

# Steven E Brenner

## List of Publications by Year in descending order

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159  
papers

45,724  
citations

17440

63  
h-index

8630

146  
g-index

181  
all docs

181  
docs citations

181  
times ranked

51198  
citing authors

#	ARTICLE	IF	CITATIONS
1	SCOPe: improvements to the structural classification of proteins – extended database to facilitate variant interpretation and machine learning. <i>Nucleic Acids Research</i> , 2022, 50, D553-D559.	14.5	59
2	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants. <i>American Journal of Human Genetics</i> , 2022, 109, 195-209.	6.2	29
3	Newborn screening for neurodevelopmental diseases: Are we there yet?. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2022, 190, 222-230.	1.6	10
4	Opportunities and challenges for the computational interpretation of rare variation in clinically important genes. <i>American Journal of Human Genetics</i> , 2021, 108, 535-548.	6.2	40
5	Revealing molecular pathways for cancer cell fitness through a genetic screen of the cancer transcriptome. <i>Cell Reports</i> , 2021, 35, 109321.	6.4	8
6	Application of full-genome analysis to diagnose rare monogenic disorders. <i>Npj Genomic Medicine</i> , 2021, 6, 77.	3.8	22
7	Precision Medicine: Using Artificial Intelligence to Improve Diagnostics and Healthcare. , 2021, , .		0
8	Computational Challenges and Artificial Intelligence in Precision Medicine. , 2020, , .		0
9	The role of exome sequencing in newborn screening for inborn errors of metabolism. <i>Nature Medicine</i> , 2020, 26, 1392-1397.	30.7	112
10	Genomic Analysis of Historical Cases with Positive Newborn Screens for Short-Chain Acyl-CoA Dehydrogenase Deficiency Shows That a Validated Second-Tier Biochemical Test Can Replace Future Sequencing. <i>International Journal of Neonatal Screening</i> , 2020, 6, 41.	3.2	9
11	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. <i>Human Mutation</i> , 2019, 40, 1373-1391.	2.5	10
12	Assessing computational predictions of the phenotypic effect of cystathionine- $\beta$ -synthase variants. <i>Human Mutation</i> , 2019, 40, 1530-1545.	2.5	5
13	VIPdb, a genetic Variant Impact Predictor Database. <i>Human Mutation</i> , 2019, 40, 1202-1214.	2.5	24
14	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019, 40, 1519-1529.	2.5	10
15	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. <i>Human Mutation</i> , 2019, 40, 1474-1485.	2.5	8
16	Back Cover, Volume 40, Issue 9. <i>Human Mutation</i> , 2019, 40, ii.	2.5	0
17	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. <i>Human Mutation</i> , 2019, 40, 1392-1399.	2.5	16
18	Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. <i>Human Mutation</i> , 2019, 40, 1612-1622.	2.5	8

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19	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019, 40, 1314-1320.	2.5	10
20	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI intellectual disability challenge. <i>Human Mutation</i> , 2019, 40, 1330-1345.	2.5	11
21	FDA oversight of NSIGHT genomic research: the need for an integrated systems approach to regulation. <i>Npj Genomic Medicine</i> , 2019, 4, 32.	3.8	6
22	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	8.8	261
23	SCOPe: classification of large macromolecular structures in the structural classification of proteins extended database. <i>Nucleic Acids Research</i> , 2019, 47, D475-D481.	14.5	122
24	Navigating ethical quandaries with the privacy dilemma of biomedical datasets. , 2019, , .		1
25	Precision Medicine: Addressing the Challenges of Sharing, Analysis, and Privacy at Scale. , 2019, , .		0
26	PRECISION MEDICINE: FROM DIPTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
27	A novel <i>PRRT2</i> pathogenic variant in a family with paroxysmal kinesigenic dyskinesia and benign familial infantile seizures. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002287.	1.2	9
28	Putting benchmarks in their rightful place: The heart of computational biology. <i>PLoS Computational Biology</i> , 2018, 14, e1006494.	3.2	20
29	Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018, 26, 1721-1731.	2.8	33
30	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	17.5	955
31	Abstract 3295: CAGI: The Critical Assessment of Genome Interpretation, a community experiment to evaluate phenotype prediction: implications for predicting impact of variants in cancer. <i>Cancer Research</i> , 2018, 78, 3295-3295.	0.9	1
32	When Biology Gets Personal: Hidden Challenges of Privacy and Ethics in Biological Big Data. , 2018, , .		3
33	Precision Medicine: Improving health through high-resolution analysis of personal data. , 2018, , .		0
34	Newborn Sequencing in Genomic Medicine and Public Health. <i>Pediatrics</i> , 2017, 139, .	2.1	174
35	Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. <i>Human Mutation</i> , 2017, 38, 460-463.	2.5	1
36	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	2.5	13

