

Todd O Yeates

List of Publications by Year in descending order

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Version: 2024-02-01

183
papers

22,974
citations

18887

64
h-index

9865

146
g-index

222
all docs

222
docs citations

222
times ranked

23193
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>AlphaFold</scp> predicts the most complex protein knot and composite protein knots. <i>Protein Science</i> , 2022, 31, .	3.1	15
2	Designing Protease-Triggered Protein Cages. <i>Journal of the American Chemical Society</i> , 2022, 144, 12681-12689.	6.6	7
3	A fragment-based protein interface design algorithm for symmetric assemblies. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	1.0	11
4	Geometric Lessons and Design Strategies for Nanoscale Protein Cages. <i>ACS Nano</i> , 2021, 15, 4277-4286.	7.3	14
5	MCPdb: The bacterial microcompartment database. <i>PLoS ONE</i> , 2021, 16, e0248269.	1.1	11
6	Advances in the World of Bacterial Microcompartments. <i>Trends in Biochemical Sciences</i> , 2021, 46, 406-416.	3.7	28
7	Recent structural insights into bacterial microcompartment shells. <i>Current Opinion in Microbiology</i> , 2021, 62, 51-60.	2.3	18
8	Structural characterization of hexameric shell proteins from two types of choline-utilization bacterial microcompartments. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 275-285.	0.4	2
9	The coronavirus disease 2019 (COVID-19) stay-at-home order's unequal effects on trauma volume by insurance status in Southern California. <i>Surgery</i> , 2021, 170, 962-968.	1.0	8
10	Designed Protein Cages as Scaffolds for Building Multienzyme Materials. <i>ACS Synthetic Biology</i> , 2020, 9, 381-391.	1.9	51
11	Design and structure of two new protein cages illustrate successes and ongoing challenges in protein engineering. <i>Protein Science</i> , 2020, 29, 919-929.	3.1	32
12	Computational design of mixed chirality peptide macrocycles with internal symmetry. <i>Protein Science</i> , 2020, 29, 2433-2445.	3.1	16
13	Symmetry breaking and structural polymorphism in a bacterial microcompartment shell protein for choline utilization. <i>Protein Science</i> , 2020, 29, 2201-2212.	3.1	11
14	Editorial overview: Engineered proteins as tools in structural biology. <i>Current Opinion in Structural Biology</i> , 2020, 60, v-vi.	2.6	0
15	Development of imaging scaffolds for cryo-electron microscopy. <i>Current Opinion in Structural Biology</i> , 2020, 60, 142-149.	2.6	21
16	Design and Characterization of an Icosahedral Protein Cage Formed by a Double-Fusion Protein Containing Three Distinct Symmetry Elements. <i>ACS Synthetic Biology</i> , 2020, 9, 517-524.	1.9	37
17	A complete rule set for designing symmetry combination materials from protein molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31817-31823.	3.3	29
18	Advances in methods for atomic resolution macromolecular structure determination. <i>F1000Research</i> , 2020, 9, 667.	0.8	22

