

Arthur M Lesk

List of Publications by Year in descending order

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177
papers

16,871
citations

24978

57
h-index

14702

127
g-index

184
all docs

184
docs citations

184
times ranked

14110
citing authors

#	ARTICLE	IF	CITATIONS
1	Canonical structures for the hypervariable regions of immunoglobulins. <i>Journal of Molecular Biology</i> , 1987, 196, 901-917.	2.0	1,358
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
3	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989, 342, 877-883.	13.7	1,199
4	Interior and surface of monomeric proteins. <i>Journal of Molecular Biology</i> , 1987, 196, 641-656.	2.0	873
5	Structural Mechanisms for Domain Movements in Proteins. <i>Biochemistry</i> , 1994, 33, 6739-6749.	1.2	770
6	How different amino acid sequences determine similar protein structures: The structure and evolutionary dynamics of the globins. <i>Journal of Molecular Biology</i> , 1980, 136, 225-270.	2.0	703
7	Standard conformations for the canonical structures of immunoglobulins 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1997, 273, 927-948.	2.0	667
8	MUSTANG: A multiple structural alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 559-574.	1.5	615
9	Determinants of a protein fold. <i>Journal of Molecular Biology</i> , 1987, 196, 199-216.	2.0	485
10	Structural repertoire of the human VH segments. <i>Journal of Molecular Biology</i> , 1992, 227, 799-817.	2.0	412
11	Prediction of protein function from protein sequence and structure. <i>Quarterly Reviews of Biophysics</i> , 2003, 36, 307-340.	2.4	376
12	Conformations of the third hypervariable region in the VH domain of immunoglobulins 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 275, 269-294.	2.0	350
13	The accessible surface area and stability of oligomeric proteins. <i>Nature</i> , 1987, 328, 834-836.	13.7	346
14	$\hat{\beta}$ -Trefoil fold. <i>Journal of Molecular Biology</i> , 1992, 223, 531-543.	2.0	318
15	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008, 456, 387-390.	13.7	283
16	Evolution of proteins formed by $\hat{\beta}$ -sheets. <i>Journal of Molecular Biology</i> , 1982, 160, 325-342.	2.0	280
17	Framework residue 71 is a major determinant of the position and conformation of the second hypervariable region in the VH domains of immunoglobulins. <i>Journal of Molecular Biology</i> , 1990, 215, 175-182.	2.0	238
18	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237

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19	NAD-binding domains of dehydrogenases. <i>Current Opinion in Structural Biology</i> , 1995, 5, 775-783.	2.6	228
20	Principles determining the structure of β^2 -sheet barrels in proteins I. A theoretical analysis. <i>Journal of Molecular Biology</i> , 1994, 236, 1369-1381.	2.0	204
21	Transmission of conformational change in insulin. <i>Nature</i> , 1983, 302, 500-505.	13.7	201
22	Functional insights from the distribution and role of homopeptide repeat-containing proteins. <i>Genome Research</i> , 2005, 15, 537-551.	2.4	189
23	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12348-12353.	3.3	189
24	Domain closure in mitochondrial aspartate aminotransferase. <i>Journal of Molecular Biology</i> , 1992, 227, 197-213.	2.0	188
25	The 2.6 Å... structure of antithrombin indicates a conformational change at the heparin binding site 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1997, 266, 601-609.	2.0	188
26	An atlas of serpin conformations. <i>Trends in Biochemical Sciences</i> , 1998, 23, 63-67.	3.7	173
27	Mechanisms of domain closure in proteins. <i>Journal of Molecular Biology</i> , 1984, 174, 175-191.	2.0	170
28	Elbow motion in the immunoglobulins involves a molecular ball-and-socket joint. <i>Nature</i> , 1988, 335, 188-190.	13.7	167
29	Evolution of Amino Acid Frequencies in Proteins Over Deep Time: Inferred Order of Introduction of Amino Acids into the Genetic Code. <i>Molecular Biology and Evolution</i> , 2002, 19, 1645-1655.	3.5	163
30	Domain Closure in Lactoferrin. <i>Journal of Molecular Biology</i> , 1993, 234, 357-372.	2.0	160
31	Structural principles of β^2 barrel proteins: The packing of the interior of the sheet. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 5, 139-148.	1.5	156
32	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8327-8332.	3.3	149
33	Conservation and Variability in the Structures of Serine Proteinases of the Chymotrypsin Family. <i>Journal of Molecular Biology</i> , 1996, 258, 501-537.	2.0	145
34	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. <i>Genome Research</i> , 2000, 10, 1845-1864.	2.4	145
35	Evolution of proteins formed by β^2 -sheets. <i>Journal of Molecular Biology</i> , 1982, 160, 309-323.	2.0	134
36	Principles determining the structure of β^2 -sheet barrels in proteins II. The observed structures. <i>Journal of Molecular Biology</i> , 1994, 236, 1382-1400.	2.0	126

