

# Maurizio Brunori

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

426  
papers

13,758  
citations

65  
h-index

89  
g-index

435  
ext. papers

14,387  
ext. citations

5.5  
avg, IF

6.05  
L-index

| #   | Paper  | IF      | Citations |
|-----|--|---------|-----------|
| 426 | From Kuru to Alzheimer: A personal outlook. <i>Protein Science</i> , <b>2021</b> , 30, 1776-1792   | 6.3     | 3         |
| 425 | Takashi Yonetani: A stellar biochemist, a man with dignity. The Roman connection. <i>IUBMB Life</i> , <b>2020</b> , 72, 1839-1842  | 4.7     |           |
| 424 | 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> , <b>2020</b> , 21, 553-572                     | 2.8     | 3         |
| 423 | 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> , <b>2020</b> , 117, 19963-19969 | 11.5    | 6         |
| 422 | Templated folding of intrinsically disordered proteins. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 6586-6593  | 5.93    | 27        |
| 421 | Ligand pathways in neuroglobin revealed by low-temperature photodissociation and docking experiments. <i>IUCrJ</i> , <b>2019</b> , 6, 832-842  | 4.7     | 4         |
| 420 | How Robust Is the Mechanism of Folding-Upon-Binding for an Intrinsically Disordered Protein?. <i>Biophysical Journal</i> , <b>2018</b> , 114, 1889-1894  | 2.9     | 27        |
| 419 | Mechanism of Folding and Binding of the N-Terminal SH2 Domain from SHP2. <i>Journal of Physical Chemistry B</i> , <b>2018</b> , 122, 11108-11114   | 3.4     | 12        |
| 418 | A Carboxylate to Amide Substitution That Switches Protein Folds. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 12977-12980   | 16.2980 |           |
| 417 | A Carboxylate to Amide Substitution That Switches Protein Folds. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 12795-12798  | 16.4    | 2         |
| 416 | Folding Mechanism of the SH3 Domain from Grb2. <i>Journal of Physical Chemistry B</i> , <b>2018</b> , 122, 11166-11173   | 3.4     | 6         |
| 415 | The Folding Pathway of the KIX Domain. <i>ACS Chemical Biology</i> , <b>2017</b> , 12, 1683-1690   | 4.9     | 5         |
| 414 | Analyzing the Folding and Binding Steps of an Intrinsically Disordered Protein by Protein Engineering. <i>Biochemistry</i> , <b>2017</b> , 56, 3780-3786   | 3.2     | 22        |
| 413 | Neuroglobin: From structure to function in health and disease. <i>Molecular Aspects of Medicine</i> , <b>2016</b> , 52, 1-48   | 16.7    | 70        |
| 412 | Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. <i>Scientific Reports</i> , <b>2016</b> , 6, 21994  | 4.9     | 77        |
| 411 | Towards a structural biology of the hydrophobic effect in protein folding. <i>Scientific Reports</i> , <b>2016</b> , 6, 28285  | 4.9     | 62        |
| 410 | Molecular medicine - To be or not to be. <i>Biophysical Chemistry</i> , <b>2016</b> , 214-215, 33-46   | 3.5     | 2         |

