

Richard C Garratt

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	UNEXPECTED PLASTICITY OF THE QUATERNARY STRUCTURE OF IRON-MANGANESE SUPEROXIDE DISMUTASES. <i>Journal of Structural Biology</i> , 2022, , 107855.	2.8	0
2	Structural Characterization of L-Galactose Dehydrogenase: An Essential Enzyme for Vitamin C Biosynthesis. <i>Plant and Cell Physiology</i> , 2022, 63, 1140-1155.	3.1	6
3	Reverse protein engineering of a novel α -domain copper nitrite reductase reveals functional regulation by protein-protein interaction. <i>FEBS Journal</i> , 2021, 288, 262-280.	4.7	12
4	Orientational Ambiguity in Septin Coiled Coils and its Structural Basis. <i>Journal of Molecular Biology</i> , 2021, 433, 166889.	4.2	18
5	An atomic model for the human septin hexamer by cryo-EM. <i>Journal of Molecular Biology</i> , 2021, 433, 167096.	4.2	26
6	A special issue of <i>Biophysical Reviews</i> dedicated to the 20th IUPAB (virtual) Congress – Foz do Iguaçu. <i>Biophysical Reviews</i> , 2021, 13, 1-5.	3.2	3
7	Protein structure, dynamics, and function – a 20th IUPAB Congress symposium. <i>Biophysical Reviews</i> , 2021, 13, 867-869.	3.2	1
8	The Structural Biology of Septins and Their Filaments: An Update. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 765085.	3.7	41
9	Molecular Recognition at Septin Interfaces: The Switches Hold the Key. <i>Journal of Molecular Biology</i> , 2020, 432, 5784-5801.	4.2	24
10	Molecular Structure and Functional Analysis of Pyocin S8 from <i>Pseudomonas aeruginosa</i> Reveals the Essential Requirement of a Glutamate Residue in the H-N-H Motif for DNase Activity. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	3
11	A complete compendium of crystal structures for the human SEPT3 subgroup reveals functional plasticity at a specific septin interface. <i>IUCr</i> , 2020, 7, 462-479.	2.2	28
12	Structures of substrate- and product-bound forms of a multi-domain copper nitrite reductase shed light on the role of domain tethering in protein complexes. <i>IUCr</i> , 2020, 7, 557-565.	2.2	5
13	A brief history of protein crystallography in Brazil. <i>Biophysical Reviews</i> , 2019, 11, 509-511.	3.2	1
14	A revised order of subunits in mammalian septin complexes. <i>Cytoskeleton</i> , 2019, 76, 457-466.	2.0	69
15	Studying the phosphoryl transfer mechanism of the <i>E. coli</i> phosphofructokinase-2: from X-ray structure to quantum mechanics/molecular mechanics simulations. <i>Chemical Science</i> , 2019, 10, 2882-2892.	7.4	15
16	Revisiting SEPT7 and the slippage of β -strands in the septin family. <i>Journal of Structural Biology</i> , 2019, 207, 67-73.	2.8	14
17	Septin 9 has Two Polybasic Domains Critical to Septin Filament Assembly and Golgi Integrity. <i>IScience</i> , 2019, 13, 138-153.	4.1	31
18	Molecular recognition and maturation of SOD1 by its evolutionarily destabilised cognate chaperone hCCS. <i>PLoS Biology</i> , 2019, 17, e3000141.	5.6	38

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19	Cover Image, Volume 76, Issue 9â€œ10. Cytoskeleton, 2019, 76, C1.	2.0	0
20	Structural characterization of a pathogenicity-related superoxide dismutase codified by a probably essential gene in <i>Xanthomonas citri</i> subsp. <i>citri</i> . PLoS ONE, 2019, 14, e0209988.	2.5	10
21	ADP-Dependent Kinases From the Archaeal Order Methanosarcinales Adapt to Salt by a Non-canonical Evolutionarily Conserved Strategy. Frontiers in Microbiology, 2018, 9, 1305.	3.5	7
22	Unusual dimerization of a Bc Csp mutant leads to reduced conformational dynamics. FEBS Journal, 2017, 284, 1882-1896.	4.7	2
23	Ohr plays a central role in bacterial responses against fatty acid hydroperoxides and peroxyxynitrite. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E132-E141.	7.1	43
24	Septin structure and filament assembly. Biophysical Reviews, 2017, 9, 481-500.	3.2	75
25	Reconstructed ancestral enzymes reveal that negative selection drove the evolution of substrate specificity in ADP-dependent kinases. Journal of Biological Chemistry, 2017, 292, 15598-15610.	3.4	22
