

Maurizio Brunori

List of Publications by Year in descending order

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428
papers

15,367
citations

13068

68
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38300

95
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435
all docs

435
docs citations

435
times ranked

8466
citing authors

#	ARTICLE	IF	CITATIONS
1	Eraldo Antonini Lectures, 1983â€“2019. <i>Biology Direct</i> , 2022, 17, .	1.9	0
2	Still quoted after half a century. <i>Molecular Aspects of Medicine</i> , 2021, , 100989.	2.7	0
3	From Kuru to Alzheimer: A personal outlook. <i>Protein Science</i> , 2021, 30, 1776-1792.	3.1	7
4	Hidden kinetic traps in multidomain folding highlight the presence of a misfolded but functionally competent intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19963-19969.	3.3	16
5	Takashi Yonetani: A stellar biochemist, a man with dignity. The Roman connection. <i>IUBMB Life</i> , 2020, 72, 1839-1842.	1.5	0
6	Templated folding of intrinsically disordered proteins. <i>Journal of Biological Chemistry</i> , 2020, 295, 6586-6593.	1.6	44
7	Control of Oxygen Affinity in Mammalian Hemoglobins: Implications for a System Biology Description of the Respiratory Properties of the Red Blood Cell. <i>Current Protein and Peptide Science</i> , 2020, 21, 553-572.	0.7	5
8	Ligand pathways in neuroglobin revealed by low-temperature photodissociation and docking experiments. <i>IUCr</i> , 2019, 6, 832-842.	1.0	8
9	How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. <i>Biophysical Journal</i> , 2018, 114, 1889-1894.	0.2	39
10	Mechanism of Folding and Binding of the N-Terminal SH2 Domain from SHP2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11108-11114.	1.2	19
11	A Carboxylate to Amide Substitution That Switches Protein Folds. <i>Angewandte Chemie</i> , 2018, 130, 12977-12980.	1.6	0
12	A Carboxylate to Amide Substitution That Switches Protein Folds. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 12795-12798.	7.2	4
13	Folding Mechanism of the SH3 Domain from Grb2. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11166-11173.	1.2	9
14	The Folding Pathway of the KIX Domain. <i>ACS Chemical Biology</i> , 2017, 12, 1683-1690.	1.6	6
15	Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. <i>Biochemistry</i> , 2017, 56, 3780-3786.	1.2	28
16	Towards a structural biology of the hydrophobic effect in protein folding. <i>Scientific Reports</i> , 2016, 6, 28285.	1.6	91
17	Molecular medicine â€“ To be or not to be. <i>Biophysical Chemistry</i> , 2016, 214-215, 33-46.	1.5	4
18	A molecule for all seasons: The heme. <i>Journal of Porphyrins and Phthalocyanines</i> , 2016, 20, 134-149.	0.4	22

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19	Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 10886-10892.	1.6	18
20	Neuroglobin: From structure to function in health and disease. <i>Molecular Aspects of Medicine</i> , 2016, 52, 1-48.	2.7	91
21	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. <i>Scientific Reports</i> , 2016, 6, 21994.	1.6	87
22	Frustration Sculptures the Early Stages of Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10867-10869.	7.2	11
23	Half a Century of Hemoglobin's Allostery. <i>Biophysical Journal</i> , 2015, 109, 1077-1079.	0.2	7
24	Variations on the theme: allosteric control in hemoglobin. <i>FEBS Journal</i> , 2014, 281, 633-643.	2.2	14
25	The mechanism of binding of the KIX domain to the mixed lineage leukemia protein and its allosteric role in the recognition of c-Myb. <i>Protein Science</i> , 2014, 23, 962-969.	3.1	38
26	The kinetics of folding of frataxin. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6391.	1.3	17
27	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14141-14146.	3.3	43
28	The centennial of X-ray diffraction (1912-2012). <i>Rendiconti Lincei</i> , 2013, 24, 1-5.	1.0	1
29	Hemoglobin Allostery: New Views on Old Players. <i>Journal of Molecular Biology</i> , 2013, 425, 1515-1526.	2.0	12
30	The Mitochondrial Italian Human Proteome Project Initiative (mt-HPP). <i>Molecular BioSystems</i> , 2013, 9, 1984-92.	2.9	10
31	The folding pathway of a functionally competent C-terminal domain of nucleophosmin: Protein stability and denatured state residual structure. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 64-68.	1.0	7
32	Structure of the transition state for the binding of c-Myb and KIX highlights an unexpected order for a disordered system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14942-14947.	3.3	99
33	Structure of Nucleophosmin DNA-binding Domain and Analysis of Its Complex with a G-quadruplex Sequence from the c-MYC Promoter. <i>Journal of Biological Chemistry</i> , 2012, 287, 26539-26548.	1.6	54
34	The Monod-Wyman-Changeux allosteric model accounts for the quaternary transition dynamics in wild type and a recombinant mutant human hemoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14894-14899.	3.3	33
35	The BOHR effect before Perutz. <i>Biochemistry and Molecular Biology Education</i> , 2012, 40, 297-299.	0.5	3
36	Reassessing the folding of the KIX domain: Evidence for a two-state mechanism. <i>Protein Science</i> , 2012, 21, 1775-1779.	3.1	2