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19	The structure of bovine Î²-lactoglobulin in crystals grown at pH 3.8 exhibiting novel threefold twinning. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 640-645.	0.4	2
20	Protein assembles into Archimedean geometry. <i>Nature</i> , 2019, 569, 340-342.	13.7	3
21	A 3.8Å resolution cryo-EM structure of a small protein bound to an imaging scaffold. <i>Nature Communications</i> , 2019, 10, 1864.	5.8	74
22	High-symmetry protein assemblies: patterns and emerging applications. <i>Current Opinion in Structural Biology</i> , 2019, 55, 77-84.	2.6	41
23	Near-atomic cryo-EM imaging of a small protein displayed on a designed scaffolding system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3362-3367.	3.3	82
24	<scp>RAF</scp>2 is a RuBisCO assembly factor in <i>Arabidopsis thaliana</i>. <i>Plant Journal</i> , 2018, 94, 146-156.	2.8	22
25	Microfocus diffraction from different regions of a protein crystal: structural variations and unit-cell polymorphism. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 411-421.	1.1	12
26	Facile methods for heterologous production of bacterial microcompartments in diverse host species. <i>Microbial Biotechnology</i> , 2018, 11, 160-162.	2.0	1
27	Geometric Principles for Designing Highly Symmetric Self-Assembling Protein Nanomaterials. <i>Annual Review of Biophysics</i> , 2017, 46, 23-42.	4.5	96
28	Molecular Dynamics Simulations of Selective Metabolite Transport across the Propanediol Bacterial Microcompartment Shell. <i>Journal of Physical Chemistry B</i> , 2017, 121, 8149-8154.	1.2	35
29	Putting the RuBisCO pieces together. <i>Science</i> , 2017, 358, 1253-1254.	6.0	4
30	The function of the PduJ microcompartment shell protein is determined by the genomic position of its encoding gene. <i>Molecular Microbiology</i> , 2016, 101, 770-783.	1.2	33
31	Designing and defining dynamic protein cage nanoassemblies in solution. <i>Science Advances</i> , 2016, 2, e1501855.	4.7	37
32	Progress in low-resolution ab initio phasing with CrowdPhase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 446-453.	1.1	3
33	A PII-Like Protein Regulated by Bicarbonate: Structural and Biochemical Studies of the Carboxysome-Associated CPII Protein. <i>Journal of Molecular Biology</i> , 2016, 428, 4013-4030.	2.0	20
34	The design of symmetric protein nanomaterials comes of age in theory and practice. <i>Current Opinion in Structural Biology</i> , 2016, 39, 134-143.	2.6	77
35	Accurate design of megadalton-scale two-component icosahedral protein complexes. <i>Science</i> , 2016, 353, 389-394.	6.0	466
36	Structure of a novel 13 nm dodecahedral nanocage assembled from a redesigned bacterial microcompartment shell protein. <i>Chemical Communications</i> , 2016, 52, 5041-5044.	2.2	31

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37	Symmetry and Computational Methods in the Design of Self-Assembling Protein Materials. FASEB Journal, 2016, 30, 250.1.	0.2	0
38	Bacterial microcompartments: widespread prokaryotic organelles for isolation and optimization of metabolic pathways. Molecular Microbiology, 2015, 98, 193-207.	1.2	120
39	Responses to Crystallography and chemistry should always go together: a cautionary tale of protein complexes with cisplatin and carboplatin. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1980-1981.	2.5	2
40	An allosteric model for control of pore opening by substrate binding in the <i>ScpE</i> microcompartment shell protein. Protein Science, 2015, 24, 956-975.	3.1	38
41	Structure of a designed tetrahedral protein assembly variant engineered to have improved soluble expression. Protein Science, 2015, 24, 1695-1701.	3.1	30
42	Diffusion accessibility as a method for visualizing macromolecular surface geometry. Protein Science, 2015, 24, 1702-1705.	3.1	3
43	Structures of potent anticancer compounds bound to tubulin. Protein Science, 2015, 24, 1164-1172.	3.1	20
44	Selective molecular transport through the protein shell of a bacterial microcompartment organelle. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2990-2995.	3.3	119
45	Exploring Bacterial Organelle Interactomes: A Model of the Protein-Protein Interaction Network in the Pdu Microcompartment. PLoS Computational Biology, 2015, 11, e1004067.	1.5	24
46	The PduL Phosphotransacylase Is Used To Recycle Coenzyme A within the Pdu Microcompartment. Journal of Bacteriology, 2015, 197, 2392-2399.	1.0	35
47	Redesigning photosynthesis to sustainably meet global food and bioenergy demand. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8529-8536.	3.3	751
48	A Suite of Engineered GFP Molecules for Oligomeric Scaffolding. Structure, 2015, 23, 1754-1768.	1.6	30
49	On the predictability of the orientation of protein domains joined by a spanning alpha-helical linker. Protein Engineering, Design and Selection, 2015, 28, 491-500.	1.0	23
50	Structure of the methanofuran/methanopterin-biosynthetic enzyme MJ1099 from <i>Methanocaldococcus jannaschii</i> . Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1472-1479.	0.4	2
51	Structure of a bacterial microcompartment shell protein bound to a cobalamin cofactor. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1584-1590.	0.4	21
52	<i>CrowdPhase</i> : crowdsourcing the phase problem. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1538-1548.	2.5	9
53	(Quasi-)Racemic X-ray Structures of Glycosylated and Non-Glycosylated Forms of the Chemokine Serpin C1L1 Prepared by Total Chemical Synthesis. Angewandte Chemie - International Edition, 2014, 53, 5194-5198.	7.2	59
54	Structure and Identification of a Pterin Dehydratase-like Protein as a Ribulose-bisphosphate Carboxylase/Oxygenase (RuBisCO) Assembly Factor in the β -Carboxysome. Journal of Biological Chemistry, 2014, 289, 7973-7981.	1.6	50