26	Filaments and fingers: Novel structural aspects of the single septin from <i>Chlamydomonas reinhardtii</i> . Journal of Biological Chemistry, 2017, 292, 10899-10911.	3.4	12
27	Heterotypic Coiled-Coil Formation is Essential for the Correct Assembly of the Septin Heterofilament. Biophysical Journal, 2016, 111, 2608-2619.	0.5	32
28	Analysis of two <i>Schistosoma mansoni</i> uridine phosphorylases isoforms suggests the emergence of a protein with a non-canonical function. Biochimie, 2016, 125, 12-22.	2.6	9
29	The structure of the giant haemoglobin from <i>Glossoscolex paulistus</i> . Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1257-1271.	2.5	12
30	Crystal Structure of a <i>Schistosoma mansoni</i> Septin Reveals the Phenomenon of Strand Slippage in Septins Dependent on the Nature of the Bound Nucleotide. Journal of Biological Chemistry, 2014, 289, 7799-7811.	3.4	32
31	Reversible paralysis of <i>Schistosoma mansoni</i> by forchlorfenuron, a phenylurea cytokinin that affects septins. International Journal for Parasitology, 2014, 44, 523-531.	3.1	15
32	The structure and properties of septin 3: a possible missing link in septin filament formation. Biochemical Journal, 2013, 450, 95-105.	3.7	39
33	On the Structural and Biochemical Properties of the Human Septins: SEPT3. Biophysical Journal, 2013, 104, 567a.	0.5	0
34	Adenosine kinase from <i>Schistosoma mansoni</i> : structural basis for the differential incorporation of nucleoside analogues. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 126-136.	2.5	13
35	X-ray crystallography and NMR studies of domain-swapped canecystatin. FEBS Journal, 2013, 280, 1028-1038.	4.7	25
36	A Ribokinase Family Conserved Monovalent Cation Binding Site Enhances the MgATP-induced Inhibition in <i>E. Coli</i> Phosphofructokinase-2. Biophysical Journal, 2013, 105, 185-193.	0.5	11

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37	Mitochondrial localization and structure-based phosphate activation mechanism of Glutaminase C with implications for cancer metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1092-1097.	7.1	225
38	Self assembly of human septin 2 into amyloid filaments. Biochimie, 2012, 94, 628-636.	2.6	22
39	Septin C-Terminal Domain Interactions: Implications for Filament Stability and Assembly. Cell Biochemistry and Biophysics, 2012, 62, 317-328.	1.8	40
40	Dissecting the Structure, Thermodynamic Stability, and Aggregation Properties of the A25T Transthyretin (A25T-TTR) Variant Involved in Leptomeningeal Amyloidosis: Identifying Protein Partners That Co-Aggregate during A25T-TTR Fibrillogenesis in Cerebrospinal Fluid. Biochemistry, 2011, 50, 11070-11083.	2.5	31
41	Using Amino Acid Correlation and Community Detection Algorithms to Identify Functional Determinants in Protein Families. PLoS ONE, 2011, 6, e27786.	2.5	25
42	Promiscuous interactions of human septins: The GTP binding domain of SEPT7 forms filaments within the crystal. FEBS Letters, 2011, 585, 3868-3873.	2.8	22
43	Purine nucleoside phosphorylase from <i>Schistosoma mansoni</i> in complex with ribose-1-phosphate. Journal of Synchrotron Radiation, 2011, 18, 62-65.	2.4	11
44	Crystallization and preliminary structural analysis of the giant haemoglobin from <i>Glossoscolex paulistus</i> at 3.2 Å. Journal of Synchrotron Radiation, 2011, 18, 24-28.	2.4	22
45	The Crystal Complex of Phosphofructokinase-2 of Escherichia coli with Fructose-6-phosphate. Journal of Biological Chemistry, 2011, 286, 5774-5783.	3.4	26
46	Adenosine binding to low-molecular-weight purine nucleoside phosphorylase: the structural basis for recognition based on its complex with the enzyme from <i>Schistosoma mansoni</i> . Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 73-79.	2.5	20
47	A Draft of the Human Septin Interactome. PLoS ONE, 2010, 5, e13799.	2.5	78
