

Arthur M Lesk

List of Publications by Year in descending order

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177
papers

16,871
citations

28736

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127
g-index

184
all docs

184
docs citations

184
times ranked

15987
citing authors

#	ARTICLE	IF	CITATIONS
1	On the reliability and the limits of inference of amino acid sequence alignments. <i>Bioinformatics</i> , 2022, 38, i255-i263.	1.8	6
2	Editorial: A Journey Through 50 Years of Structural Bioinformatics in Memoriam of Cyrus Chothia. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	0
3	Three-dimensional Structure Databases of Biological Macromolecules. <i>Methods in Molecular Biology</i> , 2022, 2449, 43-91.	0.4	2
4	Protein structure prediction improves the quality of amino acid sequence alignment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 2144-2147.	1.5	2
5	Neighbourhoods in the yeast regulatory network in different physiological states. <i>Bioinformatics</i> , 2021, 37, 551-558.	1.8	2
6	Paths Through the Yeast Regulatory Network in Different Physiological States. <i>Journal of Molecular Biology</i> , 2021, 433, 167181.	2.0	0
7	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. <i>Journal of Biological Chemistry</i> , 2021, 296, 100421.	1.6	14
8	On identifying statistical redundancy at the level of amino acid subsequences. , 2021, , .		0
9	Computer modeling of a potential agent against SARS-CoV-2 (COVID-19) protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1557-1558.	1.5	2
10	Not Enough Natural Data? Sequence and Ye Shall Find. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 65.	1.6	0
11	Universal Architectural Concepts Underlying Protein Folding Patterns. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 612920.	1.6	9
12	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. <i>Methods in Molecular Biology</i> , 2019, 1958, 123-131.	0.4	2
13	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	3.6	87
14	Statistical inference of protein structural alignments using information and compression. <i>Bioinformatics</i> , 2017, 33, 1005-1013.	1.8	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. <i>Journal of Computational Biology</i> , 2015, 22, 487-497.	0.8	4
17	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
18	How precise are reported protein coordinate data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 904-906.	2.5	3

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19	A new statistical framework to assess structural alignment quality using information compression. <i>Bioinformatics</i> , 2014, 30, i512-i518.	1.8	6
20	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Lecture Notes in Computer Science</i> , 2014, , 144-159.	1.0	3
21	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
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. <i>Bioinformatics</i> , 2012, 28, i97-i105.	1.8	37
25	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. <i>Nucleic Acids Research</i> , 2012, 40, W334-W339.	6.5	6
26	Structure Description and Identification Using the Tableau Representation of Protein Folding Patterns. <i>Methods in Molecular Biology</i> , 2012, 932, 51-59.	0.4	2
27	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
28	Piecewise linear approximation of protein structures using the principle of minimum message length. <i>Bioinformatics</i> , 2011, 27, i43-i51.	1.8	9
29	Cataloging topologies of protein folding patterns. <i>Journal of Molecular Recognition</i> , 2010, 23, 253-257.	1.1	13
30	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. <i>PLoS ONE</i> , 2010, 5, e10048.	1.1	47
31	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009, 19, 213-220.	2.4	102
32	Single and multiple input modules in regulatory networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 320-324.	1.5	14
33	On the use of overlapping lattices for screening to find pairs of nearby points in two and three dimensions. <i>Computational Biology and Chemistry</i> , 2008, 32, 212-214.	1.1	0
34	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
35	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008, 456, 387-390.	13.7	283
36	On the origin of distribution patterns of motifs in biological networks. <i>BMC Systems Biology</i> , 2008, 2, 73.	3.0	34

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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.	3.3	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.	1.8	30
40	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	2.4	237
41	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
42	The Evolution of the Globins: We Thought We Understood It. Biological and Medical Physics Series, 2007, , 57-74.	0.3	0
43	Contact patterns between helices and strands of sheet define protein folding patterns. Proteins: Structure, Function and Bioinformatics, 2007, 66, 869-876.	1.5	33
44	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	1.2	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 I ² -Helices. Journal of Molecular Biology, 2006, 358, 330-345.	2.0	46
48	What determines the spectrum of protein native state structures?. Proteins: Structure, Function and Bioinformatics, 2006, 63, 273-277.	1.5	7
49	MUSTANG: A multiple structural alignment algorithm. Proteins: Structure, Function and Bioinformatics, 2006, 64, 559-574.	1.5	615
50	Structural divergence and distant relationships in proteins: evolution of the globins. Current Opinion in Structural Biology, 2005, 15, 290-301.	2.6	75
51	Functional insights from the distribution and role of homopeptide repeat-containing proteins. Genome Research, 2005, 15, 537-551.	2.4	189
52	Molecular Forces in Antibody Maturation. Physical Review Letters, 2005, 95, 208106.	2.9	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.	1.6	29
54	Hydrophobicityâ€™ getting into hot water. Biophysical Chemistry, 2003, 105, 179-182.	1.5	9