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| 409 | A molecule for all seasons: The heme. <i>Journal of Porphyrins and Phthalocyanines</i> , <b>2016</b> , 20, 134-149  | 1.8  | 17 |
| 408 | Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 10886-92  | 5.4  | 15 |
| 407 | Half a Century of Hemoglobin's Allostery. <i>Biophysical Journal</i> , <b>2015</b> , 109, 1077-9  | 2.9  | 5  |
| 406 | Hemoglobin <b>2015</b> , 1, 100-139   |      |    |
| 405 | Frustration Sculpts the Early Stages of Protein Folding. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 10867-9   | 16.4 | 10 |
| 404 | Frustration Sculpts the Early Stages of Protein Folding. <i>Angewandte Chemie</i> , <b>2015</b> , 127, 11017-11019  | 3.6  |    |
| 403 | The kinetics of folding of frataxin. <i>Physical Chemistry Chemical Physics</i> , <b>2014</b> , 16, 6391-7  | 3.6  | 15 |
| 402 | 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> , <b>2014</b> , 111, 14141-6 | 11.5 | 36 |
| 401 | Variations on the theme: allosteric control in hemoglobin. <i>FEBS Journal</i> , <b>2014</b> , 281, 633-43  | 5.7  | 11 |
| 400 | 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> , <b>2014</b> , 23, 962-9  | 6.3  | 34 |
| 399 | The centennial of X-ray diffraction (1912-2012). <i>Rendiconti Lincei</i> , <b>2013</b> , 24, 1-5   | 1.7  | 0  |
| 398 | Hemoglobin allostery: new views on old players. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 1515-26  | 6.5  | 9  |
| 397 | The mitochondrial Italian Human Proteome Project initiative (mt-HPP). <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1984-92  |      | 8  |
| 396 | 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> , <b>2013</b> , 435, 64-8                  | 3.4  | 7  |
| 395 | 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> , <b>2013</b> , 110, 14942-7      | 11.5 | 85 |
| 394 | Moonlighting by different stressors: crystal structure of the chaperone species of a 2-Cys peroxiredoxin. <i>Structure</i> , <b>2012</b> , 20, 429-39   | 5.2  | 85 |
| 393 | On the mechanism and rate of gold incorporation into thiol-dependent flavoreductases. <i>Journal of Inorganic Biochemistry</i> , <b>2012</b> , 108, 105-11  | 4.2  | 33 |
| 392 | The Bohr effect before Perutz. <i>Biochemistry and Molecular Biology Education</i> , <b>2012</b> , 40, 297-9  | 1.3  | 2  |

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|-----|---|------|----|
| 391 | Reassessing the folding of the KIX domain: evidence for a two-state mechanism. <i>Protein Science</i> , <b>2012</b> , 21, 1775-9  | 6.3  | 2  |
| 390 | Crystal structure of Plasmodium falciparum thioredoxin reductase, a validated drug target. <i>Biochemical and Biophysical Research Communications</i> , <b>2012</b> , 425, 806-11   | 3.4  | 19 |
| 389 | Morphogenesis of a protein: folding pathways and the energy landscape. <i>Biochemical Society Transactions</i> , <b>2012</b> , 40, 429-32   | 5.1  | 8  |
| 388 | A folding-after-binding mechanism describes the recognition between the transactivation domain of c-Myb and the KIX domain of the CREB-binding protein. <i>Biochemical and Biophysical Research Communications</i> , <b>2012</b> , 428, 205-9                         | 3.4  | 65 |
| 387 | 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> , <b>2012</b> , 109, 17772-6                                  | 11.5 | 25 |
| 386 | 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> , <b>2012</b> , 287, 26539-48  | 5.4  | 43 |
| 385 | 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> , <b>2012</b> , 109, 14894-9 | 11.5 | 28 |
| 384 | GB1 is not a two-state folder: identification and characterization of an on-pathway intermediate. <i>Biophysical Journal</i> , <b>2011</b> , 101, 2053-60   | 2.9  | 25 |
| 383 | Observation of fast release of NO from ferrous dhaem allows formulation of a unified reaction mechanism for cytochrome cdhitrite reductases. <i>Biochemical Journal</i> , <b>2011</b> , 435, 217-25   | 3.8  | 23 |
| 382 | Hemoglobin allostery: variations on the theme. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2011</b> , 1807, 1262-72   | 4.6  | 30 |
| 381 | Neuroglobin-prion protein interaction: what's the function?. <i>Journal of Peptide Science</i> , <b>2011</b> , 17, 387-91   | 2.1  | 14 |
| 380 | Structural and functional characterization of Schistosoma mansoni Thioredoxin. <i>Protein Science</i> , <b>2011</b> , 20, 1069-76   | 6.3  | 20 |
| 379 | Allostery turns 50: is the vintage yet attractive?. <i>Protein Science</i> , <b>2011</b> , 20, 1097-9   | 6.3  | 7  |
| 378 | Macromolecular bases of antischistosomal therapy. <i>Current Topics in Medicinal Chemistry</i> , <b>2011</b> , 11, 2012-28  | 3.28 | 13 |
| 377 | 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> , <b>2011</b> , 286, 3863-72   | 5.4  | 34 |
| 376 | Sequence-specific long range networks in PSD-95/discs large/ZO-1 (PDZ) domains tune their binding selectivity. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 27167-75   | 5.4  | 51 |
| 375 | Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 1431-7   | 17.6 | 46 |
| 374 | 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> , <b>2010</b> , 107, 5447-52                             | 11.5 | 30 |