48	Molecular determinants of improved cathepsin B inhibition by new cystatins obtained by DNA shuffling. BMC Structural Biology, 2010, 10, 30.	2.3	6
49	Crystal structure of <i>Schistosoma</i> purine nucleoside phosphorylase complexed with a novel monocyclic inhibitor. Acta Tropica, 2010, 114, 97-102.	2.0	19
50	The CATH classification revisited—architectures reviewed and new ways to characterize structural divergence in superfamilies. Nucleic Acids Research, 2009, 37, D310-D314.	14.5	174
51	The CATH Hierarchy Revisited—Structural Divergence in Domain Superfamilies and the Continuity of Fold Space. Structure, 2009, 17, 1051-1062.	3.3	58
52	Systematic structural studies of iron superoxide dismutases from human parasites and a statistical coupling analysis of metal binding specificity. Proteins: Structure, Function and Bioinformatics, 2009, 77, 26-37.	2.6	35
53	Role of Halogen Bonds in Thyroid Hormone Receptor Selectivity: Pharmacophore-Based 3D-QSSR Studies. Journal of Chemical Information and Modeling, 2009, 49, 2606-2616.	5.4	43
54	The stability and aggregation properties of the GTPase domain from human SEPT4. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1720-1727.	2.3	10

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55	Structural modeling and mutational analysis of yeast eukaryotic translation initiation factor 5A reveal new critical residues and reinforce its involvement in protein synthesis. FEBS Journal, 2008, 275, 1874-1888.	4.7	29
56	Ligand induced interaction of thyroid hormone receptor beta with its coregulators. Journal of Steroid Biochemistry and Molecular Biology, 2008, 112, 205-212.	2.5	16
57	Crystallographic Structure of Phosphofructokinase-2 from Escherichia coli in Complex with Two ATP Molecules. Implications for Substrate Inhibition. Journal of Molecular Biology, 2008, 383, 588-602.	4.2	26
58	The three-dimensional structure of bothropasin, the main hemorrhagic factor from Bothrops jararaca venom: Insights for a new classification of snake venom metalloprotease subgroups. Toxicon, 2008, 52, 807-816.	1.6	59
59	Two- and Three-Dimensional Quantitative Structure-Activity Relationships Studies on a Series of Liver X Receptor Ligands. Open Medicinal Chemistry Journal, 2008, 2, 87-96.	2.4	10
60	Ajulemic Acid, a Synthetic Nonpsychoactive Cannabinoid Acid, Bound to the Ligand Binding Domain of the Human Peroxisome Proliferator-activated Receptor β . Journal of Biological Chemistry, 2007, 282, 18625-18633.	3.4	58
61	Crystal structure of calf spleen purine nucleoside phosphorylase complexed to a novel purine analogue. FEBS Letters, 2007, 581, 5082-5086.	2.8	10
62	An Intermediate Structure in the Thermal Unfolding of the GTPase Domain of Human Septin 4 (SEPT4/Bradeion-1 ²) Forms Amyloid-like Filaments in Vitro. Biochemistry, 2007, 46, 11101-11109.	2.5	30
63	2D QSAR studies on thyroid hormone receptor ligands. Bioorganic and Medicinal Chemistry, 2007, 15, 4609-4617.	3.0	19
64	3D QSAR comparative molecular field analysis on nonsteroidal farnesoid X receptor activators. Journal of Molecular Graphics and Modelling, 2007, 25, 921-927.	2.4	31
65	Structural flexibility in <i>Trypanosoma brucei</i> enolase revealed by X-ray crystallography and molecular dynamics. FEBS Journal, 2007, 274, 5077-5089.	4.7	41
66	Dissection of a Human Septin: Definition and Characterization of Distinct Domains within Human SEPT4. Biochemistry, 2006, 45, 13918-13931.	2.5	36
67	Structural Rearrangements in the Thyroid Hormone Receptor Hinge Domain and Their Putative Role in the Receptor Function. Journal of Molecular Biology, 2006, 360, 586-598.	4.2	106
68	GMOs: building the future on the basis of past experience. Anais Da Academia Brasileira De Ciencias, 2006, 78, 667-686.	0.8	8
69	Crystallization and preliminary crystallographic analysis of the tetrameric form of phosphofructokinase-2 from Escherichia coli, a member of the ribokinase family. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 935-937.	0.7	2
