

Luigi Vitagliano

List of Publications by Year in descending order

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133
papers

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109264

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docs citations

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times ranked

3996
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Solid-state optical properties of self-assembling amyloid-like peptides with different charged states at the terminal ends. <i>Scientific Reports</i> , 2022, 12, 759. | 1.6 | 9 |
| 2 | KCTD15 Is Overexpressed in her2+ Positive Breast Cancer Patients and Its Silencing Attenuates Proliferation in SKBR3 CELL LINE. <i>Diagnostics</i> , 2022, 12, 591. | 1.3 | 4 |
| 3 | A Protein Data Bank survey of multimodal binding of thiocyanate to proteins: Evidence for thiocyanate promiscuity. <i>International Journal of Biological Macromolecules</i> , 2022, 208, 29-36. | 3.6 | 5 |
| 4 | The temporal correlation between positive testing and death in Italy: from the first phase to the later evolution of the COVID-19 pandemic.. <i>Acta Biomedica</i> , 2022, 92, e2021395. | 0.2 | 1 |
| 5 | Molecular dynamics simulations of human $\hat{\pm}$ -thrombin in different structural contexts: evidence for an aptamer-guided cooperation between the two exosites. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 2199-2209. | 2.0 | 9 |
| 6 | Fabrication of fluorescent nanospheres by heating PEGylated tetratyrosine nanofibers. <i>Scientific Reports</i> , 2021, 11, 2470. | 1.6 | 10 |
| 7 | Monoclonal Antibodies: A Prospective and Retrospective View. <i>Current Medicinal Chemistry</i> , 2021, 28, 435-471. | 1.2 | 8 |
| 8 | Amyloid-Like Aggregation in Diseases and Biomaterials: Osmosis of Structural Information. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 641372. | 2.0 | 30 |
| 9 | Structural and functional analysis of the simultaneous binding of two duplex/quadruplex aptamers to human $\hat{\pm}$ -thrombin. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 858-867. | 3.6 | 8 |
| 10 | The lncRNA TEX41 is upregulated in pediatric B-Cells Acute Lymphoblastic Leukemia and it is necessary for leukemic cell growth. <i>Biomarker Research</i> , 2021, 9, 54. | 2.8 | 10 |
| 11 | Quaternary Structure Transitions of Human Hemoglobin: An Atomic-Level View of the Functional Intermediate States. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3988-3999. | 2.5 | 4 |
| 12 | KCTD15 deregulation is associated with alterations of the NF- $\hat{\rho}$ B signaling in both pathological and physiological model systems. <i>Scientific Reports</i> , 2021, 11, 18237. | 1.6 | 5 |
| 13 | Fluorescence Emission of Self-Assembling Amyloid-Like Peptides: Solution versus Solid State. <i>ChemPhysChem</i> , 2021, 22, 2215-2221. | 1.0 | 6 |
| 14 | Amyloid-like Prep1 peptides exhibit reversible blue-green-red fluorescence <i>in vitro</i> and in living cells. <i>Chemical Communications</i> , 2021, 57, 3720-3723. | 2.2 | 15 |
| 15 | Members of the GADD45 Protein Family Show Distinct Propensities to form Toxic Amyloid-Like Aggregates in Physiological Conditions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10700. | 1.8 | 3 |
| 16 | Exosite Binding in Thrombin: A Global Structural/Dynamic Overview of Complexes with Aptamers and Other Ligands. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10803. | 1.8 | 24 |
| 17 | Analysis of the time evolution of COVID-19 lethality during the first epidemic wave in Italy. <i>Acta Biomedica</i> , 2021, 92, e2021171. | 0.2 | 7 |
| 18 | AlphaFold-Predicted Structures of KCTD Proteins Unravel Previously Undetected Relationships among the Members of the Family. <i>Biomolecules</i> , 2021, 11, 1862. | 1.8 | 13 |