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|-----|---|------|-----|
| 373 | Mapping the catalytic cycle of <i>Schistosoma mansoni</i> thioredoxin glutathione reductase by X-ray crystallography. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 32557-67  | 5.4  | 49  |
| 372 | Nucleophosmin C-terminal leukemia-associated domain interacts with G-rich quadruplex forming DNA. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 37138-49  | 5.4  | 48  |
| 371 | 1960 Annus mirabilis: the birth of structural biology. <i>Rendiconti Lincei</i> , <b>2010</b> , 21, 335-342   | 1.7  | 1   |
| 370 | Myoglobin strikes back. <i>Protein Science</i> , <b>2010</b> , 19, 195-201  | 6.3  | 29  |
| 369 | Combining crystallography and molecular dynamics: the case of <i>Schistosoma mansoni</i> phospholipid glutathione peroxidase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 259-70                                | 4.2  | 22  |
| 368 | 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> , <b>2010</b> , 78, 2213-21 | 4.2  | 19  |
| 367 | The Folding Mechanism of c-Type Cytochromes <b>2010</b> , 13-36   |      |     |
| 366 | Inhibition of <i>Schistosoma mansoni</i> thioredoxin-glutathione reductase by auranofin: structural and kinetic aspects. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 28977-85   | 5.4  | 149 |
| 365 | Folding mechanism of the C-terminal domain of nucleophosmin: residual structure in the denatured state and its pathophysiological significance. <i>FASEB Journal</i> , <b>2009</b> , 23, 2360-5   | 0.9  | 30  |
| 364 | Pattern of cavities in globins: the case of human hemoglobin. <i>Biopolymers</i> , <b>2009</b> , 91, 1097-107   | 2.2  | 52  |
| 363 | Nitrite reduction: a ubiquitous function from a pre-aerobic past. <i>BioEssays</i> , <b>2009</b> , 31, 885-91   | 4.1  | 13  |
| 362 | Distinguishing between smooth and rough free energy barriers in protein folding. <i>Biochemistry</i> , <b>2009</b> , 48, 11825-30   | 3.2  | 9   |
| 361 | Failure of apoptosis-inducing factor to act as neuroglobin reductase. <i>Biochemical and Biophysical Research Communications</i> , <b>2009</b> , 390, 121-4   | 3.4  | 11  |
| 360 | Intramolecular electron transfer in <i>Pseudomonas aeruginosa</i> cd(1) nitrite reductase: thermodynamics and kinetics. <i>Biophysical Journal</i> , <b>2009</b> , 96, 2849-56  | 2.9  | 24  |
| 359 | The structure of neuroglobin at high Xe and Kr pressure reveals partial conservation of globin internal cavities. <i>Biophysical Journal</i> , <b>2009</b> , 97, 1700-8   | 2.9  | 31  |
| 358 | Engineered symmetric connectivity of secondary structure elements highlights malleability of protein folding pathways. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 11727-33  | 16.4 | 23  |
| 357 | Fast folding kinetics and stabilization of apo-cytochrome c. <i>FEBS Letters</i> , <b>2008</b> , 582, 1003-7  | 3.8  | 7   |
| 356 | Molecular dynamics simulation of the neuroglobin crystal: comparison with the simulation in solution. <i>Biophysical Journal</i> , <b>2008</b> , 95, 4157-62  | 2.9  | 24  |