70	Expression of Foreign Protein Epitopes at the Surface of Recombinant Yellow Fever 17D Viruses Based on Three-Dimensional Modeling of Its Envelope Protein. Cell Biochemistry and Biophysics, 2006, 44, 313-324.	1.8	14
71	Hologram QSAR Studies on Farnesoid X Receptor Activators. Letters in Drug Design and Discovery, 2006, 3, 261-267.	0.7	8
72	Solution structure of human proinsulin C-peptide. FEBS Journal, 2005, 272, 4284-4293.	4.7	29

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73	In vitro monitoring of GTPase activity and enzyme kinetics studies using capillary electrophoresis. <i>Analytical and Bioanalytical Chemistry</i> , 2005, 383, 92-97.	3.7	15
74	Hologram quantitative structure-activity relationships for a series of farnesoid X receptor activators. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2005, 15, 3119-3125.	2.2	48
75	Getting the most out of X-ray home sources. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1022-1030.	2.5	6
76	Crystallization and preliminary X-ray analysis of a novel Kunitz-type kallikrein inhibitor from <i>Bauhinia bauhinioides</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 910-913.	0.7	4
77	A Molecular Mechanism for Lys49-Phospholipase A2 Activity Based on Ligand-induced Conformational Change. <i>Journal of Biological Chemistry</i> , 2005, 280, 7326-7335.	3.4	66
78	Attenuation of Recombinant Yellow Fever 17D Viruses Expressing Foreign Protein Epitopes at the Surface. <i>Journal of Virology</i> , 2005, 79, 8602-8613.	3.4	20
79	Structures for the Potential Drug Target Purine Nucleoside Phosphorylase from <i>Schistosoma mansoni</i> Causal Agent of Schistosomiasis. <i>Journal of Molecular Biology</i> , 2005, 353, 584-599.	4.2	32
80	Structure of the cytosolic Cu,Zn superoxide dismutase from <i>Schistosoma mansoni</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1569-1578.	2.5	22
81	Overexpression, purification, biochemical characterization, and molecular modeling of recombinant GDP-mannosyltransferase (GumH) from <i>Xylella fastidiosa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 315, 485-492.	2.1	11
82	Fatty acid synthesis in <i>Xylella fastidiosa</i> : correlations between genome studies, ¹³ C NMR data, and molecular models. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 987-995.	2.1	10
83	Crystal Structures of ¹² I-Galactosidase from <i>Penicillium</i> sp. and its Complex with Galactose. <i>Journal of Molecular Biology</i> , 2004, 343, 1281-1292.	4.2	83
84	Kinetic characterization, structure modelling studies and crystallization of <i>Trypanosoma brucei</i> enolase. <i>FEBS Journal</i> , 2003, 270, 3205-3213.	0.2	64
85	Cloning, expression and preliminary crystallographic studies of the potential drug target purine nucleoside phosphorylase from <i>Schistosoma mansoni</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1096-1099.	2.5	25
86	The Crystal Structure of <i>Trypanosoma brucei</i> Enolase: Visualisation of the Inhibitory Metal Binding Site III and Potential as Target for Selective, Irreversible Inhibition. <i>Journal of Molecular Biology</i> , 2003, 331, 653-665.	4.2	34
87	An experimental bivalent peptide vaccine against schistosomiasis and fascioliasis. <i>Vaccine</i> , 2003, 22, 137-144.	3.8	37
88	Domain Motions and Quaternary Packing of Phosphofructokinase-2 from <i>Escherichia coli</i> Studied by Small Angle X-ray Scattering and Homology Modeling. <i>Journal of Biological Chemistry</i> , 2003, 278, 12913-12919.	3.4	13
89	Structural and Functional Analyses of DM43, a Snake Venom Metalloproteinase Inhibitor from <i>Didelphis marsupialis</i> Serum. <i>Journal of Biological Chemistry</i> , 2002, 277, 13129-13137.	3.4	58
90	Surface expression of an immunodominant malaria protein B cell epitope by yellow fever virus 1 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2002, 315, 873-885.	4.2	40

