

Andrei N Lupas

List of Publications by Year in descending order

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163
papers

19,240
citations

18436

62
h-index

13338

130
g-index

181
all docs

181
docs citations

181
times ranked

24275
citing authors

#	ARTICLE	IF	CITATIONS
1	The HHpred interactive server for protein homology detection and structure prediction. <i>Nucleic Acids Research</i> , 2005, 33, W244-W248.	6.5	3,246
2	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
3	CLANS: a Java application for visualizing protein families based on pairwise similarity. <i>Bioinformatics</i> , 2004, 20, 3702-3704.	1.8	641
4	The Structure of α -Helical Coiled Coils. <i>Advances in Protein Chemistry</i> , 2005, 70, 37-38.	4.4	594
5	[30] Prediction and analysis of coiled-coil structures. <i>Methods in Enzymology</i> , 1996, 266, 513-525.	0.4	539
6	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e108.	25.8	458
7	The genome sequence of the thermoacidophilic scavenger <i>Thermoplasma acidophilum</i> . <i>Nature</i> , 2000, 407, 508-513.	13.7	390
8	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
9	The HAMP Domain Structure Implies Helix Rotation in Transmembrane Signaling. <i>Cell</i> , 2006, 126, 929-940.	13.5	351
10	WIPI-1 α (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
11	AAA proteins. <i>Current Opinion in Structural Biology</i> , 2002, 12, 746-753.	2.6	319
12	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
13	Trimeric autotransporter adhesins: variable structure, common function. <i>Trends in Microbiology</i> , 2006, 14, 264-270.	3.5	275
14	Evolution of Two-Component Signal Transduction. <i>Molecular Biology and Evolution</i> , 2000, 17, 1956-1970.	3.5	269
15	The MPI Bioinformatics Toolkit for protein sequence analysis. <i>Nucleic Acids Research</i> , 2006, 34, W335-W339.	6.5	247
16	Autocatalytic processing of the 20S proteasome. <i>Nature</i> , 1996, 382, 468-470.	13.7	231
17	More than the sum of their parts: On the evolution of proteins from peptides. <i>BioEssays</i> , 2003, 25, 837-846.	1.2	229
18	Self-compartmentalizing proteases. <i>Trends in Biochemical Sciences</i> , 1997, 22, 399-404.	3.7	223

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19	High accuracy protein structure prediction in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1687-1699.	1.5	220
20	Phylogenetic analyses do not support horizontal gene transfers from bacteria to vertebrates. <i>Nature</i> , 2001, 411, 940-944.	13.7	211
21	A vocabulary of ancient peptides at the origin of folded proteins. <i>ELife</i> , 2015, 4, e09410.	2.8	199
22	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. <i>BMC Bioinformatics</i> , 2007, 8, 2.	1.2	194
23	Bartonella Adhesin A Mediates a Proangiogenic Host Cell Response. <i>Journal of Experimental Medicine</i> , 2004, 200, 1267-1278.	4.2	193
24	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
25	The first characterization of a eubacterial proteasome: the 20S complex of <i>Rhodococcus</i> . <i>Current Biology</i> , 1995, 5, 766-774.	1.8	190
26	Phylogenetic analysis of AAA proteins. <i>Journal of Structural Biology</i> , 2004, 146, 2-10.	1.3	188
27	Coiled Coils – A Model System for the 21st Century. <i>Trends in Biochemical Sciences</i> , 2017, 42, 130-140.	3.7	173
28	Salmonella Pathogenicity Island 4 encodes a giant non-fimbrial adhesin and the cognate type 1 secretion system. <i>Cellular Microbiology</i> , 2007, 9, 1834-1850.	1.1	163
29	Folding and trimerization of clathrin subunits at the triskelion hub. <i>Cell</i> , 1992, 68, 899-910.	13.5	152
30	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
31	Comparative analysis of coiled-coil prediction methods. <i>Journal of Structural Biology</i> , 2006, 155, 140-145.	1.3	150
32	Classification of AAA+ proteins. <i>Journal of Structural Biology</i> , 2006, 156, 2-11.	1.3	135
33	An endosomal tether undergoes an entropic collapse to bring vesicles together. <i>Nature</i> , 2016, 537, 107-111.	13.7	135
34	Historical review: Another 50th anniversary – new periodicities in coiled coils. <i>Trends in Biochemical Sciences</i> , 2003, 28, 679-685.	3.7	134
35	Evolution of the Î²-propeller fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 795-803.	1.5	128
36	REPPER–repeats and their periodicities in fibrous proteins. <i>Nucleic Acids Research</i> , 2005, 33, W239-W243.	6.5	118