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|----|--|-----|-----------|
| 19 | A global analysis of conservative and non-conservative mutations in SARS-CoV-2 detected in the first year of the COVID-19 world-wide diffusion. <i>Scientific Reports</i> , 2021, 11, 24495. | 1.6 | 5 |
| 20 | Guanidinium binding to proteins: The intriguing effects on the D1 and D2 domains of <i>Thermotoga maritima</i> Arginine Binding Protein and a comprehensive analysis of the Protein Data Bank. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 375-385. | 3.6 | 6 |
| 21 | Development of a Protein Scaffold for Arginine Sensing Generated through the Dissection of the Arginine-Binding Protein from <i>Thermotoga maritima</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7503. | 1.8 | 3 |
| 22 | On the extraordinary pressure stability of the <i>Thermotoga maritima</i> arginine binding protein and its folded fragments – a high-pressure FTIR spectroscopy study. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 11244-11248. | 1.3 | 2 |
| 23 | KCTD15 Protein Expression in Peripheral Blood and Acute Myeloid Leukemia. <i>Diagnostics</i> , 2020, 10, 371. | 1.3 | 4 |
| 24 | Identification and characterization of cytotoxic amyloid-like regions in human Pbx-regulating protein-1. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 618-629. | 3.6 | 6 |
| 25 | The Structural Versatility of the BTB Domains of KCTD Proteins and Their Recognition of the GABAB Receptor. <i>Biomolecules</i> , 2019, 9, 323. | 1.8 | 9 |
| 26 | Molecular basis of the scalp-ear-nipple syndrome unraveled by the characterization of disease-causing KCTD1 mutants. <i>Scientific Reports</i> , 2019, 9, 10519. | 1.6 | 18 |
| 27 | The non-swapped monomeric structure of the arginine-binding protein from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 707-713. | 0.4 | 5 |
| 28 | <i>Maleness-on-the-Y</i> (<i>MoY</i>) orchestrates male sex determination in major agricultural fruit fly pests. <i>Science</i> , 2019, 365, 1457-1460. | 6.0 | 88 |
| 29 | KCTD1: A novel modulator of adipogenesis through the interaction with the transcription factor AP2 β . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 158514. | 1.2 | 12 |
| 30 | Loop size optimization induces a strong thermal stabilization of the thioredoxin fold. <i>FEBS Journal</i> , 2019, 286, 1752-1764. | 2.2 | 17 |
| 31 | The characterization of <i>Thermotoga maritima</i> Arginine Binding Protein variants demonstrates that minimal local strains have an important impact on protein stability. <i>Scientific Reports</i> , 2019, 9, 6617. | 1.6 | 9 |
| 32 | Structure, stability and aggregation propensity of a Ribonuclease A-Onconase chimera. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 1125-1133. | 3.6 | 5 |
| 33 | The unique structural features of carbonmonoxy hemoglobin from the sub-Antarctic fish <i>Eleginops maclovinus</i> . <i>Scientific Reports</i> , 2019, 9, 18987. | 1.6 | 3 |
| 34 | KCTD15 is overexpressed in human childhood B-cell acute lymphoid leukemia. <i>Scientific Reports</i> , 2019, 9, 20108. | 1.6 | 17 |
| 35 | Amyloid-Like Fibrillary Morphology Originated by Tyrosine-Containing Aromatic Hexapeptides. <i>Chemistry - A European Journal</i> , 2018, 24, 6804-6817. | 1.7 | 28 |
| 36 | The intrinsic flexibility of the aptamer targeting the ribosomal protein S8 is a key factor for the molecular recognition. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1006-1016. | 1.1 | 19 |