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91	Fluorescence properties of tryptophan residues in the monomeric d-chain of <i>Glossoscolex paulistus</i> hemoglobin: an interpretation based on a comparative molecular model. <i>Biophysical Chemistry</i> , 2002, 97, 139-157.	2.8	28
92	A novel method for rapid production and purification of exfoliative toxin A of <i>Staphylococcus aureus</i> . <i>FEMS Microbiology Letters</i> , 2002, 212, 35-39.	1.8	32
93	Structural Basis for Low Catalytic Activity in Lys49 Phospholipases A2A Hypothesis: The Crystal Structure of Piratoxin II Complexed to Fatty Acid. <i>Biochemistry</i> , 2001, 40, 28-36.	2.5	84
94	Crystallization and preliminary crystallographic studies of a phospholipase A2 from the venom of the Brazilian snake <i>Bothrops moojeni</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 599-601.	2.5	4
95	Preliminary crystallographic studies of EcTI, a serine proteinase inhibitor from <i>Enterolobium contortisiliquum</i> seeds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 602-604.	2.5	16
96	Crystallization and preliminary X-ray analysis of jararhagin, a metalloproteinase/disintegrin from <i>Bothrops jaraca</i> snake venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1135-1137.	2.5	7
97	Expression and preliminary X-ray diffraction studies of cytosolic Cu,Zn superoxide dismutase from <i>Schistosoma mansoni</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1877-1880.	2.5	1
98	Development and Evaluation of Detection Systems for Staphylococcal Exfoliative Toxin A Responsible for Scalded-Skin Syndrome. <i>Journal of Clinical Microbiology</i> , 2001, 39, 2050-2054.	3.9	56
99	Identification of free fatty acids in maize protein bodies and purified β -zeins by ^{13}C and ^1H nuclear magnetic resonance. <i>BBA - Proteins and Proteomics</i> , 2000, 1543, 106-114.	2.1	26
100	Influence of the Histidine Tail on the Structure and Activity of Recombinant Chlorocatechol 1,2-Dioxygenase. <i>Biochemical and Biophysical Research Communications</i> , 2000, 272, 480-484.	2.1	27
101	Determination of the three-dimensional structure of toxins by protein crystallography. <i>Toxicon</i> , 2000, 38, 1307-1353.	1.6	5
102	The allosteric transition of glucosamine-6-phosphate deaminase: the structure of the T state at 2.3 Å resolution. <i>Structure</i> , 1999, 7, 527-537.	3.3	40
103	Isolation and Structural Characterization of a Cytotoxic L-Amino Acid Oxidase from <i>Agkistrodon contortrix laticinctus</i> Snake Venom: Preliminary Crystallographic Data. <i>Archives of Biochemistry and Biophysics</i> , 1999, 368, 285-290.	3.0	85
104	KM+, a mannose-binding lectin from <i>Artocarpus integrifolia</i> : Amino acid sequence, predicted tertiary structure, carbohydrate recognition, and analysis of the β -prism fold. <i>Protein Science</i> , 1999, 8, 13-24.	7.6	68
105	The reconstruction of atomic co-ordinates from a protein stereo ribbon diagram when additional information for sufficient sidechain positions is available. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 12, 605-614.		1
106	A molecular model for the d chain of the giant haemoglobin from <i>Lumbricus terrestris</i> and its implications for subunit assembly. <i>BBA - Proteins and Proteomics</i> , 1998, 1383, 130-142.	2.1	12
107	Crystallographic and spectroscopic characterization of a molecular hinge: Conformational changes in bothropstoxin I, a dimeric Lys49-phospholipase A2 homologue. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 30, 442-454.		91
108	Reduction of ortho-aminobenzoyl-proline fluorescence and formation of pyrrolobenzodiazepine-5,11-dione. <i>International Journal of Peptide Research and Therapeutics</i> , 1998, 5, 19-28.	0.1	2

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109	Set-up and Experimental Parameters of the Protein Crystallography Beamline at the Brazilian National Synchrotron Laboratory. <i>Journal of Synchrotron Radiation</i> , 1998, 5, 72-76.	2.4	62
