

Andrei N Lupas

List of Publications by Year in descending order

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163
papers

19,240
citations

18436

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130
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181
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181
docs citations

181
times ranked

24275
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring protein-protein interactions at the proteome level. <i>Structure</i> , 2022, 30, 462-475.	1.6	13
2	RpuS/R Is a Novel Two-Component Signal Transduction System That Regulates the Expression of the Pyruvate Symporter MctP in <i>Sinorhizobium fredii</i> NGR234. <i>Frontiers in Microbiology</i> , 2022, 13, 871077.	1.5	1
3	A topological refactoring design strategy yields highly stable granulopoietic proteins. <i>Nature Communications</i> , 2022, 13, .	5.8	4
4	Archaeal Connectase is a specific and efficient protein ligase related to proteasome β^2 subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	7
5	The breakthrough in protein structure prediction. <i>Biochemical Journal</i> , 2021, 478, 1885-1890.	1.7	39
6	Editorial overview: Sequences and topology: α -paths from sequence to structure TM . <i>Current Opinion in Structural Biology</i> , 2021, 68, vi-viii.	2.6	2
7	High-accuracy protein structure prediction in α -CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1687-1699.	1.5	220
8	An astonishing wealth of new proteasome homologs. <i>Bioinformatics</i> , 2021, 37, 4694-4703.	1.8	3
9	Gram-negative outer-membrane proteins with multiple β^2 -barrel domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
10	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021, 433, 167127.	2.0	36
11	Assessing the utility of α -CASP14 models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	1.5	47
12	Computational models in the service of X-ray and cryo-electron microscopy structure determination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1633-1646.	1.5	37
13	Target highlights in α -CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
14	The VCBS superfamily forms a third supercluster of β^2 -propellers that includes tachylectin and integrins. <i>Bioinformatics</i> , 2021, 36, 5618-5622.	1.8	5
15	Native display of a huge homotrimeric protein fiber on the cell surface after precise domain deletion. <i>Journal of Bioscience and Bioengineering</i> , 2020, 129, 412-417.	1.1	2
16	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020, 20, 162.	3.2	11
17	A secreted fungal histidine- and alanine-rich protein regulates metal ion homeostasis and oxidative stress. <i>New Phytologist</i> , 2020, 227, 1174-1188.	3.5	35
18	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e108.	25.8	458

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19	Design of novel granulopoietic proteins by topological rescaffolding. <i>PLoS Biology</i> , 2020, 18, e3000919.	2.6	8
20	Structural diversity of coiled coils in protein fibers of the bacterial cell envelope. <i>International Journal of Medical Microbiology</i> , 2019, 309, 351-358.	1.5	5
21	Histones predate the split between bacteria and archaea. <i>Bioinformatics</i> , 2019, 35, 2349-2353.	1.8	17
22	Characterization of MCU-Binding Proteins MCUR1 and CCDC90B – Representatives of a Protein Family Conserved in Prokaryotes and Eukaryotic Organelles. <i>Structure</i> , 2019, 27, 464-475.e6.	1.6	19
23	Auto-regulation of Rab5 GEF activity in Rabex5 by allosteric structural changes, catalytic core dynamics and ubiquitin binding. <i>ELife</i> , 2019, 8, .	2.8	26
24	Structural diversity of oligomeric β^2 -propellers with different numbers of identical blades. <i>ELife</i> , 2019, 8, .	2.8	21
25	Adenylate cyclases: Receivers, transducers, and generators of signals. <i>Cellular Signalling</i> , 2018, 46, 135-144.	1.7	58
26	From ancestral peptides to designed proteins. <i>Current Opinion in Structural Biology</i> , 2018, 48, 103-109.	2.6	46
27	A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. <i>Journal of Molecular Biology</i> , 2018, 430, 2237-2243.	2.0	1,956
28	The Origin of Mitochondria-Specific Outer Membrane β^2 -Barrels from an Ancestral Bacterial Fragment. <i>Genome Biology and Evolution</i> , 2018, 10, 2759-2765.	1.1	16
29	Asymmetric protein design from conserved supersecondary structures. <i>Journal of Structural Biology</i> , 2018, 204, 380-387.	1.3	13
30	Chemical Ligand Space of Cereblon. <i>ACS Omega</i> , 2018, 3, 11163-11171.	1.6	43
31	An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. <i>ACS Synthetic Biology</i> , 2018, 7, 2226-2235.	1.9	11
32	The ancestral KH peptide at the root of a domain family with three different folds. <i>Bioinformatics</i> , 2018, 34, 3961-3965.	1.8	12
33	Characterization of a novel signal transducer element intrinsic to class IIIa/b adenylate cyclases and guanylate cyclases. <i>FEBS Journal</i> , 2017, 284, 1204-1217.	2.2	25
34	Ribosomal proteins as documents of the transition from unstructured (poly)peptides to folded proteins. <i>Journal of Structural Biology</i> , 2017, 198, 74-81.	1.3	42
35	N@<i>a</i> and N@<i>d</i>: Oligomer and Partner Specification by Asparagine in Coiled-Coil Interfaces. <i>ACS Chemical Biology</i> , 2017, 12, 528-538.	1.6	34
36	Coiled Coils – A Model System for the 21st Century. <i>Trends in Biochemical Sciences</i> , 2017, 42, 130-140.	3.7	173

