Arthur M Lesk

List of Publications by Year
in descending order

177 papers	16,871 citations	25034 57 h-index	14759 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. Journal of Molecular Biology, 1987, 196, 901-917.	4.2	1,358
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
3	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	27.8	1,199
4	Interior and surface of monomeric proteins. Journal of Molecular Biology, 1987, 196, 641-656.	4.2	873
5	Structural Mechanisms for Domain Movements in Proteins. Biochemistry, 1994, 33, 6739-6749.	2.5	770
6	How different amino acid sequences determine similar protein structures: The structure and evolutionary dynamics of the globins. Journal of Molecular Biology, 1980, 136, 225-270.	4.2	703
7	Standard conformations for the canonical structures of immunoglobulins 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1997, 273, 927-948.	4.2	667
8	MUSTANG: A multiple structural alignment algorithm. Proteins: Structure, Function and Bioinformatics, 2006, 64, 559-574.	2.6	615
9	Determinants of a protein fold. Journal of Molecular Biology, 1987, 196, 199-216.	4.2	485
10	Structural repertoire of the human VH segments. Journal of Molecular Biology, 1992, 227, 799-817.	4.2	412
11	Prediction of protein function from protein sequence and structure. Quarterly Reviews of Biophysics, 2003, 36, 307-340.	5.7	376
12	Conformations of the third hypervariable region in the VH domain of immunoglobulins 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 275, 269-294.	4.2	350
13	The accessible surface area and stability of oligomeric proteins. Nature, 1987, 328, 834-836.	27.8	346
14	Î²-Trefoil fold. Journal of Molecular Biology, 1992, 223, 531-543.	4.2	318
15	Sequencing the nuclear genome of the extinct woolly mammoth. Nature, 2008, 456, 387-390.	27.8	283
16	Evolution of proteins formed by Î²-sheets. Journal of Molecular Biology, 1982, 160, 325-342.	4.2	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. Journal of Molecular Biology, 1990, 215, 175-182.	4.2	238
18	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237

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19	NAD-binding domains of dehydrogenases. Current Opinion in Structural Biology, 1995, 5, 775-783.	5.7	228
20	Principles determining the structure of β-sheet barrels in proteins I. A theoretical analysis. Journal of Molecular Biology, 1994, 236, 1369-1381.	4.2	204
21	Transmission of conformational change in insulin. Nature, 1983, 302, 500-505.	27.8	201
22	Functional insights from the distribution and role of homopeptide repeat-containing proteins. Genome Research, 2005, 15, 537-551.	5.5	189
23	Genetic diversity and population structure of the endangered marsupial <i>Sarcophilus harrisii</i> (Tasmanian devil). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12348-12353.	7.1	189
24	Domain closure in mitochondrial aspartate aminotransferase. Journal of Molecular Biology, 1992, 227, 197-213.	4.2	188
25	The 2.6 Ã… structure of antithrombin indicates a conformational change at the heparin binding site 1 1Edited by R. Huber. Journal of Molecular Biology, 1997, 266, 601-609.	4.2	188
26	An atlas of serpin conformations. Trends in Biochemical Sciences, 1998, 23, 63-67.	7.5	173
27	Mechanisms of domain closure in proteins. Journal of Molecular Biology, 1984, 174, 175-191.	4.2	170
28	Elbow motion in the immunoglobulins involves a molecular ball-and-socket joint. Nature, 1988, 335, 188-190.	27.8	167
29	Evolution of Amino Acid Frequencies in Proteins Over Deep Time: Inferred Order of Introduction of Amino Acids into the Genetic Code. Molecular Biology and Evolution, 2002, 19, 1645-1655.	8.9	163
30	Domain Closure in Lactoferrin. Journal of Molecular Biology, 1993, 234, 357-372.	4.2	160
31	Structural principles of α/β barrel proteins: The packing of the interior of the sheet. Proteins: Structure, Function and Bioinformatics, 1989, 5, 139-148.	2.6	156