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37	Serpins in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2002, 19, 1881-1890.	3.5	112
38	SH3 domains in prokaryotes. <i>Trends in Biochemical Sciences</i> , 1999, 24, 132-133.	3.7	110
39	Alignment of the amino acid sequences of distantly related proteins using variable gap penalties. <i>Protein Engineering, Design and Selection</i> , 1986, 1, 77-78.	1.0	108
40	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009, 19, 213-220.	2.4	102
41	Antibody Modeling: Implications for Engineering and Design. <i>Methods</i> , 2000, 20, 267-279.	1.9	98
42	Comparison of the structures of globins and phycocyanins: Evidence for evolutionary relationship. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 133-155.	1.5	93
43	Conformational changes in serpins: II. the mechanism of activation of antithrombin by heparin. <i>Journal of Molecular Biology</i> , 2000, 301, 1287-1305.	2.0	93
44	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	3.6	87
45	Structural determinants of the conformations of medium-sized loops in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 6, 382-394.	1.5	82
46	Preparative Induction and Characterization of L-Antithrombin: A Structural Homologue of Latent Plasminogen Activator Inhibitor-1. <i>Biochemistry</i> , 1997, 36, 13133-13142.	1.2	78
47	Assessment of novel fold targets in CASP4: Predictions of three-dimensional structures, secondary structures, and interresidue contacts. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 98-118.	1.5	76
48	Protein structural alignments and functional genomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 378-382.	1.5	76
49	Structural divergence and distant relationships in proteins: evolution of the globins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 290-301.	2.6	75
50	Helix movements and the reconstruction of the haem pocket during the evolution of the cytochrome c family. <i>Journal of Molecular Biology</i> , 1985, 182, 151-158.	2.0	73
51	Probing protein structure by solvent perturbation of nuclear magnetic resonance spectra. <i>Journal of Molecular Biology</i> , 1992, 224, 659-670.	2.0	73
52	Helix movements in proteins. <i>Trends in Biochemical Sciences</i> , 1985, 10, 116-118.	3.7	70
53	Quantitative sequence-function relationships in proteins based on gene ontology. <i>BMC Bioinformatics</i> , 2007, 8, 294.	1.2	68
54	Conformational changes in serpins: I. the native and cleaved conformations of α_1 -antitrypsin 1 Edited by J. M. Thornton. <i>Journal of Molecular Biology</i> , 2000, 296, 685-699.	2.0	67

