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	On the reliability and the limits of inference of amino acid sequence alignments. Bioinformatics, 2022, 38, i255-i263.	4.1	6
2	Editorial: A Journey Through 50ÂYears of Structural Bioinformatics in Memoriam of Cyrus Chothia. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	0
3	Three-dimensional Structure Databases of Biological Macromolecules. Methods in Molecular Biology, 2022, 2449, 43-91.	0.9	2
4	Protein structure prediction improves the quality of aminoâ€acid sequence alignment. Proteins: Structure, Function and Bioinformatics, 2022, 90, 2144-2147.	2.6	2
5	Neighbourhoods in the yeast regulatory network inÂdifferent physiological states. Bioinformatics, 2021, 37, 551-558.	4.1	2
6	Paths Through the Yeast Regulatory Network in Different Physiological States. Journal of Molecular Biology, 2021, 433, 167181.	4.2	0
7	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. Journal of Biological Chemistry, 2021, 296, 100421.	3.4	14
8	On identifying statistical redundancy at the level of amino acid subsequences. , 2021, , .		0
9	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
10	Not Enough Natural Data? Sequence and Ye Shall Find. Frontiers in Molecular Biosciences, 2020, 7, 65.	3.5	0
11	Universal Architectural Concepts Underlying Protein Folding Patterns. Frontiers in Molecular Biosciences, 2020, 7, 612920.	3.5	9
12	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. Methods in Molecular Biology, 2019, 1958, 123-131.	0.9	2
13	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. Nature Structural and Molecular Biology, 2018, 25, 538-545.	8.2	87
14	Statistical inference of protein structural alignments using information and compression. Bioinformatics, 2017, 33, 1005-1013.	4.1	18
15	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes. , 2017, , .		2
16	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. Journal of Computational Biology, 2015, 22, 487-497.	1.6	4
17	Sizes of interface residues account for crossâ€class binding affinity patterns in Eph receptorâ€“ephrin families. Proteins: Structure, Function and Bioinformatics, 2014, 82, 349-353.	2.6	6
18	How precise are reported protein coordinate data?. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 904-906.	2.5	3

#	Article	IF	Citations
19	A new statistical framework to assess structural alignment quality using information compression. Bioinformatics, 2014, 30, i512-i518.	4.1	6
20	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. Lecture Notes in Computer Science, 2014, , 144-159.	1.3	3
21	Comment on â€œComparing proteins by their internal dynamics: Exploring structureâ€“function relationships beyond static structural alignmentsâ€•by C. Micheletti. Physics of Life Reviews, 2013, 10, 33-34.	2.8	1
22	Statistical Inference of Protein "LEGO Bricks". , 2013, , .		1
23	Canonical Network Motifs. , 2013, , 199-201.		0
24	Minimum message length inference of secondary structure from protein coordinate data. Bioinformatics, 2012, 28, i97-i105.	4.1	37
25	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
26	Structure Description and Identification Using the Tableau Representation of Protein Folding Patterns. Methods in Molecular Biology, 2012, 932, 51-59.	0.9	2
27	Genetic diversity and population structure of the endangered marsupial Sarcophilus harrisii (Tasmanian devil). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12348-12353.	7.1	189
28	Piecewise linear approximation of protein structures using the principle of minimum message length. Bioinformatics, 2011, 27, i43-i51.	4.1	9
29	Cataloging topologies of protein folding patterns. Journal of Molecular Recognition, 2010, 23, 253-257.	2.1	13
30	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
31	The mitochondrial genome sequence of the Tasmanian tiger (Thylacinus cynocephalus). Genome Research, 2009, 19, 213-220.	5.5	102
32	Single and multiple input modules in regulatory networks. Proteins: Structure, Function and Bioinformatics, 2008, 73, 320-324.	2.6	14
33	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
34	Correspondences between lowâ€energy modes in enzymes: Dynamicsâ€based alignment of enzymatic functional families. Protein Science, 2008, 17, 918-929.	7.6	62
35	Sequencing the nuclear genome of the extinct woolly mammoth. Nature, 2008, 456, 387-390.	27.8	283
36	On the origin of distribution patterns of motifs in biological networks. BMC Systems Biology, 2008, 2, 73.	3.0	34

