StevenÂ E Brenner

List of Publications by Year
in descending order

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159 papers	45,724 citations	17405 63 h-index	8599 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 â€“ extended database to facilitate variant interpretation and machine learning. Nucleic Acids Research, 2022, 50, D553-D559.	6.5	59
2	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants. American Journal of Human Genetics, 2022, 109, 195-209.	2.6	29
3	Newborn screening for neurodevelopmental diseases: Are we there yet?. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2022, 190, 222-230.	0.7	10
4	Opportunities and challenges for the computational interpretation of rare variation in clinically important genes. American Journal of Human Genetics, 2021, 108, 535-548.	2.6	40
5	Revealing molecular pathways for cancer cell fitness through a genetic screen of the cancer translatome. Cell Reports, 2021, 35, 109321.	2.9	8
6	Application of full-genome analysis to diagnose rare monogenic disorders. Npj Genomic Medicine, 2021, 6, 77.	1.7	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. Nature Medicine, 2020, 26, 1392-1397.	15.2	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. International Journal of Neonatal Screening, 2020, 6, 41.	1.2	9
11	CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases. Human Mutation, 2019, 40, 1373-1391.	1.1	10
12	Assessing computational predictions of the phenotypic effect of cystathionineâ€betaâ€synthase variants. Human Mutation, 2019, 40, 1530-1545.	1.1	5
13	VIPdb, a genetic Variant Impact Predictor Database. Human Mutation, 2019, 40, 1202-1214.	1.1	24
14	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
15	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGIâ€5. Human Mutation, 2019, 40, 1474-1485.	1.1	8
16	Back Cover, Volume 40, Issue 9. Human Mutation, 2019, 40, ii.	1.1	0
17	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	1.1	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. Human Mutation, 2019, 40, 1612-1622.	1.1	8

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19	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2019, 40, 1314-1320.	1.1	10
20	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGIâ€5 intellectual disability challenge. Human Mutation, 2019, 40, 1330-1345.	1.1	11
21	FDA oversight of NSIGHT genomic research: the need for an integrated systems approach to regulation. Npj Genomic Medicine, 2019, 4, 32.	1.7	6
22	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	3.8	261
23	SCOPe: classification of large macromolecular structures in the structural classification of proteinsâ€"extended database. Nucleic Acids Research, 2019, 47, D475-D481.	6.5	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 DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES. , 2018, , .		3
27	A novel PRRT2 pathogenic variant in a family with paroxysmal kinesigenic dyskinesia and benign familial infantile seizures. Journal of Physical Education and Sports Management, 2018, 4, a002287.	0.5	9
28	Putting benchmarks in their rightful place: The heart of computational biology. PLoS Computational Biology, 2018, 14, e1006494.	1.5	20
29	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	1.4	33
30	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	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. Cancer Research, 2018, 78, 3295-3295.	0.4	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. Pediatrics, 2017, 139, .	1.0	174
35	Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. Human Mutation, 2017, 38, 460-463.	1.1	1
36	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13

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37	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
38	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	1.1	14
39	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins â€“ extended Database. Journal of Molecular Biology, 2017, 429, 348-355.	2.0	85
40	The evolution of function within the Nudix homology clan. Proteins: Structure, Function and Bioinformatics, 2017, 85, 775-811.	1.5	53
41	Reports from CAGI: The Critical Assessment of Genome Interpretation. Human Mutation, 2017, 38, 1039-1041.	1.1	38
42	A novel plant enzyme with dual activity: an atypical Nudix hydrolase and a dipeptidyl peptidase III. Biological Chemistry, 2017, 398, 101-112.	1.2	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 BCL11B. New England Journal of Medicine, 2016, 375, 2165-2176.	13.9	104
45	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. Molecular and Cellular Proteomics, 2016, 15, 1539-1555.	2.5	16
46	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	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. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1810-1822.	1.5	10
49	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. Molecular and Cellular Proteomics, 2016, 15, 2186-2202.	2.5	12
50	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. Journal of Experimental Medicine, 2016, 213, 155-165.	4.2	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. Journal of Allergy and Clinical Immunology, 2015, 135, AB383.	1.5	0
54	The value of protein structure classification informationâ€"Surveying the scientific literature. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2025-2038.	1.5	37