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37	Characterization of the CrbS/R Two-Component System in <i>Pseudomonas fluorescens</i> Reveals a New Set of Genes under Its Control and a DNA Motif Required for CrbR-Mediated Transcriptional Activation. <i>Frontiers in Microbiology</i> , 2017, 8, 2287.	1.5	13
38	The Structure and Topology of β -Helical Coiled Coils. <i>Sub-Cellular Biochemistry</i> , 2017, 82, 95-129.	1.0	80
39	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	1.5	16
40	An endosomal tether undergoes an entropic collapse to bring vesicles together. <i>Nature</i> , 2016, 537, 107-111.	13.7	135
41	The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis. <i>Nucleic Acids Research</i> , 2016, 44, W410-W415.	6.5	369
42	The TULIP superfamily of eukaryotic lipid-binding proteins as a mediator of lipid sensing and transport. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2016, 1861, 913-923.	1.2	68
43	Structural Basis for Toughness and Flexibility in the C-terminal Passenger Domain of an <i>Acinetobacter</i> Trimeric Autotransporter Adhesin. <i>Journal of Biological Chemistry</i> , 2016, 291, 3705-3724.	1.6	41
44	β coiled coils. <i>ELife</i> , 2016, 5, .	2.8	27
45	Origin of a folded repeat protein from an intrinsically disordered ancestor. <i>ELife</i> , 2016, 5, .	2.8	43
46	A domain dictionary of trimeric autotransporter adhesins. <i>International Journal of Medical Microbiology</i> , 2015, 305, 265-275.	1.5	50
47	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	2.0	23
48	The Thalidomide-Binding Domain of Cereblon Defines the CULT Domain Family and Is a New Member of the β -Tent Fold. <i>PLoS Computational Biology</i> , 2015, 11, e1004023.	1.5	34
49	STAC ² A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. <i>Journal of Molecular Biology</i> , 2015, 427, 3327-3339.	2.0	17
50	Structural Dynamics of the Cereblon Ligand Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0128342.	1.1	22
51	A vocabulary of ancient peptides at the origin of folded proteins. <i>ELife</i> , 2015, 4, e09410.	2.8	199
52	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	1.6	28
53	What I cannot create, I do not understand. <i>Science</i> , 2014, 346, 1455-1456.	6.0	7
54	Thalidomide mimics uridine binding to an aromatic cage in cereblon. <i>Journal of Structural Biology</i> , 2014, 188, 225-232.	1.3	54

