

Carlo Travaglini-Allocatelli

List of Publications by Year in descending order

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2,055
citations

185998

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243296

44
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63
all docs

63
docs citations

63
times ranked

1790
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of cavities in protein dynamics: Crystal structure of a photolytic intermediate of a mutant myoglobin. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 2058-2063.	3.3	143
2	Demonstration of Long-Range Interactions in a PDZ Domain by NMR, Kinetics, and Protein Engineering. Structure, 2006, 14, 1801-1809.	1.6	103
3	Controlling Ligand Binding in Myoglobin by Mutagenesis. Journal of Biological Chemistry, 2002, 277, 7509-7519.	1.6	101
4	The Kinetics of PDZ Domain-Ligand Interactions and Implications for the Binding Mechanism. Journal of Biological Chemistry, 2005, 280, 34805-34812.	1.6	87
5	Structural Dynamics of Ligand Diffusion in the Protein Matrix: A Study on a New Myoglobin Mutant Y(B10) Q(E7) R(E10). Biophysical Journal, 1999, 76, 1259-1269.	0.2	79
6	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
7	Identification and characterization of protein folding intermediates. Biophysical Chemistry, 2007, 128, 105-113.	1.5	69
8	An Obligatory Intermediate in the Folding Pathway of Cytochromec552 from Hydrogenobacterthermophilus. Journal of Biological Chemistry, 2005, 280, 25729-25734.	1.6	68
9	Molecules that target nucleophosmin for cancer treatment: an update. Oncotarget, 2016, 7, 44821-44840.	0.8	63
10	Comparison of successive transition states for folding reveals alternative early folding pathways of two homologous proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19241-19246.	3.3	59
11	Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. Nature Structural and Molecular Biology, 2010, 17, 1431-1437.	3.6	53
12	Parallel Pathways in Cytochrome c551 Folding. Journal of Molecular Biology, 2003, 330, 1145-1152.	2.0	50
13	Kinetic folding mechanism of PDZ2 from PTP-BL. Protein Engineering, Design and Selection, 2005, 18, 389-395.	1.0	50
14	A common folding mechanism in the cytochrome family. Trends in Biochemical Sciences, 2004, 29, 535-541.	3.7	48
15	A conserved folding mechanism for PDZ domains. FEBS Letters, 2007, 581, 1109-1113.	1.3	45
16	An On-pathway Intermediate in the Folding of a PDZ Domain. Journal of Biological Chemistry, 2007, 282, 8568-8572.	1.6	42
17	Interactions among residues CD3, E7, E10, and E11 in myoglobins: Attempts to simulate the ligand-binding properties of Aplysia myoglobin. Biochemistry, 1995, 34, 8715-8725.	1.2	40
18	Control and recognition of anionic ligands in myoglobin. FEBS Letters, 1991, 282, 281-284.	1.3	38

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19	Exploring the Cytochrome c Folding Mechanism. <i>Journal of Biological Chemistry</i> , 2003, 278, 41136-41140.	1.6	38
20	Engineering <i>Ascaris</i> hemoglobin oxygen affinity in sperm whale myoglobin: role of tyrosine B10. <i>FEBS Letters</i> , 1994, 352, 63-66.	1.3	37
21	The Denatured State Dictates the Topology of Two Proteins with Almost Identical Sequence but Different Native Structure and Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 3863-3872.	1.6	37
22	<i>Aplysia limacina</i> myoglobin cDNA cloning: an alternative mechanism of oxygen stabilization as studied by active-site mutagenesis. <i>Biochemical Journal</i> , 1996, 314, 83-90.	1.7	35
23	A Strategic Protein in Cytochrome c Maturation. <i>Journal of Biological Chemistry</i> , 2007, 282, 27012-27019.	1.6	35
24	Structural and functional characterization of sperm whale myoglobin mutants: Role of arginine (E10) in ligand stabilization. <i>Biochemistry</i> , 1993, 32, 6041-6049.	1.2	34
25	Unfolding of apomyoglobin from <i>Aplysia limacina</i> : the effect of salt and ph on the cooperativity of folding 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 275, 133-148.	2.0	33
26	Agitation and High Ionic Strength Induce Amyloidogenesis of a Folded PDZ Domain in Native Conditions. <i>Biophysical Journal</i> , 2009, 96, 2289-2298.	0.2	32
27	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
28	Fast Coordination Changes in Cytochrome c Do Not Necessarily Imply Folding. <i>Journal of Biological Chemistry</i> , 2001, 276, 41073-41078.	1.6	29
29	Unveiling a Hidden Folding Intermediate in c-Type Cytochromes by Protein Engineering. <i>Journal of Biological Chemistry</i> , 2006, 281, 9331-9336.	1.6	29
30	GB1 Is Not a Two-State Folder: Identification and Characterization of an On-Pathway Intermediate. <i>Biophysical Journal</i> , 2011, 101, 2053-2060.	0.2	29
31	Modulation of ligand binding in engineered human hemoglobin distal pocket. <i>Journal of Molecular Biology</i> , 1999, 290, 515-524.	2.0	27
32	Does picosecond protein dynamics have survival value?. <i>Trends in Biochemical Sciences</i> , 1999, 24, 253-255.	3.7	26
33	Folding mechanism of <i>Pseudomonas aeruginosa</i> cytochrome c 551 : role of electrostatic interactions on the hydrophobic collapse and transition state properties 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 289, 1459-1467.	2.0	25
34	Folding and Misfolding in a Naturally Occurring Circularly Permuted PDZ Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 8954-8960.	1.6	25
35	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
36	Folding pathways of proteins with increasing degree of sequence identities but different structure and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17772-17776.	3.3	25