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| 37 | The essential player in adipogenesis GRP78 is a novel KCTD15 interactor. <i>International Journal of Biological Macromolecules</i> , 2018, 115, 469-475. | 3.6 | 17 |
| 38 | Assembly modes of hexaphenylalanine variants as function of the charge states of their terminal ends. <i>Soft Matter</i> , 2018, 14, 8219-8230. | 1.2 | 18 |
| 39 | Intrinsic structural versatility of the highly conserved 412-423 epitope of the Hepatitis C Virus E2 protein. <i>International Journal of Biological Macromolecules</i> , 2018, 116, 620-632. | 3.6 | 8 |
| 40 | Domain communication in <i>Thermotoga maritima</i> Arginine Binding Protein unraveled through protein dissection. <i>International Journal of Biological Macromolecules</i> , 2018, 119, 758-769. | 3.6 | 5 |
| 41 | Local structural motifs in proteins: Detection and characterization of fragments inserted in helices. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 1924-1930. | 3.6 | 7 |
| 42 | Domain swapping dissection in <i>Thermotoga maritima</i> arginine binding protein: How structural flexibility may compensate destabilization. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 952-962. | 1.1 | 10 |
| 43 | The dynamic properties of the Hepatitis C Virus E2 envelope protein unraveled by molecular dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 805-816. | 2.0 | 11 |
| 44 | Photoluminescent Peptide-Based Nanostructures as FRET Donor for Fluorophore Dye. <i>Chemistry - A European Journal</i> , 2017, 23, 8741-8748. | 1.7 | 16 |
| 45 | Structural Characterization of PEGylated Hexaphenylalanine Nanostructures Exhibiting Green Photoluminescence Emission. <i>Chemistry - A European Journal</i> , 2017, 23, 14039-14048. | 1.7 | 34 |
| 46 | Fine Sampling of the Quaternary Structure Transition of a Tetrameric Hemoglobin. <i>Chemistry - A European Journal</i> , 2017, 23, 605-613. | 1.7 | 9 |
| 47 | Dissection of Factors Affecting the Variability of the Peptide Bond Geometry and Planarity. <i>BioMed Research International</i> , 2017, 2017, 1-9. | 0.9 | 8 |
| 48 | Structural Versatility of Hepatitis C Virus Proteins: Implications for the Design of Novel Anti-HCV Intervention Strategies. <i>Current Medicinal Chemistry</i> , 2017, 24, 4081-4101. | 1.2 | 7 |
| 49 | Factors affecting the amplitude of the β_1 angle in proteins: a revisitation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 618-625. | 1.1 | 15 |
| 50 | A peptide antagonist of Prep1-p160 interaction improves ceramide-induced insulin resistance in skeletal muscle cells. <i>Oncotarget</i> , 2017, 8, 71845-71858. | 0.8 | 14 |
| 51 | The BTB domains of the potassium channel tetramerization domain proteins prevalently assume pentameric states. <i>FEBS Letters</i> , 2016, 590, 1663-1671. | 1.3 | 25 |
| 52 | Proline 235 plays a key role in the regulation of the oligomeric states of <i>Thermotoga maritima</i> Arginine Binding Protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 814-824. | 1.1 | 13 |
| 53 | Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114. | 1.3 | 6 |
| 54 | Hierarchical Analysis of Self-Assembled PEGylated Hexaphenylalanine Photoluminescent Nanostructures. <i>Chemistry - A European Journal</i> , 2016, 22, 16586-16597. | 1.7 | 38 |