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55	Ten Years of PLoSâ€¡ Computational Biology: A Decade of Appreciation and Innovation. PLoS Computational Biology, 2015, 11, e1004317.	1.5	1
56	SIFTER search: a web server for accurate phylogeny-based protein function prediction. Nucleic Acids Research, 2015, 43, W141-W147.	6.5	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.	1.5	1
58	Nijmegen Breakage Syndrome Detected by Newborn Screening for T Cell Receptor Excision Circles (TRECs). Journal of Clinical Immunology, 2015, 35, 227-233.	2.0	34
59	Combined Immunodeficiency Due to MALT1 Mutations, Treated by Hematopoietic Cell Transplantation. Journal of Clinical Immunology, 2015, 35, 135-146.	2.0	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.	3.5	143
61	Regulation of alternative splicing in Drosophila by 56 RNA binding proteins. Genome Research, 2015, 25, 1771-1780.	2.4	77
62	Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. Human Molecular Genetics, 2015, 24, 7421-7431.	1.4	24
63	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
64	Comparison of D. melanogaster and C. elegans developmental stages, tissues, and cells by modENCODE RNA-seq data. Genome Research, 2014, 24, 1086-1101.	2.4	88
65	SCOPe: Structural Classification of Proteinsâ€"extended, integrating SCOP and ASTRAL data and classification of new structures. Nucleic Acids Research, 2014, 42, D304-D309.	6.5	627
66	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
67	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
68	Automated particle correspondence and accurate tilt-axis detection in tilted-image pairs. Journal of Structural Biology, 2014, 187, 66-75.	1.3	4
69	Newborn Screening for SCID Identifies Patients with Ataxia Telangiectasia. Journal of Clinical Immunology, 2013, 33, 540-549.	2.0	92
70	A continuous fluorescence assay for the characterization of Nudix hydrolases. Analytical Biochemistry, 2013, 437, 178-184.	1.1	4
71	Optimal and fast rotational alignment of volumes with missing data in Fourier space. Journal of Structural Biology, 2013, 184, 345-347.	1.3	1
72	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789

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73	Association of gut microbiota with post-operative clinical course in Crohnâ€™s disease. BMC Gastroenterology, 2013, 13, 131.	0.8	95
74	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
75	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Îł subfamily. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1593-1609.	1.5	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. Nature, 2013, 498, 139-139.	13.7	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 Desulfovibrio vulgaris. Journal of Proteome Research, 2012, 11, 5720-5735.	1.8	22
80	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. ISME Journal, 2012, 6, 1440-1444.	4.4	326
81	Characterization of Illumina Sequencing Errors: Implications for Investigations of the Gut Microbiota. Gastroenterology, 2011, 140, S-331.	0.6	0
82	The developmental transcriptome of Drosophila melanogaster. Nature, 2011, 471, 473-479.	13.7	1,379
83	Identification and experimental validation of splicing regulatory elements in Drosophila melanogaster reveals functionally conserved splicing enhancers in metazoans. Rna, 2011, 17, 1884-1894.	1.6	14
84	Genome-scale phylogenetic function annotation of large and diverse protein families. Genome Research, 2011, 21, 1969-1980.	2.4	54
85	Conservation of an RNA regulatory map between Drosophila and mammals. Genome Research, 2011, 21, 193-202.	2.4	208
86	An SF1 affinity model to identify branch point sequences in human introns. Nucleic Acids Research, 2011, 39, 2344-2356.	6.5	10
87	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
88	Automated multi-model reconstruction from single-particle electron microscopy data. Journal of Structural Biology, 2010, 170, 98-108.	1.3	34
89	Biases in Illumina transcriptome sequencing caused by random hexamer priming. Nucleic Acids Research, 2010, 38, e131-e131.	6.5	573
90	Alignment-free local structural search by writhe decomposition. Bioinformatics, 2010, 26, 1176-1184.	1.8	11