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55	The role of distant mutations and allosteric regulation on LovD active site dynamics. <i>Nature Chemical Biology</i> , 2014, 10, 431-436.	3.9	166
56	Structure of Dihydrmethanopterin Reductase, a Cubic Protein Cage for Redox Transfer. <i>Journal of Biological Chemistry</i> , 2014, 289, 8852-8864.	1.6	11
57	Accurate design of co-assembling multi-component protein nanomaterials. <i>Nature</i> , 2014, 510, 103-108.	13.7	504
58	Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014, 6, 1065-1071.	6.6	267
59	Diverse Bacterial Microcompartment Organelles. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 438-468.	2.9	197
60	Identification of a Unique Fe-S Cluster Binding Site in a Glycyl-Radical Type Microcompartment Shell Protein. <i>Journal of Molecular Biology</i> , 2014, 426, 3287-3304.	2.0	23
61	Alanine Scanning Mutagenesis Identifies an Asparagine-Arginine-Lysine Triad Essential to Assembly of the Shell of the Pdu Microcompartment. <i>Journal of Molecular Biology</i> , 2014, 426, 2328-2345.	2.0	66
62	A challenging interpretation of a hexagonally layered protein structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 203-208.	2.5	4
63	Using comparative genomics to uncover new kinds of protein-based metabolic organelles in bacteria. <i>Protein Science</i> , 2013, 22, 179-195.	3.1	108
64	Structure and Flexibility of Nanoscale Protein Cages Designed by Symmetric Self-Assembly. <i>Journal of the American Chemical Society</i> , 2013, 135, 7738-7743.	6.6	82
65	The Shells of BMC-Type Microcompartment Organelles in Bacteria. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 290-299.	1.0	56
66	Split green fluorescent protein as a modular binding partner for protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2513-2523.	2.5	29
67	Bacterial microcompartment shells of diverse functional types possess pentameric vertex proteins. <i>Protein Science</i> , 2013, 22, 660-665.	3.1	69
68	Crystal Pathologies. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 23-31.	0.5	0
69	Structure of a 16-nm Cage Designed by Using Protein Oligomers. <i>Science</i> , 2012, 336, 1129-1129.	6.0	260
70	Principles for designing ordered protein assemblies. <i>Trends in Cell Biology</i> , 2012, 22, 653-661.	3.6	120
71	Racemic Protein Crystallography. <i>Annual Review of Biophysics</i> , 2012, 41, 41-61.	4.5	151
72	Single-wavelength phasing strategy for quasi-racemic protein crystal diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 62-68.	2.5	9

