

# Luigi Vitagliano

## List of Publications by Year in descending order

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133  
papers

4,053  
citations

109264

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133  
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133  
docs citations

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times ranked

3996  
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone deacetylase and Cullin3-RENKCTD11 ubiquitin ligase interplay regulates Hedgehog signalling through Gli acetylation. <i>Nature Cell Biology</i> , 2010, 12, 132-142.	4.6	292
2	Crystal structure of the collagen triple helix model [(Pro-Pro-Gly) <sub>10</sub> ] <sub>3</sub> . <i>Protein Science</i> , 2009, 11, 262-270.	3.1	245
3	Structural bases of collagen stabilization induced by proline hydroxylation. <i>Biopolymers</i> , 2001, 58, 459-464.	1.2	202
4	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
5	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
6	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
7	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
8	<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
9	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
10	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
11	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
12	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
13	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
14	Global and local motions in ribonuclease A: A molecular dynamics study. <i>Biopolymers</i> , 2002, 65, 274-283.	1.2	56
15	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
16	Recent Progress on Collagen Triple Helix Structure, Stability and Assembly. <i>Protein and Peptide Letters</i> , 2002, 9, 107-116.	0.4	53
17	Stabilization of the triple-helical structure of natural collagen by side-chain interactions. <i>Biochemistry</i> , 1993, 32, 7354-7359.	1.2	51
18	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

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19	Role of hydration in collagen triple helix stabilization. <i>Biochemical and Biophysical Research Communications</i> , 2008, 372, 121-125.	1.0	50
20	Molecular organization of the cullin E3 ligase adaptor KCTD11. <i>Biochimie</i> , 2011, 93, 715-724.	1.3	50
21	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
22	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
23	The oxidation process of Antarctic fish hemoglobins. <i>FEBS Journal</i> , 2004, 271, 1651-1659.	0.2	48
24	Dynamic Properties of the N-Terminal Swapped Dimer of Ribonuclease A. <i>Biophysical Journal</i> , 2004, 86, 2383-2391.	0.2	48
25	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
26	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
27	Correlation between $\phi$ and $\psi$ Dihedral Angles in Protein Structures. <i>Journal of Molecular Biology</i> , 2005, 347, 483-487.	2.0	45
28	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
29	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
30	Cullin 3 Recognition Is Not a Universal Property among KCTD Proteins. <i>PLoS ONE</i> , 2015, 10, e0126808.	1.1	43
31	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
32	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
33	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
34	Hierarchical Analysis of Self-Assembled PEGylated Hexaphenylalanine Photoluminescent Nanostructures. <i>Chemistry - A European Journal</i> , 2016, 22, 16586-16597.	1.7	38
35	Polyproline Helices in Protein Structures: A Statistical Survey. <i>Protein and Peptide Letters</i> , 2006, 13, 847-854.	0.4	37
36	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

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37	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
38	Polyproline and Triple Helix Motifs in Host-Pathogen Recognition. <i>Current Protein and Peptide Science</i> , 2012, 13, 855-865.	0.7	34
39	Structural Characterization of PEGylated Hexaphenylalanine Nanostructures Exhibiting Green Photoluminescence Emission. <i>Chemistry - A European Journal</i> , 2017, 23, 14039-14048.	1.7	34
40	Contribution of dipole-dipole interactions to the stability of the collagen triple helix. <i>Protein Science</i> , 2008, 17, 955-961.	3.1	33
41	Cullin3 - BTB Interface: A Novel Target for Stapled Peptides. <i>PLoS ONE</i> , 2015, 10, e0121149.	1.1	33
42	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
43	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
44	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
45	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
46	Spectroscopic and Crystallographic Characterization of bis-Histidyl Adducts in Tetrameric Hemoglobins. <i>Methods in Enzymology</i> , 2008, 436, 425-444.	0.4	30
47	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
48	Amyloid-Like Aggregation in Diseases and Biomaterials: Osmosis of Structural Information. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 641372.	2.0	30
49	Amyloid-Like Fibrillary Morphology Originated by Tyrosine-Containing Aromatic Hexapeptides. <i>Chemistry - A European Journal</i> , 2018, 24, 6804-6817.	1.7	28
50	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
51	Role of Hydration in Collagen Recognition by Bacterial Adhesins. <i>Biophysical Journal</i> , 2011, 100, 2253-2261.	0.2	26
52	A biophysical characterization of the folded domains of KCTD12: insights into interaction with the GABA <sub>B2</sub> receptor. <i>Journal of Molecular Recognition</i> , 2013, 26, 488-495.	1.1	26
53	Dynamics and stability of amyloid-like steric zipper assemblies with hydrophobic dry interfaces. <i>Biopolymers</i> , 2009, 91, 1161-1171.	1.2	25
54	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