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37	Crystal structure of Plasmodium falciparum thioredoxin reductase, a validated drug target. Biochemical and Biophysical Research Communications, 2012, 425, 806-811.	1.0	25
38	Morphogenesis of a protein: folding pathways and the energy landscape ¹ . Biochemical Society Transactions, 2012, 40, 429-432.	1.6	10
39	A folding-after-binding mechanism describes the recognition between the transactivation domain of c-Myb and the KIX domain of the CREB-binding protein. Biochemical and Biophysical Research Communications, 2012, 428, 205-209.	1.0	71
40	Folding pathways of proteins with increasing degree of sequence identities but different structure and function. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17772-17776.	3.3	25
41	Moonlighting by Different Stressors: Crystal Structure of the Chaperone Species of a 2-Cys Peroxiredoxin. Structure, 2012, 20, 429-439.	1.6	102
42	On the mechanism and rate of gold incorporation into thiol-dependent flavoreductases. Journal of Inorganic Biochemistry, 2012, 108, 105-111.	1.5	48
43	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. Biophysical Journal, 2011, 101, 2053-2060.	0.2	29
44	Observation of fast release of NO from ferrous heme allows formulation of a unified reaction mechanism for cytochrome c heme nitrite reductases. Biochemical Journal, 2011, 435, 217-225.	1.7	28
45	Hemoglobin allostery: Variations on the theme. Biochimica Et Biophysica Acta - Bioenergetics, 2011, 1807, 1262-1272.	0.5	31
46	Allosteric cooperativity in respiratory proteins. Biochimica Et Biophysica Acta - Bioenergetics, 2011, 1807, 1251-1252.	0.5	2
47	Neuroglobin-prion protein interaction: what's the function?. Journal of Peptide Science, 2011, 17, 387-391.	0.8	14
48	Structural and functional characterization of Schistosoma mansoni Thioredoxin. Protein Science, 2011, 20, 1069-1076.	3.1	23
49	Allostery turns 50: Is the vintage yet attractive?. Protein Science, 2011, 20, 1097-1099.	3.1	8
50	Macromolecular Bases of Antischistosomal Therapy. Current Topics in Medicinal Chemistry, 2011, 11, 2012-2028.	1.0	19
51	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. Journal of Biological Chemistry, 2011, 286, 3863-3872.	1.6	37
52	Sequence-specific Long Range Networks in PSD-95/Discs Large/ZO-1 (PDZ) Domains Tune Their Binding Selectivity. Journal of Biological Chemistry, 2011, 286, 27167-27175.	1.6	62
53	1960 Annus mirabilis: the birth of structural biology. Rendiconti Lincei, 2010, 21, 335-342.	1.0	2
54	Myoglobin strikes back. Protein Science, 2010, 19, 195-201.	3.1	35