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73	Inward facing conformations of the MetNI methionine ABC transporter: Implications for the mechanism of transinhibition. <i>Protein Science</i> , 2012, 21, 84-96.	3.1	39
74	Computational Design of Self-Assembling Protein Nanomaterials with Atomic Level Accuracy. <i>Science</i> , 2012, 336, 1171-1174.	6.0	588
75	Structure and function in complex macromolecular assemblies: Some evolutionary themes. <i>Current Opinion in Structural Biology</i> , 2012, 22, 197-199.	2.6	8
76	Protein arrays made to order. <i>Nature Nanotechnology</i> , 2011, 6, 541-542.	15.6	23
77	Widespread Disulfide Bonding in Proteins from Thermophilic Archaea. <i>Archaea</i> , 2011, 2011, 1-9.	2.3	41
78	The protein shells of bacterial microcompartment organelles. <i>Current Opinion in Structural Biology</i> , 2011, 21, 223-231.	2.6	128
79	Synthetic symmetrization in the crystallization and structure determination of CelA from <i>Thermotoga maritima</i> . <i>Protein Science</i> , 2011, 20, 168-178.	3.1	20
80	An approach to crystallizing proteins by metal-mediated synthetic symmetrization. <i>Protein Science</i> , 2011, 20, 1876-1890.	3.1	63
81	Protein stabilization in a highly knotted protein polymer. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 627-630.	1.0	52
82	Structural and Biochemical Characterization of the Salicyl-acyltransferase SsfX3 from a Tetracycline Biosynthetic Pathway. <i>Journal of Biological Chemistry</i> , 2011, 286, 41539-41551.	1.6	14
83	Bacterial Microcompartments. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 103, 1-20.	0.9	17
84	Structure of a putative NTP pyrophosphohydrolase: YP_001813558.1 from <i>Exiguobacterium sibiricum</i> 255-15. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1237-1244.	0.7	2
85	Determination of the X-ray structure of the snake venom protein omwaprin by total chemical synthesis and racemic protein crystallography. <i>Protein Science</i> , 2010, 19, 1840-1849.	3.1	48
86	Structural Insight into the Mechanisms of Transport across the <i>Salmonella enterica</i> Pdu Microcompartment Shell. <i>Journal of Biological Chemistry</i> , 2010, 285, 37838-37846.	1.6	127
87	Structure and folding of a designed knotted protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20732-20737.	3.3	123
88	Short N-terminal sequences package proteins into bacterial microcompartments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7509-7514.	3.3	214
89	Structure and Mechanisms of a Protein-Based Organelle in <i>Escherichia coli</i> . <i>Science</i> , 2010, 327, 81-84.	6.0	205
90	Total chemical synthesis and X-ray structure of kalitoxin by racemic protein crystallography. <i>Chemical Communications</i> , 2010, 46, 8174.	2.2	47

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91	Bacterial Microcompartment Organelles: Protein Shell Structure and Evolution. <i>Annual Review of Biophysics</i> , 2010, 39, 185-205.	4.5	162
92	Exploiting genomic patterns to discover new supramolecular protein assemblies. <i>Protein Science</i> , 2009, 18, 69-79.	3.1	31
93	Insights from multiple structures of the shell proteins from the β^2 -carboxysome. <i>Protein Science</i> , 2009, 18, 108-120.	3.1	98
94	Detecting coordinated regulation of multi-protein complexes using logic analysis of gene expression. <i>BMC Systems Biology</i> , 2009, 3, 115.	3.0	15
95	Rational improvement of simvastatin synthase solubility in <i>Escherichia coli</i> leads to higher whole-cell biocatalytic activity. <i>Biotechnology and Bioengineering</i> , 2009, 102, 20-28.	1.7	31
96	Two-dimensional crystals of carboxysome shell proteins recapitulate the hexagonal packing of three-dimensional crystals. <i>Protein Science</i> , 2009, 18, 2629-2635.	3.1	42
97	Determining the DUF55-domain structure of human thymocyte nuclear protein 1 from crystals partially twinned by tetartohedry. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 212-219.	2.5	11
98	Analysis of lattice-translocation disorder in the layered hexagonal structure of carboxysome shell protein CsoS1C. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 980-988.	2.5	35
99	Directed Evolution and Structural Characterization of a Simvastatin Synthase. <i>Chemistry and Biology</i> , 2009, 16, 1064-1074.	6.2	79
100	Multiple crystal structures of actin dimers and their implications for interactions in the actin filament. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 454-465.	2.5	18
101	Bacterial microcompartments: their properties and paradoxes. <i>BioEssays</i> , 2008, 30, 1084-1095.	1.2	169
102	Equations for determining tetartohedral twin fractions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 1158-1164.	2.5	3
103	Protein-based organelles in bacteria: carboxysomes and related microcompartments. <i>Nature Reviews Microbiology</i> , 2008, 6, 681-691.	13.6	421
104	Structure of the PduU Shell Protein from the Pdu Microcompartment of Salmonella. <i>Structure</i> , 2008, 16, 1324-1332.	1.6	102
105	Atomic-Level Models of the Bacterial Carboxysome Shell. <i>Science</i> , 2008, 319, 1083-1086.	6.0	367
106	Structures and Functional Implications of an AMP-Binding Cystathionine β^2 -Synthase Domain Protein from a Hyperthermophilic Archaeon. <i>Journal of Molecular Biology</i> , 2008, 380, 181-192.	2.0	24
107	Generation of Oxide Nanopatterns by Combining Self-Assembly of S-Layer Proteins and Area-Selective Atomic Layer Deposition. <i>Journal of the American Chemical Society</i> , 2008, 130, 16908-16913.	6.6	47
108	Connecting actin monomers by iso-peptide bond is a toxicity mechanism of the <i>Vibrio cholerae</i> MARTX toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18537-18542.	3.3	68