#	Article	IF	Citations
37	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
38	Bioinformatics of Protein Function. , 2008, , 79-119.		0
39	Structural search and retrieval using a tableau representation of protein folding patterns. Bioinformatics, 2008, 24, 645-651.	4.1	30
40	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
41	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
42	The Evolution of the Globins: We Thought We Understood It. Biological and Medical Physics Series, 2007, , 57-74.	0.4	0
43	Contact patterns between helices and strands of sheet define protein folding patterns. Proteins: Structure, Function and Bioinformatics, 2007, 66, 869-876.	2.6	33
44	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	2.6	68
45	Serpin Conformations. , 2007, , 35-66.		5
46	Serpins in Prokaryotes. , 2007, , 131-162.		6
47	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
48	What determines the spectrum of protein native state structures?. Proteins: Structure, Function and Bioinformatics, 2006, 63, 273-277.	2.6	7
49	MUSTANG: A multiple structural alignment algorithm. Proteins: Structure, Function and Bioinformatics, 2006, 64, 559-574.	2.6	615
50	Structural divergence and distant relationships in proteins: evolution of the globins. Current Opinion in Structural Biology, 2005, 15, 290-301.	5.7	75
51	Functional insights from the distribution and role of homopeptide repeat-containing proteins. Genome Research, 2005, 15, 537-551.	5.5	189
52	Molecular Forces in Antibody Maturation. Physical Review Letters, 2005, 95, 208106.	7.8	15
53	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
54	Hydrophobicityâ€"getting into hot water. Biophysical Chemistry, 2003, 105, 179-182.	2.8	9

#	Article	IF	Citations
55	From electrons to proteins and back again. International Journal of Quantum Chemistry, 2003, 95, 678-682.	2.0	2
56	Prediction of protein function from protein sequence and structure. Quarterly Reviews of Biophysics, 2003, 36, 307-340.	5.7	376
57	Serpins in Prokaryotes. Molecular Biology and Evolution, 2002, 19, 1881-1890.	8.9	112
58	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
59	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
60	Modularity and homology: modelling of the titin type I modules and their interfaces. Journal of Molecular Biology, 2001, 311, 283-296.	4.2	29
61	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
62	Protein structural alignments and functional genomics. Proteins: Structure, Function and Bioinformatics, 2001, 42, 378-382.	2.6	76
63	The unreasonable effectiveness of mathematics in molecular biology. Mathematical Intelligencer, 2000, 22, 28-37.	0.2	22
64	Canonical structures for the hypervariable regions of T cell Î±Î² receptors. Journal of Molecular Biology, 2000, 295, 979-995.	4.2	56
65	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
66	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
67	Conformational changes in serpins: II. the mechanism of activation of antithrombin by heparin. Journal of Molecular Biology, 2000, 301, 1287-1305.	4.2	93
68	Antibody Modeling: Implications for Engineering and Design. Methods, 2000, 20, 267-279.	3.8	98
69	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
70	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
71	Tendamistat surface accessibility to the TEMPOL paramagnetic probe. Journal of Biomolecular NMR, 1999, 15, 125-133.	2.8	30
72	SH3 domains in prokaryotes. Trends in Biochemical Sciences, 1999, 24, 132-133.	7.5	110

#	Article	IF	Citations
73	Serpins in theCaenorhabditis elegans genome. , 1999, 36, 31-41.		18
74	An atlas of serpin conformations. Trends in Biochemical Sciences, 1998, 23, 63-67.	7.5	173
75	Extraction of geometrically similar substructures: Least-squares and Chebyshev fitting and the difference distance matrix. , 1998, 33, 320-328.		13
76	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
77	Assessment of ab initio protein structure prediction. , 1998, , .		0
78	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
79	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
80	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
81	Extraction of well-fitting substructures: root-mean-square deviation and the difference distance matrix. Folding & Design, 1997, 2, S12-S14.	4.5	7
82	Importance of the release of strand 1C to the polymerization mechanism of inhibitory serpins. Protein Science, 1997, 6, 89-98.	7.6	64
83	CASP2: Report on ab initio predictions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 151-166.	2.6	54
84	CASP2: Report on ab initio predictions. Proteins: Structure, Function and Bioinformatics, 1997, 29, 151-166.	2.6	4
85	Conservation and Variability in the Structures of Serine Proteinases of the Chymotrypsin Family. Journal of Molecular Biology, 1996, 258, 501-537.	4.2	145
86	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
87	Systematic representation of protein folding patterns. Journal of Molecular Graphics, 1995, 13, 159-164.	1.1	35
88	NAD-binding domains of dehydrogenases. Current Opinion in Structural Biology, 1995, 5, 775-783.	5.7	228
89	Three-dimensional pattern matching in protein structure analysis. Lecture Notes in Computer Science, 1995, , 248-260.	1.3	8
90	Three-Dimensional Searching for Recurrent Structural Motifs in Data Bases of Protein Structures. Journal of Computational Biology, 1994, 1, 121-132.	1.6	11

