Geoffrey J Barton

List of Publications by Year
in descending order

152 papers	30,879 citations	14644 66 h-index	9090 144 g-index
173 all docs	173 docs citations	173 times ranked	43281 citing authors

#	Article	IF	Citations
1	Jalview Version 2â€"a multiple sequence alignment editor and analysis workbench. Bioinformatics, 2009, 25, 1189-1191.	1.8	8,091
2	JPred4: a protein secondary structure prediction server. Nucleic Acids Research, 2015, 43, W389-W394.	6.5	1,546
3	The Jalview Java alignment editor. Bioinformatics, 2004, 20, 426-427.	1.8	1,342
4	The Jpred 3 secondary structure prediction server. Nucleic Acids Research, 2008, 36, W197-W201.	6.5	1,308
5	ALSCRIPT: a tool to format multiple sequence alignments. Protein Engineering, Design and Selection, 1993, 6, 37-40.	1.0	1,104
6	JPred: a consensus secondary structure prediction server. Bioinformatics, 1998, 14, 892-893.	1.8	982
7	Draft Genome Sequence of the Sexually Transmitted Pathogen Trichomonas vaginalis. Science, 2007, 315, 207-212.	6.0	731
8	Application of multiple sequence alignment profiles to improve protein secondary structure prediction. Proteins: Structure, Function and Bioinformatics, 2000, 40, 502-511.	1.5	714
9	Multiple protein sequence alignment from tertiary structure comparison: Assignment of global and residue confidence levels. Proteins: Structure, Function and Bioinformatics, 1992, 14, 309-323.	1.5	622
10	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. Rna, 2016, 22, 839-851.	1.6	622
11	Identification of multiple distinct Snf2 subfamilies with conserved structural motifs. Nucleic Acids Research, 2006, 34, 2887-2905.	6.5	612
12	Draft Genome of the Filarial Nematode Parasite <i>Brugia malayi</i>. Science, 2007, 317, 1756-1760.	6.0	571
13	Evaluation and improvement of multiple sequence methods for protein secondary structure prediction. , 1999, 34, 508-519.		548
14	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. Rna, 2009, 15, 2147-2160.	1.6	525
15	Emerging roles of pseudokinases. Trends in Cell Biology, 2006, 16, 443-452.	3.6	475
16	A strategy for the rapid multiple alignment of protein sequences. Journal of Molecular Biology, 1987, 198, 327-337.	2.0	463
17	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
18	Crystal structure of isopenicillin N synthase is the first from a new structural family of enzymes. Nature, 1995, 375, 700-704.	13.7	434

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19	System-Wide Changes to SUMO Modifications in Response to Heat Shock. Science Signaling, 2009, 2, ra24.	1.6	415
20	Protein sequence alignments: a strategy for the hierarchical analysis of residue conservation. Bioinformatics, 1993, 9, 745-756.	1.8	354
21	A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells. Molecular and Cellular Proteomics, 2012, 11, M111.011429.	2.5	332
22	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. ELife, 2020, 9, .	2.8	312
23	Effects of common mutations in the SARS-CoV-2 Spike RBD and its ligand, the human ACE2 receptor on binding affinity and kinetics. ELife, 2021, 10, .	2.8	267
24	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. Science, 2011, 333, 1758-1760.	6.0	260
25	PIPs: human protein-protein interaction prediction database. Nucleic Acids Research, 2009, 37, D651-D656.	6.5	206
26	GOtcha: a new method for prediction of protein function assessed by the annotation of seven genomes. BMC Bioinformatics, 2004, 5, 178.	1.2	205
27	PGE2 Induces Macrophage IL-10 Production and a Regulatory-like Phenotype via a Protein Kinase Aâ€"SIKâ€"CRTC3 Pathway. Journal of Immunology, 2013, 190, 565-577.	0.4	197
28	Regulation of the miR-212/132 locus by MSK1 and CREB in response to neurotrophins. Biochemical Journal, 2010, 428, 281-291.	1.7	195
29	14-3-3-Pred: improved methods to predict 14-3-3-binding phosphopeptides. Bioinformatics, 2015, 31, 2276-2283.	1.8	177
30	OXBench: a benchmark for evaluation of protein multiple sequence alignment accuracy. BMC Bioinformatics, 2003, 4, 47.	1.2	173
31	[25] Protein multiple sequence alignment and flexible pattern matching. Methods in Enzymology, 1990, 183, 403-428.	0.4	169
32	Structural Features can be Unconserved in Proteins with Similar Folds. Journal of Molecular Biology, 1994, 244, 332-350.	2.0	169
33	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
34	Human miRNA Precursors with Box H/ACA snoRNA Features. PLoS Computational Biology, 2009, 5, e1000507.	1.5	167
35	Characterization and prediction of protein nucleolar localization sequences. Nucleic Acids Research, 2010, 38, 7388-7399.	6.5	167
36	Structural similarity between the p17 matrix protein of HIV-1 and interferon-Î³. Nature, 1994, 370, 666-668.	13.7	158

