

Geoffrey J Barton

List of Publications by Year in descending order

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152
papers

30,879
citations

16791

66
h-index

10399

144
g-index

173
all docs

173
docs citations

173
times ranked

47949
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
2	Missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike providing a mechanism for ACE2 mediated genetic risk in Covid-19: A case study in affinity predictions of interface variants. <i>PLoS Computational Biology</i> , 2022, 18, e1009922.	1.5	9
3	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. <i>Nature Communications</i> , 2022, 13, 2001.	5.8	35
4	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	5.8	44
5	2passtools: two-pass alignment using machine-learning-filtered splice junctions increases the accuracy of intron detection in long-read RNA sequencing. <i>Genome Biology</i> , 2021, 22, 72.	3.8	16
6	Widespread premature transcription termination of <i>Arabidopsis thaliana</i> NLR genes by the spen protein FPA. <i>ELife</i> , 2021, 10, .	2.8	36
7	Ankyrin repeats in context with human population variation. <i>PLoS Computational Biology</i> , 2021, 17, e1009335.	1.5	5
8	Effects of common mutations in the SARS-CoV-2 Spike RBD and its ligand, the human ACE2 receptor on binding affinity and kinetics. <i>ELife</i> , 2021, 10, .	2.8	267
9	Alignment of Biological Sequences with Jalview. <i>Methods in Molecular Biology</i> , 2021, 2231, 203-224.	0.4	83
10	Disease related single point mutations alter the global dynamics of a tetratricopeptide (TPR) $\hat{\pm}$ -solenoid domain. <i>Journal of Structural Biology</i> , 2020, 209, 107405.	1.3	7
11	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
12	The Dundee Resource for Sequence Analysis and Structure Prediction. <i>Protein Science</i> , 2020, 29, 277-297.	3.1	14
13	Nanopore direct RNA sequencing maps the complexity of <i>Arabidopsis</i> mRNA processing and m6A modification. <i>ELife</i> , 2020, 9, .	2.8	312
14	Relative Abundance of Transcripts (RATs): Identifying differential isoform abundance from RNA-seq. <i>F1000Research</i> , 2019, 8, 213.	0.8	20
15	How well do RNA-Seq differential gene expression tools perform in a complex eukaryote? A case study in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2019, 35, 3372-3377.	1.8	9
16	JABAWS 2.2 distributed web services for Bioinformatics: protein disorder, conservation and RNA secondary structure. <i>Bioinformatics</i> , 2018, 34, 1939-1940.	1.8	29
17	Adenylate cyclase A acting on PKA mediates induction of stalk formation by cyclic diguanylate at the <i>Dictyostelium</i> organizer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 516-521.	3.3	22
18	Improved annotation with de novo transcriptome assembly in four social amoeba species. <i>BMC Genomics</i> , 2017, 18, 120.	1.2	7

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19	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017, 9, 113.	3.6	47
20	A study of the structural properties of sites modified by the O-linked 6-N-acetylglucosamine transferase. <i>PLoS ONE</i> , 2017, 12, e0184405.	1.1	6
21	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	1.6	622
22	AlmostSignificant: simplifying quality control of high-throughput sequencing data. <i>Bioinformatics</i> , 2016, 32, 3850-3851.	1.8	6
23	14-3-3-Pred: improved methods to predict 14-3-3-binding phosphopeptides. <i>Bioinformatics</i> , 2015, 31, 2276-2283.	1.8	177
24	JPred4: a protein secondary structure prediction server. <i>Nucleic Acids Research</i> , 2015, 43, W389-W394.	6.5	1,546
25	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	1.8	76
26	Proteotoxic stress reprograms the chromatin landscape of SUMO modification. <i>Science Signaling</i> , 2015, 8, rs7.	1.6	81
27	Improved Annotation of 3' UTRs and Complex Loci by Combination of Strand-Specific Direct RNA Sequencing, RNA-Seq and ESTs. <i>PLoS ONE</i> , 2014, 9, e94270.	1.1	27
28	Major transcriptome re-organisation and abrupt changes in signalling, cell cycle and chromatin regulation at neural differentiation <i>in vivo</i> . <i>Development (Cambridge)</i> , 2014, 141, 3266-3276.	1.2	54
29	Elevated O-GlcNAc Levels Activate Epigenetically Repressed Genes and Delay Mouse ESC Differentiation Without Affecting Naïve to Primed Cell Transition. <i>Stem Cells</i> , 2014, 32, 2605-2615.	1.4	50
30	Filaggrin-stratified transcriptomic analysis of pediatric skin identifies mechanistic pathways in patients with atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 82-91.	1.5	118
31	Tmem79/Matt is the matted mouse gene and is a predisposing gene for atopic dermatitis in human subjects. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 132, 1121-1129.	1.5	135
32	Transcription Termination and Chimeric RNA Formation Controlled by Arabidopsis thaliana FPA. <i>PLoS Genetics</i> , 2013, 9, e1003867.	1.5	67
33	PGE2 Induces Macrophage IL-10 Production and a Regulatory-like Phenotype via a Protein Kinase A-SIK-CRTC3 Pathway. <i>Journal of Immunology</i> , 2013, 190, 565-577.	0.4	197
34	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. <i>Scientific Reports</i> , 2013, 3, 2866.	1.6	58
35	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.011429.	2.5	332
36	Haploinsufficiency for AAGAB causes clinically heterogeneous forms of punctate palmoplantar keratoderma. <i>Nature Genetics</i> , 2012, 44, 1272-1276.	9.4	78