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55	Combining crystallography and molecular dynamics: The case of <i>Schistosoma mansoni</i> phospholipid glutathione peroxidase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 259-270.	1.5	30
56	Structural and functional characterization of CcmG from <i>Pseudomonas aeruginosa</i> , a key component of the bacterial cytochrome c maturation apparatus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2213-2221.	1.5	19
57	Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1431-1437.	3.6	53
58	Deciphering the folding transition state structure and denatured state properties of Nucleophosmin C-terminal domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5447-5452.	3.3	33
59	Mapping the Catalytic Cycle of <i>Schistosoma mansoni</i> Thioredoxin Glutathione Reductase by X-ray Crystallography. <i>Journal of Biological Chemistry</i> , 2010, 285, 32557-32567.	1.6	63
60	Nucleophosmin C-terminal Leukemia-associated Domain Interacts with G-rich Quadruplex Forming DNA. <i>Journal of Biological Chemistry</i> , 2010, 285, 37138-37149.	1.6	54
61	The Folding Mechanism of c-Type Cytochromes. , 2010, , 13-36.		0
62	Inhibition of <i>Schistosoma mansoni</i> Thioredoxin-glutathione Reductase by Auranofin. <i>Journal of Biological Chemistry</i> , 2009, 284, 28977-28985.	1.6	184
63	Folding mechanism of the C-terminal domain of nucleophosmin: residual structure in the denatured state and its pathophysiological significance. <i>FASEB Journal</i> , 2009, 23, 2360-2365.	0.2	31
64	Pattern of cavities in globins: The case of human hemoglobin. <i>Biopolymers</i> , 2009, 91, 1097-1107.	1.2	57
65	Nitrite reduction: a ubiquitous function from a pre-aerobic past. <i>BioEssays</i> , 2009, 31, 885-891.	1.2	13
66	Distinguishing between Smooth and Rough Free Energy Barriers in Protein Folding. <i>Biochemistry</i> , 2009, 48, 11825-11830.	1.2	10
67	Failure of apoptosis-inducing factor to act as neuroglobin reductase. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 121-124.	1.0	13
68	Intramolecular Electron Transfer in <i>Pseudomonas aeruginosa</i> cd1 Nitrite Reductase: Thermodynamics and Kinetics. <i>Biophysical Journal</i> , 2009, 96, 2849-2856.	0.2	29
69	The Structure of Neuroglobin at High Xe and Kr Pressure Reveals Partial Conservation of Globin Internal Cavities. <i>Biophysical Journal</i> , 2009, 97, 1700-1708.	0.2	32
70	Engineered Symmetric Connectivity of Secondary Structure Elements Highlights Malleability of Protein Folding Pathways. <i>Journal of the American Chemical Society</i> , 2009, 131, 11727-11733.	6.6	25
71	Mechanisms of protein folding. <i>European Biophysics Journal</i> , 2008, 37, 721-728.	1.2	20
72	Glutathione reductase and thioredoxin reductase at the crossroad: The structure of <i>Schistosoma mansoni</i> thioredoxin glutathione reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 936-945.	1.5	63

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73	Is neuroglobin a signal transducer?. IUBMB Life, 2008, 60, 410-413.	1.5	13
74	Fast folding kinetics and stabilization of apo-cytochrome c. FEBS Letters, 2008, 582, 1003-1007.	1.3	7
75	Molecular Dynamics Simulation of the Neuroglobin Crystal: Comparison with the Simulation in Solution. Biophysical Journal, 2008, 95, 4157-4162.	0.2	26
76	Kinetic Characterization of the Escherichia coli Nitric Oxide Reductase Flavorubredoxin. Methods in Enzymology, 2008, 437, 47-62.	0.4	10
77	NO sensing in Pseudomonas aeruginosa: Structure of the Transcriptional Regulator DNR. Journal of Molecular Biology, 2008, 378, 1002-1015.	2.0	80
78	An X-ray diffraction and X-ray absorption spectroscopy joint study of neuroglobin. Archives of Biochemistry and Biophysics, 2008, 475, 7-13.	1.4	50
79	Neuroglobin: Enzymatic reduction and oxygen affinity. Biochemical and Biophysical Research Communications, 2008, 367, 893-898.	1.0	43
80	Ancient hemes for ancient catalysts. Plant Signaling and Behavior, 2008, 3, 135-136.	1.2	9
81	The O ₂ -scavenging Flavodiiron Protein in the Human Parasite Giardia intestinalis. Journal of Biological Chemistry, 2008, 283, 4061-4068.	1.6	107
82	Folding and Misfolding in a Naturally Occurring Circularly Permuted PDZ Domain. Journal of Biological Chemistry, 2008, 283, 8954-8960.	1.6	25
83	The folding pathway of an engineered circularly permuted PDZ domain. Protein Engineering, Design and Selection, 2008, 21, 155-160.	1.0	20
84	New insights into the activity of Pseudomonas aeruginosa cd1 nitrite reductase. Biochemical Society Transactions, 2008, 36, 1155-1159.	1.6	17
85	Myoglobin Strikes Back. , 2008, , 183-189.		0
86	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	1.6	42
87	The Three-dimensional Structure of Two Redox States of Cyclophilin A from Schistosoma mansoni. Journal of Biological Chemistry, 2007, 282, 24851-24857.	1.6	29
88	Fast Dissociation of Nitric Oxide from Ferrous Pseudomonas aeruginosa cd1 Nitrite Reductase. Journal of Biological Chemistry, 2007, 282, 14761-14767.	1.6	46
89	A Strategic Protein in Cytochrome c Maturation. Journal of Biological Chemistry, 2007, 282, 27012-27019.	1.6	35
90	Plasticity of the protein folding landscape: Switching between on- and off-pathway intermediates. Archives of Biochemistry and Biophysics, 2007, 466, 172-176.	1.4	5