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|-----|--|------|----|
| 355 | Kinetic characterization of the Escherichia coli nitric oxide reductase flavorubredoxin. <i>Methods in Enzymology</i> , <b>2008</b> , 437, 47-62   | 1.7  | 10 |
| 354 | NO sensing in Pseudomonas aeruginosa: structure of the transcriptional regulator DNR. <i>Journal of Molecular Biology</i> , <b>2008</b> , 378, 1002-15   | 6.5  | 69 |
| 353 | An X-ray diffraction and X-ray absorption spectroscopy joint study of neuroglobin. <i>Archives of Biochemistry and Biophysics</i> , <b>2008</b> , 475, 7-13  | 4.1  | 44 |
| 352 | Neuroglobin: enzymatic reduction and oxygen affinity. <i>Biochemical and Biophysical Research Communications</i> , <b>2008</b> , 367, 893-8  | 3.4  | 40 |
| 351 | Ancient hemes for ancient catalysts. <i>Plant Signaling and Behavior</i> , <b>2008</b> , 3, 135-6  | 2.5  | 8  |
| 350 | The O <sub>2</sub> -scavenging flavodiiron protein in the human parasite Giardia intestinalis. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 4061-8  | 5.4  | 93 |
| 349 | Folding and misfolding in a naturally occurring circularly permuted PDZ domain. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 8954-60  | 5.4  | 24 |
| 348 | The folding pathway of an engineered circularly permuted PDZ domain. <i>Protein Engineering, Design and Selection</i> , <b>2008</b> , 21, 155-60   | 1.9  | 18 |
| 347 | New insights into the activity of Pseudomonas aeruginosa cd1 nitrite reductase. <i>Biochemical Society Transactions</i> , <b>2008</b> , 36, 1155-9   | 5.1  | 16 |
| 346 | Mechanisms of protein folding. <i>European Biophysics Journal</i> , <b>2008</b> , 37, 721-8  | 1.9  | 16 |
| 345 | Glutathione reductase and thioredoxin reductase at the crossroad: the structure of Schistosoma mansoni thioredoxin glutathione reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2008</b> , 72, 936-45 | 4.2  | 49 |
| 344 | Is neuroglobin a signal transducer?. <i>IUBMB Life</i> , <b>2008</b> , 60, 410-3   | 4.7  | 13 |
| 343 | Myoglobin Strikes Back <b>2008</b> , 183-189   |      |    |
| 342 | Molecular dynamics simulation of deoxy and carboxy murine neuroglobin in water. <i>Biophysical Journal</i> , <b>2007</b> , 93, 434-41  | 2.9  | 42 |
| 341 | Identification and characterization of protein folding intermediates. <i>Biophysical Chemistry</i> , <b>2007</b> , 128, 105-13   | 3.5  | 59 |
| 340 | Kinetics of electron transfer from NADH to the Escherichia coli nitric oxide reductase flavorubredoxin. <i>FEBS Journal</i> , <b>2007</b> , 274, 677-86  | 5.7  | 15 |
| 339 | Neuroglobin, seven years after. <i>Cellular and Molecular Life Sciences</i> , <b>2007</b> , 64, 1259-68  | 10.3 | 85 |
| 338 | An on-pathway intermediate in the folding of a PDZ domain. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 8568-72   | 5.4  | 38 |