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37	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017, 38, 1182-1192.	2.5	39
38	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	2.5	14
39	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins “ extended Database. <i>Journal of Molecular Biology</i> , 2017, 429, 348-355.	4.2	85
40	The evolution of function within the Nudix homology clan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 775-811.	2.6	53
41	Reports from CAGI: The Critical Assessment of Genome Interpretation. <i>Human Mutation</i> , 2017, 38, 1039-1041.	2.5	38
42	A novel plant enzyme with dual activity: an atypical Nudix hydrolase and a dipeptidyl peptidase III. <i>Biological Chemistry</i> , 2017, 398, 101-112.	2.5	14
43	USE OF GENOME DATA IN NEWBORNS AS A STARTING POINT FOR LIFE-LONG PRECISION MEDICINE. , 2016, , .		1
44	Multisystem Anomalies in Severe Combined Immunodeficiency with Mutant <i>BCL11B</i> . <i>New England Journal of Medicine</i> , 2016, 375, 2165-2176.	27.0	104
45	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1539-1555.	3.8	16
46	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
47	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. , 2016, , .		2
48	Substrate specificity characterization for eight putative nudix hydrolases. Evaluation of criteria for substrate identification within the Nudix family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1810-1822.	2.6	10
49	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2186-2202.	3.8	12
50	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. <i>Journal of Experimental Medicine</i> , 2016, 213, 155-165.	8.5	83
51	REGULATORY RNA. , 2016, , .		0
52	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 243-8.	0.7	4
53	Novel Presentation of Recurrent Infection in a Family with NOD2 Mutation. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, AB383.	2.9	0
54	The value of protein structure classification information“Surveying the scientific literature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2025-2038.	2.6	37

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55	Ten Years of PLoS Computational Biology: A Decade of Appreciation and Innovation. PLoS Computational Biology, 2015, 11, e1004317.	3.2	1
56	SIFTER search: a web server for accurate phylogeny-based protein function prediction. Nucleic Acids Research, 2015, 43, W141-W147.	14.5	39
57	Nijmegen Breakage Syndrome Detected By Newborn Screening for T Cell Receptor Excision Circles (TRECs). Journal of Allergy and Clinical Immunology, 2015, 135, AB14.	2.9	1
58	Nijmegen Breakage Syndrome Detected by Newborn Screening for T Cell Receptor Excision Circles (TRECs). Journal of Clinical Immunology, 2015, 35, 227-233.	3.8	34
59	Combined Immunodeficiency Due to MALT1 Mutations, Treated by Hematopoietic Cell Transplantation. Journal of Clinical Immunology, 2015, 35, 135-146.	3.8	94
60	Regulation of Splicing Factors by Alternative Splicing and NMD Is Conserved between Kingdoms Yet Evolutionarily Flexible. Molecular Biology and Evolution, 2015, 32, 1072-1079.	8.9	143
61	Regulation of alternative splicing in <i>Drosophila</i> by 56 RNA binding proteins. Genome Research, 2015, 25, 1771-1780.	5.5	77
62	Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. Human Molecular Genetics, 2015, 24, 7421-7431.	2.9	24
63	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
64	Comparison of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages, tissues, and cells by modENCODE RNA-seq data. Genome Research, 2014, 24, 1086-1101.	5.5	88
65	SCOPe: Structural Classification of Proteins extended, integrating SCOP and ASTRAL data and classification of new structures. Nucleic Acids Research, 2014, 42, D304-D309.	14.5	627
66	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
67	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
68	Automated particle correspondence and accurate tilt-axis detection in tilted-image pairs. Journal of Structural Biology, 2014, 187, 66-75.	2.8	4
69	Newborn Screening for SCID Identifies Patients with Ataxia Telangiectasia. Journal of Clinical Immunology, 2013, 33, 540-549.	3.8	92
70	A continuous fluorescence assay for the characterization of Nudix hydrolases. Analytical Biochemistry, 2013, 437, 178-184.	2.4	4
71	Optimal and fast rotational alignment of volumes with missing data in Fourier space. Journal of Structural Biology, 2013, 184, 345-347.	2.8	1
72	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789