32	Intraspecific phylogenetic analysis of Siberian woolly mammoths using complete mitochondrial genomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8327-8332.	7.1	149
33	Conservation and Variability in the Structures of Serine Proteinases of the Chymotrypsin Family. Journal of Molecular Biology, 1996, 258, 501-537.	4.2	145
34	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. Genome Research, 2000, 10, 1845-1864.	5.5	145
35	Evolution of proteins formed by β-sheets. Journal of Molecular Biology, 1982, 160, 309-323.	4.2	134
36	Principles determining the structure of β-sheet barrels in proteins II. The observed structures. Journal of Molecular Biology, 1994, 236, 1382-1400.	4.2	126

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37	Serpins in Prokaryotes. Molecular Biology and Evolution, 2002, 19, 1881-1890.	8.9	112
38	SH3 domains in prokaryotes. Trends in Biochemical Sciences, 1999, 24, 132-133.	7.5	110
39	Alignment of the amino acid sequences of distantly related proteins using variable gap penalties. Protein Engineering, Design and Selection, 1986, 1, 77-78.	2.1	108
40	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). Genome Research, 2009, 19, 213-220.	5.5	102
41	Antibody Modeling: Implications for Engineering and Design. Methods, 2000, 20, 267-279.	3.8	98
42	Comparison of the structures of globins and phycocyanins: Evidence for evolutionary relationship. Proteins: Structure, Function and Bioinformatics, 1990, 8, 133-155.	2.6	93
43	Conformational changes in serpins: II. the mechanism of activation of antithrombin by heparin. Journal of Molecular Biology, 2000, 301, 1287-1305.	4.2	93
44	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. Nature Structural and Molecular Biology, 2018, 25, 538-545.	8.2	87
45	Structural determinants of the conformations of medium-sized loops in proteins. Proteins: Structure, Function and Bioinformatics, 1989, 6, 382-394.	2.6	82
46	Preparative Induction and Characterization of L-Antithrombin:â€‰ A Structural Homologue of Latent Plasminogen Activator Inhibitor-1. Biochemistry, 1997, 36, 13133-13142.	2.5	78
47	Assessment of novel fold targets in CASP4: Predictions of three-dimensional structures, secondary structures, and interresidue contacts. Proteins: Structure, Function and Bioinformatics, 2001, 45, 98-118.	2.6	76
48	Protein structural alignments and functional genomics. Proteins: Structure, Function and Bioinformatics, 2001, 42, 378-382.	2.6	76
49	Structural divergence and distant relationships in proteins: evolution of the globins. Current Opinion in Structural Biology, 2005, 15, 290-301.	5.7	75
50	Helix movements and the reconstruction of the haem pocket during the evolution of the cytochrome c family. Journal of Molecular Biology, 1985, 182, 151-158.	4.2	73
51	Probing protein structure by solvent perturbation of nuclear magnetic resonance spectra. Journal of Molecular Biology, 1992, 224, 659-670.	4.2	73
52	Helix movements in proteins. Trends in Biochemical Sciences, 1985, 10, 116-118.	7.5	70
53	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	2.6	68
54	Conformational changes in serpins: I. the native and cleaved conformations of Î± 1 -antitrypsin 1 1Edited by J. M. Thornton. Journal of Molecular Biology, 2000, 296, 685-699.	4.2	67

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55	Importance of the release of strand 1C to the polymerization mechanism of inhibitory serpins. Protein Science, 1997, 6, 89-98.	7.6	64
56	Common features of the conformations of antigen-binding loops in immunoglobulins and application to modeling loop conformations. Proteins: Structure, Function and Bioinformatics, 1992, 13, 231-245.	2.6	63
57	Conformational changes in serpins: I. the native and cleaved conformations of Î± 1 -antitrypsin 1 1Edited by J. M. Thornton. Journal of Molecular Biology, 2000, 295, 651-665.	4.2	62
