

Emilia Maria Pedone

List of Publications by Year in descending order

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118
papers

2,776
citations

185998

28
h-index

264894

42
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119
all docs

119
docs citations

119
times ranked

3514
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective Photo-Assisted Eradication of Triple-Negative Breast Cancer Cells through Aptamer Decoration of Doped Conjugated Polymer Nanoparticles. <i>Pharmaceutics</i> , 2022, 14, 626.	2.0	24
2	Targeting Ship2-Sam with peptide ligands: Novel insights from a multidisciplinary approach. <i>Bioorganic Chemistry</i> , 2022, 122, 105680.	2.0	3
3	Design, Synthesis, and Anticancer Activity of a Selenium-Containing Galectin-3 and Galectin-9N Inhibitor. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2581.	1.8	7
4	Pomegranate Peel Extract as an Inhibitor of SARS-CoV-2 Spike Binding to Human ACE2 Receptor (in) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	60
5	The TBC1D31/praja2 complex controls primary ciliogenesis through PKA-directed OFD1 ubiquitylation. <i>EMBO Journal</i> , 2021, 40, e106503.	3.5	15
6	More Is Always Better Than One: The N-Terminal Domain of the Spike Protein as Another Emerging Target for Hampering the SARS-CoV-2 Attachment to Host Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6462.	1.8	14
7	Impact of a Single Point Mutation on the Antimicrobial and Fibrillogenic Properties of Cryptides from Human Apolipoprotein B. <i>Pharmaceutics</i> , 2021, 14, 631.	1.7	11
8	Exploring the Ability of Cyclic Peptides to Target SAM Domains: A Computational and Experimental Study. <i>ChemBioChem</i> , 2020, 21, 702-711.	1.3	9
9	Enzymatic Antioxidant Signatures in Hyperthermophilic Archaea. <i>Antioxidants</i> , 2020, 9, 703.	2.2	19
10	A Multi-Targeting Approach to Fight SARS-CoV-2 Attachment. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 186.	1.6	24
11	Structural Insight of the Full-Length Ros Protein: A Prototype of the Prokaryotic Zinc-Finger Family. <i>Scientific Reports</i> , 2020, 10, 9283.	1.6	11
12	Ultra-rapid glutathionylation of chymotrypsinogen in its molten globule-like conformation: A comparison to archaeal proteins. <i>Scientific Reports</i> , 2020, 10, 8943.	1.6	6
13	Insights into PPAR γ Phosphorylation and Its Inhibition Mechanism. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 4811-4823.	2.9	21
14	Synthesis of diglycosylated (di)sulfides and comparative evaluation of their antiproliferative effect against tumor cell lines: A focus on the nature of sugar-recognizing mediators involved. <i>Carbohydrate Research</i> , 2019, 482, 107740.	1.1	10
15	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
16	Investigating the properties of TBA variants with twin thrombin binding domains. <i>Scientific Reports</i> , 2019, 9, 9184.	1.6	17
17	Cystatin B Involvement in Synapse Physiology of Rodent Brains and Human Cerebral Organoids. <i>Frontiers in Molecular Neuroscience</i> , 2019, 12, 195.	1.4	47
18	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

