

Arthur M Lesk

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

169
papers

14,831
citations

56
h-index

121
g-index

184
ext. papers

15,877
ext. citations

8.1
avg, IF

6.08
L-index

#	Paper	IF	Citations
169	Three-dimensional Structure Databases of Biological Macromolecules.. <i>Methods in Molecular Biology</i> , 2022 , 2449, 43-91	1.4	
168	Neighbourhoods in the yeast regulatory network in different physiological states. <i>Bioinformatics</i> , 2021 , 37, 551-558	7.2	2
167	Paths Through the Yeast Regulatory Network in Different Physiological States. <i>Journal of Molecular Biology</i> , 2021 , 433, 167181	6.5	
166	Invisible leashes: The tethering VAPs from infectious diseases to neurodegeneration. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100421	5.4	4
165	Not Enough Natural Data? Sequence and Ye Shall Find. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 65	5.6	
164	Computer modeling of a potential agent against SARS-Cov-2 (COVID-19) protease. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1557-1558	4.2	1
163	Universal Architectural Concepts Underlying Protein Folding Patterns. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 612920	5.6	4
162	Information-Theoretic Inference of an Optimal Dictionary of Protein Supersecondary Structures. <i>Methods in Molecular Biology</i> , 2019 , 1958, 123-131	1.4	1
161	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 538-545	17.6	57
160	Statistical inference of protein structural alignments using information and compression. <i>Bioinformatics</i> , 2017 , 33, 1005-1013	7.2	7
159	Statistical Compression of Protein Folding Patterns for Inference of Recurrent Substructural Themes 2017 ,		2
158	On sufficient statistics of least-squares superposition of vector sets. <i>Journal of Computational Biology</i> , 2015 , 22, 487-97	1.7	2
157	A new statistical framework to assess structural alignment quality using information compression. <i>Bioinformatics</i> , 2014 , 30, i512-8	7.2	5
156	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, 349-53	4.2	5
155	How precise are reported protein coordinate data?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 904-6		2
154	On Sufficient Statistics of Least-Squares Superposition of Vector Sets. <i>Lecture Notes in Computer Science</i> , 2014 , 144-159	0.9	3
153	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, 33-4; discussion 39-40	2.1	1

152	Structure description and identification using the tableau representation of protein folding patterns. <i>Methods in Molecular Biology</i> , 2013 , 932, 51-9	1.4	2
151	The Globin Family 2013 , 207-235		
150	Statistical Inference of Protein "LEGO Bricks" 2013 ,		1
149	Minimum message length inference of secondary structure from protein coordinate data. <i>Bioinformatics</i> , 2012 , 28, i97-105	7.2	31
148	Super: a web server to rapidly screen superposable oligopeptide fragments from the protein data bank. <i>Nucleic Acids Research</i> , 2012 , 40, W334-9	20.1	6
147	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, 12348-53	11.5	164
146	Piecewise linear approximation of protein structures using the principle of minimum message length. <i>Bioinformatics</i> , 2011 , 27, i43-51	7.2	4
145	MUSTANG-MR structural sieving server: applications in protein structural analysis and crystallography. <i>PLoS ONE</i> , 2010 , 5, e10048	3.7	40
144	Cataloging topologies of protein folding patterns. <i>Journal of Molecular Recognition</i> , 2010 , 23, 253-7	2.6	9
143	The mitochondrial genome sequence of the Tasmanian tiger (<i>Thylacinus cynocephalus</i>). <i>Genome Research</i> , 2009 , 19, 213-20	9.7	83
142	Sequencing the nuclear genome of the extinct woolly mammoth. <i>Nature</i> , 2008 , 456, 387-90	50.4	242
141	On the origin of distribution patterns of motifs in biological networks. <i>BMC Systems Biology</i> , 2008 , 2, 73	3.5	29
140	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, 8327-32	11.5	130
139	Bioinformatics of Protein Function 2008 , 79-119		
138	Structural search and retrieval using a tableau representation of protein folding patterns. <i>Bioinformatics</i> , 2008 , 24, 645-51	7.2	25
137	Single and multiple input modules in regulatory networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 320-4	4.2	10
136	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, 212-4	3.6	
135	Correspondences between low-energy modes in enzymes: dynamics-based alignment of enzymatic functional families. <i>Protein Science</i> , 2008 , 17, 918-29	6.3	56