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| 55 | The Interacting Domains of PREP1 and p160 are Endowed with a Remarkable Structural Stability. <i>Molecular Biotechnology</i> , 2016, 58, 328-339. | 1.3 | 9 |
| 56 | Generation and Characterization of Monoclonal Antibodies against a Cyclic Variant of Hepatitis C Virus E2 Epitope 412-422. <i>Journal of Virology</i> , 2016, 90, 3745-3759. | 1.5 | 39 |
| 57 | The structure of Resuscitation promoting factor B from <i>M. tuberculosis</i> reveals unexpected ubiquitin-like domains. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 445-451. | 1.1 | 22 |
| 58 | KCTD5 is endowed with large, functionally relevant, interdomain motions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1725-1735. | 2.0 | 9 |
| 59 | The determinants of bond angle variability in protein/peptide backbones: A comprehensive statistical/quantum mechanics analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1973-1986. | 1.5 | 11 |
| 60 | Cullin3 - BTB Interface: A Novel Target for Stapled Peptides. <i>PLoS ONE</i> , 2015, 10, e0121149. | 1.1 | 33 |
| 61 | Cullin 3 Recognition Is Not a Universal Property among KCTD Proteins. <i>PLoS ONE</i> , 2015, 10, e0126808. | 1.1 | 43 |
| 62 | Bond distances in polypeptide backbones depend on the local conformation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1272-1283. | 2.5 | 11 |
| 63 | Nucleophosmin contains amyloidogenic regions that are able to form toxic aggregates under physiological conditions. <i>FASEB Journal</i> , 2015, 29, 3689-3701. | 0.2 | 53 |
| 64 | Structural conversion of the transformer protein RfaH: new insights derived from protein structure prediction and molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2173-2179. | 2.0 | 30 |
| 65 | Molecular recognition of Cullin3 by KCTDs: Insights from experimental and computational investigations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1289-1298. | 1.1 | 31 |
| 66 | A Loose Domain Swapping Organization Confers a Remarkable Stability to the Dimeric Structure of the Arginine Binding Protein from <i>Thermotoga maritima</i> . <i>PLoS ONE</i> , 2014, 9, e96560. | 1.1 | 31 |
| 67 | Role of loops connecting secondary structure elements in the stabilization of proteins isolated from thermophilic organisms. <i>Protein Science</i> , 2013, 22, 1016-1023. | 3.1 | 20 |
| 68 | A biophysical characterization of the folded domains of KCTD12: insights into interaction with the GABA _{B2} receptor. <i>Journal of Molecular Recognition</i> , 2013, 26, 488-495. | 1.1 | 26 |
| 69 | The intrinsic stability of the human prion $\hat{\imath}^2$ -sheet region investigated by molecular dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 441-452. | 2.0 | 2 |
| 70 | Carbohydrate Recognition by RpfB from <i>Mycobacterium tuberculosis</i> Unveiled by Crystallographic and Molecular Dynamics Analyses. <i>Biophysical Journal</i> , 2013, 104, 2530-2539. | 0.2 | 37 |
| 71 | Thermal and Chemical Stability of Two Homologous POZ/BTB Domains of KCTD Proteins Characterized by a Different Oligomeric Organization. <i>BioMed Research International</i> , 2013, 2013, 1-8. | 0.9 | 13 |
| 72 | Interplay between Peptide Bond Geometrical Parameters in Nonglobular Structural Contexts. <i>BioMed Research International</i> , 2013, 2013, 1-8. | 0.9 | 14 |