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55	From electrons to proteins and back again. <i>International Journal of Quantum Chemistry</i> , 2003, 95, 678-682.	1.0	2
56	Prediction of protein function from protein sequence and structure. <i>Quarterly Reviews of Biophysics</i> , 2003, 36, 307-340.	2.4	376
57	Serpins in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2002, 19, 1881-1890.	3.5	112
58	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
59	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
60	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
61	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
62	Protein structural alignments and functional genomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 378-382.	1.5	76
63	The unreasonable effectiveness of mathematics in molecular biology. <i>Mathematical Intelligencer</i> , 2000, 22, 28-37.	0.1	22
64	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
65	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
66	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
67	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
68	Antibody Modeling: Implications for Engineering and Design. <i>Methods</i> , 2000, 20, 267-279.	1.9	98
69	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
70	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
71	Tendamistat surface accessibility to the TEMPOL paramagnetic probe. <i>Journal of Biomolecular NMR</i> , 1999, 15, 125-133.	1.6	30
72	SH3 domains in prokaryotes. <i>Trends in Biochemical Sciences</i> , 1999, 24, 132-133.	3.7	110

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73	Serpins in the <i>Caenorhabditis elegans</i> genome. , 1999, 36, 31-41.		18
74	An atlas of serpin conformations. <i>Trends in Biochemical Sciences</i> , 1998, 23, 63-67.	3.7	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 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1998, 275, 269-294.	2.0	350
77	Assessment of ab initio protein structure prediction. , 1998, , .		0
78	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
79	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
80	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
81	Extraction of well-fitting substructures: root-mean-square deviation and the difference distance matrix. <i>Folding & Design</i> , 1997, 2, S12-S14.	4.5	7
82	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
83	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 151-166.	1.5	54
84	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 151-166.	1.5	4
85	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
86	Modeling of serpin-protease complexes: Antithrombin-thrombin, $\hat{1}$ -antitrypsin (358Met $\hat{1}$ Arg)-thrombin, $\hat{1}$ -antitrypsin (358Met $\hat{1}$ Arg)-trypsin, and antitrypsin-elastase. , 1996, 26, 288-303.		26
87	Systematic representation of protein folding patterns. <i>Journal of Molecular Graphics</i> , 1995, 13, 159-164.	1.7	35
88	NAD-binding domains of dehydrogenases. <i>Current Opinion in Structural Biology</i> , 1995, 5, 775-783.	2.6	228
89	Three-dimensional pattern matching in protein structure analysis. <i>Lecture Notes in Computer Science</i> , 1995, , 248-260.	1.0	8
90	Three-Dimensional Searching for Recurrent Structural Motifs in Data Bases of Protein Structures. <i>Journal of Computational Biology</i> , 1994, 1, 121-132.	0.8	11

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91	AprÃ©s moi l'Ã© deluge. Nature, 1994, 371, 440-441.	13.7	0
92	Structural Mechanisms for Domain Movements in Proteins. Biochemistry, 1994, 33, 6739-6749.	1.2	770
93	Principles determining the structure of β^2 -sheet barrels in proteins I. A theoretical analysis. Journal of Molecular Biology, 1994, 236, 1369-1381.	2.0	204
94	Principles determining the structure of β^2 -sheet barrels in proteins II. The observed structures. Journal of Molecular Biology, 1994, 236, 1382-1400.	2.0	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.	1.2	10
96	Domain Closure in Lactoferrin. Journal of Molecular Biology, 1993, 234, 357-372.	2.0	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.	2.6	15
99	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	1.5	26
100	Structural repertoire of the human VH segments. Journal of Molecular Biology, 1992, 227, 799-817.	2.0	412
101	Probing protein structure by solvent perturbation of nuclear magnetic resonance spectra. Journal of Molecular Biology, 1992, 224, 659-670.	2.0	73
102	β^2 -Trefoil fold. Journal of Molecular Biology, 1992, 223, 531-543.	2.0	318
103	Domain closure in mitochondrial aspartate aminotransferase. Journal of Molecular Biology, 1992, 227, 197-213.	2.0	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.	1.5	63
105	What the papers say: Does protein structure determine amino acid sequence?. BioEssays, 1992, 14, 407-410.	1.2	15
106	Brave new proteins: What evolution reveals about protein structure. Current Opinion in Biotechnology, 1991, 2, 592-598.	3.3	7
107	Alarums and diversions. Nature, 1991, 352, 379-380.	13.7	7
108	Comparison of the structures of globins and phycocyanins: Evidence for evolutionary relationship. Proteins: Structure, Function and Bioinformatics, 1990, 8, 133-155.	1.5	93