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55	Importance of the release of strand 1C to the polymerization mechanism of inhibitory serpins. <i>Protein Science</i> , 1997, 6, 89-98.	3.1	64
56	Common features of the conformations of antigen-binding loops in immunoglobulins and application to modeling loop conformations. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 13, 231-245.	1.5	63
57	Conformational changes in serpins: I. the native and cleaved conformations of α_1 -antitrypsin 1 Edited by J. M. Thornton. <i>Journal of Molecular Biology</i> , 2000, 295, 651-665.	2.0	62
58	Correspondences between low-energy modes in enzymes: Dynamics-based alignment of enzymatic functional families. <i>Protein Science</i> , 2008, 17, 918-929.	3.1	62
59	Canonical structures for the hypervariable regions of T cell $\alpha\beta$ receptors. <i>Journal of Molecular Biology</i> , 2000, 295, 979-995.	2.0	56
60	Detection of three-dimensional patterns of atoms in chemical structures. <i>Communications of the ACM</i> , 1979, 22, 219-224.	3.3	55
61	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 151-166.	1.5	54
62	Computer-generated pictures of proteins. <i>Methods in Enzymology</i> , 1985, 115, 381-390.	0.4	49
63	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. <i>PLoS ONE</i> , 2010, 5, e10048.	1.1	47
64	Haemoglobin: The surface buried between the $\alpha_1\alpha_1$ and $\alpha_2\alpha_2$ dimers in the deoxy and oxy structures. <i>Journal of Molecular Biology</i> , 1985, 183, 267-270.	2.0	46
65	Computational Study of the Fibril Organization of Polyglutamine Repeats Reveals a Common Motif Identified in β -Helices. <i>Journal of Molecular Biology</i> , 2006, 358, 330-345.	2.0	46
66	Fix L, a haemoglobin that acts as an oxygen sensor: signalling mechanism and structural basis of its homology with PAS domains. <i>Chemistry and Biology</i> , 1999, 6, R291-R297.	6.2	37
67	Minimum message length inference of secondary structure from protein coordinate data. <i>Bioinformatics</i> , 2012, 28, i97-i105.	1.8	37
68	Systematic representation of protein folding patterns. <i>Journal of Molecular Graphics</i> , 1995, 13, 159-164.	1.7	35
69	On the origin of distribution patterns of motifs in biological networks. <i>BMC Systems Biology</i> , 2008, 2, 73.	3.0	34
70	Contact patterns between helices and strands of sheet define protein folding patterns. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 66, 869-876.	1.5	33
71	Tendamistat surface accessibility to the TEMPOL paramagnetic probe. <i>Journal of Biomolecular NMR</i> , 1999, 15, 125-133.	1.6	30
72	Structural search and retrieval using a tableau representation of protein folding patterns. <i>Bioinformatics</i> , 2008, 24, 645-651.	1.8	30

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73	Modularity and homology: modelling of the titin type I modules and their interfaces. <i>Journal of Molecular Biology</i> , 2001, 311, 283-296.	2.0	29
74	The High Resolution Crystal Structure of a Native Thermostable Serpin Reveals the Complex Mechanism Underpinning the Stressed to Relaxed Transition. <i>Journal of Biological Chemistry</i> , 2005, 280, 8435-8442.	1.6	29
75	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 105-110.	1.5	26
76	Modeling of serpin-protease complexes: Antithrombin-thrombin, α_1 -antitrypsin (358Met \rightarrow Arg)-thrombin, α_1 -antitrypsin (358Met \rightarrow Arg)-trypsin, and antitrypsin-elastase. , 1996, 26, 288-303.		26
77	ROTATORY DISPERSION OF NUCLEIC ACIDS IN THE NEAR-ULTRAVIOLET REGION. <i>Journal of the American Chemical Society</i> , 1961, 83, 3155-3156.	6.6	24
78	The unreasonable effectiveness of mathematics in molecular biology. <i>Mathematical Intelligencer</i> , 2000, 22, 28-37.	0.1	22
79	Serpins in the <i>Caenorhabditis elegans</i> genome. , 1999, 36, 31-41.		18
80	Statistical inference of protein structural alignments using information and compression. <i>Bioinformatics</i> , 2017, 33, 1005-1013.	1.8	18
81	Macromolecular marionettes. <i>Computers in Biology and Medicine</i> , 1977, 7, 113-129.	3.9	15
82	Homology modelling: inferences from tables of aligned sequences. <i>Current Opinion in Structural Biology</i> , 1992, 2, 242-247.	2.6	15
83	What the papers say: Does protein structure determine amino acid sequence?. <i>BioEssays</i> , 1992, 14, 407-410.	1.2	15
84	Molecular Forces in Antibody Maturation. <i>Physical Review Letters</i> , 2005, 95, 208106.	2.9	15
85	The Fluorides and Oxides of Helium and Neon ¹ . <i>Journal of the American Chemical Society</i> , 1966, 88, 615-616.	6.6	14
86	Lower bound to the long-range interaction energy of two identical rare gas atoms in the restricted Hartree-Fock approximation. <i>Journal of Chemical Physics</i> , 1973, 59, 44-46.	1.2	14
87	Single and multiple input modules in regulatory networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 320-324.	1.5	14
88	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. <i>Journal of Biological Chemistry</i> , 2021, 296, 100421.	1.6	14
89	Extraction of geometrically similar substructures: Least-squares and Chebyshev fitting and the difference distance matrix. , 1998, 33, 320-328.		13
90	Cataloging topologies of protein folding patterns. <i>Journal of Molecular Recognition</i> , 2010, 23, 253-257.	1.1	13