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37	Structure and Activity of the N-Terminal Substrate Recognition Domains in Proteasomal ATPases. <i>Molecular Cell</i> , 2009, 34, 580-590.	4.5	116
38	Hyperthermostable Surface Layer Protein Tetrabrachion from the Archaeobacterium <i>Staphylothermus marinus</i> : Evidence for the Presence of a Right-handed Coiled Coil Derived from the Primary Structure. <i>Journal of Molecular Biology</i> , 1996, 257, 1031-1041.	2.0	115
39	Tetrabrachion: A Filamentous Archaeobacterial Surface Protein Assembly of Unusual Structure and Extreme Stability. <i>Journal of Molecular Biology</i> , 1995, 245, 385-401.	2.0	112
40	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
41	PhyloGenie: automated phylome generation and analysis. <i>Nucleic Acids Research</i> , 2004, 32, 5231-5238.	6.5	98
42	Domain annotation of trimeric autotransporter adhesins. <i>Bioinformatics</i> , 2008, 24, 1251-1256.	1.8	98
43	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
44	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
45	prf and yhaV Encode a New Toxin-Antitoxin System in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 894-905.	2.0	87
46	Mechanism of Regulation of Receptor Histidine Kinases. <i>Structure</i> , 2012, 20, 56-66.	1.6	87
47	Gene Duplication of the Eight-stranded β -Barrel OmpX Produces a Functional Pore: A Scenario for the Evolution of Transmembrane β -Barrels. <i>Journal of Molecular Biology</i> , 2007, 366, 1174-1184.	2.0	86
48	HHomoprediction and classification of outer membrane proteins. <i>Nucleic Acids Research</i> , 2009, 37, W446-W451.	6.5	86
49	The Mechanisms of HAMP-Mediated Signaling in Transmembrane Receptors. <i>Structure</i> , 2011, 19, 378-385.	1.6	86
50	The Structure and Topology of α -Helical Coiled Coils. <i>Sub-Cellular Biochemistry</i> , 2017, 82, 95-129.	1.0	80
51	Comprehensive Analysis of HAMP Domains: Implications for Transmembrane Signal Transduction. <i>Journal of Molecular Biology</i> , 2010, 397, 1156-1174.	2.0	79
52	AbrB-like Transcription Factors Assume a Swapped Hairpin Fold that Is Evolutionarily Related to Double- β Barrels. <i>Structure</i> , 2005, 13, 919-928.	1.6	78
53	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
54	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

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55	Î²-Propeller Blades as Ancestral Peptides in Protein Evolution. PLoS ONE, 2013, 8, e77074.	1.1	77
56	Evolutionary Relationships of Microbial Aromatic Prenyltransferases. PLoS ONE, 2011, 6, e27336.	1.1	73
57	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. Nucleic Acids Research, 2006, 34, W374-W378.	6.5	72
58	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
59	A galaxy of folds. Protein Science, 2010, 19, 124-130.	3.1	71
60	Structure of the Head of the Bartonella Adhesin BadA. PLoS Pathogens, 2008, 4, e1000119.	2.1	70
61	A polycystin-2 (TRPP2) dimerization domain essential for the function of heteromeric polycystin complexes. EMBO Journal, 2010, 29, 1176-1191.	3.5	70
62	Structure and mechanism of ATP-dependent proteases. Current Opinion in Chemical Biology, 1999, 3, 584-591.	2.8	68
63	The TULIP superfamily of eukaryotic lipid-binding proteins as a mediator of lipid sensing and transport. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 913-923.	1.2	68
64	Proteasome sequences in eubacteria. Trends in Biochemical Sciences, 1994, 19, 533-534.	3.7	67
65	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
66	The head of <i>Bartonella</i> adhesin A is crucial for host cell interaction of <i>Bartonella henselae</i> . Cellular Microbiology, 2008, 10, 2223-2234.	1.1	66
67	The Structure of E. coli IgG-Binding Protein D Suggests a General Model for Bending and Binding in Trimeric Autotransporter Adhesins. Structure, 2011, 19, 1021-1030.	1.6	66
68	Model structure of the prototypical non-fimbrial adhesin YadA of <i>Yersinia enterocolitica</i> . Journal of Structural Biology, 2006, 155, 154-161.	1.3	65
69	SMG6 interacts with the exon junction complex via two conserved EJC-binding motifs (EBMs) required for nonsense-mediated mRNA decay. Genes and Development, 2010, 24, 2440-2450.	2.7	63
70	Cloning, sequencing and expression of VAT, a CDC48/p97 ATPase homologue from the archaeon <i>Thermoplasma acidophilum</i> . FEBS Letters, 1997, 404, 263-268.	1.3	59
71	Model Structure of the OmpA Rod, a Parallel Four-stranded Coiled Coil from the Hyperthermophilic Eubacterium <i>Thermotoga maritima</i> . Journal of Molecular Biology, 1995, 248, 180-189.	2.0	58
72	Modeling AAA+ ring complexes from monomeric structures. Journal of Structural Biology, 2006, 156, 230-243.	1.3	58