58	Correspondences between lowâ€energy modes in enzymes: Dynamicsâ€based alignment of enzymatic functional families. Protein Science, 2008, 17, 918-929.	7.6	62
59	Canonical structures for the hypervariable regions of T cell Î±Î² receptors. Journal of Molecular Biology, 2000, 295, 979-995.	4.2	56
60	Detection of three-dimensional patterns of atoms in chemical structures. Communications of the ACM, 1979, 22, 219-224.	4.5	55
61	CASP2: Report on ab initio predictions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 151-166.	2.6	54
62	Computer-generated pictures of proteins. Methods in Enzymology, 1985, 115, 381-390.	1.0	49
63	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
64	Haemoglobin: The surface buried between the Î±1Î²1 and Î±2Î²2 dimers in the deoxy and oxy structures. Journal of Molecular Biology, 1985, 183, 267-270.	4.2	46
65	Computational Study of the Fibril Organization of Polyglutamine Repeats Reveals a Common Motif Identified in Î²-Helices. Journal of Molecular Biology, 2006, 358, 330-345.	4.2	46
66	Fix L, a haemoglobin that acts as an oxygen sensor: signalling mechanism and structural basis of its homology with PAS domains. Chemistry and Biology, 1999, 6, R291-R297.	6.0	37
67	Minimum message length inference of secondary structure from protein coordinate data. Bioinformatics, 2012, 28, i97-i105.	4.1	37
68	Systematic representation of protein folding patterns. Journal of Molecular Graphics, 1995, 13, 159-164.	1.1	35
69	On the origin of distribution patterns of motifs in biological networks. BMC Systems Biology, 2008, 2, 73.	3.0	34
70	Contact patterns between helices and strands of sheet define protein folding patterns. Proteins: Structure, Function and Bioinformatics, 2007, 66, 869-876.	2.6	33
71	Tendamistat surface accessibility to the TEMPOL paramagnetic probe. Journal of Biomolecular NMR, 1999, 15, 125-133.	2.8	30
72	Structural search and retrieval using a tableau representation of protein folding patterns. Bioinformatics, 2008, 24, 645-651.	4.1	30

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73	Modularity and homology: modelling of the titin type I modules and their interfaces. Journal of Molecular Biology, 2001, 311, 283-296.	4.2	29
74	The High Resolution Crystal Structure of a Native Thermostable Serpin Reveals the Complex Mechanism Underpinning the Stressed to Relaxed Transition. Journal of Biological Chemistry, 2005, 280, 8435-8442.	3.4	29
75	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	2.6	26
76	Modeling of serpin-protease complexes: Antithrombin-thrombin, Î±1-antitrypsin (358Metâ†'Arg)-thrombin, Î±1-antitrypsin (358Metâ†'Arg)-trypsin, and antitrypsin-elastase. , 1996, 26, 288-303.		26
77	ROTATORY DISPERSION OF NUCLEIC ACIDS IN THE NEAR-ULTRAVIOLET REGION. Journal of the American Chemical Society, 1961, 83, 3155-3156.	13.7	24
78	The unreasonable effectiveness of mathematics in molecular biology. Mathematical Intelligencer, 2000, 22, 28-37.	0.2	22
79	Serpins in theCaenorhabditis elegans genome. , 1999, 36, 31-41.		18
80	Statistical inference of protein structural alignments using information and compression. Bioinformatics, 2017, 33, 1005-1013.	4.1	18
81	Macromolecular marionettes. Computers in Biology and Medicine, 1977, 7, 113-129.	7.0	15
82	Homology modelling: inferences from tables of aligned sequences. Current Opinion in Structural Biology, 1992, 2, 242-247.	5.7	15
83	What the papers say: Does protein structure determine amino acid sequence?. BioEssays, 1992, 14, 407-410.	2.5	15
84	Molecular Forces in Antibody Maturation. Physical Review Letters, 2005, 95, 208106.	7.8	15
85	The Fluorides and Oxides of Helium and Neon1. Journal of the American Chemical Society, 1966, 88, 615-616.	13.7	14
86	Lower bound to the longâ€range interaction energy of two identical rare gas atoms in the restricted Hartreeâ€Fock approximation. Journal of Chemical Physics, 1973, 59, 44-46.	3.0	14