134	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34	33.3	1072
133	The Evolution of the Globins: We Thought We Understood It 2007 , 57-74		
132	Contact patterns between helices and strands of sheet define protein folding patterns. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 66, 869-76	4.2	33
131	Quantitative sequence-function relationships in proteins based on gene ontology. <i>BMC Bioinformatics</i> , 2007 , 8, 294	3.6	54
130	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007 , 17, 1797-808	9.7	204
129	Serpin Conformations 2007 , 35-66		4
128	Serpins in Prokaryotes 2007 , 131-162		2
127	Computational study of the fibril organization of polyglutamine repeats reveals a common motif identified in beta-helices. <i>Journal of Molecular Biology</i> , 2006 , 358, 330-45	6.5	44
126	What determines the spectrum of protein native state structures?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 273-7	4.2	7
125	MUSTANG: a multiple structural alignment algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 559-74	4.2	527
124	Structural divergence and distant relationships in proteins: evolution of the globins. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 290-301	8.1	65
123	Functional insights from the distribution and role of homopeptide repeat-containing proteins. <i>Genome Research</i> , 2005 , 15, 537-51	9.7	147
122	Molecular forces in antibody maturation. <i>Physical Review Letters</i> , 2005 , 95, 208106	7.4	12
121	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, 8435-42	5.4	26
120	Hydrophobicity--getting into hot water. <i>Biophysical Chemistry</i> , 2003 , 105, 179-82	3.5	8
119	From electrons to proteins and back again. <i>International Journal of Quantum Chemistry</i> , 2003 , 95, 678-682.1		1
118	Prediction of protein function from protein sequence and structure. <i>Quarterly Reviews of Biophysics</i> , 2003 , 36, 307-40	7	300
117	Serpins in prokaryotes. <i>Molecular Biology and Evolution</i> , 2002 , 19, 1881-90	8.3	91

116	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, 1645-55	8.3	140
115	A cluster of familial Creutzfeldt-Jakob disease mutations recapitulate conserved residues in Doppel: a case of molecular mimicry?. <i>FEBS Letters</i> , 2002 , 532, 21-6	3.8	4
114	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 , Suppl 5, 98-113	4.3	66
113	Protein structural alignments and functional genomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 378-82	4.2	66
112	Modularity and homology: modelling of the titin type I modules and their interfaces. <i>Journal of Molecular Biology</i> , 2001 , 311, 283-96	6.5	25
111	The unreasonable effectiveness of mathematics in molecular biology. <i>Mathematical Intelligencer</i> , 2000 , 22, 28-37	0.2	16
110	Canonical structures for the hypervariable regions of T cell alphabeta receptors. <i>Journal of Molecular Biology</i> , 2000 , 295, 979-95	6.5	48
109	Conformational changes in serpins: I. The native and cleaved conformations of alpha(1)-antitrypsin. <i>Journal of Molecular Biology</i> , 2000 , 295, 651-65	6.5	47
108	Conformational changes in serpins: I. The native and cleaved conformations of alpha(1)-antitrypsin. <i>Journal of Molecular Biology</i> , 2000 , 296, 685-99	6.5	60
107	Conformational changes in serpins: II. The mechanism of activation of antithrombin by heparin. <i>Journal of Molecular Biology</i> , 2000 , 301, 1287-305	6.5	81
106	Antibody modeling: implications for engineering and design. <i>Methods</i> , 2000 , 20, 267-79	4.6	84
105	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. <i>Genome Research</i> , 2000 , 10, 1845-1864	9.7	92
104	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, R291-7		33
103	Tendamistat surface accessibility to the TEMPOL paramagnetic probe. <i>Journal of Biomolecular NMR</i> , 1999 , 15, 125-33	3	26
102	SH3 domains in prokaryotes. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 132-3	10.3	86
101	Serpins in the <i>Caenorhabditis elegans</i> genome 1999 , 36, 31-41		17
100	An atlas of serpin conformations. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 63-7	10.3	157
99	Extraction of geometrically similar substructures: Least-squares and Chebyshev fitting and the difference distance matrix 1998 , 33, 320-328		12