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73	Association of gut microbiota with post-operative clinical course in Crohn's disease. <i>BMC Gastroenterology</i> , 2013, 13, 131.	2.0	95
74	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	5.6	54
75	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Î± subfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1593-1609.	2.6	6
76	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
77	Be prepared for the big genome leak. <i>Nature</i> , 2013, 498, 139-139.	27.8	24
78	THE FUTURE OF GENOME-BASED MEDICINE. , 2012, , .		0
79	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of <i>Desulfovibrio vulgaris</i> . <i>Journal of Proteome Research</i> , 2012, 11, 5720-5735.	3.7	22
80	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. <i>ISME Journal</i> , 2012, 6, 1440-1444.	9.8	326
81	Characterization of Illumina Sequencing Errors: Implications for Investigations of the Gut Microbiota. <i>Gastroenterology</i> , 2011, 140, S-331.	1.3	0
82	The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011, 471, 473-479.	27.8	1,379
83	Identification and experimental validation of splicing regulatory elements in <i>Drosophila melanogaster</i> reveals functionally conserved splicing enhancers in metazoans. <i>Rna</i> , 2011, 17, 1884-1894.	3.5	14
84	Genome-scale phylogenetic function annotation of large and diverse protein families. <i>Genome Research</i> , 2011, 21, 1969-1980.	5.5	54
85	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. <i>Genome Research</i> , 2011, 21, 193-202.	5.5	208
86	An SF1 affinity model to identify branch point sequences in human introns. <i>Nucleic Acids Research</i> , 2011, 39, 2344-2356.	14.5	10
87	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
88	Automated multi-model reconstruction from single-particle electron microscopy data. <i>Journal of Structural Biology</i> , 2010, 170, 98-108.	2.8	34
89	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	14.5	573
90	Alignment-free local structural search by writhe decomposition. <i>Bioinformatics</i> , 2010, 26, 1176-1184.	4.1	11