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55	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
56	The Crystal Structure of <i>Sulfolobus solfataricus</i> Elongation Factor 1 $\pm$ in Complex with Magnesium and GDP. <i>Biochemistry</i> , 2004, 43, 6630-6636.	1.2	22
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	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
59	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
60	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
61	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
62	Characterization of collagen-like heterotrimers: Implications for triple-helix stability. <i>Biopolymers</i> , 2004, 73, 682-688.	1.2	18
63	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
64	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
65	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
66	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
67	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
68	Loop size optimization induces a strong thermal stabilization of the thioredoxin fold. <i>FEBS Journal</i> , 2019, 286, 1752-1764.	2.2	17
69	KCTD15 is overexpressed in human childhood B-cell acute lymphoid leukemia. <i>Scientific Reports</i> , 2019, 9, 20108.	1.6	17
70	Photoluminescent Peptide-Based Nanostructures as FRET Donor for Fluorophore Dye. <i>Chemistry - A European Journal</i> , 2017, 23, 8741-8748.	1.7	16
71	Design, synthesis and characterization of a peptide able to bind proteins of the KCTD family: implications for KCTD $\epsilon$ cullin 3 recognition. <i>Journal of Peptide Science</i> , 2011, 17, 373-376.	0.8	15
72	Factors affecting the amplitude of the $\psi$ , angle in proteins: a revisitiation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 618-625.	1.1	15

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73	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
74	Interplay between Peptide Bond Geometrical Parameters in Nonglobular Structural Contexts. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	14
75	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
76	Chemical Denaturation of the Elongation Factor 1 $\pm$ Isolated from the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Biochemistry</i> , 2006, 45, 719-726.	1.2	13
77	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
78	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
79	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
80	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
81	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
82	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
83	KCTD1: A novel modulator of adipogenesis through the interaction with the transcription factor AP2 $\pm$ . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 158514.	1.2	12
84	Stability against temperature of <i>Sulfolobus solfataricus</i> elongation factor 1 $\pm$ , a multi-domain protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 573-581.	1.1	11
85	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
86	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
87	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
88	Limited tendency of $\pm$ -helical residues to form disulfide bridges: a structural explanation. <i>Journal of Peptide Science</i> , 2006, 12, 740-747.	0.8	10
89	Structural and Dynamic Properties of Incomplete Immunoglobulin-like Fold Domains. <i>Protein and Peptide Letters</i> , 2012, 19, 1045-1053.	0.4	10
90	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

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91	Fabrication of fluorescent nanospheres by heating PEGylated tetratyrosine nanofibers. <i>Scientific Reports</i> , 2021, 11, 2470.	1.6	10
92	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
93	Elongation Factors EF1A and EF2u: Their Role in Translation and Beyond. <i>Israel Journal of Chemistry</i> , 2010, 50, 71-79.	1.0	9
94	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
95	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
96	KCTD5 is endowed with large, functionally relevant, interdomain motions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1725-1735.	2.0	9
97	Fine Sampling of the R $\alpha$ T Quaternary Structure Transition of a Tetrameric Hemoglobin. <i>Chemistry - A European Journal</i> , 2017, 23, 605-613.	1.7	9
98	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
99	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
100	Molecular dynamics simulations of human $\alpha$ -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
101	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
102	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
103	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
104	Monoclonal Antibodies: A Prospective and Retrospective View. <i>Current Medicinal Chemistry</i> , 2021, 28, 435-471.	1.2	8
105	Structural and functional analysis of the simultaneous binding of two duplex/quadruplex aptamers to human $\alpha$ -thrombin. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 858-867.	3.6	8
106	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
107	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
108	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



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109	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
110	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114.	1.3	6
111	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
112	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
113	Fluorescence Emission of Self-assembling Amyloid-like Peptides: Solution versus Solid State. <i>ChemPhysChem</i> , 2021, 22, 2215-2221.	1.0	6
114	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
115	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
116	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
117	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
118	KCTD15 deregulation is associated with alterations of the NF- $\kappa$ B signaling in both pathological and physiological model systems. <i>Scientific Reports</i> , 2021, 11, 18237.	1.6	5
119	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
120	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
121	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
122	KCTD15 Protein Expression in Peripheral Blood and Acute Myeloid Leukemia. <i>Diagnostics</i> , 2020, 10, 371.	1.3	4
123	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
124	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
125	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
126	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



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127	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
128	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
129	The intrinsic stability of the human prion $\beta$ -sheet region investigated by molecular dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 441-452.	2.0	2
130	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
131	Biochemical characterisation of the D60A mutant of the elongation factor $\beta$ from the archaeon <i>Sulfolobus solfataricus</i> . <i>Biochimie</i> , 2009, 91, 835-842.	1.3	1
132	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
133	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