98	Conformations of the third hypervariable region in the VH domain of immunoglobulins. <i>Journal of Molecular Biology</i> , 1998 , 275, 269-94	6.5	313
97	Preparative induction and characterization of L-antithrombin: a structural homologue of latent plasminogen activator inhibitor-1. <i>Biochemistry</i> , 1997 , 36, 13133-42	3.2	71
96	The 2.6 Å structure of antithrombin indicates a conformational change at the heparin binding site. <i>Journal of Molecular Biology</i> , 1997 , 266, 601-9	6.5	177
95	Standard conformations for the canonical structures of immunoglobulins. <i>Journal of Molecular Biology</i> , 1997 , 273, 927-48	6.5	603
94	Extraction of well-fitting substructures: root-mean-square deviation and the difference distance matrix. <i>Folding & Design</i> , 1997 , 2, S12-4		6
93	Importance of the release of strand 1C to the polymerization mechanism of inhibitory serpins. <i>Protein Science</i> , 1997 , 6, 89-98	6.3	58
92	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 151-166	4.2	41
91	CASP2: Report on ab initio predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 151-166	4.2	3
90	Conservation and variability in the structures of serine proteinases of the chymotrypsin family. <i>Journal of Molecular Biology</i> , 1996 , 258, 501-37	6.5	127
89	Modeling of serpin-protease complexes: antithrombin-thrombin, alpha 1-antitrypsin (358Met-->Arg)-thrombin, alpha 1-antitrypsin (358Met-->Arg)-trypsin, and antitrypsin-elastase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 288-303	4.2	25
88	Systematic representation of protein folding patterns. <i>Journal of Molecular Graphics</i> , 1995 , 13, 159-64		30
87	NAD-binding domains of dehydrogenases. <i>Current Opinion in Structural Biology</i> , 1995 , 5, 775-83	8.1	202
86	Three-dimensional pattern matching in protein structure analysis. <i>Lecture Notes in Computer Science</i> , 1995 , 248-260	0.9	7
85	Three-dimensional searching for recurrent structural motifs in data bases of protein structures. <i>Journal of Computational Biology</i> , 1994 , 1, 121-32	1.7	11
84	Structural mechanisms for domain movements in proteins. <i>Biochemistry</i> , 1994 , 33, 6739-49	3.2	697
83	Principles determining the structure of beta-sheet barrels in proteins. I. A theoretical analysis. <i>Journal of Molecular Biology</i> , 1994 , 236, 1369-81	6.5	184
82	Principles determining the structure of beta-sheet barrels in proteins. II. The observed structures. <i>Journal of Molecular Biology</i> , 1994 , 236, 1382-400	6.5	120
81	Domain closure in lactoferrin. Two hinges produce a see-saw motion between alternative close-packed interfaces. <i>Journal of Molecular Biology</i> , 1993 , 234, 357-72	6.5	146