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|----|---|-----|-----------|
| 73 | Dynamical Properties of Steric Zipper Polymorphs Formed by a IAPP-Derived Peptide. <i>Protein and Peptide Letters</i> , 2012, 19, 846-851. | 0.4 | 1 |
| 74 | Structural and Dynamic Properties of Incomplete Immunoglobulin-like Fold Domains. <i>Protein and Peptide Letters</i> , 2012, 19, 1045-1053. | 0.4 | 10 |
| 75 | Polyproline and Triple Helix Motifs in Host-Pathogen Recognition. <i>Current Protein and Peptide Science</i> , 2012, 13, 855-865. | 0.7 | 34 |
| 76 | ATP regulation of the ligand-binding properties in temperate and cold-adapted haemoglobins. X-ray structure and ligand-binding kinetics in the sub-Antarctic fish <i>Eleginops maclovinus</i> . <i>Molecular BioSystems</i> , 2012, 8, 3295. | 2.9 | 12 |
| 77 | Crystallographic and spectroscopic characterizations of <i>Sulfolobus solfataricus</i> TrxA1 provide insights into the determinants of thioredoxin fold stability. <i>Journal of Structural Biology</i> , 2012, 177, 506-512. | 1.3 | 6 |
| 78 | Role of Hydration in Collagen Recognition by Bacterial Adhesins. <i>Biophysical Journal</i> , 2011, 100, 2253-2261. | 0.2 | 26 |
| 79 | Molecular organization of the cullin E3 ligase adaptor KCTD11. <i>Biochimie</i> , 2011, 93, 715-724. | 1.3 | 50 |
| 80 | Crystallization and preliminary X-ray crystallographic analysis of ligand-free and arginine-bound forms of <i>Thermotoga maritima</i> arginine-binding protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1462-1465. | 0.7 | 12 |
| 81 | Design, synthesis and characterization of a peptide able to bind proteins of the KCTD family: implications for KCTD cullin 3 recognition. <i>Journal of Peptide Science</i> , 2011, 17, 373-376. | 0.8 | 15 |
| 82 | Peptide Bond Distortions from Planarity: New Insights from Quantum Mechanical Calculations and Peptide/Protein Crystal Structures. <i>PLoS ONE</i> , 2011, 6, e24533. | 1.1 | 40 |
| 83 | Elongation Factors EFIA and EF4u: Their Role in Translation and Beyond. <i>Israel Journal of Chemistry</i> , 2010, 50, 71-79. | 1.0 | 9 |
| 84 | Crystallization, preliminary X-ray diffraction studies and Raman microscopy of the major haemoglobin from the sub-Antarctic fish <i>Eleginops maclovinus</i> in the carbomonoxy form. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1536-1540. | 0.7 | 9 |
| 85 | Histone deacetylase and Cullin3-RNKCTD11 ubiquitin ligase interplay regulates Hedgehog signalling through Gli acetylation. <i>Nature Cell Biology</i> , 2010, 12, 132-142. | 4.6 | 292 |
| 86 | An Order-Disorder Transition Plays a Role in Switching Off the Root Effect in Fish Hemoglobins. <i>Journal of Biological Chemistry</i> , 2010, 285, 32568-32575. | 1.6 | 31 |
| 87 | Dynamics and stability of amyloid-like steric zipper assemblies with hydrophobic dry interfaces. <i>Biopolymers</i> , 2009, 91, 1161-1171. | 1.2 | 25 |
| 88 | Combined crystallographic and spectroscopic analysis of <i>Trematomus bernacchii</i> hemoglobin highlights analogies and differences in the peculiar oxidation pathway of Antarctic fish hemoglobins. <i>Biopolymers</i> , 2009, 91, 1117-1125. | 1.2 | 21 |
| 89 | The dimeric structure of <i>Sulfolobus solfataricus</i> thioredoxin A2 and the basis of its thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 1004-1008. | 1.5 | 5 |
| 90 | Role of side chains in collagen triple helix stabilization and partner recognition. <i>Journal of Peptide Science</i> , 2009, 15, 131-140. | 0.8 | 39 |