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| 337 | The three-dimensional structure of two redox states of cyclophilin A from <i>Schistosoma mansoni</i> . Evidence for redox regulation of peptidyl-prolyl cis-trans isomerase activity. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 24851-7            | 5.4  | 23  |
| 336 | Fast dissociation of nitric oxide from ferrous <i>Pseudomonas aeruginosa</i> cd1 nitrite reductase. A novel outlook on the catalytic mechanism. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 14761-7  | 5.4  | 43  |
| 335 | A strategic protein in cytochrome c maturation: three-dimensional structure of CcmH and binding to apocytochrome c. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 27012-27019  | 5.4  | 33  |
| 334 | Plasticity of the protein folding landscape: switching between on- and off-pathway intermediates. <i>Archives of Biochemistry and Biophysics</i> , <b>2007</b> , 466, 172-6  | 4.1  | 5   |
| 333 | Redox control of fast ligand dissociation from <i>Escherichia coli</i> cytochrome bd. <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 355, 97-102   | 3.4  | 66  |
| 332 | Nitrite controls the release of nitric oxide in <i>Pseudomonas aeruginosa</i> cd1 nitrite reductase. <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 363, 662-6   | 3.4  | 19  |
| 331 | Time-resolved methods in biophysics. 6. Time-resolved Laue crystallography as a tool to investigate photo-activated protein dynamics. <i>Photochemical and Photobiological Sciences</i> , <b>2007</b> , 6, 1047-56   | 4.2  | 32  |
| 330 | A PDZ domain recapitulates a unifying mechanism for protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 128-33  | 11.5 | 65  |
| 329 | Hemoglobin is an honorary enzyme. <i>Rendiconti Lincei</i> , <b>2006</b> , 17, 51-58   | 1.7  |     |
| 328 | Demonstration of long-range interactions in a PDZ domain by NMR, kinetics, and protein engineering. <i>Structure</i> , <b>2006</b> , 14, 1801-9  | 5.2  | 93  |
| 327 | The allosteric properties of hemoglobin: insights from natural and site directed mutants. <i>Current Protein and Peptide Science</i> , <b>2006</b> , 7, 17-45  | 2.8  | 41  |
| 326 | Unveiling a hidden folding intermediate in c-type cytochromes by protein engineering. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 9331-6   | 5.4  | 27  |
| 325 | A globin for the brain. <i>FASEB Journal</i> , <b>2006</b> , 20, 2192-7  | 0.9  | 80  |
| 324 | 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> , <b>2006</b> , 103, 4924-9   | 11.5 | 104 |
| 323 | 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> , <b>2006</b> , 103, 12365-70 | 11.5 | 44  |
| 322 | Nitric oxide reacts with the ferryl-oxo catalytic intermediate of the CuB-lacking cytochrome bd terminal oxidase. <i>FEBS Letters</i> , <b>2006</b> , 580, 4823-6  | 3.8  | 40  |
| 321 | Nitric oxide and the respiratory enzyme. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2006</b> , 1757, 1144-54  | 4.6  | 61  |
| 320 | Probing the mechanism of GSH activation in <i>Schistosoma haematobium</i> glutathione-S-transferase by site-directed mutagenesis and X-ray crystallography. <i>Journal of Molecular Biology</i> , <b>2006</b> , 360, 678-89  | 6.5  | 18  |