87	Single and multiple input modules in regulatory networks. Proteins: Structure, Function and Bioinformatics, 2008, 73, 320-324.	2.6	14
88	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. Journal of Biological Chemistry, 2021, 296, 100421.	3.4	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. Journal of Molecular Recognition, 2010, 23, 253-257.	2.1	13

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91	Why does DNA contain thymine and RNA uracil?. Journal of Theoretical Biology, 1969, 22, 537-540.	1.7	12
92	Pictorial pattern recognition and the phase problem of x-ray crystallography. Communications of the ACM, 1972, 15, 3-6.	4.5	11
93	Three-Dimensional Searching for Recurrent Structural Motifs in Data Bases of Protein Structures. Journal of Computational Biology, 1994, 1, 121-132.	1.6	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.	1.4	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.	2.4	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.	2.6	9
97	Hydrophobicity â€"getting into hot water. Biophysical Chemistry, 2003, 105, 179-182.	2.8	9
98	Piecewise linear approximation of protein structures using the principle of minimum message length. Bioinformatics, 2011, 27, i43-i51.	4.1	9
99	Universal Architectural Concepts Underlying Protein Folding Patterns. Frontiers in Molecular Biosciences, 2020, 7, 612920.	3.5	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.	27.8	8
102	Three-dimensional pattern matching in protein structure analysis. Lecture Notes in Computer Science, 1995, , 248-260.	1.3	8
103	Brave new proteins: What evolution reveals about protein structure. Current Opinion in Biotechnology, 1991, 2, 592-598.	6.6	7
104	Alarums and diversions. Nature, 1991, 352, 379-380.	27.8	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.	2.6	7
107	On hypothesized selective pressure by u.v. on DNA base compositions. Journal of Theoretical Biology, 1973, 40, 201-202.	1.7	6
108	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. Nucleic Acids Research, 2012, 40, W334-W339.	14.5	6

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109	Sizes of interface residues account for cross‑class binding affinity patterns in Eph receptor–ephrin families. Proteins: Structure, Function and Bioinformatics, 2014, 82, 349-353.	2.6	6
110	A new statistical framework to assess structural alignment quality using information compression. Bioinformatics, 2014, 30, i512-i518.	4.1	6
111	Serpins in Prokaryotes. , 2007, , 131-162.		6
112	On the reliability and the limits of inference of amino acid sequence alignments. Bioinformatics, 2022, 38, i255-i263.	4.1	6
113	On the origin of the genetic code: Photochemical interaction between amino acids and nucleic acids not requiring adaptors. Journal of Theoretical Biology, 1970, 27, 171-173.	1.7	5
114	On the possibility of a stage in the evolution of the genetic message in which replication was imprecise. Biochemical and Biophysical Research Communications, 1970, 38, 855-858.	2.1	5
115	Generation of interactive displays from FORTRAN using the PDP - 10/LDS-1 computer graphics system. Software - Practice and Experience, 1972, 2, 259-273.	3.6	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. Journal of Theoretical Biology, 1974, 44, 7-17.	1.7	5
117	Recursion relations for the classical partition function of the hard‑sphere gas in two and three dimensions. Journal of Chemical Physics, 1975, 63, 5048-5049.	3.0	5
118	Serpin Conformations. , 2007, , 35-66.		5
119	Choice of Basis Set for Expansion of One‑Dimensional Oscillator Eigenfunctions. Journal of Chemical Physics, 1968, 49, 3898-3900.	3.0	4
120	A cluster of familial Creutzfeldt-Jakob disease mutations recapitulate conserved residues in Doppel: a case of molecular mimicry?. FEBS Letters, 2002, 532, 21-26.	2.8	4
121	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. Journal of Computational Biology, 2015, 22, 487-497.	1.6	4