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55	Crystallographic snapshot of the Escherichia coli EnvZ histidine kinase in an active conformation. Journal of Structural Biology, 2014, 186, 376-379.	1.3	46
56	A soluble mutant of the transmembrane receptor Af1503 features strong changes in coiled-coil periodicity. Journal of Structural Biology, 2014, 186, 357-366.	1.3	15
57	Axial helix rotation as a mechanism for signal regulation inferred from the crystallographic analysis of the E. coli serine chemoreceptor. Journal of Structural Biology, 2014, 186, 349-356.	1.3	50
58	Prokaryotic Ancestry of Eukaryotic Protein Networks Mediating Innate Immunity and Apoptosis. Journal of Molecular Biology, 2014, 426, 1568-1582.	2.0	23
59	Archaeal Proteasome. , 2013, , 3666-3671.		0
60	The First Prokaryotic Trehalose Synthase Complex Identified in the Hyperthermophilic Crenarchaeon Thermoproteus tenax. PLoS ONE, 2013, 8, e61354.	1.1	18
61	Î²-Propeller Blades as Ancestral Peptides in Protein Evolution. PLoS ONE, 2013, 8, e77074.	1.1	77
62	The Archaeal Proteasome Is Regulated by a Network of AAA ATPases. Journal of Biological Chemistry, 2012, 287, 39254-39262.	1.6	42
63	Delineation of structural domains and identification of functionally important residues in DNA repair enzyme exonuclease VII. Nucleic Acids Research, 2012, 40, 8163-8174.	6.5	13
64	Structure and function of tripeptidyl peptidase II, a giant cytosolic protease. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 237-245.	1.1	22
65	Complete fiber structures of complex trimeric autotransporter adhesins conserved in enterobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20907-20912.	3.3	57
66	HAMP Domain-mediated Signal Transduction Probed with a Mycobacterial Adenylyl Cyclase as a Reporter. Journal of Biological Chemistry, 2012, 287, 1022-1031.	1.6	27
67	Mechanism of Regulation of Receptor Histidine Kinases. Structure, 2012, 20, 56-66.	1.6	87
68	Crystal structure of a dimeric archaeal Cleavage and Polyadenylation Specificity Factor. Journal of Structural Biology, 2011, 173, 191-195.	1.3	31
69	Evolutionary Relationships of Microbial Aromatic Prenyltransferases. PLoS ONE, 2011, 6, e27336.	1.1	73
70	Bioinformatics of the TULIP domain superfamily. Biochemical Society Transactions, 2011, 39, 1033-1038.	1.6	48
71	The Mechanisms of HAMP-Mediated Signaling in Transmembrane Receptors. Structure, 2011, 19, 378-385.	1.6	86
72	The Structure of E.Âcoli IgG-Binding Protein D Suggests a General Model for Bending and Binding in Trimeric Autotransporter Adhesins. Structure, 2011, 19, 1021-1030.	1.6	66

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73	A galaxy of folds. <i>Protein Science</i> , 2010, 19, 124-130.	3.1	71
74	The use of FLP-mediated recombination for the functional analysis of an effector gene family in the biotrophic smut fungus <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2010, 187, 957-968.	3.5	93
75	A polycystin-2 (TRPP2) dimerization domain essential for the function of heteromeric polycystin complexes. <i>EMBO Journal</i> , 2010, 29, 1176-1191.	3.5	70
76	SMG6 interacts with the exon junction complex via two conserved EJC-binding motifs (EBMs) required for nonsense-mediated mRNA decay. <i>Genes and Development</i> , 2010, 24, 2440-2450.	2.7	63
77	Homology of SMP domains to the TULIP superfamily of lipid-binding proteins provides a structural basis for lipid exchange between ER and mitochondria. <i>Bioinformatics</i> , 2010, 26, 1927-1931.	1.8	192
78	Measuring the conformational space of square four-helical bundles with the program samCC. <i>Journal of Structural Biology</i> , 2010, 170, 226-235.	1.3	36
79	A transition from strong right-handed to canonical left-handed supercoiling in a conserved coiled-coil segment of trimeric autotransporter adhesins. <i>Journal of Structural Biology</i> , 2010, 170, 236-245.	1.3	41
80	Comprehensive Analysis of HAMP Domains: Implications for Transmembrane Signal Transduction. <i>Journal of Molecular Biology</i> , 2010, 397, 1156-1174.	2.0	79
81	A coiled-coil motif that sequesters ions to the hydrophobic core. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16950-16955.	3.3	77
82	The GD box: A widespread noncontiguous supersecondary structural element. <i>Protein Science</i> , 2009, 18, 1961-1966.	3.1	15
83	Crystal Structure of SpoVT, the Final Modulator of Gene Expression during Spore Development in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2009, 386, 962-975.	2.0	18
84	Structure and Activity of the N-Terminal Substrate Recognition Domains in Proteasomal ATPases. <i>Molecular Cell</i> , 2009, 34, 580-590.	4.5	116
85	HHomp prediction and classification of outer membrane proteins. <i>Nucleic Acids Research</i> , 2009, 37, W446-W451.	6.5	86
86	Two unique membrane-bound AAA proteins from <i>Sulfolobus solfataricus</i> . <i>Biochemical Society Transactions</i> , 2009, 37, 118-122.	1.6	1
87	Evolution of the Î propeller fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 795-803.	1.5	128
88	The head of <i>Bartonella</i> adhesin A is crucial for host cell interaction of <i>Bartonella henselae</i> . <i>Cellular Microbiology</i> , 2008, 10, 2223-2234.	1.1	66
89	Cradle-loop barrels and the concept of metafolds in protein classification by natural descent. <i>Current Opinion in Structural Biology</i> , 2008, 18, 358-365.	2.6	57
90	The long coming of computational structural biology. <i>Journal of Structural Biology</i> , 2008, 163, 254-257.	1.3	7