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|-----|--|-----|-----------|
| 91 | Crystallization and preliminary X-ray crystallographic analysis of two dimeric hyperthermostable thioredoxins isolated from <i>Sulfolobus solfataricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 604-607. | 0.7 | 2 |
| 92 | Structure and stability of a thioredoxin reductase from <i>Sulfolobus solfataricus</i> : A thermostable protein with two functions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 554-562. | 1.1 | 13 |
| 93 | Crystal structure of the collagen triple helix model [(Pro-Pro-Gly) ₁₀] ₃ . <i>Protein Science</i> , 2009, 11, 262-270. | 3.1 | 245 |
| 94 | Biochemical characterisation of the D60A mutant of the elongation factor λ from the archaeon <i>Sulfolobus solfataricus</i> . <i>Biochimie</i> , 2009, 91, 835-842. | 1.3 | 1 |
| 95 | Characterisation of the components of the thioredoxin system in the archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2008, 12, 553-562. | 0.9 | 17 |
| 96 | Stability against temperature of <i>Sulfolobus solfataricus</i> elongation factor λ , a multi-domain protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 573-581. | 1.1 | 11 |
| 97 | Contribution of dipole-dipole interactions to the stability of the collagen triple helix. <i>Protein Science</i> , 2008, 17, 955-961. | 3.1 | 33 |
| 98 | Insights into Structure, Stability, and Toxicity of Monomeric and Aggregated Polyglutamine Models from Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2008, 94, 4031-4040. | 0.2 | 47 |
| 99 | Insights into Stability and Toxicity of Amyloid-Like Oligomers by Replica Exchange Molecular Dynamics Analyses. <i>Biophysical Journal</i> , 2008, 95, 1965-1973. | 0.2 | 51 |
| 100 | Structure, dynamics, and stability of assemblies of the human prion fragment SNQNNF. <i>Biochemical and Biophysical Research Communications</i> , 2008, 366, 800-806. | 1.0 | 18 |
| 101 | Role of hydration in collagen triple helix stabilization. <i>Biochemical and Biophysical Research Communications</i> , 2008, 372, 121-125. | 1.0 | 50 |
| 102 | Stability of single sheet GNNQQNY aggregates analyzed by replica exchange molecular dynamics: Antiparallel versus parallel association. <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 1036-1041. | 1.0 | 32 |
| 103 | Spectroscopic and Crystallographic Characterization of a Tetrameric Hemoglobin Oxidation Reveals Structural Features of the Functional Intermediate Relaxed/Tense State. <i>Journal of the American Chemical Society</i> , 2008, 130, 10527-10535. | 6.6 | 46 |
| 104 | Spectroscopic and Crystallographic Characterization of bis-Histidyl Adducts in Tetrameric Hemoglobins. <i>Methods in Enzymology</i> , 2008, 436, 425-444. | 0.4 | 30 |
| 105 | Structural Characterization of Ferric Hemoglobins from Three Antarctic Fish Species of the Suborder Notothenioidei. <i>Biophysical Journal</i> , 2007, 93, 2822-2829. | 0.2 | 45 |
| 106 | Chemical Denaturation of the Elongation Factor λ Isolated from the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Biochemistry</i> , 2006, 45, 719-726. | 1.2 | 13 |
| 107 | Molecular dynamics analyses of cross-beta-spine steric zipper models: beta-Sheet twisting and aggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11533-11538. | 3.3 | 107 |
| 108 | High resolution crystal structure of deoxy hemoglobin from <i>Trematomus bernacchii</i> at different pH values: The role of histidine residues in modulating the strength of the root effect. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 490-498. | 1.5 | 45 |