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109	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
110	The computational analysis of protein structures: Sources, methods, systems and results. <i>Journal of Research of the National Bureau of Standards (United States)</i> , 1989, 94, 85.	0.3	3
111	Structural principles of β/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
112	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
113	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989, 342, 877-883.	13.7	1,199
114	Introduction: Protein engineering. <i>BioEssays</i> , 1988, 8, 51-52.	1.2	2
115	Structural alignment and analysis of two distantly related proteins: <i>Aplysia limacina</i> myoglobin and sea lamprey globin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 4, 240-250.	1.5	9
116	Cover blown. <i>Nature</i> , 1988, 334, 560-560.	13.7	1
117	Elbow motion in the immunoglobulins involves a molecular ball-and-socket joint. <i>Nature</i> , 1988, 335, 188-190.	13.7	167
118	Interior and surface of monomeric proteins. <i>Journal of Molecular Biology</i> , 1987, 196, 641-656.	2.0	873
119	Canonical structures for the hypervariable regions of immunoglobulins. <i>Journal of Molecular Biology</i> , 1987, 196, 901-917.	2.0	1,358
120	Determinants of a protein fold. <i>Journal of Molecular Biology</i> , 1987, 196, 199-216.	2.0	485
121	The accessible surface area and stability of oligomeric proteins. <i>Nature</i> , 1987, 328, 834-836.	13.7	346
122	On the calculation of Euler angles from a rotation matrix. <i>International Journal of Mathematical Education in Science and Technology</i> , 1986, 17, 335-337.	0.8	10
123	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
124	Molecular biology: Coordination of sequence data. <i>Nature</i> , 1985, 314, 318-319.	13.7	8
125	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
126	Computer-generated pictures of proteins. <i>Methods in Enzymology</i> , 1985, 115, 381-390.	0.4	49

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127	Helix movements in proteins. Trends in Biochemical Sciences, 1985, 10, 116-118.	3.7	70
128	Haemoglobin: The surface buried between the $\hat{1}\pm 1\hat{1}^2$ and $\hat{1}\pm 2\hat{1}^2$ dimers in the deoxy and oxy structures. Journal of Molecular Biology, 1985, 183, 267-270.	2.0	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.	2.0	73
130	The analysis of protein structures: New insights from a growing data base. BioEssays, 1984, 1, 105-110.	1.2	3
131	Mechanisms of domain closure in proteins. Journal of Molecular Biology, 1984, 174, 175-191.	2.0	170
132	Themes and contrasts in protein structures. Trends in Biochemical Sciences, 1984, 9, 290.	3.7	3
133	Transmission of conformational change in insulin. Nature, 1983, 302, 500-505.	13.7	201
134	A toolkit for computational molecular biology I: packing and unpacking of protein coordinate sets. Journal of Molecular Graphics, 1983, 1, 118-121.	1.7	3
135	Evolution of proteins formed by $\hat{1}^2$ -sheets. Journal of Molecular Biology, 1982, 160, 309-323.	2.0	134
136	Evolution of proteins formed by $\hat{1}^2$ -sheets. Journal of Molecular Biology, 1982, 160, 325-342.	2.0	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.	2.0	703
138	Reinterpretation of Moseley's experiments relating $K\hat{1}\pm$ line frequencies and atomic number. American Journal of Physics, 1980, 48, 492-493.	0.3	2
139	Detection of three-dimensional patterns of atoms in chemical structures. Communications of the ACM, 1979, 22, 219-224.	3.3	55
140	Macromolecular marionettes. Computers in Biology and Medicine, 1977, 7, 113-129.	3.9	15
141	An encoding technique to facilitate the detection of homologies in biopolymer sequences. Journal of Theoretical Biology, 1977, 69, 767-769.	0.8	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.	1.2	1
143	Treatment of nonspecular reflection in the single-particle model of an ideal gas. American Journal of Physics, 1976, 44, 1134-1135.	0.3	1
144	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.	1.2	5

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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.	0.8	5
146	Entropy Changes in Isothermal Expansions of Real Gases. American Journal of Physics, 1974, 42, 1030-1033.	0.3	2
147	On hypothesized selective pressure by u.v. on DNA base compositions. Journal of Theoretical Biology, 1973, 40, 201-202.	0.8	6
148	Lower bound to the long-range interaction energy of two identical rare gas atoms in the restricted Hartree-Fock approximation. Journal of Chemical Physics, 1973, 59, 44-46.	1.2	14
149	Pictorial pattern recognition and the phase problem of x-ray crystallography. Communications of the ACM, 1972, 15, 3-6.	3.3	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.	2.5	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.	1.0	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.	0.8	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.	1.0	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.	1.0	2
155	Why does DNA contain thymine and RNA uracil?. Journal of Theoretical Biology, 1969, 22, 537-540.	0.8	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.	1.0	1
157	A corrected valence electron approximation. Molecular Physics, 1968, 15, 453-458.	0.8	1
158	Choice of Basis Set for Expansion of One-Dimensional Oscillator Eigenfunctions. Journal of Chemical Physics, 1968, 49, 3898-3900.	1.2	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.	3.3	2
161	The Fluorides and Oxides of Helium and Neon ¹ . Journal of the American Chemical Society, 1966, 88, 615-616.	6.6	14
162	ROTATORY DISPERSION OF NUCLEIC ACIDS IN THE NEAR-ULTRAVIOLET REGION. Journal of the American Chemical Society, 1961, 83, 3155-3156.	6.6	24

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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