letters, 1988, 240, 196-200.	1.3	38
134	Crystal structure of the trigonal form of bovine beta-lactoglobulin and of its complex with retinol at 2.5 Å... resolution. Journal of Molecular Biology, 1987, 197, 695-706.	2.0	348
135	Crystallographic Studies on Retinol-Binding Protein and Beta Lactoglobulin. , 1987, , 69-79.		0
136	Crystallization of human plasma apo-retinol-binding protein. Journal of Molecular Biology, 1984, 178, 477-479.	2.0	9
137	Crystallization of hen eggwhite riboflavin-binding protein. Journal of Molecular Biology, 1984, 180, 1185-1187.	2.0	15
138	Crystallization and preliminary X-ray data of human plasma retinol-binding protein. Journal of Molecular Biology, 1983, 163, 679-681.	2.0	11