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37	Refolding kinetics of cytochrome c551 reveals a mechanistic difference between urea and guanidine. <i>Protein Science</i> , 2001, 10, 1685-1688.	3.1	23
38	Folding and stability of globular proteins and implications for function. <i>Current Opinion in Structural Biology</i> , 2009, 19, 3-7.	2.6	22
39	Mechanisms of protein folding. <i>European Biophysics Journal</i> , 2008, 37, 721-728.	1.2	20
40	The folding pathway of an engineered circularly permuted PDZ domain. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 155-160.	1.0	20
41	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
42	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
43	Equilibrium unfolding of a small bacterial cytochrome, cytochrome c 551 from <i>Pseudomonas aeruginosa</i> . <i>FEBS Letters</i> , 1998, 425, 385-390.	1.3	17
44	Protein Machineries Involved in the Attachment of Heme to Cytochrome c: Protein Structures and Molecular Mechanisms. <i>Scientifica</i> , 2013, 2013, 1-17.	0.6	16
45	A myoglobin mutant designed to mimic the oxygen-avid <i>Ascaris suum</i> hemoglobin: elucidation of the distal hydrogen bonding network by solution NMR. <i>Biophysical Journal</i> , 1997, 73, 1019-1030.	0.2	15
46	Folding of <i>Aplysia limacina</i> Apomyoglobin Involves an Intermediate in Common with Other Evolutionarily Distant Globins. <i>Biochemistry</i> , 2004, 43, 230-236.	1.2	14
47	The Folding Process of Acylphosphatase from <i>Escherichia coli</i> is Remarkably Accelerated by the Presence of a Disulfide Bond. <i>Journal of Molecular Biology</i> , 2008, 379, 1107-1118.	2.0	14
48	A new folding intermediate of apomyoglobin from <i>Aplysia limacina</i> : stepwise formation of a molten globule. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 297, 1231-1244.	2.0	13
49	Recognition and binding of apocytochrome c to <i>P. aeruginosa</i> CcmI, a component of cytochrome c maturation machinery. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1554-1561.	1.1	13
50	Solution 1H NMR Study of the Influence of Distal Hydrogen Bonding and N Terminus Acetylation on the Active Site Electronic and Molecular Structure of <i>Aplysia limacina</i> Cyanomet Myoglobin. <i>Journal of Biological Chemistry</i> , 2000, 275, 742-751.	1.6	12
51	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
52	Morphogenesis of a protein: folding pathways and the energy landscape. <i>Biochemical Society Transactions</i> , 2012, 40, 429-432.	1.6	10
53	Structural and functional investigation of the Small Ribosomal Subunit Biogenesis GTPase A (RsgA) from <i>Pseudomonas Aeruginosa</i> . <i>FEBS Journal</i> , 2019, 286, 4245-4260.	2.2	9
54	Cytochrome c551 as a model system for protein folding. <i>Biophysical Chemistry</i> , 2002, 100, 409-419.	1.5	7

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55	Fast folding kinetics and stabilization of apo-cytochrome c. FEBS Letters, 2008, 582, 1003-1007.	1.3	7
56	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
57	Engineering His(E7) Affects the Control of Heme Reactivity in Aplysia limacina Myoglobin. Biochemical and Biophysical Research Communications, 2000, 269, 58-63.	1.0	4
58	Conformational states of hemoproteins by XANES: The mutant VR myoglobin. Physica B: Condensed Matter, 1995, 208-209, 743-745.	1.3	3
59	Construction and characterization of a chimeric myoglobin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1645, 139-145.	1.1	1
60	Unveiling the folding mechanism of the Bromodomains. Biochemistry and Biophysics Reports, 2017, 11, 99-104.	0.7	1
61	A Glimpse into the Structural Properties of the Intermediate and Transition State in the Folding of Bromodomain 2 Domain 2 by \hat{I} Value Analysis. International Journal of Molecular Sciences, 2021, 22, 5953.	1.8	1
62	Studies of cytochrome c-551 unfolding using fluorescence correlation spectroscopy and other biophysical techniques. Physical Chemistry Chemical Physics, 2016, 18, 24537-24548.	1.3	0
63	The Folding Mechanism of c-Type Cytochromes. , 2010, , 13-36.		0