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19	A physicochemical investigation on the metal binding properties of TtSmtB, a thermophilic member of the ArsR/SmtB transcription factor family. <i>International Journal of Biological Macromolecules</i> , 2019, 138, 1056-1063.	3.6	7
20	Ubiquitin binds the amyloid β peptide and interferes with its clearance pathways. <i>Chemical Science</i> , 2019, 10, 2732-2742.	3.7	46
21	Molecular insights into the role of the polyalanine region in mediating α -synuclein aggregation. <i>FEBS Journal</i> , 2019, 286, 2505-2521.	2.2	9
22	Focusing on the functional characterization of the anserinase from <i>Oreochromis niloticus</i> . <i>International Journal of Biological Macromolecules</i> , 2019, 130, 158-165.	3.6	2
23	Design and analysis of EphA2-SAM peptide ligands: A multi-disciplinary screening approach. <i>Bioorganic Chemistry</i> , 2019, 84, 434-443.	2.0	11
24	A selective α -v β 5 integrin antagonist hidden into the anophelin family protein cE5 from the malaria vector <i>Anopheles gambiae</i> . <i>Peptide Science</i> , 2018, 110, e24054.	1.0	7
25	Biochemical characterization of a novel thermostable β -glucosidase from <i>Dictyoglomus turgidum</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 113, 783-791.	3.6	54
26	Metastatic group 3 medulloblastoma is driven by PRUNE1 targeting NME1 \rightarrow TGF- β \rightarrow OTX2 \rightarrow SNAIL via PTEN inhibition. <i>Brain</i> , 2018, 141, 1300-1319.	3.7	22
27	Folding mechanisms steer the amyloid fibril formation propensity of highly homologous proteins. <i>Chemical Science</i> , 2018, 9, 3290-3298.	3.7	18
28	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
29	MucR binds multiple target sites in the promoter of its own gene and is a heat-stable protein: Is MucR a H α -NS-like protein?. <i>FEBS Open Bio</i> , 2018, 8, 711-718.	1.0	15
30	Biochemical characterization of a thermostable endomannanase/endoglucanase from <i>Dictyoglomus turgidum</i> . <i>Extremophiles</i> , 2018, 22, 131-140.	0.9	19
31	Cell milieu significantly affects the fate of AApoAI amyloidogenic variants: predestination or serendipity?. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 377-384.	1.1	15
32	Identifying the region responsible for <i>Brucella abortus</i> MucR higher-order oligomer formation and examining its role in gene regulation. <i>Scientific Reports</i> , 2018, 8, 17238.	1.6	14
33	Sam domain-based stapled peptides: Structural analysis and interaction studies with the Sam domains from the EphA2 receptor and the lipid phosphatase Ship2. <i>Bioorganic Chemistry</i> , 2018, 80, 602-610.	2.0	17
34	Elucidating the role of the pLG72 R30K substitution in schizophrenia susceptibility. <i>FEBS Letters</i> , 2017, 591, 646-655.	1.3	8
35	A new cryptic host defense peptide identified in human 11-hydroxysteroid dehydrogenase-1 β -like: from in silico identification to experimental evidence. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2342-2353.	1.1	26
36	Insights into the anticancer properties of the first antimicrobial peptide from Archaea. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2155-2164.	1.1	29

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37	Structural investigation of a C-terminal EphA2 receptor mutant: Does mutation affect the structure and interaction properties of the Sam domain?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1095-1104.	1.1	3
38	Functional analyses yield detailed insight into the mechanism of thrombin inhibition by the antihemostatic salivary protein cE5 from <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 12632-12642.	1.6	20
39	Novel propanamides as fatty acid amide hydrolase inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2017, 136, 523-542.	2.6	10
40	The Sam-Sam interaction between Ship2 and the EphA2 receptor: design and analysis of peptide inhibitors. <i>Scientific Reports</i> , 2017, 7, 17474.	1.6	17
41	Ml proteins from <i>Mesorhizobium loti</i> and MucR from <i>Brucella abortus</i> : an AT-rich core DNA-target site and oligomerization ability. <i>Scientific Reports</i> , 2017, 7, 15805.	1.6	13
42	<i>Thermus thermophilus</i> as source of thermozymes for biotechnological applications: homologous expression and biochemical characterization of an L-galactosidase. <i>Microbial Cell Factories</i> , 2017, 16, 28.	1.9	38
43	The <sc>BTB</sc> domains of the potassium channel tetramerization domain proteins prevalently assume pentameric states. <i>FEBS Letters</i> , 2016, 590, 1663-1671.	1.3	25
44	Exploring the binding of d(GGGT) ₄ to the HIV-1 integrase: An approach to investigate G-quadruplex aptamer/target protein interactions. <i>Biochimie</i> , 2016, 127, 19-22.	1.3	25
45	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114.	1.3	6
46	Regulating levels of the neuromodulator <sc>d</sc>-serine in human brain: structural insight into pLG72 and <sc>d</sc>-amino acid oxidase interaction. <i>FEBS Journal</i> , 2016, 283, 3353-3370.	2.2	15
47	Targeting EphA2-Sam and Its Interactome: Design and Evaluation of Helical Peptides Enriched in Charged Residues. <i>ChemBioChem</i> , 2016, 17, 2179-2188.	1.3	14
48	A new cryptic cationic antimicrobial peptide from human apolipoprotein E with antibacterial activity and immunomodulatory effects on human cells. <i>FEBS Journal</i> , 2016, 283, 2115-2131.	2.2	54
49	A trans-kingdom antimicrobial peptide targeting cystic fibrosis pathogens. <i>Journal of Genetic Syndromes & Gene Therapy</i> , 2016, 7, .	0.2	0
50	The identification of a novel <i>Sulfolobus islandicus</i> CAMP-like peptide points to archaeal microorganisms as cell factories for the production of antimicrobial molecules. <i>Microbial Cell Factories</i> , 2015, 14, 126.	1.9	24
51	Peptide Fragments of Odin-Sam1: Conformational Analysis and Interaction Studies with EphA2-Sam. <i>ChemBioChem</i> , 2015, 16, 1629-1636.	1.3	13
52	Cullin3 - BTB Interface: A Novel Target for Stapled Peptides. <i>PLoS ONE</i> , 2015, 10, e0121149.	1.1	33
53	Cullin 3 Recognition Is Not a Universal Property among KCTD Proteins. <i>PLoS ONE</i> , 2015, 10, e0126808.	1.1	43
54	A therapeutic approach to treat prostate cancer by targeting Nm23-H1/h-Prune interaction. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2015, 388, 257-269.	1.4	20