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37	Classification and functional annotation of eukaryotic protein kinases. Proteins: Structure, Function and Bioinformatics, 2007, 68, 893-914.	1.5	154
38	Continuous and discontinuous domains: An algorithm for the automatic generation of reliable protein domain definitions. Protein Science, 1995, 4, 872-884.	3.1	151
39	NoD: a Nucleolar localization sequence detector for eukaryotic and viral proteins. BMC Bioinformatics, 2011, 12, 317.	1.2	149
40	Direct sequencing of Arabidopsis thaliana RNA reveals patterns of cleavage and polyadenylation. Nature Structural and Molecular Biology, 2012, 19, 845-852.	3.6	142
41	Amino acid sequence analysis of the annexin super-gene family of proteins. FEBS Journal, 1991, 198, 749-760.	0.2	141
42	Tmem79/Matt is the matted mouse gene and is a predisposing gene for atopic dermatitis in human subjects. Journal of Allergy and Clinical Immunology, 2013, 132, 1121-1129.	1.5	135
43	Protein Fold Recognition by Mapping Predicted Secondary Structures. Journal of Molecular Biology, 1996, 259, 349-365.	2.0	134
44	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
45	Flexible protein sequence patterns. Journal of Molecular Biology, 1990, 212, 389-402.	2.0	131
46	The Structure of Serine Palmitoyltransferase; Gateway to Sphingolipid Biosynthesis. Journal of Molecular Biology, 2007, 370, 870-886.	2.0	124
47	Identification of human miRNA precursors that resemble box C/D snoRNAs. Nucleic Acids Research, 2011, 39, 3879-3891.	6.5	123
48	Filaggrin-stratified transcriptomic analysis of pediatric skin identifies mechanistic pathways in patients with atopic dermatitis. Journal of Allergy and Clinical Immunology, 2014, 134, 82-91.	1.5	118
49	Probabilistic prediction and ranking of human protein-protein interactions. BMC Bioinformatics, 2007, 8, 239.	1.2	115
50	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
51	Evaluation and improvements in the automatic alignment of protein sequences. Protein Engineering, Design and Selection, 1987, 1, 89-94.	1.0	110
52	Java bioinformatics analysis web services for multiple sequence alignment—JABAWS:MSA. Bioinformatics, 2011, 27, 2001-2002.	1.8	110
53	The Scottish Structural Proteomics Facility: targets, methods and outputs. Journal of Structural and Functional Genomics, 2010, 11, 167-180.	1.2	107
54	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