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91	Structure of the Head of the Bartonella Adhesin BadA. PLoS Pathogens, 2008, 4, e1000119.	2.1	70
92	Domain annotation of trimeric autotransporter adhesins daTAA. Bioinformatics, 2008, 24, 1251-1256.	1.8	98
93	Functional Mapping of YadA- and Ail-Mediated Binding of Human Factor H to <i>Yersinia enterocolitica</i> Serotype O:3. Infection and Immunity, 2008, 76, 5016-5027.	1.0	55
94	The <i>Sulfolobus solfataricus</i> AAA protein Sso0909, a homologue of the eukaryotic ESCRT Vps4 ATPase. Biochemical Society Transactions, 2008, 36, 94-98.	1.6	30
95	A Conserved Glycine Residue of Trimeric Autotransporter Domains Plays a Key Role in <i>Yersinia</i> Adhesin A Autotransport. Journal of Bacteriology, 2007, 189, 9011-9019.	1.0	67
96	A new expression system for protein crystallization using trimeric coiled-coil adaptors. Protein Engineering, Design and Selection, 2007, 21, 11-18.	1.0	36
97	Gene Duplication of the Eight-stranded β -Barrel OmpX Produces a Functional Pore: A Scenario for the Evolution of Transmembrane β -Barrels. Journal of Molecular Biology, 2007, 366, 1174-1184.	2.0	86
98	prfF and yhaV Encode a New Toxin-Antitoxin System in Escherichia coli. Journal of Molecular Biology, 2007, 372, 894-905.	2.0	87
99	On the origin of the histone fold. BMC Structural Biology, 2007, 7, 17.	2.3	45
100	Salmonella Pathogenicity Island 4 encodes a giant non-fimbrial adhesin and the cognate type 1 secretion system. Cellular Microbiology, 2007, 9, 1834-1850.	1.1	163
101	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. BMC Bioinformatics, 2007, 8, 2.	1.2	194
102	A CTP-Dependent Archaeal Riboflavin Kinase Forms a Bridge in the Evolution of Cradle-Loop Barrels. Structure, 2007, 15, 1577-1590.	1.6	29
103	Inherent chaperone-like activity of aspartic proteases reveals a distant evolutionary relation to double- β barrel domains of AAA-ATPases. Protein Science, 2007, 16, 644-653.	3.1	11
104	The HAMP Domain Structure Implies Helix Rotation in Transmembrane Signaling. Cell, 2006, 126, 929-940.	13.5	351
105	Purification of the YadA membrane anchor for secondary structure analysis and crystallization. International Journal of Biological Macromolecules, 2006, 39, 3-9.	3.6	52
106	Comparative analysis of coiled-coil prediction methods. Journal of Structural Biology, 2006, 155, 140-145.	1.3	150
107	Characterization of AMA, a new AAA protein from Archaeoglobus and methanogenic archaea. Journal of Structural Biology, 2006, 156, 130-138.	1.3	5
108	Model structure of the prototypical non-fimbrial adhesin YadA of Yersinia enterocolitica. Journal of Structural Biology, 2006, 155, 154-161.	1.3	65