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|-----|---|------|-----|
| 319 | The Structural and Functional Properties of Hemoglobin and their Relevance for a Hemoglobin-Based Blood Substitute <b>2006</b> , 327-340  |      | 1   |
| 318 | Large-scale purification and crystallization of the endoribonuclease XendoU: troubleshooting with His-tagged proteins. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2006</b> , 62, 298-301                           |      | 18  |
| 317 | Critical role of His369 in the reactivity of <i>Pseudomonas aeruginosa</i> cytochrome cd1 nitrite reductase with oxygen. <i>FEBS Journal</i> , <b>2006</b> , 273, 4495-503  | 5.7  | 3   |
| 316 | Nitric oxide, cytochrome c oxidase and myoglobin: competition and reaction pathways. <i>FEBS Letters</i> , <b>2005</b> , 579, 2528-32   | 3.8  | 32  |
| 315 | Molecular dynamics simulation of sperm whale myoglobin: effects of mutations and trapped CO on the structure and dynamics of cavities. <i>Biophysical Journal</i> , <b>2005</b> , 89, 465-74  | 2.9  | 91  |
| 314 | <sup>1</sup> 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> , <b>2005</b> , 89, 4149-58 | 2.9  | 5   |
| 313 | Insights into the catalytic mechanism of glutathione S-transferase: the lesson from <i>Schistosoma haematobium</i> . <i>Structure</i> , <b>2005</b> , 13, 1241-6  | 5.2  | 31  |
| 312 | Cytochrome c oxidase, ligands and electrons. <i>Journal of Inorganic Biochemistry</i> , <b>2005</b> , 99, 324-36  | 4.2  | 102 |
| 311 | An obligatory intermediate in the folding pathway of cytochrome c552 from <i>Hydrogenobacter thermophilus</i> . <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 25729-34  | 5.4  | 64  |
| 310 | 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> , <b>2005</b> , 102, 8483-8   | 11.5 | 213 |
| 309 | Kinetic folding mechanism of PDZ2 from PTP-BL. <i>Protein Engineering, Design and Selection</i> , <b>2005</b> , 18, 389-95  | 1.9  | 44  |
| 308 | The structure of carbonmonoxy 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> , <b>2004</b> , 101, 17351-6                          | 11.5 | 175 |
| 307 | A common folding mechanism in the cytochrome c family. <i>Trends in Biochemical Sciences</i> , <b>2004</b> , 29, 535-41   | 10.3 | 46  |
| 306 | The structure of murine neuroglobin: Novel pathways for ligand migration and binding. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 56, 85-92   | 4.2  | 154 |
| 305 | Structural dynamics of myoglobin: an infrared kinetic study of ligand migration in mutants YQR and YQRF. <i>Biophysical Chemistry</i> , <b>2004</b> , 109, 41-58  | 3.5  | 15  |
| 304 | 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> , <b>2004</b> , 43, 2957-63   | 3.2  | 18  |
| 303 | Folding of <i>Aplysia limacina</i> apomyoglobin involves an intermediate in common with other evolutionarily distant globins. <i>Biochemistry</i> , <b>2004</b> , 43, 230-6   | 3.2  | 13  |
| 302 | <i>Schistosoma mansoni</i> fatty acid binding protein: specificity and functional control as revealed by crystallographic structure. <i>Biochemistry</i> , <b>2004</b> , 43, 13000-11   | 3.2  | 25  |



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|-----|---|------|-----|
| 301 | Extended molecular dynamics simulation of the carbon monoxide migration in sperm whale myoglobin. <i>Biophysical Journal</i> , <b>2004</b> , 86, 3855-62  | 2.9  | 121 |
| 300 | Control of cytochrome c oxidase activity by nitric oxide. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2004</b> , 1655, 365-71   | 4.6  | 80  |
| 299 | The structural dynamics of myoglobin. <i>Journal of Structural Biology</i> , <b>2004</b> , 147, 223-34  | 3.4  | 75  |
| 298 | Kinetics of NO and O2 binding to a maleimide poly(ethylene glycol)-conjugated human haemoglobin. <i>Biochemical Journal</i> , <b>2004</b> , 382, 183-9  | 3.8  | 37  |
| 297 | Roles for holes: are cavities in proteins mere packing defects?. <i>Italian Journal of Biochemistry</i> , <b>2004</b> , 53, 46-52   |      | 4   |
| 296 | Exploring the cytochrome c folding mechanism: cytochrome c552 from thermus thermophilus folds through an on-pathway intermediate. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 41136-40                    | 5.4  | 35  |
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