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73	Adenylate cyclases: Receivers, transducers, and generators of signals. <i>Cellular Signalling</i> , 2018, 46, 135-144.	1.7	58
74	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
75	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
76	Complete fiber structures of complex trimeric autotransporter adhesins conserved in enterobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20907-20912.	3.3	57
77	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
78	Functional Mapping of YadA- and Ail-Mediated Binding of Human Factor H to <i>Yersinia enterocolitica</i> Serotype O:3. <i>Infection and Immunity</i> , 2008, 76, 5016-5027.	1.0	55
79	Do G protein subunits associate via a three-stranded coiled coil?. <i>FEBS Letters</i> , 1992, 314, 105-108.	1.3	54
80	Thalidomide mimics uridine binding to an aromatic cage in cereblon. <i>Journal of Structural Biology</i> , 2014, 188, 225-232.	1.3	54
81	Purification of the YadA membrane anchor for secondary structure analysis and crystallization. <i>International Journal of Biological Macromolecules</i> , 2006, 39, 3-9.	3.6	52
82	Axial helix rotation as a mechanism for signal regulation inferred from the crystallographic analysis of the <i>E. coli</i> serine chemoreceptor. <i>Journal of Structural Biology</i> , 2014, 186, 349-356.	1.3	50
83	A domain dictionary of trimeric autotransporter adhesins. <i>International Journal of Medical Microbiology</i> , 2015, 305, 265-275.	1.5	50
84	The proteasome from <i>Thermoplasma acidophilum</i> is neither a cysteine nor a serine protease. <i>FEBS Letters</i> , 1995, 359, 173-178.	1.3	48
85	Eubacterial proteasomes. <i>Molecular Biology Reports</i> , 1997, 24, 125-131.	1.0	48
86	Bioinformatics of the TULIP domain superfamily. <i>Biochemical Society Transactions</i> , 2011, 39, 1033-1038.	1.6	48
87	Assessing the utility of <i>CASP14</i> models for molecular replacement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1752-1769.	1.5	47
88	Crystallographic snapshot of the <i>Escherichia coli</i> EnvZ histidine kinase in an active conformation. <i>Journal of Structural Biology</i> , 2014, 186, 376-379.	1.3	46
89	From ancestral peptides to designed proteins. <i>Current Opinion in Structural Biology</i> , 2018, 48, 103-109.	2.6	46
90	On the origin of the histone fold. <i>BMC Structural Biology</i> , 2007, 7, 17.	2.3	45