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|-----|--|-----|-----------|
| 109 | Limited tendency of α -helical residues to form disulfide bridges: a structural explanation. <i>Journal of Peptide Science</i> , 2006, 12, 740-747. | 0.8 | 10 |
| 110 | Polyproline Helices in Protein Structures: A Statistical Survey. <i>Protein and Peptide Letters</i> , 2006, 13, 847-854. | 0.4 | 37 |
| 111 | Crystallization and preliminary X-ray crystallographic analysis of <i>Sulfolobus solfataricus</i> thioredoxin reductase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 906-909. | 0.7 | 4 |
| 112 | Minimal structural requirements for root effect: Crystal structure of the cathodic hemoglobin isolated from the antarctic fish <i>Trematomus newnesi</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 316-321. | 1.5 | 49 |
| 113 | Correlation between ϕ and ψ Dihedral Angles in Protein Structures. <i>Journal of Molecular Biology</i> , 2005, 347, 483-487. | 2.0 | 45 |
| 114 | Open Interface and Large Quaternary Structure Movements in 3D Domain Swapped Proteins: Insights from Molecular Dynamics Simulations of the C-Terminal Swapped Dimer of Ribonuclease A. <i>Biophysical Journal</i> , 2005, 88, 2003-2012. | 0.2 | 26 |
| 115 | The oxidation process of Antarctic fish hemoglobins. <i>FEBS Journal</i> , 2004, 271, 1651-1659. | 0.2 | 48 |
| 116 | Characterization of collagen-like heterotrimers: Implications for triple-helix stability. <i>Biopolymers</i> , 2004, 73, 682-688. | 1.2 | 18 |
| 117 | Imino Acids and Collagen Triple Helix Stability: Characterization of Collagen-like Polypeptides Containing Hyp-Hyp-Gly Sequence Repeats. <i>Journal of the American Chemical Society</i> , 2004, 126, 11402-11403. | 6.6 | 62 |
| 118 | The Crystal Structure of <i>Sulfolobus solfataricus</i> Elongation Factor τ in Complex with Magnesium and GDP. <i>Biochemistry</i> , 2004, 43, 6630-6636. | 1.2 | 22 |
| 119 | Dynamic Properties of the N-Terminal Swapped Dimer of Ribonuclease A. <i>Biophysical Journal</i> , 2004, 86, 2383-2391. | 0.2 | 48 |
| 120 | Subtle functional collective motions in pancreatic-like ribonucleases: From ribonuclease A to angiogenin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 101-110. | 1.5 | 64 |
| 121 | The crystal structure of a tetrameric hemoglobin in a partial hemichrome state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9801-9806. | 3.3 | 71 |
| 122 | Global and local motions in ribonuclease A: A molecular dynamics study. <i>Biopolymers</i> , 2002, 65, 274-283. | 1.2 | 56 |
| 123 | Recent Progress on Collagen Triple Helix Structure, Stability and Assembly. <i>Protein and Peptide Letters</i> , 2002, 9, 107-116. | 0.4 | 53 |
| 124 | Structural bases of collagen stabilization induced by proline hydroxylation. <i>Biopolymers</i> , 2001, 58, 459-464. | 1.2 | 202 |
| 125 | Preferred proline puckerings in <i>cis</i> and <i>trans</i> peptide groups: Implications for collagen stability. <i>Protein Science</i> , 2001, 10, 2627-2632. | 3.1 | 120 |
| 126 | Crystal structure of a collagen-like polypeptide with repeating sequence Pro-Hyp-Gly at 1.4 Å resolution: Implications for collagen hydration. <i>Biopolymers</i> , 2000, 56, 8-13. | 1.2 | 98 |

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| 127 | Productive and nonproductive binding to ribonuclease A: X-ray structure of two complexes with uridylyl(2',5')guanosine. <i>Protein Science</i> , 2000, 9, 1217-1225. | 3.1 | 62 |
| 128 | Experimental evidence for the correlation of bond distances in peptide groups detected in ultrahigh-resolution protein structures. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 825-828. | 1.0 | 21 |
| 129 | Crystal structure of <i>Trematomus newnesi</i> haemoglobin re-opens the root effect question. <i>Journal of Molecular Biology</i> , 1999, 287, 897-906. | 2.0 | 71 |
| 130 | A potential allosteric subsite generated by domain swapping in bovine seminal ribonuclease 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 293, 569-577. | 2.0 | 48 |
| 131 | Binding of a substrate analog to a domain swapping protein: X-ray structure of the complex of bovine seminal ribonuclease with uridylyl(2',5')adenosine. <i>Protein Science</i> , 1998, 7, 1691-1699. | 3.1 | 36 |
| 132 | X-ray crystallographic determination of a collagen-like peptide with the repeating sequence (Pro-Pro-Gly). <i>Journal of Molecular Biology</i> , 1998, 280, 623-638. | 2.0 | 166 |
| 133 | Stabilization of the triple-helical structure of natural collagen by side-chain interactions. <i>Biochemistry</i> , 1993, 32, 7354-7359. | 1.2 | 51 |