

Steven E Brenner

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | WebLogo: a sequence logo generator. <i>Genome Research</i> , 2004 , 14, 1188-90 | 9.7 | 7896 |
| 144 | SCOP: a structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995 , 247, 536-40 | 6.5 | 5115 |
| 143 | The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63 | 33.3 | 2807 |
| 142 | SCOP: A structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995 , 247, 536-540 | 6.5 | 2645 |
| 141 | The Bioperl toolkit: Perl modules for the life sciences. <i>Genome Research</i> , 2002 , 12, 1611-8 | 9.7 | 1234 |
| 140 | The developmental transcriptome of <i>Drosophila melanogaster</i> . <i>Nature</i> , 2011 , 471, 473-9 | 50.4 | 1094 |
| 139 | Identification of functional elements and regulatory circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010 , 330, 1787-97 | 33.3 | 892 |
| 138 | Data growth and its impact on the SCOP database: new developments. <i>Nucleic Acids Research</i> , 2008 , 36, D419-25 | 20.1 | 768 |
| 137 | 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, 189-92 | 11.5 | 768 |
| 136 | SCOP database in 2004: refinements integrate structure and sequence family data. <i>Nucleic Acids Research</i> , 2004 , 32, D226-9 | 20.1 | 733 |
| 135 | The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16 | 9.7 | 638 |
| 134 | Unlocking the secrets of the genome. <i>Nature</i> , 2009 , 459, 927-30 | 50.4 | 620 |
| 133 | A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7 | 21.6 | 587 |
| 132 | Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010 , 38, e131 | 20.1 | 471 |
| 131 | Unproductive splicing of SR genes associated with highly conserved and ultraconserved DNA elements. <i>Nature</i> , 2007 , 446, 926-9 | 50.4 | 469 |
| 130 | SCOP: a structural classification of proteins database. <i>Nucleic Acids Research</i> , 2000 , 28, 257-9 | 20.1 | 468 |
| 129 | SCOPE: Structural Classification of Proteins--extended, integrating SCOP and ASTRAL data and classification of new structures. <i>Nucleic Acids Research</i> , 2014 , 42, D304-9 | 20.1 | 438 |

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| 128 | 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, 6073-8 | 11.5 | 438 |
| 127 | The ASTRAL Compendium in 2004. <i>Nucleic Acids Research</i> , 2004 , 32, D189-92 | 20.1 | 433 |
| 126 | KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018 , 36, 566-569 | 44.5 | 419 |
| 125 | SCOP database in 2002: refinements accommodate structural genomics. <i>Nucleic Acids Research</i> , 2002 , 30, 264-7 | 20.1 | 348 |
| 124 | The ASTRAL compendium for protein structure and sequence analysis. <i>Nucleic Acids Research</i> , 2000 , 28, 254-6 | 20.1 | 348 |
| 123 | The impact of structural genomics: expectations and outcomes. <i>Science</i> , 2006 , 311, 347-51 | 33.3 | 316 |
| 122 | Errors in genome annotation. <i>Trends in Genetics</i> , 1999 , 15, 132-3 | 8.5 | 271 |
| 121 | The evolving roles of alternative splicing. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 273-82 | 8.1 | 263 |
| 120 | Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. <i>ISME Journal</i> , 2012 , 6, 1440-4 | 11.9 | 243 |
| 119 | An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184 | 18.3 | 218 |
| 118 | Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8 | 50.4 | 207 |
| 117 | SCOP: a Structural Classification of Proteins database. <i>Nucleic Acids Research</i> , 1999 , 27, 254-6 | 20.1 | 191 |
| 116 | Conservation of an RNA regulatory map between Drosophila and mammals. <i>Genome Research</i> , 2011 , 21, 193-202 | 9.7 | 165 |
| 115 | The coupling of alternative splicing and nonsense-mediated mRNA decay. <i>Advances in Experimental Medicine and Biology</i> , 2007 , 623, 190-211 | 3.6 | 162 |
| 114 | Population statistics of protein structures: lessons from structural classifications. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 369-76 | 8.1 | 158 |
| 113 | RNA structural motifs: building blocks of a modular biomolecule. <i>Quarterly Reviews of Biophysics</i> , 2005 , 38, 221-43 | 7 | 151 |
| 112 | An unappreciated role for RNA surveillance. <i>Genome Biology</i> , 2004 , 5, R8 | 18.3 | 145 |
| 111 | Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. <i>Bioinformatics</i> , 2003 , 19 Suppl 1, i118-21 | 7.2 | 138 |