#	Article	IF	Citations
91	AprÃ©s moi lÃ© deluge. Nature, 1994, 371, 440-441.	27.8	0
92	Structural Mechanisms for Domain Movements in Proteins. Biochemistry, 1994, 33, 6739-6749.	2.5	770
93	Principles determining the structure of Î²-sheet barrels in proteins I. A theoretical analysis. Journal of Molecular Biology, 1994, 236, 1369-1381.	4.2	204
94	Principles determining the structure of Î²-sheet barrels in proteins II. The observed structures. Journal of Molecular Biology, 1994, 236, 1382-1400.	4.2	126
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	Domain Closure in Lactoferrin. Journal of Molecular Biology, 1993, 234, 357-372.	4.2	160
97	Boolean programming formulation of some pattern-matching problems in molecular biology. Journal of the Chemical Society, Faraday Transactions, 1993, 89, 2603.	1.7	3
98	Homology modelling: inferences from tables of aligned sequences. Current Opinion in Structural Biology, 1992, 2, 242-247.	5.7	15
99	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
100	Structural repertoire of the human VH segments. Journal of Molecular Biology, 1992, 227, 799-817.	4.2	412
101	Probing protein structure by solvent perturbation of nuclear magnetic resonance spectra. Journal of Molecular Biology, 1992, 224, 659-670.	4.2	73
102	Î²-Trefoil fold. Journal of Molecular Biology, 1992, 223, 531-543.	4.2	318
103	Domain closure in mitochondrial aspartate aminotransferase. Journal of Molecular Biology, 1992, 227, 197-213.	4.2	188
104	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
105	What the papers say: Does protein structure determine amino acid sequence?. BioEssays, 1992, 14, 407-410.	2.5	15
106	Brave new proteins: What evolution reveals about protein structure. Current Opinion in Biotechnology, 1991, 2, 592-598.	6.6	7
107	Alarums and diversions. Nature, 1991, 352, 379-380.	27.8	7
108	Comparison of the structures of globins and phycocyanins: Evidence for evolutionary relationship. Proteins: Structure, Function and Bioinformatics, 1990, 8, 133-155.	2.6	93

#	Article	IF	Citations
109	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
110	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
111	Structural principles of Î±/Î² barrel proteins: The packing of the interior of the sheet. Proteins: Structure, Function and Bioinformatics, 1989, 5, 139-148.	2.6	156
112	Structural determinants of the conformations of medium-sized loops in proteins. Proteins: Structure, Function and Bioinformatics, 1989, 6, 382-394.	2.6	82
113	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	27.8	1,199
114	Introduction: Protein engineering. BioEssays, 1988, 8, 51-52.	2.5	2
115	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
116	Cover blown. Nature, 1988, 334, 560-560.	27.8	1
117	Elbow motion in the immunoglobulins involves a molecular ball-and-socket joint. Nature, 1988, 335, 188-190.	27.8	167
118	Interior and surface of monomeric proteins. Journal of Molecular Biology, 1987, 196, 641-656.	4.2	873
119	Canonical structures for the hypervariable regions of immunoglobulins. Journal of Molecular Biology, 1987, 196, 901-917.	4.2	1,358
120	Determinants of a protein fold. Journal of Molecular Biology, 1987, 196, 199-216.	4.2	485
121	The accessible surface area and stability of oligomeric proteins. Nature, 1987, 328, 834-836.	27.8	346
122	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
123	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
124	Molecular biology: Coordination of sequence data. Nature, 1985, 314, 318-319.	27.8	8
125	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
126	Computer-generated pictures of proteins. Methods in Enzymology, 1985, 115, 381-390.	1.0	49