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91	Redox control of fast ligand dissociation from Escherichia coli cytochrome bd. Biochemical and Biophysical Research Communications, 2007, 355, 97-102.	1.0	79
92	Nitrite controls the release of nitric oxide in Pseudomonas aeruginosa cd1 nitrite reductase. Biochemical and Biophysical Research Communications, 2007, 363, 662-666.	1.0	20
93	Time-resolved methods in biophysics. 6. Time-resolved Laue crystallography as a tool to investigate photo-activated protein dynamics. Photochemical and Photobiological Sciences, 2007, 6, 1047-1056.	1.6	42
94	A PDZ domain recapitulates a unifying mechanism for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 128-133.	3.3	69
95	Molecular Dynamics Simulation of Deoxy and Carboxy Murine Neuroglobin in Water. Biophysical Journal, 2007, 93, 434-441.	0.2	42
96	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	1.5	69
97	Kinetics of electron transfer from NADH to the Escherichia coli nitric oxide reductase flavorubredoxin. FEBS Journal, 2007, 274, 677-686.	2.2	15
98	Neuroglobin, seven years after. Cellular and Molecular Life Sciences, 2007, 64, 1259-1268.	2.4	94
99	Nitric oxide reacts with the ferryl-oxo catalytic intermediate of the CuB-lacking cytochrome bd terminal oxidase. FEBS Letters, 2006, 580, 4823-4826.	1.3	46
100	Nitric oxide and the respiratory enzyme. Biochimica Et Biophysica Acta - Bioenergetics, 2006, 1757, 1144-1154.	0.5	66
101	Probing the Mechanism of GSH Activation in Schistosoma haematobium Glutathione-S-transferase by Site-directed Mutagenesis and X-ray Crystallography. Journal of Molecular Biology, 2006, 360, 678-689.	2.0	20
102	The Structural and Functional Properties of Hemoglobin and their Relevance for a Hemoglobin-Based Blood Substitute. , 2006, , 327-340.		1
103	Large-scale purification and crystallization of the endoribonuclease XendoU: troubleshooting with His-tagged proteins. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 298-301.	0.7	19
104	Critical role of His369 in the reactivity of Pseudomonas aeruginosa cytochrome cd1 nitrite reductase with oxygen. FEBS Journal, 2006, 273, 4495-4503.	2.2	3
105	Hemoglobin is an honorary enzyme. Rendiconti Lincei, 2006, 17, 51-58.	1.0	0
106	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	1.6	103
107	The Allosteric Properties of Hemoglobin: Insights from Natural and Site Directed Mutants. Current Protein and Peptide Science, 2006, 7, 17-45.	0.7	46
108	Unveiling a Hidden Folding Intermediate in c-Type Cytochromes by Protein Engineering. Journal of Biological Chemistry, 2006, 281, 9331-9336.	1.6	29