80	Boolean programming formulation of some pattern-matching problems in molecular biology. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1993 , 89, 2603		3
79	Probing protein structure by solvent perturbation of NMR spectra. II. Determination of surface and buried residues in homologous proteins. <i>Biopolymers</i> , 1993 , 33, 839-46	2.2	8
78	Homology modelling: inferences from tables of aligned sequences. <i>Current Opinion in Structural Biology</i> , 1992 , 2, 242-247	8.1	14
77	Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 12, 105-10	4.2	25
76	Structural repertoire of the human VH segments. <i>Journal of Molecular Biology</i> , 1992 , 227, 799-817	6.5	377
75	Probing protein structure by solvent perturbation of nuclear magnetic resonance spectra. Nuclear magnetic resonance spectral editing and topological mapping in proteins by paramagnetic relaxation filtering. <i>Journal of Molecular Biology</i> , 1992 , 224, 659-70	6.5	66
74	beta-Trefoil fold. Patterns of structure and sequence in the Kunitz inhibitors interleukins-1 beta and 1 alpha and fibroblast growth factors. <i>Journal of Molecular Biology</i> , 1992 , 223, 531-43	6.5	290
73	Domain closure in mitochondrial aspartate aminotransferase. <i>Journal of Molecular Biology</i> , 1992 , 227, 197-213	6.5	172
72	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, 231-45	4.2	61
71	Does protein structure determine amino acid sequence?. <i>BioEssays</i> , 1992 , 14, 407-10	4.1	14
70	Brave new proteins: what evolution reveals about protein structure. <i>Current Opinion in Biotechnology</i> , 1991 , 2, 592-8	11.4	5
69	Comparison of the structures of globins and phycocyanins: evidence for evolutionary relationship. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990 , 8, 133-55	4.2	81
68	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, 175-82	6.5	218
67	Structural principles of alpha/beta barrel proteins: the packing of the interior of the sheet. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989 , 5, 139-48	4.2	144
66	Structural determinants of the conformations of medium-sized loops in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989 , 6, 382-94	4.2	75
65	Conformations of immunoglobulin hypervariable regions. <i>Nature</i> , 1989 , 342, 877-83	50.4	1091
64	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, 85-92		3
63	Introduction: Protein engineering. <i>BioEssays</i> , 1988 , 8, 51-52	4.1	2

62	Structural alignment and analysis of two distantly related proteins: Aplysia limacina myoglobin and sea lamprey globin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988 , 4, 240-50	4.2	9
61	Cover blown. <i>Nature</i> , 1988 , 334, 560-560	50.4	
60	Elbow motion in the immunoglobulins involves a molecular ball-and-socket joint. <i>Nature</i> , 1988 , 335, 188-190	50.4	149
59	Interior and surface of monomeric proteins. <i>Journal of Molecular Biology</i> , 1987 , 196, 641-56	6.5	784
58	Canonical structures for the hypervariable regions of immunoglobulins. <i>Journal of Molecular Biology</i> , 1987 , 196, 901-17	6.5	1195
57	Determinants of a protein fold. Unique features of the globin amino acid sequences. <i>Journal of Molecular Biology</i> , 1987 , 196, 199-216	6.5	455
56	The accessible surface area and stability of oligomeric proteins. <i>Nature</i> , 1987 , 328, 834-6	50.4	314
55	Alignment of the amino acid sequences of distantly related proteins using variable gap penalties. <i>Protein Engineering, Design and Selection</i> , 1986 , 1, 77-8	1.9	87
54	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	0.5	9
53	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	4.1	3
52	Computer-generated pictures of proteins. <i>Methods in Enzymology</i> , 1985 , 115, 381-90	1.7	41
51	Helix movements in proteins. <i>Trends in Biochemical Sciences</i> , 1985 , 10, 116-118	10.3	64
50	Haemoglobin: the surface buried between the alpha 1 beta 1 and alpha 2 beta 2 dimers in the deoxy and oxy structures. <i>Journal of Molecular Biology</i> , 1985 , 183, 267-70	6.5	41
49	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, 151-8	6.5	67
48	The analysis of protein structures: New insights from a growing data base. <i>BioEssays</i> , 1984 , 1, 105-110	4.1	2
47	Mechanisms of domain closure in proteins. <i>Journal of Molecular Biology</i> , 1984 , 174, 175-91	6.5	162
46	Themes and contrasts in protein structures. <i>Trends in Biochemical Sciences</i> , 1984 , 9, 290	10.3	2
45	A toolkit for computational molecular biology I: packing and unpacking of protein coordinate sets. <i>Journal of Molecular Graphics</i> , 1983 , 1, 118-121		3