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109	Modeling AAA+ ring complexes from monomeric structures. <i>Journal of Structural Biology</i> , 2006, 156, 230-243.	1.3	58
110	Classification of AAA+ proteins. <i>Journal of Structural Biology</i> , 2006, 156, 2-11.	1.3	135
111	Trimeric autotransporter adhesins: variable structure, common function. <i>Trends in Microbiology</i> , 2006, 14, 264-270.	3.5	275
112	Common Evolutionary Origin of Swapped-Hairpin and Double-Psi $\hat{\Gamma}^2$ Barrels. <i>Structure</i> , 2006, 14, 1489-1498.	1.6	36
113	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. <i>Nucleic Acids Research</i> , 2006, 34, W374-W378.	6.5	72
114	The MPI Bioinformatics Toolkit for protein sequence analysis. <i>Nucleic Acids Research</i> , 2006, 34, W335-W339.	6.5	247
115	AbrB-like Transcription Factors Assume a Swapped Hairpin Fold that Is Evolutionarily Related to Double-Psi $\hat{\Gamma}^2$ Barrels. <i>Structure</i> , 2005, 13, 919-928.	1.6	78
116	The HHpred interactive server for protein homology detection and structure prediction. <i>Nucleic Acids Research</i> , 2005, 33, W244-W248.	6.5	3,246
117	REPPER—repeats and their periodicities in fibrous proteins. <i>Nucleic Acids Research</i> , 2005, 33, W239-W243.	6.5	118
118	The Structure of $\hat{\Gamma}^{\pm}$ -Helical Coiled Coils. <i>Advances in Protein Chemistry</i> , 2005, 70, 37-38.	4.4	594
119	Bartonella Adhesin A Mediates a Proangiogenic Host Cell Response. <i>Journal of Experimental Medicine</i> , 2004, 200, 1267-1278.	4.2	193
120	PhyloGenie: automated phylome generation and analysis. <i>Nucleic Acids Research</i> , 2004, 32, 5231-5238.	6.5	98
121	<i>Thermoplasma acidophilum</i> TAA43 is an archaeal member of the eukaryotic meiotic branch of AAA ATPases. <i>Biological Chemistry</i> , 2004, 385, 1105-11.	1.2	7
122	WIPI-1 $\hat{\Gamma}^{\pm}$ (WIPI49), a member of the novel 7-bladed WIPI protein family, is aberrantly expressed in human cancer and is linked to starvation-induced autophagy. <i>Oncogene</i> , 2004, 23, 9314-9325.	2.6	322
123	Coiled coils meet the chaperone world. <i>Trends in Biochemical Sciences</i> , 2004, 29, 455-458.	3.7	35
124	Phylogenetic analysis of AAA proteins. <i>Journal of Structural Biology</i> , 2004, 146, 2-10.	1.3	188
125	CLANS: a Java application for visualizing protein families based on pairwise similarity. <i>Bioinformatics</i> , 2004, 20, 3702-3704.	1.8	641
126	Historical review: Another 50th anniversary — new periodicities in coiled coils. <i>Trends in Biochemical Sciences</i> , 2003, 28, 679-685.	3.7	134

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127	More than the sum of their parts: On the evolution of proteins from peptides. <i>BioEssays</i> , 2003, 25, 837-846.	1.2	229
128	Bioinformatic analysis of ClpS, a protein module involved in prokaryotic and eukaryotic protein degradation. <i>Journal of Structural Biology</i> , 2003, 141, 77-83.	1.3	57
129	Barentsz, a New Component of the Staufen-Containing Ribonucleoprotein Particles in Mammalian Cells, Interacts with Staufen in an RNA-Dependent Manner. <i>Journal of Neuroscience</i> , 2003, 23, 5778-5788.	1.7	88
130	AAA proteins. <i>Current Opinion in Structural Biology</i> , 2002, 12, 746-753.	2.6	319
131	Fold recognition without folds. <i>Protein Science</i> , 2002, 11, 1575-1579.	3.1	20
132	On the Evolution of Protein Folds: Are Similar Motifs in Different Protein Folds the Result of Convergence, Insertion, or Relics of an Ancient Peptide World?. <i>Journal of Structural Biology</i> , 2001, 134, 191-203.	1.3	276
133	Phylogenetic analyses do not support horizontal gene transfers from bacteria to vertebrates. <i>Nature</i> , 2001, 411, 940-944.	13.7	211
134	Systematic Identification of Selective Essential Genes in <i>Helicobacter pylori</i> by Genome Prioritization and Allelic Replacement Mutagenesis. <i>Journal of Bacteriology</i> , 2001, 183, 1259-1268.	1.0	151
135	Evolution of Two-Component Signal Transduction. <i>Molecular Biology and Evolution</i> , 2000, 17, 1956-1970.	3.5	269
136	The genome sequence of the thermoacidophilic scavenger <i>Thermoplasma acidophilum</i> . <i>Nature</i> , 2000, 407, 508-513.	13.7	390
137	The Janus Face of the Archaeal Cdc48/p97 Homologue VAT: Protein Folding versus Unfolding. <i>Biological Chemistry</i> , 1999, 380, 1049-62.	1.2	77
138	Structure and mechanism of ATP-dependent proteases. <i>Current Opinion in Chemical Biology</i> , 1999, 3, 584-591.	2.8	68
139	Fold recognition using sequence and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 141-148.	1.5	43
140	Novel molecular architecture of the multimeric archaeal PEP-synthase homologue (MAPS) from <i>Staphylothermus marinus</i> 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 290, 347-361.	2.0	14
141	What makes a thermophile?. <i>Trends in Microbiology</i> , 1998, 6, 349-351.	3.5	5
142	Characterization of ARC, a divergent member of the AAA ATPase family from <i>Rhodococcus erythropolis</i> . <i>Journal of Molecular Biology</i> , 1998, 277, 13-25.	2.0	107
143	The thermosome: alternating $\hat{1}\pm$ and $\hat{1}^2$ -subunits within the chaperonin of the archaeon <i>Thermoplasma acidophilum</i> . <i>Journal of Molecular Biology</i> , 1997, 267, 142-149.	2.0	56
144	Cloning, sequencing and expression of VAT, a CDC48/p97 ATPase homologue from the archaeon <i>Thermoplasma acidophilum</i> . <i>FEBS Letters</i> , 1997, 404, 263-268.	1.3	59