110	Trypanosoma cruzi glycosomal glyceraldehyde-3-phosphate dehydrogenase: structure, catalytic mechanism and targeted inhibitor design. <i>FEBS Letters</i> , 1998, 424, 131-135.	2.8	80
111	Characterization of a Schistosoma mansoni gene encoding a homologue of the Y-box binding protein. <i>Gene</i> , 1997, 198, 5-16.	2.2	22
112	Plural Origins of Molecular Homochirality in Our Biota Part II. The Relative Stabilities of Homochiral and Mixed Oligoribotides and Peptides. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 1997, 52, 89-96.	1.4	7
113	Crystallization and preliminary crystallographic studies of calgranulin C, an S100-like calcium-binding protein from pig granulocytes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 200-202.	2.5	4
114	Crystallization and preliminary crystallographic data of a neutrophil migration-inducing lectin (KM+) extracted from the seed of <i>Artocarpus integrifolia</i> . , 1997, 27, 157-159.		4
115	A Schistosoma mansoni fatty acid-binding protein, Sm14, is the potential basis of a dual-purpose anti-helminth vaccine.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 269-273.	7.1	213
116	Novel features of serine protease active sites and specificity pockets: sequence analysis and modelling studies of glutamate-specific endopeptidases and epidermolytic toxins. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 591-601.	2.1	35
117	Structure and catalytic mechanism of glucosamine 6-phosphate deaminase from <i>Escherichia coli</i> at 2.1 Å resolution. <i>Structure</i> , 1995, 3, 1323-1332.	3.3	84
118	Characterization and Structural Analysis of a Functional Human Serum Transferrin Variant and Implications for Receptor Recognition. <i>Biochemistry</i> , 1994, 33, 12512-12520.	2.5	28
119	Studies of the zein-like β -prolamins based on an analysis of amino acid sequences: Implications for their evolution and three-dimensional structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 88-99.	2.6	48
120	A structural model for the glutamate-specific endopeptidase from <i>Streptomyces griseus</i> that explains substrate specificity. <i>FEBS Letters</i> , 1993, 324, 45-50.	2.8	5
121	A molecular model for the tumour-associated antigen, p97, suggests a Zn-binding function. <i>FEBS Letters</i> , 1992, 305, 55-61.	2.8	16
122	Crystallization and preliminary crystallographic studies of glucosamine-6-phosphate deaminase from <i>Escherichia coli</i> K12. <i>Journal of Molecular Biology</i> , 1992, 226, 1283-1286.	4.2	10
123	An extension of secondary structure prediction towards the production of tertiary structure. <i>FEBS Letters</i> , 1991, 280, 141-146.	2.8	14
124	High-resolution X-ray studies on rabbit serum transferrin: preliminary structure analysis of the N-terminal half-molecule at 2.3 Å... resolution. <i>Acta Crystallographica Section B: Structural Science</i> , 1990, 46, 763-771.	1.8	76
125	The epidermolytic toxins are serine proteases. <i>FEBS Letters</i> , 1990, 268, 129-132.	2.8	88
126	Molecular structure of serum transferrin at 3.3-Å resolution. <i>Biochemistry</i> , 1988, 27, 5804-5812.	2.5	413

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127	Structural studies on transferrins: the anion-binding sites. Biochemical Society Transactions, 1988, 16, 825-826.	3.4	1
128	Characterization of the amino acid change in a transferrin variant. Biochemical Society Transactions, 1988, 16, 834-835.	3.4	9
129	Transferrin: a study of the iron-binding sites using extended X-ray absorption fine structure and anomalous dispersion techniques. Biochemical Society Transactions, 1986, 14, 542-545.	3.4	1
130	The influence of tertiary structure on secondary structure prediction. FEBS Letters, 1985, 188, 59-62.	2.8	20
131	Abnormal in vitro function of a variant human transferrin. British Journal of Haematology, 1984, 56, 581-587.	2.5	17
132	Effect of cis-9, trans-11 Conjugated Linoleic Acid (CLA) on the Metabolism Profile of Breast Cancer Cells Determined by ¹ H HR-MAS NMR Spectroscopy. Journal of the Brazilian Chemical Society, 0, , .	0.6	2