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91	Survey of large protein complexes in <i>D. vulgaris</i> reveals great structural diversity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16580-16585.	7.1	29
92	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in <i>Drosophila</i> . PLoS Genetics, 2009, 5, e1000525.	3.5	87
93	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	27.8	744
94	A method for the alignment of heterogeneous macromolecules from electron microscopy. Journal of Structural Biology, 2009, 166, 67-78.	2.8	40
95	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the <i>Drosophila</i> hnRNP A/B Family Members. Molecular Cell, 2009, 33, 438-449.	9.7	79
96	Phylogenetic molecular function annotation. Journal of Physics: Conference Series, 2009, 180, 012024.	0.4	12
97	Data growth and its impact on the SCOP database: new developments. Nucleic Acids Research, 2007, 36, D419-D425.	14.5	854
98	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	5.6	736
99	Common sense for our genomes. Nature, 2007, 449, 783-784.	27.8	27
100	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. Nature, 2007, 446, 926-929.	27.8	593
101	The Coupling of Alternative Splicing and Nonsense-Mediated mRNA Decay. Advances in Experimental Medicine and Biology, 2007, 623, 190-211.	1.6	202
102	Developing Computational Biology. PLoS Computational Biology, 2007, 3, e157.	3.2	0
103	The Impact of Structural Genomics: Expectations and Outcomes. Science, 2006, 311, 347-351.	12.6	366
104	The RNA Ontology Consortium: An open invitation to the RNA community. Rna, 2006, 12, 533-541.	3.5	59
105	ANDY: a general, fault-tolerant tool for database searching on computer clusters. Bioinformatics, 2006, 22, 618-620.	4.1	3
106	MeRNA: a database of metal ion binding sites in RNA structures. Nucleic Acids Research, 2006, 34, D131-D134.	14.5	67
107	A graphical model for predicting protein molecular function. , 2006, , .		7
108	Structural Genomics of Minimal Organisms and Protein Fold Space. Journal of Structural and Functional Genomics, 2005, 6, 63-70.	1.2	29

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109	Target selection and deselection at the Berkeley Structural Genomics Center. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 356-370.	2.6	27
110	An alternative model of amino acid replacement. <i>Bioinformatics</i> , 2005, 21, 975-980.	4.1	19
111	Protein Molecular Function Prediction by Bayesian Phylogenomics. <i>PLoS Computational Biology</i> , 2005, 1, e45.	3.2	162
112	Global analysis of positive and negative pre-mRNA splicing regulators in <i>Drosophila</i> . <i>Genes and Development</i> , 2005, 19, 1306-1314.	5.9	106
113	Pairwise alignment incorporating dipeptide covariation. <i>Bioinformatics</i> , 2005, 21, 3704-3710.	4.1	13
114	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. <i>Bioinformatics</i> , 2005, 21, 3824-3831.	4.1	22
115	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
116	RNA structural motifs: building blocks of a modular biomolecule. <i>Quarterly Reviews of Biophysics</i> , 2005, 38, 221-243.	5.7	184
117	<i>PLoS Computational Biology: A New Community Journal</i> . <i>PLoS Computational Biology</i> , 2005, 1, e4.	3.2	7
118	Three-dimensional motifs from the SCOR, structural classification of RNA database: extruded strands, base triples, tetraloops and U-turns. <i>Nucleic Acids Research</i> , 2004, 32, 2342-2352.	14.5	60
119	The ASTRAL Compendium in 2004. <i>Nucleic Acids Research</i> , 2004, 32, 189D-192.	14.5	480
120	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004, 14, 273-282.	5.7	304
121	SCOR: Structural Classification of RNA, version 2.0. <i>Nucleic Acids Research</i> , 2004, 32, 182D-184.	14.5	98
122	Measurements of protein sequence-structure correlations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 804-810.	2.6	39
123	Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 166-179.	2.6	61
124	A generalized affine gap model significantly improves protein sequence alignment accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 329-338.	2.6	29
125	Protein secondary structure: entropy, correlations and prediction. <i>Bioinformatics</i> , 2004, 20, 1603-1611.	4.1	71
126	SCOP database in 2004: refinements integrate structure and sequence family data. <i>Nucleic Acids Research</i> , 2004, 32, 226D-229.	14.5	815