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91	Why does DNA contain thymine and RNA uracil?. Journal of Theoretical Biology, 1969, 22, 537-540.	0.8	12
92	Pictorial pattern recognition and the phase problem of x-ray crystallography. Communications of the ACM, 1972, 15, 3-6.	3.3	11
93	Three-Dimensional Searching for Recurrent Structural Motifs in Data Bases of Protein Structures. Journal of Computational Biology, 1994, 1, 121-132.	0.8	11
94	On the calculation of Euler angles from a rotation matrix. International Journal of Mathematical Education in Science and Technology, 1986, 17, 335-337.	0.8	10
95	Probing protein structure by solvent perturbation of nmr spectra. II. Determination of surface and buried residues in homologous proteins. Biopolymers, 1993, 33, 839-846.	1.2	10
96	Structural alignment and analysis of two distantly related proteins:Aplysia limacina myoglobin and sea lamprey globin. Proteins: Structure, Function and Bioinformatics, 1988, 4, 240-250.	1.5	9
97	Hydrophobicityâ€”getting into hot water. Biophysical Chemistry, 2003, 105, 179-182.	1.5	9
98	Piecewise linear approximation of protein structures using the principle of minimum message length. Bioinformatics, 2011, 27, i43-i51.	1.8	9
99	Universal Architectural Concepts Underlying Protein Folding Patterns. Frontiers in Molecular Biosciences, 2020, 7, 612920.	1.6	9
100	Use of the Hartree-Fock Approximation in Computing Electron Affinities. Physical Review, 1968, 171, 7-10.	2.7	8
101	Molecular biology: Coordination of sequence data. Nature, 1985, 314, 318-319.	13.7	8
102	Three-dimensional pattern matching in protein structure analysis. Lecture Notes in Computer Science, 1995, , 248-260.	1.0	8
103	Brave new proteins: What evolution reveals about protein structure. Current Opinion in Biotechnology, 1991, 2, 592-598.	3.3	7
104	Alarums and diversions. Nature, 1991, 352, 379-380.	13.7	7
105	Extraction of well-fitting substructures: root-mean-square deviation and the difference distance matrix. Folding & Design, 1997, 2, S12-S14.	4.5	7
106	What determines the spectrum of protein native state structures?. Proteins: Structure, Function and Bioinformatics, 2006, 63, 273-277.	1.5	7
107	On hypothesized selective pressure by u.v. on DNA base compositions. Journal of Theoretical Biology, 1973, 40, 201-202.	0.8	6
108	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. Nucleic Acids Research, 2012, 40, W334-W339.	6.5	6