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55	Insight into conformational modification of alpha-synuclein in the presence of neuronal whole cells and of their isolated membranes. <i>FEBS Letters</i> , 2015, 589, 798-804.	1.3	6
56	Interaction of the N-(3-Methylpyridin-2-yl)amide Derivatives of Flurbiprofen and Ibuprofen with FAAH: Enantiomeric Selectivity and Binding Mode. <i>PLoS ONE</i> , 2015, 10, e0142711.	1.1	12
57	Structural Model of the hUbA1-UbcH10 Quaternary Complex: In Silico and Experimental Analysis of the Protein-Protein Interactions between E1, E2 and Ubiquitin. <i>PLoS ONE</i> , 2014, 9, e112082.	1.1	7
58	Structural and functional studies of Stf76 from the <i>Sulfolobus islandicus</i> plasmid virus pSSVx: a novel peculiar member of the winged helix-turn-helix transcription factor family. <i>Nucleic Acids Research</i> , 2014, 42, 5993-6011.	6.5	24
59	<i>Sulfolobus solfataricus</i> thiol redox puzzle: characterization of an atypical protein disulfide oxidoreductase. <i>Extremophiles</i> , 2014, 18, 219-228.	0.9	13
60	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
61	Functional and structural characterization of protein disulfide oxidoreductase from <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2014, 18, 723-731.	0.9	4
62	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
63	A novel arsenate reductase from the bacterium <i>Thermus thermophilus</i> HB27: Its role in arsenic detoxification. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2071-2079.	1.1	48
64	Molecular basis of the PED/PEA15 interaction with the C-terminal fragment of phospholipase D1 revealed by NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1572-1580.	1.1	10
65	Heterotypic Sam-Sam Association between Odin-Sam1 and Arap3-Sam: Binding Affinity and Structural Insights. <i>ChemBioChem</i> , 2013, 14, 100-106.	1.3	19
66	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
67	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of the L, D-transpeptidase LdtMt1 from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 253-256.	0.7	5
68	Biochemical phenotype of a common disease-causing mutation and a possible therapeutic approach for the phosphomannomutase 2-associated disorder of glycosylation. <i>Molecular Genetics & Genomic Medicine</i> , 2013, 1, 32-44.	0.6	20
69	Structures of free and inhibited forms of the L, D-transpeptidase LdtMt1 from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1697-1706.	2.5	58
70	Mapping Functional Interaction Sites of Human Prune C-terminal Domain by NMR Spectroscopy in Human Cell Lysates. <i>Chemistry - A European Journal</i> , 2013, 19, 12217-12220.	1.7	12
71	Neuroblastoma tumorigenesis is regulated through the Nm23-H1/h-Prune C-terminal interaction. <i>Scientific Reports</i> , 2013, 3, 1351.	1.6	34
72	gH625 is a viral derived peptide for effective delivery of intrinsically disordered proteins. <i>International Journal of Nanomedicine</i> , 2013, 8, 2555.	3.3	20