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91	Survey of large protein complexes in D. vulgaris reveals great structural diversity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16580-16585.	3.3	29
92	Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in Drosophila. PLoS Genetics, 2009, 5, e1000525.	1.5	87
93	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744
94	A method for the alignment of heterogeneous macromolecules from electron microscopy. Journal of Structural Biology, 2009, 166, 67-78.	1.3	40
95	Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the Drosophila hnRNP A/B Family Members. Molecular Cell, 2009, 33, 438-449.	4.5	79
96	Phylogenetic molecular function annotation. Journal of Physics: Conference Series, 2009, 180, 012024.	0.3	12
97	Data growth and its impact on the SCOP database: new developments. Nucleic Acids Research, 2007, 36, D419-D425.	6.5	854
98	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
99	Common sense for our genomes. Nature, 2007, 449, 783-784.	13.7	27
100	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. Nature, 2007, 446, 926-929.	13.7	593
101	The Coupling of Alternative Splicing and Nonsense-Mediated mRNA Decay. Advances in Experimental Medicine and Biology, 2007, 623, 190-211.	0.8	202
102	Developing Computational Biology. PLoS Computational Biology, 2007, 3, e157.	1.5	0
103	The Impact of Structural Genomics: Expectations and Outcomes. Science, 2006, 311, 347-351.	6.0	366
104	The RNA Ontology Consortium: An open invitation to the RNA community. Rna, 2006, 12, 533-541.	1.6	59
105	ANDY: a general, fault-tolerant tool for database searching on computer clusters. Bioinformatics, 2006, 22, 618-620.	1.8	3
106	MeRNA: a database of metal ion binding sites in RNA structures. Nucleic Acids Research, 2006, 34, D131-D134.	6.5	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. Proteins: Structure, Function and Bioinformatics, 2005, 62, 356-370.	1.5	27
110	An alternative model of amino acid replacement. Bioinformatics, 2005, 21, 975-980.	1.8	19
111	Protein Molecular Function Prediction by Bayesian Phylogenomics. PLoS Computational Biology, 2005, 1, e45.	1.5	162
112	Global analysis of positive and negative pre-mRNA splicing regulators in Drosophila. Genes and Development, 2005, 19, 1306-1314.	2.7	106
113	Pairwise alignment incorporating dipeptide covariation. Bioinformatics, 2005, 21, 3704-3710.	1.8	13
114	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. Bioinformatics, 2005, 21, 3824-3831.	1.8	22
115	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	6.0	3,227
116	RNA structural motifs: building blocks of a modular biomolecule. Quarterly Reviews of Biophysics, 2005, 38, 221-243.	2.4	184
117	PLoS Computational Biology: A New Community Journal. PLoS Computational Biology, 2005, 1, e4.	1.5	7
118	Three-dimensional motifs from the SCOR, structural classification of RNA database: extruded strands, base triples, tetraloops and U-turns. Nucleic Acids Research, 2004, 32, 2342-2352.	6.5	60
119	The ASTRAL Compendium in 2004. Nucleic Acids Research, 2004, 32, 189D-192.	6.5	480
120	The evolving roles of alternative splicing. Current Opinion in Structural Biology, 2004, 14, 273-282.	2.6	304
121	SCOR: Structural Classification of RNA, version 2.0. Nucleic Acids Research, 2004, 32, 182D-184.	6.5	98
122	Measurements of protein sequence-structure correlations. Proteins: Structure, Function and Bioinformatics, 2004, 57, 804-810.	1.5	39
123	Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. Proteins: Structure, Function and Bioinformatics, 2004, 58, 166-179.	1.5	61
124	A generalized affine gap model significantly improves protein sequence alignment accuracy. Proteins: Structure, Function and Bioinformatics, 2004, 58, 329-338.	1.5	29
125	Protein secondary structure: entropy, correlations and prediction. Bioinformatics, 2004, 20, 1603-1611.	1.8	71
126	SCOP database in 2004: refinements integrate structure and sequence family data. Nucleic Acids Research, 2004, 32, 226D-229.	6.5	815