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127	The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004, 14, 273-273.	5.7	1
128	Structural genomics and structural biology: compare and contrast. <i>Genome Biology</i> , 2004, 5, 343.	9.6	8
129	An unappreciated role for RNA surveillance. <i>Genome Biology</i> , 2004, 5, R8.	9.6	159
130	Genome-Wide Analysis Reveals an Unexpected Function for the Drosophila Splicing Factor U2AF50 in the Nuclear Export of Intronless mRNAs. <i>Molecular Cell</i> , 2004, 14, 775-786.	9.7	56
131	Structural Studies of the Nudix Hydrolase DR1025 From <i>Deinococcus radiodurans</i> and its Ligand Complexes. <i>Journal of Molecular Biology</i> , 2004, 339, 103-116.	4.2	25
132	WebLogo: A Sequence Logo Generator: Figure 1. <i>Genome Research</i> , 2004, 14, 1188-1190.	5.5	10,751
133	Evidence for the widespread coupling of alternative splicing and nonsense-mediated mRNA decay in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 189-192.	7.1	920
134	Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. <i>Bioinformatics</i> , 2003, 19, i118-i121.	4.1	155
135	SCOP database in 2002: refinements accommodate structural genomics. <i>Nucleic Acids Research</i> , 2002, 30, 264-267.	14.5	403
136	ASTRAL compendium enhancements. <i>Nucleic Acids Research</i> , 2002, 30, 260-263.	14.5	117
137	The Bioperl Toolkit: Perl Modules for the Life Sciences. <i>Genome Research</i> , 2002, 12, 1611-1618.	5.5	1,427
138	Sulfotransferases and Sulfatases in Mycobacteria. <i>Chemistry and Biology</i> , 2002, 9, 767-776.	6.0	109
139	SCOR: a Structural Classification of RNA database. <i>Nucleic Acids Research</i> , 2002, 30, 392-394.	14.5	103
140	A tour of structural genomics. <i>Nature Reviews Genetics</i> , 2001, 2, 801-809.	16.3	152
141	Target selection for structural genomics. , 2000, 7, 967-969.		108
142	SCOP: a Structural Classification of Proteins database. <i>Nucleic Acids Research</i> , 2000, 28, 257-259.	14.5	533
143	The ASTRAL compendium for protein structure and sequence analysis. <i>Nucleic Acids Research</i> , 2000, 28, 254-256.	14.5	432
144	Expectations from structural genomics. <i>Protein Science</i> , 2000, 9, 197-200.	7.6	99

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145	SCOP: a Structural Classification of Proteins database. <i>Nucleic Acids Research</i> , 1999, 27, 254-256.	14.5	208
146	The PRESAGE database for structural genomics. <i>Nucleic Acids Research</i> , 1999, 27, 251-253.	14.5	48
147	Errors in genome annotation. <i>Trends in Genetics</i> , 1999, 15, 132-133.	6.7	335
148	Using metabolic pathway databases for functional annotation. <i>Trends in Genetics</i> , 1998, 14, 332-333.	6.7	19
149	SCOP, Structural Classification of Proteins Database: Applications to Evaluation of the Effectiveness of Sequence Alignment Methods and Statistics of Protein Structural Data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1147-1154.	2.5	31
150	Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 6073-6078.	7.1	493
151	Population statistics of protein structures: lessons from structural classifications. <i>Current Opinion in Structural Biology</i> , 1997, 7, 369-376.	5.7	173
152	[37] Understanding protein structure: Using scop for fold interpretation. <i>Methods in Enzymology</i> , 1996, 266, 635-643.	1.0	80
153	Blast, blitz, blocks and beauty; sequence comparison on the net. <i>Trends in Genetics</i> , 1995, 11, 330-331.	6.7	12
154	Gene duplications in <i>H. influenzae</i> . <i>Nature</i> , 1995, 378, 140-140.	27.8	82
155	DNA recognition code of transcription factors. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 319-328.	2.1	78
156	Classification of multi-helical DNA-binding domains and application to predict the DBD structures of $\lambda$ factor, LysR, OmpR/PhoB, CENP-B, Rap1, and XylS/Ada/AraC. <i>FEBS Letters</i> , 1995, 372, 215-221.	2.8	30
157	SCOP: A structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995, 247, 536-540.	4.2	3,952
158	SCOP: a structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995, 247, 536-540.	4.2	5,400
159	A quantitative methodology for the de novo design of proteins. <i>Protein Science</i> , 1994, 3, 1871-1882.	7.6	11