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37	Direct sequencing of Arabidopsis thaliana RNA reveals patterns of cleavage and polyadenylation. Nature Structural and Molecular Biology, 2012, 19, 845-852.	3.6	142
38	Live imaging of nascent RNA dynamics reveals distinct types of transcriptional pulse regulation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7350-7355.	3.3	111
39	PTEN Protein Phosphatase Activity Correlates with Control of Gene Expression and Invasion, a Tumor-Suppressing Phenotype, But Not with AKT Activity. Science Signaling, 2012, 5, ra18.	1.6	107
40	Human box C/D snoRNA processing conservation across multiple cell types. Nucleic Acids Research, 2012, 40, 3676-3688.	6.5	79
41	The kinomes of apicomplexan parasites. Microbes and Infection, 2012, 14, 796-810.	1.0	61
42	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. Science, 2011, 333, 1758-1760.	6.0	260
43	A Dictyostelium SH2 adaptor protein required for correct DIF-1 signaling and pattern formation. Developmental Biology, 2011, 353, 290-301.	0.9	3
44	Computational approaches to selecting and optimising targets for structural biology. Methods, 2011, 55, 3-11.	1.9	7
45	The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4. EMBO Journal, 2011, 30, 1919-1927.	3.5	47
46	PIMS sequencing extension: a laboratory information management system for DNA sequencing facilities. BMC Research Notes, 2011, 4, 48.	0.6	7
47	Global network analysis of drug tolerance, mode of action and virulence in methicillin-resistant S. aureus. BMC Systems Biology, 2011, 5, 68.	3.0	36
48	NoD: a Nucleolar localization sequence detector for eukaryotic and viral proteins. BMC Bioinformatics, 2011, 12, 317.	1.2	149
49	PNAC: a protein nucleolar association classifier. BMC Genomics, 2011, 12, 74.	1.2	8
50	XANNpred: Neural nets that predict the propensity of a protein to yield diffraction-quality crystals. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1027-1033.	1.5	21
51	Java bioinformatics analysis web services for multiple sequence alignment "JABAWS:MSA. Bioinformatics, 2011, 27, 2001-2002.	1.8	110
52	Identification of human miRNA precursors that resemble box C/D snoRNAs. Nucleic Acids Research, 2011, 39, 3879-3891.	6.5	123
53	The Scottish Structural Proteomics Facility: targets, methods and outputs. Journal of Structural and Functional Genomics, 2010, 11, 167-180.	1.2	107
54	Human protein-protein interaction prediction. BMC Bioinformatics, 2010, 11, .	1.2	3