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109	Structural Analysis of CsoS1A and the Protein Shell of the Halothiobacillus neapolitanus Carboxysome. PLoS Biology, 2007, 5, e144.	2.6	145
110	How Some Pili Pull. Science, 2007, 318, 1558-1559.	6.0	17
111	Self-assembly in the carboxysome: a viral capsid-like protein shell in bacterial cells. Biochemical Society Transactions, 2007, 35, 508-511.	1.6	51
112	Discovery of a Thermophilic Protein Complex Stabilized by Topologically Interlinked Chains. Journal of Molecular Biology, 2007, 368, 1332-1344.	2.0	110
113	Identification of Rare Slipknots in Proteins and Their Implications for Stability and Folding. Journal of Molecular Biology, 2007, 373, 153-166.	2.0	120
114	Knotted and topologically complex proteins as models for studying folding and stability. Current Opinion in Chemical Biology, 2007, 11, 595-603.	2.8	93
115	Structure of the RuBisCO chaperone RbcX from <i>Synechocystis</i> sp. PCC6803. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1109-1112.	2.5	16
116	Protein Structure: Evolutionary Bridges to New Folds. Current Biology, 2007, 17, R48-R50.	1.8	12
117	Conformational Change and Assembly through Edge β Strands in Transthyretin and Other Amyloid Proteins. Accounts of Chemical Research, 2006, 39, 576-583.	7.6	31
118	A Framework for Describing Topological Frustration in Models of Protein Folding. Journal of Molecular Biology, 2006, 362, 605-621.	2.0	27
119	An approach to crystallizing proteins by synthetic symmetrization. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16230-16235.	3.3	86
120	Proteins in a Small World. Science, 2006, 314, 1882-1883.	6.0	12
121	The Structure of β -Carbonic Anhydrase from the Carboxysomal Shell Reveals a Distinct Subclass with One Active Site for the Price of Two. Journal of Biological Chemistry, 2006, 281, 7546-7555.	1.6	159
122	Phylogenetic profiling. , 2005, , .		0
123	Utilizing logical relationships in genomic data to decipher cellular processes. FEBS Journal, 2005, 272, 5110-5118.	2.2	33
124	The crystal structure of a cross-linked actin dimer suggests a detailed molecular interface in F-actin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13105-13110.	3.3	54
125	The Genomics of Disulfide Bonding and Protein Stabilization in Thermophiles. PLoS Biology, 2005, 3, e309.	2.6	180
126	Protein Structures Forming the Shell of Primitive Bacterial Organelles. Science, 2005, 309, 936-938.	6.0	420

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127	Crystal Structure of the Apo Forms of γ -55 tRNA Pseudouridine Synthase from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2004, 279, 24585-24591.	1.6	23
128	GDAP: a web tool for genome-wide protein disulfide bond prediction. <i>Nucleic Acids Research</i> , 2004, 32, W360-W364.	6.5	31
129	Use of Logic Relationships to Decipher Protein Network Organization. <i>Science</i> , 2004, 306, 2246-2249.	6.0	140
130	Prolinks: a database of protein functional linkages derived from coevolution. <i>Genome Biology</i> , 2004, 5, R35.	13.9	276
131	The 1.6Å resolution structure of Fe-superoxide dismutase from the thermophilic cyanobacterium <i>Thermosynechococcus elongatus</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2003, 8, 707-714.	1.1	25
132	The Crystal Structure of a Cyanobacterial Water-Soluble Carotenoid Binding Protein. <i>Structure</i> , 2003, 11, 55-65.	1.6	267
133	The Crystal Structure of the First Enzyme in the Pantothenate Biosynthetic Pathway, Ketopantoate Hydroxymethyltransferase, from <i>M. tuberculosis</i> . <i>Structure</i> , 2003, 11, 753-764.	1.6	38
134	Use of multiple anomalous dispersion to phase highly merohedrally twinned crystals of interleukin-1 β . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 290-298.	2.5	14
135	A statistic for local intensity differences: robustness to anisotropy and pseudo-centering and utility for detecting twinning. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1124-1130.	2.5	234
136	Amyloid-like filaments and water-filled nanotubes formed by SOD1 mutant proteins linked to familial ALS. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 461-467.	3.6	311
137	Visualization and interpretation of protein networks in Mycobacterium tuberculosis based on hierarchical clustering of genome-wide functional linkage maps. <i>Nucleic Acids Research</i> , 2003, 31, 7099-7109.	6.5	55
138	Structural and EPR Characterization of the Soluble Form of Cytochrome c-550 and of the psbV2 Gene Product from the Cyanobacterium <i>Thermosynechococcus elongatus</i> . <i>Plant and Cell Physiology</i> , 2003, 44, 697-706.	1.5	39
139	Computational Genomics: Prediction of Protein Functional Linkages and Networks. , 2003, , 15-19.		0
140	Genomic evidence that the intracellular proteins of archaeal microbes contain disulfide bonds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9679-9684.	3.3	167
141	Crystal Structure of Human l-Isoaspartyl Methyltransferase. <i>Journal of Biological Chemistry</i> , 2002, 277, 10642-10646.	1.6	25
142	Protein Repair Methyltransferase from the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 1058-1065.	1.6	23
143	Structures of SET Domain Proteins. <i>Cell</i> , 2002, 111, 5-7.	13.5	73
144	Designing supramolecular protein assemblies. <i>Current Opinion in Structural Biology</i> , 2002, 12, 464-470.	2.6	167

