Steven E Brenner

List of Publications by Year in Descending Order

145 papers	35,997 citations	59 h-index	181 g-index
181 ext. papers	41,428 ext. citations	12.4 avg, IF	6.99 L-index

#	Paper	IF	Citations
145	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants.. *American Journal of Human Genetics*, **2022**,	11	4
144	Opportunities and challenges for the computational interpretation of rare variation in clinically important genes. *American Journal of Human Genetics*, **2021**, 108, 535-548	11	10
143	Revealing molecular pathways for cancer cell fitness through a genetic screen of the cancer translatome. *Cell Reports*, **2021**, 35, 109321	10.6	3
142	Application of full-genome analysis to diagnose rare monogenic disorders. *Npj Genomic Medicine*, **2021**, 6, 77	6.2	0
141	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,	2.6	1
140	The role of exome sequencing in newborn screening for inborn errors of metabolism. *Nature Medicine*, **2020**, 26, 1392-1397	50.5	41
139	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. *Human Mutation*, **2019**, 40, 1392-1399	4.7	11
138	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	4.7	4
137	Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Human Mutation*, **2019**, 40, 1314-1320	4.7	5
136	Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI-5 intellectual disability challenge. *Human Mutation*, **2019**, 40, 1330-1345	4.7	4
135	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	4.7	5
134	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. *Human Mutation*, **2019**, 40, 1530-1545	4.7	3
133	VIPdb, a genetic Variant Impact Predictor Database. *Human Mutation*, **2019**, 40, 1202-1214	4.7	13
132	Assessment of predicted enzymatic activity of N-acetylglucosaminidase variants of unknown significance for CAGI 2016. *Human Mutation*, **2019**, 40, 1519-1529	4.7	4
131	Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. *Human Mutation*, **2019**, 40, 1474-1485	4.7	5
130	FDA oversight of NSIGHT genomic research: the need for an integrated systems approach to regulation. *Npj Genomic Medicine*, **2019**, 4, 32	6.2	2
129	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111

128	SCOPe: classification of large macromolecular structures in the structural classification of proteins-extended database. *Nucleic Acids Research*, **2019**, 47, D475-D481	20.1	57
127	PRECISION MEDICINE: FROM DIPLOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES **2018**,		2
126	Registered access: authorizing data access. *European Journal of Human Genetics*, **2018**, 26, 1721-1731	5.3	17
125	KBase: The United States Department of Energy Systems Biology Knowledgebase. *Nature Biotechnology*, **2018**, 36, 566-569	44.5	419
124	A novel pathogenic variant in a family with paroxysmal kinesigenic dyskinesia and benign familial infantile seizures. *Journal of Physical Education and Sports Management*, **2018**, 4,	2.8	5
123	Newborn Sequencing in Genomic Medicine and Public Health. *Pediatrics*, **2017**, 139,	7.4	109
122	Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. *Human Mutation*, **2017**, 38, 460-463	4.7	1
121	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. *Human Mutation*, **2017**, 38, 1042-1050	4.7	9
120	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Human Mutation*, **2017**, 38, 1182-1192	4.7	28
119	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. *Human Mutation*, **2017**, 38, 1266-1276	4.7	9
118	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins - extended Database. *Journal of Molecular Biology*, **2017**, 429, 348-355	6.5	59
117	The evolution of function within the Nudix homology clan. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 775-811	4.2	33
116	Reports from CAGI: The Critical Assessment of Genome Interpretation. *Human Mutation*, **2017**, 38, 1039-1041	4.7	28
115	A novel plant enzyme with dual activity: an atypical Nudix hydrolase and a dipeptidyl peptidase III. *Biological Chemistry*, **2017**, 398, 101-112	4.5	9
114	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY **2016**,		2
113	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	4.2	8
112	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. *Molecular and Cellular Proteomics*, **2016**, 15, 2186-202	7.6	10
111	A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. *Journal of Experimental Medicine*, **2016**, 213, 155-65	16.6	60