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73	Responding to toxic compounds: a genomic and functional overview of Archaea. <i>Frontiers in Bioscience - Landmark</i> , 2013, 18, 165.	3.0	31
74	Solution Structure of the First Sam Domain of Odin and Binding Studies with the EphA2 Receptor. <i>Biochemistry</i> , 2012, 51, 2136-2145.	1.2	34
75	Mapping key interactions in the dimerization process of HBHA from <i>Mycobacterium tuberculosis</i> , insights into bacterial agglutination. <i>FEBS Letters</i> , 2012, 586, 659-667.	1.3	15
76	Molecular organization of the cullin E3 ligase adaptor KCTD11. <i>Biochimie</i> , 2011, 93, 715-724.	1.3	50
77	Heparin-binding hemagglutinin HBHA from <i>Mycobacterium tuberculosis</i> affects actin polymerisation. <i>Biochemical and Biophysical Research Communications</i> , 2011, 410, 339-344.	1.0	28
78	C68 from the <i>Sulfolobus islandicus</i> plasmid virus pSSVx is a novel member of the AbrB-like transcription factor family. <i>Biochemical Journal</i> , 2011, 435, 157-166.	1.7	24
79	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
80	Expression, Purification, Crystallization and Preliminary X-Ray Crystallographic Analysis of the Resuscitation Promoting Factor Interacting Protein RipA from <i>M. tuberculosis</i> . <i>Protein and Peptide Letters</i> , 2010, 17, 70-73.	0.4	10
81	Multiple catalytically active thioredoxin folds: a winning strategy for many functions. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3797-3814.	2.4	28
82	Structure and Functional Regulation of RipA, a Mycobacterial Enzyme Essential for Daughter Cell Separation. <i>Structure</i> , 2010, 18, 1184-1190.	1.6	73
83	Dimerisation and structural integrity of Heparin Binding Hemagglutinin A from <i>Mycobacterium tuberculosis</i> : Implications for bacterial agglutination. <i>FEBS Letters</i> , 2010, 584, 1091-1096.	1.3	16
84	NMR backbone dynamics studies of human PED/PEA15 outline protein functional sites. <i>FEBS Journal</i> , 2010, 277, 4229-4240.	2.2	10
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	Corrigendum for Pedone E, Limauro D, and Bartolucci S. The Machinery for Oxidative Protein Folding in Thermophiles. <i>Antioxid Redox Signal</i> 10:157-169, 2008. <i>Antioxidants and Redox Signaling</i> , 2010, 12, 171-179.	2.5	2
87	Exploring the catalytic mechanism of the first dimeric Bcp: Functional, structural and docking analyses of Bcp4 from <i>Sulfolobus solfataricus</i> . <i>Biochimie</i> , 2010, 92, 1435-1444.	1.3	20
88	Dynamical properties of cold shock protein A from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 402, 693-698.	1.0	13
89	High hydrostatic pressure-induced conformational changes in protein disulfide oxidoreductase from the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . A Fourier-transform infrared spectroscopic study. <i>Molecular BioSystems</i> , 2010, 6, 2015.	2.9	9
90	Insights into the catalytic mechanism of the Bcp family: Functional and structural analysis of Bcp1 from <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 995-1006.	1.5	25