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109	A globin for the brain. <i>FASEB Journal</i> , 2006, 20, 2192-2197.	0.2	87
110	Extended subnanosecond structural dynamics of myoglobin revealed by Laue crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4924-4929.	3.3	111
111	The structure of the endoribonuclease XendoU: From small nucleolar RNA processing to severe acute respiratory syndrome coronavirus replication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12365-12370.	3.3	51
112	Insights into the Catalytic Mechanism of Glutathione S-Transferase: The Lesson from <i>Schistosoma haematobium</i> . <i>Structure</i> , 2005, 13, 1241-1246.	1.6	46
113	Cytochrome oxidase, ligands and electrons. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 324-336.	1.5	119
114	An Obligatory Intermediate in the Folding Pathway of Cytochrome c552 from <i>Hydrogenobacter thermophilus</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25729-25734.	1.6	68
115	Neuroglobin, nitric oxide, and oxygen: Functional pathways and conformational changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8483-8488.	3.3	233
116	Kinetic folding mechanism of PDZ2 from PTP-BL. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 389-395.	1.0	50
117	Nitric oxide, cytochrome oxidase and myoglobin: Competition and reaction pathways. <i>FEBS Letters</i> , 2005, 579, 2528-2532.	1.3	34
118	Molecular Dynamics Simulation of Sperm Whale Myoglobin: Effects of Mutations and Trapped CO on the Structure and Dynamics of Cavities. <i>Biophysical Journal</i> , 2005, 89, 465-474.	0.2	93
119	¹ H-NMR Study of the Effect of Temperature through Reversible Unfolding on the Heme Pocket Molecular Structure and Magnetic Properties of <i>Aplysia limacina</i> Cyano-Metmyoglobin. <i>Biophysical Journal</i> , 2005, 89, 4149-4158.	0.2	7
120	The structure of carbon monoxide neuroglobin reveals a heme-sliding mechanism for control of ligand affinity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17351-17356.	3.3	182
121	A common folding mechanism in the cytochrome family. <i>Trends in Biochemical Sciences</i> , 2004, 29, 535-541.	3.7	48
122	NO Production by <i>Pseudomonas aeruginosa</i> cd1 Nitrite Reductase. <i>IUBMB Life</i> , 2004, 55, 617-621.	1.5	19
123	Nitric Oxide and Mitochondrial Complex IV. <i>IUBMB Life</i> , 2004, 55, 605-611.	1.5	43
124	The structure of murine neuroglobin: Novel pathways for ligand migration and binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 85-92.	1.5	170
125	Structural dynamics of myoglobin: an infrared kinetic study of ligand migration in mutants YQR and YQRF. <i>Biophysical Chemistry</i> , 2004, 109, 41-58.	1.5	16
126	Proton Uptake upon Anaerobic Reduction of the <i>Paracoccus denitrificans</i> Cytochrome c Oxidase: A Kinetic Investigation of the K354M and D124N Mutants. <i>Biochemistry</i> , 2004, 43, 2957-2963.	1.2	20

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127	Folding of Aplysia limacina Apomyoglobin Involves an Intermediate in Common with Other Evolutionarily Distant Globins. <i>Biochemistry</i> , 2004, 43, 230-236.	1.2	14
128	Schistosoma mansoni Fatty Acid Binding Protein: Specificity and Functional Control as Revealed by Crystallographic Structure. <i>Biochemistry</i> , 2004, 43, 13000-13011.	1.2	29
129	Extended Molecular Dynamics Simulation of the Carbon Monoxide Migration in Sperm Whale Myoglobin. <i>Biophysical Journal</i> , 2004, 86, 3855-3862.	0.2	129
130	Control of cytochrome c oxidase activity by nitric oxide. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004, 1655, 365-371.	0.5	91
131	The structural dynamics of myoglobin. <i>Journal of Structural Biology</i> , 2004, 147, 223-234.	1.3	81
132	Kinetics of NO and O ₂ binding to a maleimide poly(ethylene glycol)-conjugated human haemoglobin. <i>Biochemical Journal</i> , 2004, 382, 183-189.	1.7	38
133	Roles for holes: are cavities in proteins mere packing defects?. <i>Italian Journal of Biochemistry</i> , 2004, 53, 46-52.	0.3	4
134	Nitric oxide and cytochrome oxidase: reaction mechanisms from the enzyme to the cell. <i>Free Radical Biology and Medicine</i> , 2003, 34, 509-520.	1.3	87
135	Construction and characterization of a chimeric myoglobin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1645, 139-145.	1.1	1
136	Analysis of the effect of microgravity on protein crystal quality: the case of a myoglobin triple mutant. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 982-988.	2.5	13
137	Parallel Pathways in Cytochrome c551 Folding. <i>Journal of Molecular Biology</i> , 2003, 330, 1145-1152.	2.0	50
138	Crystal Structure of the 28 kDa Glutathione S-Transferase from Schistosoma haematobium. <i>Biochemistry</i> , 2003, 42, 10084-10094.	1.2	45
139	Exploring the Cytochrome c Folding Mechanism. <i>Journal of Biological Chemistry</i> , 2003, 278, 41136-41140.	1.6	38
140	Complex landscape of protein structural dynamics unveiled by nanosecond Laue crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8704-8709.	3.3	195
141	Structural Dynamics of Myoglobin. <i>Journal of Biological Chemistry</i> , 2002, 277, 11636-11644.	1.6	69
142	Controlling Ligand Binding in Myoglobin by Mutagenesis. <i>Journal of Biological Chemistry</i> , 2002, 277, 7509-7519.	1.6	101
143	Nitric Oxide Reacts with the Single-electron Reduced Active Site of Cytochrome c Oxidase. <i>Journal of Biological Chemistry</i> , 2002, 277, 22402-22406.	1.6	31
144	A Novel Type of Nitric-oxide Reductase. <i>Journal of Biological Chemistry</i> , 2002, 277, 25273-25276.	1.6	176