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55	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	9.0	73
56	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. <i>Molecular Biology of the Cell</i> , 2010, 21, 1569-1584.	0.9	40
57	Characterization and prediction of protein nucleolar localization sequences. <i>Nucleic Acids Research</i> , 2010, 38, 7388-7399.	6.5	167
58	Regulation of the miR-212/132 locus by MSK1 and CREB in response to neurotrophins. <i>Biochemical Journal</i> , 2010, 428, 281-291.	1.7	195
59	Jalview Version 2.2.1 a multiple sequence alignment editor and analysis workbench. <i>Bioinformatics</i> , 2009, 25, 1189-1191.	1.8	8,091
60	Kinomer v. 1.0: a database of systematically classified eukaryotic protein kinases. <i>Nucleic Acids Research</i> , 2009, 37, D244-D250.	6.5	83
61	Human miRNA Precursors with Box H/ACA snoRNA Features. <i>PLoS Computational Biology</i> , 2009, 5, e1000507.	1.5	167
62	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. <i>Rna</i> , 2009, 15, 2147-2160.	1.6	525
63	Identification of a glycosylphosphatidylinositol anchor-modifying N-acetylglucosaminyl transferase in <i>Trypanosoma brucei</i> . <i>Molecular Microbiology</i> , 2009, 71, 478-491.	1.2	35
64	Distinct donor and acceptor specificities of <i>Trypanosoma brucei</i> oligosaccharyltransferases. <i>EMBO Journal</i> , 2009, 28, 2650-2661.	3.5	96
65	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 2009, 2, ra24.	1.6	415
66	PIPs: human protein-protein interaction prediction database. <i>Nucleic Acids Research</i> , 2009, 37, D651-D656.	6.5	206
67	A comparison of SCOP and CATH with respect to domain-domain interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 54-62.	1.5	10
68	Sequence alignment for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 25-32.	2.5	7
69	The contrasting properties of conservation and correlated phylogeny in protein functional residue prediction. <i>BMC Bioinformatics</i> , 2008, 9, 51.	1.2	38
70	The Jpred 3 secondary structure prediction server. <i>Nucleic Acids Research</i> , 2008, 36, W197-W201.	6.5	1,308
71	TarO: a target optimisation system for structural biology. <i>Nucleic Acids Research</i> , 2008, 36, W190-W196.	6.5	79
72	SCANPS: a web server for iterative protein sequence database searching by dynamic programming, with display in a hierarchical SCOP browser. <i>Nucleic Acids Research</i> , 2008, 36, W25-W29.	6.5	32

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73	A new family of transcription factors. <i>Development (Cambridge)</i> , 2008, 135, 3093-3101.	1.2	20
74	Genome Analysis of the Unicellular Green Alga <i>Chlamydomonas reinhardtii</i> Indicates an Ancient Evolutionary Origin for Key Pattern Recognition and Cell-Signaling Protein Families. <i>Genetics</i> , 2008, 179, 193-197.	1.2	40
75	ParCrys: a Parzen window density estimation approach to protein crystallization propensity prediction. <i>Bioinformatics</i> , 2008, 24, 901-907.	1.8	64
76	SNAPPI-DB: a database and API of Structures, iNterfaces and Alignments for Protein-Protein Interactions. <i>Nucleic Acids Research</i> , 2007, 35, D580-D589.	6.5	58
77	The Structure of Serine Palmitoyltransferase; Gateway to Sphingolipid Biosynthesis. <i>Journal of Molecular Biology</i> , 2007, 370, 870-886.	2.0	124
78	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	6.0	731
79	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i> . <i>Science</i> , 2007, 317, 1756-1760.	6.0	571
80	Expression, purification, crystallization, data collection and preliminary biochemical characterization of methicillin-resistant <i>Staphylococcus aureus</i> Sar2028, an aspartate/tyrosine/phenylalanine pyridoxal-5-phosphate-dependent aminotransferase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 452-456.	0.7	5
81	Purification, crystallization and data collection of methicillin-resistant <i>Staphylococcus aureus</i> Sar2676, a pantothenate synthetase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 488-491.	0.7	4
82	Classification and functional annotation of eukaryotic protein kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 893-914.	1.5	154
83	The relationship between domain-domain interaction orientation and sequence similarity. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	0
84	Probabilistic prediction and ranking of human protein-protein interactions. <i>BMC Bioinformatics</i> , 2007, 8, 239.	1.2	115
85	The complement of protein kinases of the microsporidium <i>Encephalitozoon cuniculi</i> in relation to those of <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>BMC Genomics</i> , 2007, 8, 309.	1.2	68
86	Identification of multiple distinct Snf2 subfamilies with conserved structural motifs. <i>Nucleic Acids Research</i> , 2006, 34, 2887-2905.	6.5	612
87	A normalised scale for structural genomics target ranking: The OB-Score. <i>FEBS Letters</i> , 2006, 580, 4005-4009.	1.3	54
88	Biological Units and their Effect upon the Properties and Prediction of Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2006, 364, 1118-1129.	2.0	23
89	Emerging roles of pseudokinases. <i>Trends in Cell Biology</i> , 2006, 16, 443-452.	3.6	475
90	MACSIMS : multiple alignment of complete sequences information management system. <i>BMC Bioinformatics</i> , 2006, 7, 318.	1.2	38