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55	Conservation analysis and structure prediction of the SH2 family of phosphotyrosine binding domains. FEBS Letters, 1992, 304, 15-20.	1.3	96
56	Distinct donor and acceptor specificities of Trypanosoma brucei oligosaccharyltransferases. EMBO Journal, 2009, 28, 2650-2661.	3.5	96
57	E-MSD: an integrated data resource for bioinformatics. Nucleic Acids Research, 2004, 32, 211D-216.	6.5	90
58	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	6.5	87
59	Kinomer v. 1.0: a database of systematically classified eukaryotic protein kinases. Nucleic Acids Research, 2009, 37, D244-D250.	6.5	83
60	Alignment of Biological Sequences with Jalview. Methods in Molecular Biology, 2021, 2231, 203-224.	0.4	83
61	Protein secondary structure prediction. Current Opinion in Structural Biology, 1995, 5, 372-376.	2.6	81
62	Proteotoxic stress reprograms the chromatin landscape of SUMO modification. Science Signaling, 2015, 8, rs7.	1.6	81
63	TarO: a target optimisation system for structural biology. Nucleic Acids Research, 2008, 36, W190-W196.	6.5	79
64	Human box C/D snoRNA processing conservation across multiple cell types. Nucleic Acids Research, 2012, 40, 3676-3688.	6.5	79
65	Haploinsufficiency for AAGAB causes clinically heterogeneous forms of punctate palmoplantar keratoderma. Nature Genetics, 2012, 44, 1272-1276.	9.4	78
66	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. Bioinformatics, 2015, 31, 3625-3630.	1.8	76
67	The Limits of Protein Secondary Structure Prediction Accuracy from Multiple Sequence Alignment. Journal of Molecular Biology, 1993, 234, 951-957.	2.0	75
68	Visualization of multiple alignments, phylogenies and gene family evolution. Nature Methods, 2010, 7, S16-S25.	9.0	73
69	The complement of protein kinases of the microsporidium Encephalitozoon cuniculi in relation to those of Saccharomyces cerevisiae and Schizosaccharomyces pombe. BMC Genomics, 2007, 8, 309.	1.2	68
70	Mast cell tryptases: Examination of unusual characteristics by multiple sequence alignment and molecular modeling. Protein Science, 1992, 1, 370-377.	3.1	67
71	Transcription Termination and Chimeric RNA Formation Controlled by Arabidopsis thaliana FPA. PLoS Genetics, 2013, 9, e1003867.	1.5	67
72	[29] Identification of functional residues and secondary structure from protein multiple sequence alignment. Methods in Enzymology, 1996, 266, 497-512.	0.4	65

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73	ParCrys: a Parzen window density estimation approach to protein crystallization propensity prediction. Bioinformatics, 2008, 24, 901-907.	1.8	64
74	The kinomes of apicomplexan parasites. Microbes and Infection, 2012, 14, 796-810.	1.0	61
75	SNAPPI-DB: a database and API of Structures, iNterfaces and Alignments for Protein-Protein Interactions. Nucleic Acids Research, 2007, 35, D580-D589.	6.5	58
76	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. Scientific Reports, 2013, 3, 2866.	1.6	58
77	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
78	A Structural Analysis of Phosphate and Sulphate Binding Sites in Proteins. Journal of Molecular Biology, 1994, 242, 321-329.	2.0	54
79	A normalised scale for structural genomics target ranking: The OB-Score. FEBS Letters, 2006, 580, 4005-4009.	1.3	54
80	Major transcriptome re-organisation and abrupt changes in signalling, cell cycle and chromatin regulation at neural differentiation *in vivo*. Development (Cambridge), 2014, 141, 3266-3276.	1.2	54
81	AIDS vaccine predictions. Nature, 1987, 326, 549-550.	13.7	50
82	Elevated *O*-GlcNAc Levels Activate Epigenetically Repressed Genes and Delay Mouse ESC Differentiation Without Affecting Naïve to Primed Cell Transition. Stem Cells, 2014, 32, 2605-2615.	1.4	50
83	The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4. EMBO Journal, 2011, 30, 1919-1927.	3.5	47
84	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
85	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
86	Quantification of the variation in percentage identity for protein sequence alignments. BMC Bioinformatics, 2006, 7, 415.	1.2	45
87	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	5.8	44
88	Genome Analysis of the Unicellular Green Alga *Chlamydomonas reinhardtii* Indicates an Ancient Evolutionary Origin for Key Pattern Recognition and Cell-Signaling Protein Families. Genetics, 2008, 179, 193-197.	1.2	40
89	Analysis of Human Small Nucleolar RNAs (snoRNA) and the Development of snoRNA Modulator of Gene Expression Vectors. Molecular Biology of the Cell, 2010, 21, 1569-1584.	0.9	40
90	Human platelet€derived endothelial cell growth factor is homologous to *Escherichia coli* thymidine phosphorylase. Protein Science, 1992, 1, 688-690.	3.1	39