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127	The evolving roles of alternative splicing. Current Opinion in Structural Biology, 2004, 14, 273-273.	2.6	1
128	Structural genomics and structural biology: compare and contrast. Genome Biology, 2004, 5, 343.	13.9	8
129	An unappreciated role for RNA surveillance. Genome Biology, 2004, 5, R8.	13.9	159
130	Genome-Wide Analysis Reveals an Unexpected Function for the Drosophila Splicing Factor U2AF50 in the Nuclear Export of Intronless mRNAs. Molecular Cell, 2004, 14, 775-786.	4.5	56
131	Structural Studies of the Nudix Hydrolase DR1025 From Deinococcus radiodurans and its Ligand Complexes. Journal of Molecular Biology, 2004, 339, 103-116.	2.0	25
132	WebLogo: A Sequence Logo Generator. Genome Research, 2004, 14, 1188-1190.	2.4	10,751
133	Evidence for the widespread coupling of alternative splicing and nonsense-mediated mRNA decay in humans. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 189-192.	3.3	920
134	Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. Bioinformatics, 2003, 19, i118-i121.	1.8	155
135	SCOP database in 2002: refinements accommodate structural genomics. Nucleic Acids Research, 2002, 30, 264-267.	6.5	403
136	ASTRAL compendium enhancements. Nucleic Acids Research, 2002, 30, 260-263.	6.5	117
137	The Bioperl Toolkit: Perl Modules for the Life Sciences. Genome Research, 2002, 12, 1611-1618.	2.4	1,427
138	Sulfotransferases and Sulfatases in Mycobacteria. Chemistry and Biology, 2002, 9, 767-776.	6.2	109
139	SCOR: a Structural Classification of RNA database. Nucleic Acids Research, 2002, 30, 392-394.	6.5	103
140	A tour of structural genomics. Nature Reviews Genetics, 2001, 2, 801-809.	7.7	152
141	Target selection for structural genomics. , 2000, 7, 967-969.		108
142	SCOP: a Structural Classification of Proteins database. Nucleic Acids Research, 2000, 28, 257-259.	6.5	533
143	The ASTRAL compendium for protein structure and sequence analysis. Nucleic Acids Research, 2000, 28, 254-256.	6.5	432
144	Expectations from structural genomics. Protein Science, 2000, 9, 197-200.	3.1	99

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145	SCOP: a Structural Classification of Proteins database. Nucleic Acids Research, 1999, 27, 254-256.	6.5	208
146	The PRESAGE database for structural genomics. Nucleic Acids Research, 1999, 27, 251-253.	6.5	48
147	Errors in genome annotation. Trends in Genetics, 1999, 15, 132-133.	2.9	335
148	Using metabolic pathway databases for functional annotation. Trends in Genetics, 1998, 14, 332-333.	2.9	19
149	SCOP, Structural Classification of Proteins Database: Applications to Evaluation of the Effectiveness of Sequence Alignment Methods and Statistics of Protein Structural Data. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1147-1154.	2.5	31
150	Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 6073-6078.	3.3	493
151	Population statistics of protein structures: lessons from structural classifications. Current Opinion in Structural Biology, 1997, 7, 369-376.	2.6	173
152	[37] Understanding protein structure: Using scop for fold interpretation. Methods in Enzymology, 1996, 266, 635-643.	0.4	80
153	Blast, blitz, blocks and beauty; sequence comparison on the net. Trends in Genetics, 1995, 11, 330-331.	2.9	12
154	Gene duplications in H. influenzae. Nature, 1995, 378, 140-140.	13.7	82
155	DNA recognition code of transcription factors. Protein Engineering, Design and Selection, 1995, 8, 319-328.	1.0	78
156	Classification of multi-helical DNA-binding domains and application to predict the DBD structures of Ïƒ factor, LysR, OmpR/PhoB, CENP-B, Rap1, and XylS/Ada/AraC. FEBS Letters, 1995, 372, 215-221.	1.3	30
157	SCOP: A structural classification of proteins database for the investigation of sequences and structures. Journal of Molecular Biology, 1995, 247, 536-540.	2.0	3,952
158	SCOP: a structural classification of proteins database for the investigation of sequences and structures. Journal of Molecular Biology, 1995, 247, 536-540.	2.0	5,400
159	A quantitative methodology for the de novo design of proteins. Protein Science, 1994, 3, 1871-1882.	3.1	11