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| 110 | Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014 , 512, 453-6 | 50.4 | 135 |
| 109 | Protein molecular function prediction by Bayesian phylogenomics. <i>PLoS Computational Biology</i> , 2005 , 1, e45 | 5 | 131 |
| 108 | A tour of structural genomics. <i>Nature Reviews Genetics</i> , 2001 , 2, 801-9 | 30.1 | 131 |
| 107 | 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 | 18.3 | 111 |
| 106 | Newborn Sequencing in Genomic Medicine and Public Health. <i>Pediatrics</i> , 2017 , 139, | 7.4 | 109 |
| 105 | Global analysis of positive and negative pre-mRNA splicing regulators in Drosophila. <i>Genes and Development</i> , 2005 , 19, 1306-14 | 12.6 | 97 |
| 104 | ASTRAL compendium enhancements. <i>Nucleic Acids Research</i> , 2002 , 30, 260-3 | 20.1 | 93 |
| 103 | Sulfotransferases and sulfatases in mycobacteria. <i>Chemistry and Biology</i> , 2002 , 9, 767-76 | | 92 |
| 102 | Target selection for structural genomics. <i>Nature Structural Biology</i> , 2000 , 7 Suppl, 967-9 | | 88 |
| 101 | Expectations from structural genomics. <i>Protein Science</i> , 2000 , 9, 197-200 | 6.3 | 85 |
| 100 | SCOR: Structural Classification of RNA, version 2.0. <i>Nucleic Acids Research</i> , 2004 , 32, D182-4 | 20.1 | 85 |
| 99 | SCOR: a Structural Classification of RNA database. <i>Nucleic Acids Research</i> , 2002 , 30, 392-4 | 20.1 | 85 |
| 98 | Regulation of splicing factors by alternative splicing and NMD is conserved between kingdoms yet evolutionarily flexible. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1072-9 | 8.3 | 82 |
| 97 | Combined immunodeficiency due to MALT1 mutations, treated by hematopoietic cell transplantation. <i>Journal of Clinical Immunology</i> , 2015 , 35, 135-46 | 5.7 | 72 |
| 96 | Gene duplications in H. influenzae. <i>Nature</i> , 1995 , 378, 140 | 50.4 | 71 |
| 95 | Genome-wide analysis of alternative pre-mRNA splicing and RNA-binding specificities of the Drosophila hnRNP A/B family members. <i>Molecular Cell</i> , 2009 , 33, 438-49 | 17.6 | 70 |
| 94 | Newborn screening for SCID identifies patients with ataxia telangiectasia. <i>Journal of Clinical Immunology</i> , 2013 , 33, 540-9 | 5.7 | 69 |
| 93 | Understanding protein structure: using scop for fold interpretation. <i>Methods in Enzymology</i> , 1996 , 266, 635-43 | 1.7 | 69 |

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|----|--|------|----|
| 92 | Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000525 | 6 | 68 |
| 91 | DNA recognition code of transcription factors. <i>Protein Engineering, Design and Selection</i> , 1995 , 8, 319-28 | 1.9 | 67 |
| 90 | Association of gut microbiota with post-operative clinical course in Crohn's disease. <i>BMC Gastroenterology</i> , 2013 , 13, 131 | 3 | 63 |
| 89 | Protein secondary structure: entropy, correlations and prediction. <i>Bioinformatics</i> , 2004 , 20, 1603-11 | 7.2 | 62 |
| 88 | A novel human autoimmune syndrome caused by combined hypomorphic and activating mutations in ZAP-70. <i>Journal of Experimental Medicine</i> , 2016 , 213, 155-65 | 16.6 | 60 |
| 87 | SCOPE: Manual Curation and Artifact Removal in the Structural Classification of Proteins - extended Database. <i>Journal of Molecular Biology</i> , 2017 , 429, 348-355 | 6.5 | 59 |
| 86 | Comparison of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages, tissues, and cells by modENCODE RNA-seq data. <i>Genome Research</i> , 2014 , 24, 1086-101 | 9.7 | 59 |
| 85 | MeRNA: a database of metal ion binding sites in RNA structures. <i>Nucleic Acids Research</i> , 2006 , 34, D131-4 | 10.1 | 57 |
| 84 | Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 166-79 | 4.2 | 57 |
| 83 | Multisystem Anomalies in Severe Combined Immunodeficiency with Mutant BCL11B. <i>New England Journal of Medicine</i> , 2016 , 375, 2165-2176 | 59.2 | 57 |
| 82 | SCOPE: classification of large macromolecular structures in the structural classification of proteins-extended database. <i>Nucleic Acids Research</i> , 2019 , 47, D475-D481 | 20.1 | 57 |
| 81 | 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, 2342-52 | 20.1 | 54 |
| 80 | Genome-wide analysis reveals an unexpected function for the <i>Drosophila</i> splicing factor U2AF50 in the nuclear export of intronless mRNAs. <i>Molecular Cell</i> , 2004 , 14, 775-86 | 17.6 | 54 |
| 79 | Regulation of alternative splicing in <i>Drosophila</i> by 56 RNA binding proteins. <i>Genome Research</i> , 2015 , 25, 1771-80 | 9.7 | 51 |
| 78 | The RNA Ontology Consortium: an open invitation to the RNA community. <i>Rna</i> , 2006 , 12, 533-41 | 5.8 | 49 |
| 77 | The COMBREX project: design, methodology, and initial results. <i>PLoS Biology</i> , 2013 , 11, e1001638 | 9.7 | 47 |
| 76 | Genome-scale phylogenetic function annotation of large and diverse protein families. <i>Genome Research</i> , 2011 , 21, 1969-80 | 9.7 | 43 |
| 75 | The PRESAGE database for structural genomics. <i>Nucleic Acids Research</i> , 1999 , 27, 251-3 | 20.1 | 43 |