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91	MACSIMS : multiple alignment of complete sequences information management system. BMC Bioinformatics, 2006, 7, 318.	1.2	38
92	The contrasting properties of conservation and correlated phylogeny in protein functional residue prediction. BMC Bioinformatics, 2008, 9, 51.	1.2	38
93	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
94	Widespread premature transcription termination of Arabidopsis thaliana NLR genes by the spen protein FPA. ELife, 2021, 10, .	2.8	36
95	Identification of a glycosylphosphatidylinositol anchor–modifying Î²1–3 N–acetylglucosaminyl transferase in <i>Trypanosoma brucei</i>. Molecular Microbiology, 2009, 71, 478-491.	1.2	35
96	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. Nature Communications, 2022, 13, 2001.	5.8	35
97	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
98	SCANPS: a web server for iterative protein sequence database searching by dynamic programing, with display in a hierarchical SCOP browser. Nucleic Acids Research, 2008, 36, W25-W29.	6.5	32
99	Protein structural domains: Analysis of the 3Dee domains database. Proteins: Structure, Function and Bioinformatics, 2001, 42, 332-344.	1.5	31
100	JABAWS 2.2 distributed web services for Bioinformatics: protein disorder, conservation and RNA secondary structure. Bioinformatics, 2018, 34, 1939-1940.	1.8	29
101	Improved Annotation of 3′ Untranslated Regions and Complex Loci by Combination of Strand-Specific Direct RNA Sequencing, RNA-Seq and ESTs. PLoS ONE, 2014, 9, e94270.	1.1	27
102	An SH2–SH3 domain hybrid. Nature, 1993, 364, 765-765.	13.7	26
103	Protein structure prediction. Nature, 1993, 361, 505-506.	13.7	24
104	Conservation of amino acids in multiple alignments: aspartic acid has unexpected conservation. FEBS Letters, 1996, 397, 225-229.	1.3	24
105	Biological Units and their Effect upon the Properties and Prediction of Protein–Protein Interactions. Journal of Molecular Biology, 2006, 364, 1118-1129.	2.0	23
106	Prediction of antigenic determinants and secondary structures of the major AIDS virus proteins. FEBS Letters, 1987, 218, 231-237.	1.3	22
107	scop: structural classification of proteins. Trends in Biochemical Sciences, 1994, 19, 554-555.	3.7	22
108	Adenylate cyclase A acting on PKA mediates induction of stalk formation by cyclic diguanylate at the <i>Dictyostelium</i> organizer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 516-521.	3.3	22

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109	LOPAL and SCAMP: techniques for the comparison and display of protein structures. Journal of Molecular Graphics, 1988, 6, 190-196.	1.7	21
110	XANNpred: Neural nets that predict the propensity of a protein to yield diffractionâ€quality crystals. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1027-1033.	1.5	21
111	A new family of transcription factors. Development (Cambridge), 2008, 135, 3093-3101.	1.2	20
112	Relative Abundance of Transcripts (RATs): Identifying differential isoform abundance from RNA-seq. F1000Research, 2019, 8, 213.	0.8	20
113	Secondary structure prediction for modelling by homology. Protein Engineering, Design and Selection, 1993, 6, 261-266.	1.0	19
114	An efficient algorithm to locate all locally optimal alignments between two sequences allowing for gaps. Bioinformatics, 1993, 9, 729-734.	1.8	18
115	2passtools: two-pass alignment using machine-learning-filtered splice junctions increases the accuracy of intron detection in long-read RNA sequencing. Genome Biology, 2021, 22, 72.	3.8	16
116	Jalview: Visualization and Analysis of Molecular Sequences, Alignments, and Structures. BMC Bioinformatics, 2005, 6, P28.	1.2	15
117	Secondary structure prediction from multiple sequence data: blood clotting factor XIII and *Yersinia* proteinâ€tyrosine phosphatase. International Journal of Peptide and Protein Research, 1994, 44, 239-244.	0.1	15
118	The Dundee Resource for Sequence Analysis and Structure Prediction. Protein Science, 2020, 29, 277-297.	3.1	14
119	The AMPS Package for Multiple Protein Sequence Alignment. , 1994, 25, 327-347.		13
120	Protein Sequence Alignment Techniques. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1139-1146.	2.5	13
121	Deposition of Macromolecular Structures. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1105-1108.	2.5	13
122	Detection and mitigation of spurious antisense expression with RoSA. F1000Research, 0, 8, 819.	0.8	13
123	A knowledge-based architecture for protein sequence analysis and structure prediction. Journal of Molecular Graphics, 1990, 8, 94-107.	1.7	12
124	A comparison of SCOP and CATH with respect to domainâ€"domain interactions. Proteins: Structure, Function and Bioinformatics, 2008, 70, 54-62.	1.5	10
125	How well do RNA-Seq differential gene expression tools perform in a complex eukaryote? A case study in *Arabidopsis thaliana*. Bioinformatics, 2019, 35, 3372-3377.	1.8	9
126	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. PLoS Computational Biology, 2022, 18, e1009922.	1.5	9