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145	Structure of cytochromec6fromArthrospira maxima: an assembly of 24 subunits in a nearly symmetric shell. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1104-1110.	2.5	4
146	Structure determination of a cocaine hydrolytic antibody from a pseudomerohedrally twinned crystal. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2055-2059.	2.5	14
147	Arrangement of subunits and ordering of β^2 -strands in an amyloid sheet. Nature Structural Biology, 2002, 9, 734-739.	9.7	108
148	Crystal structure of a protein repair methyltransferase from Pyrococcus furiosus with its l-isoaspartyl peptide substrate 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 313, 1103-1116.	2.0	55
149	Nanohedra: Using symmetry to design self assembling protein cages, layers, crystals, and filaments. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 2217-2221.	3.3	426
150	Structures of Cytochrome c-549 and Cytochrome c6 from the Cyanobacterium Arthrospira maxima,. Biochemistry, 2001, 40, 9215-9225.	1.2	65
151	Identification of a Subunit Interface in Transthyretin Amyloid Fibrils: Evidence for Self-Assembly from Oligomeric Building Blocks. Biochemistry, 2001, 40, 9089-9096.	1.2	69
152	Evaluation of phase accuracyviatopological and geometrical analysis of electron-density maps. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1421-1429.	2.5	4
153	Protein function in the post-genomic era. Nature, 2000, 405, 823-826.	13.7	690
154	The structure of adenylosuccinate lyase, an enzyme with dual activity in the de novo purine biosynthetic pathway. Structure, 2000, 8, 163-174.	1.6	77
155	The crystal structure of adenylosuccinate lyase from Pyrobaculum aerophilum reveals an intracellular protein with three disulfide bonds 1 Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 301, 433-450.	2.0	75
156	A combined algorithm for genome-wide prediction of protein function. Nature, 1999, 402, 83-86.	13.7	879
157	Detecting Protein Function and Protein-Protein Interactions from Genome Sequences. Science, 1999, 285, 751-753.	6.0	1,595
158	Protein crystals and their evil twins. Structure, 1999, 7, R25-R29.	1.6	46
159	A fast algorithm for genome-wide analysis of proteins with repeated sequences. Proteins: Structure, Function and Bioinformatics, 1999, 35, 440-446.	1.5	71
160	Searching for frameshift evolutionary relationships between protein sequence families. Proteins: Structure, Function and Bioinformatics, 1999, 37, 278-283.	1.5	11
161	Assigning protein functions by comparative genome analysis: Protein phylogenetic profiles. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 4285-4288.	3.3	1,653
162	A census of protein repeats. Journal of Molecular Biology, 1999, 293, 151-160.	2.0	385

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163	The 1.8 Å crystal structure of the ycaC gene product from Escherichia coli reveals an octameric hydrolase of unknown specificity. Structure, 1998, 6, 1329-1337.	1.6	49
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