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145	Redox-Linked Protonation of Cytochrome c Oxidase: The Effect of Chloride Bound to CuB. <i>Biochemistry</i> , 2002, 41, 13046-13052.	1.2	26
146	Cyanide Binding to cd1 Nitrite Reductase from <i>Pseudomonas aeruginosa</i> : Role of the Active-Site His369 in Ligand Stabilization. <i>Biochemical and Biophysical Research Communications</i> , 2002, 291, 1-7.	1.0	19
147	<i>Pseudomonas aeruginosa</i> cytochrome C551: probing the role of the hydrophobic patch in electron transfer. <i>Journal of Inorganic Biochemistry</i> , 2002, 88, 353-361.	1.5	38
148	Cytochrome c551 as a model system for protein folding. <i>Biophysical Chemistry</i> , 2002, 100, 409-419.	1.5	7
149	Cavities and packing defects in the structural dynamics of myoglobin. <i>EMBO Reports</i> , 2001, 2, 674-679.	2.0	165
150	Snapshots of protein folding. A study on the multiple transition state pathway of cytochrome c551 from <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2001, 309, 1177-1187.	2.0	30
151	Domain Swing Upon His to Ala Mutation in Nitrite Reductase of <i>Pseudomonas aeruginosa</i> . <i>Journal of Molecular Biology</i> , 2001, 312, 541-554.	2.0	22
152	Photochemically Induced Electron Transfer. <i>Methods</i> , 2001, 24, 139-152.	1.9	18
153	Does myoglobin protect <i>Trypanosoma cruzi</i> from the antiparasitic effects of nitric oxide? <i>FEBS Letters</i> , 2001, 501, 103-105.	1.3	26
154	Binding of NO and CO to the d1 Heme of cd1 Nitrite Reductase from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 2001, 40, 10774-10781.	1.2	26
155	Control of Heme Reactivity by Diffusion: A Structural Basis and Functional Characterization in Hemoglobin Mutants. <i>Biochemistry</i> , 2001, 40, 14449-14458.	1.2	12
156	The cytochrome cbb 3 from <i>Pseudomonas stutzeri</i> displays nitric oxide reductase activity. <i>FEBS Journal</i> , 2001, 268, 6486-6491.	0.2	110
157	Refolding kinetics of cytochrome c551 reveals a mechanistic difference between urea and guanidine. <i>Protein Science</i> , 2001, 10, 1685-1688.	3.1	23
158	Article Myoglobin: a pseudo-enzymatic scavenger of nitric oxide. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 183-185.	0.5	4
159	Nitric oxide, cytochrome-c oxidase and myoglobin. <i>Trends in Biochemical Sciences</i> , 2001, 26, 21-23.	3.7	186
160	Nitric oxide moves myoglobin centre stage. <i>Trends in Biochemical Sciences</i> , 2001, 26, 209-210.	3.7	207
161	Myoglobin: a pseudo-enzymatic scavenger of nitric oxide. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 183-185.	0.5	7
162	Fast Coordination Changes in Cytochrome c Do Not Necessarily Imply Folding. <i>Journal of Biological Chemistry</i> , 2001, 276, 41073-41078.	1.6	29

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163	Structural dynamics of myoglobin. <i>Biophysical Chemistry</i> , 2000, 86, 221-230.	1.5	73
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