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91	Fold recognition using sequence and secondary structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 141-148.	1.5	43
92	Chemical Ligand Space of Cereblon. <i>ACS Omega</i> , 2018, 3, 11163-11171.	1.6	43
93	Origin of a folded repeat protein from an intrinsically disordered ancestor. <i>ELife</i> , 2016, 5, .	2.8	43
94	The Archaeal Proteasome Is Regulated by a Network of AAA ATPases. <i>Journal of Biological Chemistry</i> , 2012, 287, 39254-39262.	1.6	42
95	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
96	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
97	Structural Basis for Toughness and Flexibility in the C-terminal Passenger Domain of an Acinetobacter Trimeric Autotransporter Adhesin. <i>Journal of Biological Chemistry</i> , 2016, 291, 3705-3724.	1.6	41
98	The breakthrough in protein structure prediction. <i>Biochemical Journal</i> , 2021, 478, 1885-1890.	1.7	39
99	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
100	Common Evolutionary Origin of Swapped-Hairpin and Double-Psi β^2 Barrels. <i>Structure</i> , 2006, 14, 1489-1498.	1.6	36
101	A new expression system for protein crystallization using trimeric coiled-coil adaptors. <i>Protein Engineering, Design and Selection</i> , 2007, 21, 11-18.	1.0	36
102	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
103	Integrative Structural Biology in the Era of Accurate Structure Prediction. <i>Journal of Molecular Biology</i> , 2021, 433, 167127.	2.0	36
104	Coiled coils meet the chaperone world. <i>Trends in Biochemical Sciences</i> , 2004, 29, 455-458.	3.7	35
105	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
106	The Thalidomide-Binding Domain of Cereblon Defines the CULT Domain Family and Is a New Member of the β^2 -Tent Fold. <i>PLoS Computational Biology</i> , 2015, 11, e1004023.	1.5	34
107	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
108	A circular permutation event in the evolution of the SLH domain?. <i>Molecular Microbiology</i> , 1996, 20, 897-898.	1.2	31

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109	Crystal structure of a dimeric archaeal Cleavage and Polyadenylation Specificity Factor. <i>Journal of Structural Biology</i> , 2011, 173, 191-195.	1.3	31
110	The <i>Sulfolobus solfataricus</i> AAA protein Sso0909, a homologue of the eukaryotic ESCRT Vps4 ATPase. <i>Biochemical Society Transactions</i> , 2008, 36, 94-98.	1.6	30
111	A CTP-Dependent Archaeal Riboflavin Kinase Forms a Bridge in the Evolution of Cradle-Loop Barrels. <i>Structure</i> , 2007, 15, 1577-1590.	1.6	29
112	Classification of tyrosine kinases from <i>Dictyostelium discoideum</i> with two distinct, complete or incomplete catalytic domains. <i>FEBS Letters</i> , 1996, 395, 286-292.	1.3	28
113	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	1.6	28
114	HAMP Domain-mediated Signal Transduction Probed with a Mycobacterial Adenylyl Cyclase as a Reporter. <i>Journal of Biological Chemistry</i> , 2012, 287, 1022-1031.	1.6	27
115	Target highlights in CASP14: Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
116	$\hat{1}\pm/\hat{1}^2$ coiled coils. <i>ELife</i> , 2016, 5, .	2.8	27
117	Structural features of archaeobacterial and eukaryotic proteasomes. <i>Molecular Biology Reports</i> , 1995, 21, 11-20.	1.0	26
118	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
119	Characterization of a novel signal transducer element intrinsic to class IIIa/b adenylyl cyclases and guanylyl cyclases. <i>FEBS Journal</i> , 2017, 284, 1204-1217.	2.2	25
120	Prokaryotic Ancestry of Eukaryotic Protein Networks Mediating Innate Immunity and Apoptosis. <i>Journal of Molecular Biology</i> , 2014, 426, 1568-1582.	2.0	23
121	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	2.0	23
122	Structure and function of tripeptidyl peptidase II, a giant cytosolic protease. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 237-245.	1.1	22
123	Structural Dynamics of the Cereblon Ligand Binding Domain. <i>PLoS ONE</i> , 2015, 10, e0128342.	1.1	22
124	Structural diversity of oligomeric $\hat{1}^2$ -propellers with different numbers of identical blades. <i>ELife</i> , 2019, 8, .	2.8	21
125	Fold recognition without folds. <i>Protein Science</i> , 2002, 11, 1575-1579.	3.1	20
126	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