122	CASP2: Report on ab initio predictions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 151-166.	2.6	4
123	A toolkit for computational molecular biology I: packing and unpacking of protein coordinate sets. Journal of Molecular Graphics, 1983, 1, 118-121.	1.1	3
124	The analysis of protein structures: New insights from a growing data base. BioEssays, 1984, 1, 105-110.	2.5	3
125	Themes and contrasts in protein structures. Trends in Biochemical Sciences, 1984, 9, 290.	7.5	3
126	What the papers say: Protein structure and evolution: Similar amino acid sequences sometimes produce strikingly different three-dimensional structures. BioEssays, 1985, 2, 213-214.	2.5	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.	0.4	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.	1.3	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.	2.0	2
132	Entropy Changes in Isothermal Expansions of Real Gases. American Journal of Physics, 1974, 42, 1030-1033.	0.7	2
133	Reinterpretation of Moseleyâ€™s experiments relating Kα line frequencies and atomic number. American Journal of Physics, 1980, 48, 492-493.	0.7	2
134	Introduction: Protein engineering. BioEssays, 1988, 8, 51-52.	2.5	2
135	From electrons to proteins and back again. International Journal of Quantum Chemistry, 2003, 95, 678-682.	2.0	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.	0.9	2
138	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes. , 2017, , .		2
139	Computer modeling of a potential agent against <scp>SARSâ€Cov</scp>â€2 (<scp>COVID</scp>â€19) protease. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1557-1558.	2.6	2
140	Neighbourhoods in the yeast regulatory network inÂdifferent physiological states. Bioinformatics, 2021, 37, 551-558.	4.1	2
141	Dynamic computation of derivatives. Communications of the ACM, 1967, 10, 571-572.	4.5	2
142	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. Methods in Molecular Biology, 2019, 1958, 123-131.	0.9	2
143	Three-dimensional Structure Databases of Biological Macromolecules. Methods in Molecular Biology, 2022, 2449, 43-91.	0.9	2
144	Protein structure prediction improves the quality of aminoâ€acid sequence alignment. Proteins: Structure, Function and Bioinformatics, 2022, 90, 2144-2147.	2.6	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. International Journal of Quantum Chemistry, 1968, 2, 801-805.	2.0	1
146	A corrected valence electron approximation. Molecular Physics, 1968, 15, 453-458.	1.7	1
147	Application of the common features of transfer RNAs to the determination of their nucleotide sequences. Biochemical and Biophysical Research Communications, 1971, 45, 676-680.	2.1	1
148	Expansion of eigenfunctions of a morse oscillator in a nonorthogonal basis of displaced harmonic oscillator functions. Chemical Physics Letters, 1976, 38, 113-116.	2.6	1
149	Treatment of nonspecular reflection in the single€particle model of an ideal gas. American Journal of Physics, 1976, 44, 1134-1135.	0.7	1
150	Cover blown. Nature, 1988, 334, 560-560.	27.8	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. Physics of Life Reviews, 2013, 10, 33-34.	2.8	1
153	Statistical Inference of Protein "LEGO Bricks". , 2013, , .		1
154	An encoding technique to facilitate the detection of homologies in biopolymer sequences. Journal of Theoretical Biology, 1977, 69, 767-769.	1.7	0
155	AprÃ©s moi lÃ© deluge. Nature, 1994, 371, 440-441.	27.8	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.	0.4	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.	2.3	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.	3.5	0
174	Paths Through the Yeast Regulatory Network in Different Physiological States. Journal of Molecular Biology, 2021, 433, 167181.	4.2	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 50ÂYears of Structural Bioinformatics in Memoriam of Cyrus Chothia. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	0