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91	Quantification of the variation in percentage identity for protein sequence alignments. BMC Bioinformatics, 2006, 7, 415.	1.2	45
92	Jalview: Visualization and Analysis of Molecular Sequences, Alignments, and Structures. BMC Bioinformatics, 2005, 6, P28.	1.2	15
93	The Jalview Java alignment editor. Bioinformatics, 2004, 20, 426-427.	1.8	1,342
94	E-MSD: an integrated data resource for bioinformatics. Nucleic Acids Research, 2004, 32, 211D-216.	6.5	90
95	GOtcha: a new method for prediction of protein function assessed by the annotation of seven genomes. BMC Bioinformatics, 2004, 5, 178.	1.2	205
96	OXBench: a benchmark for evaluation of protein multiple sequence alignment accuracy. BMC Bioinformatics, 2003, 4, 47.	1.2	173
97	Visual representation of database search results: the RHIMS Plot. Bioinformatics, 2003, 19, 1037-1038.	1.8	2
98	Increased coverage obtained by combination of methods for protein sequence database searching. Bioinformatics, 2003, 19, 1397-1403.	1.8	7
99	Creation and Analysis of Protein Multiple Sequence Alignments. Methods of Biochemical Analysis, 2002, 43, 215-232.	0.2	2
100	Protein structural domains: Analysis of the 3Dee domains database. Proteins: Structure, Function and Bioinformatics, 2001, 42, 332-344.	1.5	31
101	Application of multiple sequence alignment profiles to improve protein secondary structure prediction. Proteins: Structure, Function and Bioinformatics, 2000, 40, 502-511.	1.5	714
102	Application of multiple sequence alignment profiles to improve protein secondary structure prediction. , 2000, 40, 502.		2
103	Evaluation and improvement of multiple sequence methods for protein secondary structure prediction. , 1999, 34, 508-519.		548
104	Protein Sequence Alignment Techniques. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1139-1146.	2.5	13
105	Deposition of Macromolecular Structures. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1105-1108.	2.5	13
106	Re: Letter to the Editor Regarding Deposition of 3D Structural Studies of Biological Macromolecules. Biochemical and Biophysical Research Communications, 1998, 245, 946.	1.0	0
107	JPred: a consensus secondary structure prediction server. Bioinformatics, 1998, 14, 892-893.	1.8	982
108	Protein Fold Recognition by Mapping Predicted Secondary Structures. Journal of Molecular Biology, 1996, 259, 349-365.	2.0	134

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109	Conservation of amino acids in multiple alignments: aspartic acid has unexpected conservation. FEBS Letters, 1996, 397, 225-229.	1.3	24
110	[29] Identification of functional residues and secondary structure from protein multiple sequence alignment. Methods in Enzymology, 1996, 266, 497-512.	0.4	65
111	Crystal structure of isopenicillin N synthase is the first from a new structural family of enzymes. Nature, 1995, 375, 700-704.	13.7	434
112	Protein secondary structure prediction. Current Opinion in Structural Biology, 1995, 5, 372-376.	2.6	81
113	Continuous and discontinuous domains: An algorithm for the automatic generation of reliable protein domain definitions. Protein Science, 1995, 4, 872-884.	3.1	151
114	The AMPS Package for Multiple Protein Sequence Alignment. , 1994, 25, 327-347.		13
115	scop: structural classification of proteins. Trends in Biochemical Sciences, 1994, 19, 554-555.	3.7	22
116	Structural similarity between the p17 matrix protein of HIV-1 and interferon- β . Nature, 1994, 370, 666-668.	13.7	158
117	Conservation analysis and structure prediction of the protein serine/threonine phosphatases. Sequence similarity with diadenosine tetraphosphatase from Escherichia coli suggests homology to the protein phosphatases. FEBS Journal, 1994, 220, 225-237.	0.2	167
118	A Structural Analysis of Phosphate and Sulphate Binding Sites in Proteins. Journal of Molecular Biology, 1994, 242, 321-329.	2.0	54
119	Structural Features can be Unconserved in Proteins with Similar Folds. Journal of Molecular Biology, 1994, 244, 332-350.	2.0	169
120	A Structural Analysis of Phosphate and Sulphate Binding Sites in Proteins Estimation of Propensities for Binding and Conservation of Phosphate Binding Sites. Journal of Molecular Biology, 1994, 242, 321-329.	2.0	133
121	Secondary structure prediction from multiple sequence data: blood clotting factor XIII and Yersinia protein tyrosine phosphatase. International Journal of Peptide and Protein Research, 1994, 44, 239-244.	0.1	15
122	Mutational analysis of human papillomavirus E4 proteins: identification of structural features important in the formation of cytoplasmic E4/cytokeratin networks in epithelial cells. Journal of Virology, 1994, 68, 6432-6445.	1.5	58
123	An SH2-SH3 domain hybrid. Nature, 1993, 364, 765-765.	13.7	26
124	Protein structure prediction. Nature, 1993, 361, 505-506.	13.7	24
125	Protein sequence alignments: a strategy for the hierarchical analysis of residue conservation. Bioinformatics, 1993, 9, 745-756.	1.8	354
126	ALSCRIPT: a tool to format multiple sequence alignments. Protein Engineering, Design and Selection, 1993, 6, 37-40.	1.0	1,104