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109	Sizes of interface residues account for cross-class binding affinity patterns in Eph receptor-ephrin families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 349-353.	1.5	6
110	A new statistical framework to assess structural alignment quality using information compression. <i>Bioinformatics</i> , 2014, 30, i512-i518.	1.8	6
111	Serpins in Prokaryotes. , 2007, , 131-162.		6
112	On the reliability and the limits of inference of amino acid sequence alignments. <i>Bioinformatics</i> , 2022, 38, i255-i263.	1.8	6
113	On the origin of the genetic code: Photochemical interaction between amino acids and nucleic acids not requiring adaptors. <i>Journal of Theoretical Biology</i> , 1970, 27, 171-173.	0.8	5
114	On the possibility of a stage in the evolution of the genetic message in which replication was imprecise. <i>Biochemical and Biophysical Research Communications</i> , 1970, 38, 855-858.	1.0	5
115	Generation of interactive displays from FORTRAN using the PDP - 10/LDS-1 computer graphics system. <i>Software - Practice and Experience</i> , 1972, 2, 259-273.	2.5	5
116	A combinatorial study of the effects of admitting non-watson-crick base pairings and of base composition on the helix-forming potential of polynucleotides of random sequence. <i>Journal of Theoretical Biology</i> , 1974, 44, 7-17.	0.8	5
117	Recursion relations for the classical partition function of the hard-sphere gas in two and three dimensions. <i>Journal of Chemical Physics</i> , 1975, 63, 5048-5049.	1.2	5
118	Serpin Conformations. , 2007, , 35-66.		5
119	Choice of Basis Set for Expansion of One-Dimensional Oscillator Eigenfunctions. <i>Journal of Chemical Physics</i> , 1968, 49, 3898-3900.	1.2	4
120	A cluster of familial Creutzfeldt-Jakob disease mutations recapitulate conserved residues in Doppel: a case of molecular mimicry?. <i>FEBS Letters</i> , 2002, 532, 21-26.	1.3	4
121	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Journal of Computational Biology</i> , 2015, 22, 487-497.	0.8	4
122	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 151-166.	1.5	4
123	A toolkit for computational molecular biology I: packing and unpacking of protein coordinate sets. <i>Journal of Molecular Graphics</i> , 1983, 1, 118-121.	1.7	3
124	The analysis of protein structures: New insights from a growing data base. <i>BioEssays</i> , 1984, 1, 105-110.	1.2	3
125	Themes and contrasts in protein structures. <i>Trends in Biochemical Sciences</i> , 1984, 9, 290.	3.7	3
126	What the papers say: Protein structure and evolution: Similar amino acid sequences sometimes produce strikingly different three-dimensional structures. <i>BioEssays</i> , 1985, 2, 213-214.	1.2	3

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127	The computational analysis of protein structures: Sources, methods, systems and results. Journal of Research of the National Bureau of Standards (United States), 1989, 94, 85.	0.3	3
128	Boolean programming formulation of some pattern-matching problems in molecular biology. Journal of the Chemical Society, Faraday Transactions, 1993, 89, 2603.	1.7	3
129	How precise are reported protein coordinate data?. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 904-906.	2.5	3
130	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. Lecture Notes in Computer Science, 2014, , 144-159.	1.0	3
131	Expansion of linear combinations of slater-type orbitals in eigenfunctions of the three-dimensional isotropic harmonic oscillator. International Journal of Quantum Chemistry, 1969, 3, 289-295.	1.0	2
132	Entropy Changes in Isothermal Expansions of Real Gases. American Journal of Physics, 1974, 42, 1030-1033.	0.3	2
133	Reinterpretation of Moseley's experiments relating $K\alpha$ line frequencies and atomic number. American Journal of Physics, 1980, 48, 492-493.	0.3	2
134	Introduction: Protein engineering. BioEssays, 1988, 8, 51-52.	1.2	2
135	From electrons to proteins and back again. International Journal of Quantum Chemistry, 2003, 95, 678-682.	1.0	2
136	The European Bioinformatics Institute Macromolecular Structure Relational Database Technology. , 0, , 223-240.		2
137	Structure Description and Identification Using the Tableau Representation of Protein Folding Patterns. Methods in Molecular Biology, 2012, 932, 51-59.	0.4	2
138	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes. , 2017, , .		2
139	Computer modeling of a potential agent against SARS-CoV-2 (COVID-19) protease. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1557-1558.	1.5	2
140	Neighbourhoods in the yeast regulatory network in different physiological states. Bioinformatics, 2021, 37, 551-558.	1.8	2
141	Dynamic computation of derivatives. Communications of the ACM, 1967, 10, 571-572.	3.3	2
142	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. Methods in Molecular Biology, 2019, 1958, 123-131.	0.4	2
143	Three-dimensional Structure Databases of Biological Macromolecules. Methods in Molecular Biology, 2022, 2449, 43-91.	0.4	2
144	Protein structure prediction improves the quality of amino acid sequence alignment. Proteins: Structure, Function and Bioinformatics, 2022, 90, 2144-2147.	1.5	2