110	PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2016**, 21, 243-8	1.3	3
109	Multisystem Anomalies in Severe Combined Immunodeficiency with Mutant BCL11B. *New England Journal of Medicine*, **2016**, 375, 2165-2176	59.2	57
108	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, 1539-55	7.6	12
107	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
106	Combined immunodeficiency due to MALT1 mutations, treated by hematopoietic cell transplantation. *Journal of Clinical Immunology*, **2015**, 35, 135-46	5.7	72
105	Regulation of splicing factors by alternative splicing and NMD is conserved between kingdoms yet evolutionarily flexible. *Molecular Biology and Evolution*, **2015**, 32, 1072-9	8.3	82
104	Regulation of alternative splicing in Drosophila by 56 RNA binding proteins. *Genome Research*, **2015** , 25, 1771-80	9.7	51
103	Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. *Human Molecular Genetics*, **2015**, 24, 7421-31	5.6	13
102	The value of protein structure classification information-Surveying the scientific literature. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 2025-38	4.2	14
101	SIFTER search: a web server for accurate phylogeny-based protein function prediction. *Nucleic Acids Research*, **2015**, 43, W141-7	20.1	31
100	Nijmegen breakage syndrome detected by newborn screening for T cell receptor excision circles (TRECs). *Journal of Clinical Immunology*, **2015**, 35, 227-33	5.7	21
99	Comparative analysis of the transcriptome across distant species. *Nature*, **2014**, 512, 445-8	50.4	207
98	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135
97	Automated particle correspondence and accurate tilt-axis detection in tilted-image pairs. *Journal of Structural Biology*, **2014**, 187, 66-75	3.4	4
96	Personalized medicine: from genotypes and molecular phenotypes towards therapy- session introduction. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2014**, 19, 224-8	1.3	1
95	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE **2014**,		4
94	Comparison of D. melanogaster and C. elegans developmental stages, tissues, and cells by modENCODE RNA-seq data. *Genome Research*, **2014**, 24, 1086-101	9.7	59
93	SCOPe: Structural Classification of Proteins--extended, integrating SCOP and ASTRAL data and classification of new structures. *Nucleic Acids Research*, **2014**, 42, D304-9	20.1	438

92	Newborn screening for SCID identifies patients with ataxia telangiectasia. *Journal of Clinical Immunology*, **2013**, 33, 540-9	5.7	69
91	A continuous fluorescence assay for the characterization of Nudix hydrolases. *Analytical Biochemistry*, **2013**, 437, 178-84	3.1	3
90	Optimal and fast rotational alignment of volumes with missing data in Fourier space. *Journal of Structural Biology*, **2013**, 184, 345-7	3.4	1
89	A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7	21.6	587
88	Association of gut microbiota with post-operative clinical course in Crohn's disease. *BMC Gastroenterology*, **2013**, 13, 131	3	63
87	The COMBREX project: design, methodology, and initial results. *PLoS Biology*, **2013**, 11, e1001638	9.7	47
86	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: recurrence of tyrosine aminotransferase activity in the I subfamily. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1593-609	4.2	5
85	Be prepared for the big genome leak. *Nature*, **2013**, 498, 139	50.4	18
84	High-throughput isolation and characterization of untagged membrane protein complexes: outer membrane complexes of Desulfovibrio vulgaris. *Journal of Proteome Research*, **2012**, 11, 5720-35	5.6	15
83	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. *ISME Journal*, **2012**, 6, 1440-4	11.9	243
82	The developmental transcriptome of Drosophila melanogaster. *Nature*, **2011**, 471, 473-9	50.4	1094
81	Identification and experimental validation of splicing regulatory elements in Drosophila melanogaster reveals functionally conserved splicing enhancers in metazoans. *Rna*, **2011**, 17, 1884-94	5.8	11
80	Genome-scale phylogenetic function annotation of large and diverse protein families. *Genome Research*, **2011**, 21, 1969-80	9.7	43
79	Conservation of an RNA regulatory map between Drosophila and mammals. *Genome Research*, **2011**, 21, 193-202	9.7	165
78	An SF1 affinity model to identify branch point sequences in human introns. *Nucleic Acids Research*, **2011**, 39, 2344-56	20.1	9
77	Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, **2010**, 330, 1787-97	33.3	892
76	Automated multi-model reconstruction from single-particle electron microscopy data. *Journal of Structural Biology*, **2010**, 170, 98-108	3.4	30
75	Biases in Illumina transcriptome sequencing caused by random hexamer priming. *Nucleic Acids Research*, **2010**, 38, e131	20.1	471