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145	Self-compartmentalizing proteases. Trends in Biochemical Sciences, 1997, 22, 399-404.	3.7	223
146	Eubacterial proteasomes. Molecular Biology Reports, 1997, 24, 125-131.	1.0	48
147	Classification of tyrosine kinases from Dictyostelium discoideum with two distinct, complete or incomplete catalytic domains. FEBS Letters, 1996, 395, 286-292.	1.3	28
148	Hyperthermostable Surface Layer Protein Tetrabrachion from the Archaeobacterium Staphylothermus marinus: Evidence for the Presence of a Right-handed Coiled Coil Derived from the Primary Structure. Journal of Molecular Biology, 1996, 257, 1031-1041.	2.0	115
149	[30] Prediction and analysis of coiled-coil structures. Methods in Enzymology, 1996, 266, 513-525.	0.4	539
150	A hyperthermostable protease of the subtilisin family bound to the surface layer of the Archaeon Staphylothermus marinus. Current Biology, 1996, 6, 739-749.	1.8	71
151	A circular permutation event in the evolution of the SLH domain?. Molecular Microbiology, 1996, 20, 897-898.	1.2	31
152	Autocatalytic processing of the 20S proteasome. Nature, 1996, 382, 468-470.	13.7	231
153	The first characterization of a eubacterial proteasome: the 20S complex of Rhodococcus. Current Biology, 1995, 5, 766-774.	1.8	190
154	Structural features of archaeobacterial and eukaryotic proteasomes. Molecular Biology Reports, 1995, 21, 11-20.	1.0	26
155	A Mouse Ig \hat{H} Domain of Very Unusual Framework Structure Loses Function when Converted to the Consensus. Journal of Biological Chemistry, 1995, 270, 12446-12451.	1.6	6
156	Tetrabrachion: A Filamentous Archaeobacterial Surface Protein Assembly of Unusual Structure and Extreme Stability. Journal of Molecular Biology, 1995, 245, 385-401.	2.0	112
157	Model Structure of the Omp $\hat{\pm}$ Rod, a Parallel Four-stranded Coiled Coil from the Hyperthermophilic Eubacterium Thermotoga maritima. Journal of Molecular Biology, 1995, 248, 180-189.	2.0	58
158	The proteasome from Thermoplasma acidophilum is neither a cysteine nor a serine protease. FEBS Letters, 1995, 359, 173-178.	1.3	48
159	Proteasome sequences in eubacteria. Trends in Biochemical Sciences, 1994, 19, 533-534.	3.7	67
160	Predicted secondary structure of the 20 S proteasome and model structure of the putative peptide channel. FEBS Letters, 1994, 354, 45-49.	1.3	18
161	Folding and trimerization of clathrin subunits at the triskelion hub. Cell, 1992, 68, 899-910.	13.5	152
162	Do G protein subunits associate via a three-stranded coiled coil?. FEBS Letters, 1992, 314, 105-108.	1.3	54

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163	New Î ² -Propellers Are Continuously Amplified From Single Blades in all Major Lineages of the Î ² -Propeller Superfamily. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	1