#	Article	IF	Citations
127	Helix movements in proteins. Trends in Biochemical Sciences, 1985, 10, 116-118.	7.5	70
128	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
129	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
130	The analysis of protein structures: New insights from a growing data base. BioEssays, 1984, 1, 105-110.	2.5	3
131	Mechanisms of domain closure in proteins. Journal of Molecular Biology, 1984, 174, 175-191.	4.2	170
132	Themes and contrasts in protein structures. Trends in Biochemical Sciences, 1984, 9, 290.	7.5	3
133	Transmission of conformational change in insulin. Nature, 1983, 302, 500-505.	27.8	201
134	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
135	Evolution of proteins formed by Î²-sheets. Journal of Molecular Biology, 1982, 160, 309-323.	4.2	134
136	Evolution of proteins formed by Î²-sheets. Journal of Molecular Biology, 1982, 160, 325-342.	4.2	280
137	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
138	Reinterpretation of Moseleyâ€™s experiments relating KÎ± line frequencies and atomic number. American Journal of Physics, 1980, 48, 492-493.	0.7	2
139	Detection of three-dimensional patterns of atoms in chemical structures. Communications of the ACM, 1979, 22, 219-224.	4.5	55
140	Macromolecular marionettes. Computers in Biology and Medicine, 1977, 7, 113-129.	7.0	15
141	An encoding technique to facilitate the detection of homologies in biopolymer sequences. Journal of Theoretical Biology, 1977, 69, 767-769.	1.7	0
142	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
143	Treatment of nonspecular reflection in the singleâ€particle model of an ideal gas. American Journal of Physics, 1976, 44, 1134-1135.	0.7	1
144	Recursion relations for the classical partition function of the hardâ€sphere gas in two and three dimensions. Journal of Chemical Physics, 1975, 63, 5048-5049.	3.0	5

#	Article	IF	Citations
145	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
146	Entropy Changes in Isothermal Expansions of Real Gases. American Journal of Physics, 1974, 42, 1030-1033.	0.7	2
147	On hypothesized selective pressure by u.v. on DNA base compositions. Journal of Theoretical Biology, 1973, 40, 201-202.	1.7	6
148	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
149	Pictorial pattern recognition and the phase problem of x-ray crystallography. Communications of the ACM, 1972, 15, 3-6.	4.5	11
150	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
151	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
152	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
153	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
154	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
155	Why does DNA contain thymine and RNA uracil?. Journal of Theoretical Biology, 1969, 22, 537-540.	1.7	12
156	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
157	A corrected valence electron approximation. Molecular Physics, 1968, 15, 453-458.	1.7	1
158	Choice of Basis Set for Expansion of Oneâ€Dimensional Oscillator Eigenfunctions. Journal of Chemical Physics, 1968, 49, 3898-3900.	3.0	4
159	Use of the Hartree-Fock Approximation in Computing Electron Affinities. Physical Review, 1968, 171, 7-10.	2.7	8
160	Dynamic computation of derivatives. Communications of the ACM, 1967, 10, 571-572.	4.5	2
161	The Fluorides and Oxides of Helium and Neon1. Journal of the American Chemical Society, 1966, 88, 615-616.	13.7	14
162	ROTATORY DISPERSION OF NUCLEIC ACIDS IN THE NEAR-ULTRAVIOLET REGION. Journal of the American Chemical Society, 1961, 83, 3155-3156.	13.7	24

#	Article	IF	Citations
163	Modelling Protein Structures. , 0, , 9-35.		1
164	Classification of Protein Function. , 0, , 167-183.		0
165	Models of Database Interconnectivity. , 0, , 203-221.		0
166	The European Bioinformatics Institute Macromolecular Structure Relational Database Technology. , 0, , 223-240.		2
167	Looking Around, Looking Ahead. , 0, , 242-244.		0
168	Survey of Sequence Databases: Archival Projects. , 0, , 24-44.		0
169	Survey of Sequence Databases: Derived Databases. , 0, , 45-62.		0
170	Databanks of Macromolecular Structure. , 0, , 63-79.		0
171	Taxonomy: a Moving Target for Sequence Data. , 0, , 100-112.		0
172	Genomics and Proteomics: Design and Sources of Annotation. , 0, , 113-130.		0
173	Issues in the Annotation of Protein Structures. , 0, , 149-165.		0
174	Annotation of Protein Sequences. , 0, , 131-147.		0
175	Information Flow and Data Integration of Databanks. , 0, , 186-201.		0
176	Gene Expression Databases. , 0, , 81-97.		0
177	Annotation and Databases: Status and Prospects. , 0, , 1-21.		0