74	Alignment-free local structural search by writhe decomposition. *Bioinformatics*, **2010**, 26, 1176-84	7.2	6
73	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, 16580-5	11.5	24
72	Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in Drosophila. *PLoS Genetics*, **2009**, 5, e1000525	6	68
71	Unlocking the secrets of the genome. *Nature*, **2009**, 459, 927-30	50.4	620
70	A method for the alignment of heterogeneous macromolecules from electron microscopy. *Journal of Structural Biology*, **2009**, 166, 67-78	3.4	32
69	Genome-wide analysis of alternative pre-mRNA splicing and RNA-binding specificities of the Drosophila hnRNP A/B family members. *Molecular Cell*, **2009**, 33, 438-49	17.6	70
68	Phylogenetic molecular function annotation. *Journal of Physics: Conference Series*, **2009**, 180, 12024	0.3	7
67	Data growth and its impact on the SCOP database: new developments. *Nucleic Acids Research*, **2008**, 36, D419-25	20.1	768
66	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. *PLoS Biology*, **2007**, 5, e16	9.7	638
65	Common sense for our genomes. *Nature*, **2007**, 449, 783-4	50.4	18
64	Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. *Nature*, **2007**, 446, 926-9	50.4	469
63	The coupling of alternative splicing and nonsense-mediated mRNA decay. *Advances in Experimental Medicine and Biology*, **2007**, 623, 190-211	3.6	162
62	The RNA Ontology Consortium: an open invitation to the RNA community. *Rna*, **2006**, 12, 533-41	5.8	49
61	ANDY: a general, fault-tolerant tool for database searching on computer clusters. *Bioinformatics*, **2006**, 22, 618-20	7.2	1
60	MeRNA: a database of metal ion binding sites in RNA structures. *Nucleic Acids Research*, **2006**, 34, D131-4	20.1	57
59	A graphical model for predicting protein molecular function **2006**,		3
58	The impact of structural genomics: expectations and outcomes. *Science*, **2006**, 311, 347-51	33.3	316
57	Target selection and deselection at the Berkeley Structural Genomics Center. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 356-70	4.2	24

56	Pairwise alignment incorporating dipeptide covariation. *Bioinformatics*, **2005**, 21, 3704-10	7.2	13
55	Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. *Bioinformatics*, **2005**, 21, 3824-31	7.2	21
54	The transcriptional landscape of the mammalian genome. *Science*, **2005**, 309, 1559-63	33.3	2807
53	RNA structural motifs: building blocks of a modular biomolecule. *Quarterly Reviews of Biophysics*, **2005**, 38, 221-43	7	151
52	Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 166-79	4.2	57
51	A generalized affine gap model significantly improves protein sequence alignment accuracy. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 329-38	4.2	22
50	Structural genomics of minimal organisms and protein fold space. *Journal of Structural and Functional Genomics*, **2005**, 6, 63-70		26
49	An alternative model of amino acid replacement. *Bioinformatics*, **2005**, 21, 975-80	7.2	16
48	Protein molecular function prediction by Bayesian phylogenomics. *PLoS Computational Biology*, **2005**, 1, e45	5	131
47	Global analysis of positive and negative pre-mRNA splicing regulators in Drosophila. *Genes and Development*, **2005**, 19, 1306-14	12.6	97
46	Three-dimensional motifs from the SCOR, structural classification of RNA database: extruded strands, base triples, tetraloops and U-turns. *Nucleic Acids Research*, **2004**, 32, 2342-52	20.1	54
45	The ASTRAL Compendium in 2004. *Nucleic Acids Research*, **2004**, 32, D189-92	20.1	433
44	The evolving roles of alternative splicing. *Current Opinion in Structural Biology*, **2004**, 14, 273-82	8.1	263
43	SCOR: Structural Classification of RNA, version 2.0. *Nucleic Acids Research*, **2004**, 32, D182-4	20.1	85
42	Measurements of protein sequence-structure correlations. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 804-10	4.2	32
41	Protein secondary structure: entropy, correlations and prediction. *Bioinformatics*, **2004**, 20, 1603-11	7.2	62
40	SCOP database in 2004: refinements integrate structure and sequence family data. *Nucleic Acids Research*, **2004**, 32, D226-9	20.1	733
39	The evolving roles of alternative splicing. *Current Opinion in Structural Biology*, **2004**, 14, 273-273	8.1	0