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127	The Limits of Protein Secondary Structure Prediction Accuracy from Multiple Sequence Alignment. <i>Journal of Molecular Biology</i> , 1993, 234, 951-957.	2.0	75
128	Secondary structure prediction for modelling by homology. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 261-266.	1.0	19
129	An efficient algorithm to locate all locally optimal alignments between two sequences allowing for gaps. <i>Bioinformatics</i> , 1993, 9, 729-734.	1.8	18
130	Prediction of Protein Structure from Multiple Sequence Alignment. , 1993, , 209-220.		0
131	Structural and Functional Analysis of the S-Layer Protein from <i>Bacillus stearothermophilus</i> . , 1993, , 143-149.		1
132	Conservation analysis and structure prediction of the SH2 family of phosphotyrosine binding domains. <i>FEBS Letters</i> , 1992, 304, 15-20.	1.3	96
133	Mast cell tryptases: Examination of unusual characteristics by multiple sequence alignment and molecular modeling. <i>Protein Science</i> , 1992, 1, 370-377.	3.1	67
134	Human platelet-derived endothelial cell growth factor is homologous to <i>Escherichia coli</i> thymidine phosphorylase. <i>Protein Science</i> , 1992, 1, 688-690.	3.1	39
135	Multiple protein sequence alignment from tertiary structure comparison: Assignment of global and residue confidence levels. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 14, 309-323.	1.5	622
136	Generation and interpretation of protein sequence and structural multiple alignments. <i>The Protein Journal</i> , 1992, 11, 389-389.	1.1	2
137	Multiple Sequence Alignment and Flexible Pattern Matching. <i>Springer Series in Biophysics</i> , 1992, , 29-52.	0.4	2
138	Amino acid sequence analysis of the annexin super-gene family of proteins. <i>FEBS Journal</i> , 1991, 198, 749-760.	0.2	141
139	Scanning protein sequence databanks using a distributed processing workstation network. <i>Bioinformatics</i> , 1991, 7, 85-88.	1.8	7
140	Interaction of synthetic peptides from annexin I and uteroglobin with lipid monolayers and their effect on phospholipase A2 activity. <i>Biochemical Society Transactions</i> , 1990, 18, 1233-1234.	1.6	8
141	[25] Protein multiple sequence alignment and flexible pattern matching. <i>Methods in Enzymology</i> , 1990, 183, 403-428.	0.4	169
142	A PROLOG approach to analysing protein structure. <i>Tetrahedron Computer Methodology</i> , 1990, 3, 739-756.	0.2	7
143	A knowledge-based architecture for protein sequence analysis and structure prediction. <i>Journal of Molecular Graphics</i> , 1990, 8, 94-107.	1.7	12
144	Flexible protein sequence patterns. <i>Journal of Molecular Biology</i> , 1990, 212, 389-402.	2.0	131

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145	Prediction of domain organisation and secondary structure of thyroid peroxidase, a human autoantigen involved in destructive thyroiditis. FEBS Letters, 1990, 266, 133-141.	1.3	33
146	LOPAL and SCAMP: techniques for the comparison and display of protein structures. Journal of Molecular Graphics, 1988, 6, 190-196.	1.7	21
147	Evaluation and improvements in the automatic alignment of protein sequences. Protein Engineering, Design and Selection, 1987, 1, 89-94.	1.0	110
148	Prediction of antigenic determinants and secondary structures of the major AIDS virus proteins. FEBS Letters, 1987, 218, 231-237.	1.3	22
149	A strategy for the rapid multiple alignment of protein sequences. Journal of Molecular Biology, 1987, 198, 327-337.	2.0	463
150	Prediction of protein secondary structure and active sites using the alignment of homologous sequences. Journal of Molecular Biology, 1987, 195, 957-961.	2.0	439
151	AIDS vaccine predictions. Nature, 1987, 326, 549-550.	13.7	50
152	Detection and mitigation of spurious antisense expression with RoSA. F1000Research, 0, 8, 819.	0.8	13