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127	Interaction of synthetic peptides from annexin I and uteroglobin with lipid monolayers and their effect on phospholipase A2 activity. Biochemical Society Transactions, 1990, 18, 1233-1234.	1.6	8
128	PNAC: a protein nucleolar association classifier. BMC Genomics, 2011, 12, 74.	1.2	8
129	A PROLOG approach to analysing protein structure. Tetrahedron Computer Methodology, 1990, 3, 739-756.	0.2	7
130	Scanning protein sequence databanks using a distributed processing workstation network. Bioinformatics, 1991, 7, 85-88.	1.8	7
131	Increased coverage obtained by combination of methods for protein sequence database searching. Bioinformatics, 2003, 19, 1397-1403.	1.8	7
132	Sequence alignment for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 25-32.	2.5	7
133	Computational approaches to selecting and optimising targets for structural biology. Methods, 2011, 55, 3-11.	1.9	7
134	PIMS sequencing extension: a laboratory information management system for DNA sequencing facilities. BMC Research Notes, 2011, 4, 48.	0.6	7
135	Improved annotation with de novo transcriptome assembly in four social amoeba species. BMC Genomics, 2017, 18, 120.	1.2	7
136	Disease related single point mutations alter the global dynamics of a tetratricopeptide (TPR) α-solenoid domain. Journal of Structural Biology, 2020, 209, 107405.	1.3	7
137	AlmostSignificant: simplifying quality control of high-throughput sequencing data. Bioinformatics, 2016, 32, 3850-3851.	1.8	6
138	A study of the structural properties of sites modified by the O-linked 6-N-acetylglucosamine transferase. PLoS ONE, 2017, 12, e0184405.	1.1	6
139	Expression, purification, crystallization, data collection and preliminary biochemical characterization of methicillin-resistantStaphylococcus aureusSar2028, an aspartate/tyrosine/phenylalanine pyridoxal-5â€²-phosphate-dependent aminotransferase. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 452-456.	0.7	5
140	Ankyrin repeats in context with human population variation. PLoS Computational Biology, 2021, 17, e1009335.	1.5	5
141	Purification, crystallization and data collection of methicillin-resistantStaphylococcus aureusSar2676, a pantothenate synthetase. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 488-491.	0.7	4
142	Human protein-protein interaction prediction. BMC Bioinformatics, 2010, 11, .	1.2	3
143	A Dictyostelium SH2 adaptor protein required for correct DIF-1 signaling and pattern formation. Developmental Biology, 2011, 353, 290-301.	0.9	3
144	Generation and interpretation of protein sequence and structural multiple alignments. The Protein Journal, 1992, 11, 389-389.	1.1	2

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145	Creation and Analysis of Protein Multiple Sequence Alignments. Methods of Biochemical Analysis, 2002, 43, 215-232.	0.2	2
146	Visual representation of database search results: the RHIMS Plot. Bioinformatics, 2003, 19, 1037-1038.	1.8	2
147	Application of multiple sequence alignment profiles to improve protein secondary structure prediction. , 2000, 40, 502.		2
148	Multiple Sequence Alignment and Flexible Pattern Matching. Springer Series in Biophysics, 1992, , 29-52.	0.4	2
149	Structural and Functional Analysis of the S-Layer Protein from Bacillus stearothermophilus. , 1993, , 143-149.		1
150	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
151	The relationship between domain-domain interaction orientation and sequence similarity. BMC Systems Biology, 2007, 1, .	3.0	0
152	Prediction of Protein Structure from Multiple Sequence Alignment. , 1993, , 209-220.		0