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91	Crystal Structure of the Resuscitation-Promoting Factor $\hat{\Gamma}$ DUFpFB from <i>M. tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2009, 385, 153-162.	2.0	72
92	Peroxiredoxins as cellular guardians in <i>Sulfolobus solfataricus</i> characterization of Bcp1, Bcp3 and Bcp4. <i>FEBS Journal</i> , 2008, 275, 2067-2077.	2.2	35
93	The Machinery for Oxidative Protein Folding in Thermophiles. <i>Antioxidants and Redox Signaling</i> , 2008, 10, 157-170.	2.5	31
94	Evidence for an Elongated Dimeric Structure of Heparin-Binding Hemagglutinin from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2008, 190, 4749-4753.	1.0	28
95	<i>Sulfolobus solfataricus</i> protein disulphide oxidoreductase: insight into the roles of its redox sites. <i>Protein Engineering, Design and Selection</i> , 2008, 22, 19-26.	1.0	17
96	The prokaryotic Cys ₂ His ₂ zinc-finger adopts a novel fold as revealed by the NMR structure of <i>Agrobacterium tumefaciens</i> Ros DNA-binding domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17341-17346.	3.3	47
97	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of a resuscitation-promoting factor from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 870-873.	0.7	6
98	Insights on a New PDI-like Family: Structural and Functional Analysis of a Protein Disulfide Oxidoreductase from the Bacterium <i>Aquifex aeolicus</i> . <i>Journal of Molecular Biology</i> , 2006, 356, 155-164.	2.0	26
99	A Novel Member of the Protein Disulfide Oxidoreductase Family from <i>Aeropyrum pernix</i> K1: Structure, Function and Electrostatics. <i>Journal of Molecular Biology</i> , 2006, 362, 743-752.	2.0	21
100	Identification and characterization of 1-Cys peroxiredoxin from <i>Sulfolobus solfataricus</i> and its involvement in the response to oxidative stress. <i>FEBS Journal</i> , 2006, 273, 721-731.	2.2	36
101	Characterization of a multifunctional protein disulfide oxidoreductase from <i>Sulfolobus solfataricus</i> . <i>FEBS Journal</i> , 2006, 273, 5407-5420.	2.2	38
102	Crystallization and preliminary X-ray diffraction studies of a protein disulfide oxidoreductase from <i>Aeropyrum pernix</i> K1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 335-336.	0.7	4
103	Temperature-, SDS-, and pH-Induced Conformational Changes in Protein Disulfide Oxidoreductase from the Archaeon <i>Pyrococcus furiosus</i> : A Dynamic Simulation and Fourier Transform Infrared Spectroscopic Study. <i>Journal of Proteome Research</i> , 2005, 4, 1972-1980.	1.8	16
104	Sensing and adapting to environmental stress: the archaeal tactic. <i>Frontiers in Bioscience - Landmark</i> , 2004, 9, 2909.	3.0	37
105	Functional properties of the protein disulfide oxidoreductase from the archaeon <i>Pyrococcus furiosus</i> . <i>FEBS Journal</i> , 2004, 271, 3437-3448.	0.2	47
106	Crystallization and preliminary X-ray diffraction studies of a protein disulfide oxidoreductase from <i>Aquifex aeolicus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2076-2077.	2.5	6
107	Solution Structure and Backbone Dynamics of the K18G/R82E <i>Alicyclobacillus acidocaldarius</i> Thioredoxin Mutant: A Molecular Analysis of Its Reduced Thermal Stability. <i>Biochemistry</i> , 2004, 43, 6043-6058.	1.2	22
108	High-level expression of <i>Alicyclobacillus acidocaldarius</i> thioredoxin in <i>Pichia pastoris</i> and <i>Bacillus subtilis</i> . <i>Protein Expression and Purification</i> , 2003, 30, 179-184.	0.6	7

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109	An Integrated Structural and Computational Study of the Thermostability of Two Thioredoxin Mutants from <i>Alicyclobacillus acidocaldarius</i> . <i>Journal of Bacteriology</i> , 2003, 185, 4285-4289.	1.0	8
110	Structural and thermal stability analysis of <i>Escherichia coli</i> and <i>Alicyclobacillus acidocaldarius</i> thioredoxin revealed a molten globule-like state in thermal denaturation pathway of the proteins: an infrared spectroscopic study. <i>Biochemical Journal</i> , 2003, 373, 875-883.	1.7	37
111	A single point mutation (Glu85Arg) increases the stability of the thioredoxin from <i>Escherichia coli</i> . <i>Protein Engineering, Design and Selection</i> , 2001, 14, 255-260.	1.0	28
112	NMR solution structure of a novel thioredoxin from <i>Bacillus acidocaldarius</i> . <i>FEBS Journal</i> , 2000, 267, 403-413.	0.2	22
113	Prediction and experimental testing of <i>Bacillus acidocaldarius</i> thioredoxin stability1. <i>Biochemical Journal</i> , 1999, 339, 309-317.	1.7	18
114	Prediction and experimental testing of <i>Bacillus acidocaldarius</i> thioredoxin stability1. <i>Biochemical Journal</i> , 1999, 339, 309.	1.7	9
115	Prediction and experimental testing of <i>Bacillus acidocaldarius</i> thioredoxin stability. <i>Biochemical Journal</i> , 1999, 339 (Pt 2), 309-17.	1.7	7
116	Computational Analysis of the Thermal Stability in Thioredoxins: A Molecular Dynamics Approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 437-446.	2.0	14
117	Thioredoxin from <i>Bacillus acidocaldarius</i> : characterization, high-level expression in <i>Escherichia coli</i> and molecular modelling. <i>Biochemical Journal</i> , 1997, 328, 277-285.	1.7	27
118	Conformational studies of retro-inverso peptides: The crystal and molecular structure of the hydantoin from H-Ala-G-Ala-mGly-OBzl. <i>Biopolymers</i> , 1995, 36, 659-667.	1.2	11