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145	Computation of derivatives for parameter optimization in least-squares fitting of linear combinations of Slater-type orbitals by Gaussians. <i>International Journal of Quantum Chemistry</i> , 1968, 2, 801-805.	1.0	1
146	A corrected valence electron approximation. <i>Molecular Physics</i> , 1968, 15, 453-458.	0.8	1
147	Application of the common features of transfer RNAs to the determination of their nucleotide sequences. <i>Biochemical and Biophysical Research Communications</i> , 1971, 45, 676-680.	1.0	1
148	Expansion of eigenfunctions of a morse oscillator in a nonorthogonal basis of displaced harmonic oscillator functions. <i>Chemical Physics Letters</i> , 1976, 38, 113-116.	1.2	1
149	Treatment of nonspecular reflection in the single-particle model of an ideal gas. <i>American Journal of Physics</i> , 1976, 44, 1134-1135.	0.3	1
150	Cover blown. <i>Nature</i> , 1988, 334, 560-560.	13.7	1
151	Modelling Protein Structures. , 0, , 9-35.		1
152	Comment on "Comparing proteins by their internal dynamics: Exploring structure-function relationships beyond static structural alignments" by C. Micheletti. <i>Physics of Life Reviews</i> , 2013, 10, 33-34.	1.5	1
153	Statistical Inference of Protein "LEGO Bricks". , 2013, , .		1
154	An encoding technique to facilitate the detection of homologies in biopolymer sequences. <i>Journal of Theoretical Biology</i> , 1977, 69, 767-769.	0.8	0
155	Apr�s moi l� deluge. <i>Nature</i> , 1994, 371, 440-441.	13.7	0
156	Assessment of ab initio protein structure prediction. , 1998, , .		0
157	Classification of Protein Function. , 0, , 167-183.		0
158	Models of Database Interconnectivity. , 0, , 203-221.		0
159	Looking Around, Looking Ahead. , 0, , 242-244.		0
160	Survey of Sequence Databases: Archival Projects. , 0, , 24-44.		0
161	Survey of Sequence Databases: Derived Databases. , 0, , 45-62.		0
162	Databanks of Macromolecular Structure. , 0, , 63-79.		0

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163	Taxonomy: a Moving Target for Sequence Data. , 0, , 100-112.		0
164	Genomics and Proteomics: Design and Sources of Annotation. , 0, , 113-130.		0
165	Issues in the Annotation of Protein Structures. , 0, , 149-165.		0
166	Annotation of Protein Sequences. , 0, , 131-147.		0
167	Information Flow and Data Integration of Databanks. , 0, , 186-201.		0
168	Gene Expression Databases. , 0, , 81-97.		0
169	Annotation and Databases: Status and Prospects. , 0, , 1-21.		0
170	The Evolution of the Globins: We Thought We Understood It. Biological and Medical Physics Series, 2007, , 57-74.	0.3	0
171	On the use of overlapping lattices for screening to find pairs of nearby points in two and three dimensions. Computational Biology and Chemistry, 2008, 32, 212-214.	1.1	0
172	Bioinformatics of Protein Function. , 2008, , 79-119.		0
173	Not Enough Natural Data? Sequence and Ye Shall Find. Frontiers in Molecular Biosciences, 2020, 7, 65.	1.6	0
174	Paths Through the Yeast Regulatory Network in Different Physiological States. Journal of Molecular Biology, 2021, 433, 167181.	2.0	0
175	Canonical Network Motifs. , 2013, , 199-201.		0
176	On identifying statistical redundancy at the level of amino acid subsequences. , 2021, , .		0
177	Editorial: A Journey Through 50 Years of Structural Bioinformatics in Memoriam of Cyrus Chothia. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	0