44	Transmission of conformational change in insulin. <i>Nature</i> , 1983 , 302, 500-5	50.4	186
43	Evolution of proteins formed by beta-sheets. I. Plastocyanin and azurin. <i>Journal of Molecular Biology</i> , 1982 , 160, 309-23	6.5	121
42	Evolution of proteins formed by beta-sheets. II. The core of the immunoglobulin domains. <i>Journal of Molecular Biology</i> , 1982 , 160, 325-42	6.5	259
41	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, 225-70	6.5	633
40	Reinterpretation of Moseley's experiments relating K α line frequencies and atomic number. <i>American Journal of Physics</i> , 1980 , 48, 492-493	0.7	2
39	Detection of three-dimensional patterns of atoms in chemical structures. <i>Communications of the ACM</i> , 1979 , 22, 219-224	2.5	45
38	Macromolecular marionettes. <i>Computers in Biology and Medicine</i> , 1977 , 7, 113-29	7	14
37	An encoding technique to facilitate the detection of homologies in biopolymer sequences. <i>Journal of Theoretical Biology</i> , 1977 , 69, 767-9	2.3	
36	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	2.5	1
35	Treatment of nonspecular reflection in the single-particle model of an ideal gas. <i>American Journal of Physics</i> , 1976 , 44, 1134-1135	0.7	1
34	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	3.9	5
33	Entropy Changes in Isothermal Expansions of Real Gases. <i>American Journal of Physics</i> , 1974 , 42, 1030-1033	3.7	2
32	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	2.3	5
31	On hypothesized selective pressure by u.v. on DNA base compositions. <i>Journal of Theoretical Biology</i> , 1973 , 40, 201-2	2.3	5
30	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	3.9	14
29	Pictorial pattern recognition and the phase problem of x-ray crystallography. <i>Communications of the ACM</i> , 1972 , 15, 3-6	2.5	7
28	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	3
27	Application of the common features of transfer RNAs to the determination of their nucleotide sequences. <i>Biochemical and Biophysical Research Communications</i> , 1971 , 45, 676-80	3.4	1

26	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	2.3	5
25	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, 855-8	3.4	5
24	Expansion of linear combinations of slater-type orbitals in eigenfunctions of the three-dimensional isotropic harmonic oscillator. <i>International Journal of Quantum Chemistry</i> , 1969 , 3, 289-295	2.1	2
23	Why does DNA contain thymine and RNA uracil?. <i>Journal of Theoretical Biology</i> , 1969 , 22, 537-40	2.3	10
22	A corrected valence electron approximation. <i>Molecular Physics</i> , 1968 , 15, 453-458	1.7	1
21	Choice of Basis Set for Expansion of One-Dimensional Oscillator Eigenfunctions. <i>Journal of Chemical Physics</i> , 1968 , 49, 3898-3900	3.9	4
20	Use of the Hartree-Fock Approximation in Computing Electron Affinities. <i>Physical Review</i> , 1968 , 171, 7-10		8
19	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	2.1	1
18	Dynamic computation of derivatives. <i>Communications of the ACM</i> , 1967 , 10, 571-572	2.5	1
17	The Fluorides and Oxides of Helium and Neon ¹ . <i>Journal of the American Chemical Society</i> , 1966 , 88, 615-616	16.4	13
16	ROTATORY DISPERSION OF NUCLEIC ACIDS IN THE NEAR-ULTRAVIOLET REGION. <i>Journal of the American Chemical Society</i> , 1961 , 83, 3155-3156	16.4	18
15	Classification of Protein Function	167-183	
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