38	Structural genomics and structural biology: compare and contrast. *Genome Biology*, **2004**, 5, 343	18.3	8
37	An unappreciated role for RNA surveillance. *Genome Biology*, **2004**, 5, R8	18.3	145
36	Genome-wide analysis reveals an unexpected function for the Drosophila splicing factor U2AF50 in the nuclear export of intronless mRNAs. *Molecular Cell*, **2004**, 14, 775-86	17.6	54
35	Structural studies of the Nudix hydrolase DR1025 from Deinococcus radiodurans and its ligand complexes. *Journal of Molecular Biology*, **2004**, 339, 103-16	6.5	24
34	WebLogo: a sequence logo generator. *Genome Research*, **2004**, 14, 1188-90	9.7	7896
33	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, 189-92	11.5	768
32	Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. *Bioinformatics*, **2003**, 19 Suppl 1, i118-21	7.2	138
31	Sulfotransferases and sulfatases in mycobacteria. *Chemistry and Biology*, **2002**, 9, 767-76		92
30	SCOR: a Structural Classification of RNA database. *Nucleic Acids Research*, **2002**, 30, 392-4	20.1	85
29	SCOP database in 2002: refinements accommodate structural genomics. *Nucleic Acids Research*, **2002**, 30, 264-7	20.1	348
28	ASTRAL compendium enhancements. *Nucleic Acids Research*, **2002**, 30, 260-3	20.1	93
27	The Bioperl toolkit: Perl modules for the life sciences. *Genome Research*, **2002**, 12, 1611-8	9.7	1234
26	A tour of structural genomics. *Nature Reviews Genetics*, **2001**, 2, 801-9	30.1	131
25	Expectations from structural genomics. *Protein Science*, **2000**, 9, 197-200	6.3	85
24	Target selection for structural genomics. *Nature Structural Biology*, **2000**, 7 Suppl, 967-9		88
23	SCOP: a structural classification of proteins database. *Nucleic Acids Research*, **2000**, 28, 257-9	20.1	468
22	The ASTRAL compendium for protein structure and sequence analysis. *Nucleic Acids Research*, **2000**, 28, 254-6	20.1	348
21	SCOP: a Structural Classification of Proteins database. *Nucleic Acids Research*, **1999**, 27, 254-6	20.1	191

20	The PRESAGE database for structural genomics. *Nucleic Acids Research*, **1999**, 27, 251-3	20.1	43
19	Errors in genome annotation. *Trends in Genetics*, **1999**, 15, 132-3	8.5	271
18	Using metabolic pathway databases for functional annotation. *Trends in Genetics*, **1998**, 14, 332-3	8.5	17
17	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, 1147-54		26
16	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, 6073-8	11.5	438
15	Population statistics of protein structures: lessons from structural classifications. *Current Opinion in Structural Biology*, **1997**, 7, 369-76	8.1	158
14	Understanding protein structure: using scop for fold interpretation. *Methods in Enzymology*, **1996**, 266, 635-43	1.7	69
13	Gene duplications in H. influenzae. *Nature*, **1995**, 378, 140	50.4	71
12	DNA recognition code of transcription factors. *Protein Engineering, Design and Selection*, **1995**, 8, 319-28	1.9	67
11	Classification of multi-helical DNA-binding domains and application to predict the DBD structures of sigma factor, LysR, OmpR/PhoB, CENP-B, Rapl, and Xy1S/Ada/AraC. *FEBS Letters*, **1995**, 372, 215-21	3.8	22
10	SCOP: A structural classification of proteins database for the investigation of sequences and structures. *Journal of Molecular Biology*, **1995**, 247, 536-540	6.5	2645
9	BLAST, Blitz, BLOCKS and BEAUTY: sequence comparison on the net. *Trends in Genetics*, **1995**, 11, 330-1	8.5	12
8	SCOP: a structural classification of proteins database for the investigation of sequences and structures. *Journal of Molecular Biology*, **1995**, 247, 536-40	6.5	5115
7	A quantitative methodology for the de novo design of proteins. *Protein Science*, **1994**, 3, 1871-82	6.3	10
6	Networks of Splice Factor Regulation by Unproductive Splicing Coupled With Nonsense Mediated mRNA Decay		1
5	Polysome fractionation analysis reveals features important for human nonsense-mediated mRNA decay		1
4	StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants		5
3	DNA from dried blood spots yields high quality sequences for exome analysis		2