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127	Predicted secondary structure of the 20 S proteasome and model structure of the putative peptide channel. <i>FEBS Letters</i> , 1994, 354, 45-49.	1.3	18
128	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
129	The First Prokaryotic Trehalose Synthase Complex Identified in the Hyperthermophilic Crenarchaeon <i>Thermoproteus tenax</i> . <i>PLoS ONE</i> , 2013, 8, e61354.	1.1	18
130	STAC—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
131	Histones predate the split between bacteria and archaea. <i>Bioinformatics</i> , 2019, 35, 2349-2353.	1.8	17
132	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
133	The Origin of Mitochondria-Specific Outer Membrane β -Barrels from an Ancestral Bacterial Fragment. <i>Genome Biology and Evolution</i> , 2018, 10, 2759-2765.	1.1	16
134	The GD box: A widespread noncontiguous supersecondary structural element. <i>Protein Science</i> , 2009, 18, 1961-1966.	3.1	15
135	A soluble mutant of the transmembrane receptor Af1503 features strong changes in coiled-coil periodicity. <i>Journal of Structural Biology</i> , 2014, 186, 357-366.	1.3	15
136	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
137	Delineation of structural domains and identification of functionally important residues in DNA repair enzyme exonuclease VII. <i>Nucleic Acids Research</i> , 2012, 40, 8163-8174.	6.5	13
138	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
139	Asymmetric protein design from conserved supersecondary structures. <i>Journal of Structural Biology</i> , 2018, 204, 380-387.	1.3	13
140	Exploring protein-protein interactions at the proteome level. <i>Structure</i> , 2022, 30, 462-475.	1.6	13
141	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
142	Inherent chaperone-like activity of aspartic proteases reveals a distant evolutionary relation to double- β barrel domains of AAA-ATPases. <i>Protein Science</i> , 2007, 16, 644-653.	3.1	11
143	An Interface-Driven Design Strategy Yields a Novel, Corrugated Protein Architecture. <i>ACS Synthetic Biology</i> , 2018, 7, 2226-2235.	1.9	11
144	The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. <i>BMC Evolutionary Biology</i> , 2020, 20, 162.	3.2	11

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145	Gram-negative outer-membrane proteins with multiple β -barrel domains. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	10
146	Design of novel granulopoietic proteins by topological rescaffolding. PLoS Biology, 2020, 18, e3000919.	2.6	8
147	Thermoplasma acidophilum TAA43 is an archaeal member of the eukaryotic meiotic branch of AAA ATPases. Biological Chemistry, 2004, 385, 1105-11.	1.2	7
148	The long coming of computational structural biology. Journal of Structural Biology, 2008, 163, 254-257.	1.3	7
149	What I cannot create, I do not understand. Science, 2014, 346, 1455-1456.	6.0	7
150	Archaeal Connectase is a specific and efficient protein ligase related to proteasome β subunits. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7
151	A Mouse Ig β Domain of Very Unusual Framework Structure Loses Function when Converted to the Consensus. Journal of Biological Chemistry, 1995, 270, 12446-12451.	1.6	6
152	What makes a thermophile?. Trends in Microbiology, 1998, 6, 349-351.	3.5	5
153	Characterization of AMA, a new AAA protein from Archaeoglobus and methanogenic archaea. Journal of Structural Biology, 2006, 156, 130-138.	1.3	5
154	Structural diversity of coiled coils in protein fibers of the bacterial cell envelope. International Journal of Medical Microbiology, 2019, 309, 351-358.	1.5	5
155	The VCBS superfamily forms a third supercluster of β -propellers that includes tachylectin and integrins. Bioinformatics, 2021, 36, 5618-5622.	1.8	5
156	A topological refactoring design strategy yields highly stable granulopoietic proteins. Nature Communications, 2022, 13, .	5.8	4
157	An astonishing wealth of new proteasome homologs. Bioinformatics, 2021, 37, 4694-4703.	1.8	3
158	Native display of a huge homotrimeric protein fiber on the cell surface after precise domain deletion. Journal of Bioscience and Bioengineering, 2020, 129, 412-417.	1.1	2
159	Editorial overview: Sequences and topology: β -paths from sequence to structure TM . Current Opinion in Structural Biology, 2021, 68, vi-viii.	2.6	2
160	Two unique membrane-bound AAA proteins from Sulfolobus solfataricus. Biochemical Society Transactions, 2009, 37, 118-122.	1.6	1
161	RpuS/R Is a Novel Two-Component Signal Transduction System That Regulates the Expression of the Pyruvate Symporter MctP in Sinorhizobium fredii NGR234. Frontiers in Microbiology, 2022, 13, 871077.	1.5	1
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