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| 74 | The role of exome sequencing in newborn screening for inborn errors of metabolism. <i>Nature Medicine</i> , 2020 , 26, 1392-1397 | 50.5 | 41 |
| 73 | The evolution of function within the Nudix homology clan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 775-811 | 4.2 | 33 |
| 72 | A method for the alignment of heterogeneous macromolecules from electron microscopy. <i>Journal of Structural Biology</i> , 2009 , 166, 67-78 | 3.4 | 32 |
| 71 | Measurements of protein sequence-structure correlations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 804-10 | 4.2 | 32 |
| 70 | SIFTER search: a web server for accurate phylogeny-based protein function prediction. <i>Nucleic Acids Research</i> , 2015 , 43, W141-7 | 20.1 | 31 |
| 69 | Automated multi-model reconstruction from single-particle electron microscopy data. <i>Journal of Structural Biology</i> , 2010 , 170, 98-108 | 3.4 | 30 |
| 68 | 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 | 4.7 | 28 |
| 67 | Reports from CAGI: The Critical Assessment of Genome Interpretation. <i>Human Mutation</i> , 2017 , 38, 1039-1041 | 4.4 | 28 |
| 66 | 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, 1147-54 | | 26 |
| 65 | Structural genomics of minimal organisms and protein fold space. <i>Journal of Structural and Functional Genomics</i> , 2005 , 6, 63-70 | | 26 |
| 64 | Survey of large protein complexes in <i>D. vulgaris</i> reveals great structural diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 16580-5 | 11.5 | 24 |
| 63 | Structural studies of the Nudix hydrolase DR1025 from <i>Deinococcus radiodurans</i> and its ligand complexes. <i>Journal of Molecular Biology</i> , 2004 , 339, 103-16 | 6.5 | 24 |
| 62 | Target selection and deselection at the Berkeley Structural Genomics Center. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 356-70 | 4.2 | 24 |
| 61 | A generalized affine gap model significantly improves protein sequence alignment accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 329-38 | 4.2 | 22 |
| 60 | Classification of multi-helical DNA-binding domains and application to predict the DBD structures of sigma factor, LysR, OmpR/PhoB, CENP-B, RapI, and Xy1S/Ada/AraC. <i>FEBS Letters</i> , 1995 , 372, 215-21 | 3.8 | 22 |
| 59 | Nijmegen breakage syndrome detected by newborn screening for T cell receptor excision circles (TRECs). <i>Journal of Clinical Immunology</i> , 2015 , 35, 227-33 | 5.7 | 21 |
| 58 | Statistical evaluation of pairwise protein sequence comparison with the Bayesian bootstrap. <i>Bioinformatics</i> , 2005 , 21, 3824-31 | 7.2 | 21 |
| 57 | Common sense for our genomes. <i>Nature</i> , 2007 , 449, 783-4 | 50.4 | 18 |

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|----|--|------|----|
| 56 | Be prepared for the big genome leak. <i>Nature</i> , 2013 , 498, 139 | 50.4 | 18 |
| 55 | Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018 , 26, 1721-1731 | 5.3 | 17 |
| 54 | Using metabolic pathway databases for functional annotation. <i>Trends in Genetics</i> , 1998 , 14, 332-3 | 8.5 | 17 |
| 53 | An alternative model of amino acid replacement. <i>Bioinformatics</i> , 2005 , 21, 975-80 | 7.2 | 16 |
| 52 | 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, 5720-35 | 5.6 | 15 |
| 51 | The value of protein structure classification information-Surveying the scientific literature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 2025-38 | 4.2 | 14 |
| 50 | Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. <i>Human Molecular Genetics</i> , 2015 , 24, 7421-31 | 5.6 | 13 |
| 49 | VIPdb, a genetic Variant Impact Predictor Database. <i>Human Mutation</i> , 2019 , 40, 1202-1214 | 4.7 | 13 |
| 48 | Pairwise alignment incorporating dipeptide covariation. <i>Bioinformatics</i> , 2005 , 21, 3704-10 | 7.2 | 13 |
| 47 | BLAST, Blitz, BLOCKS and BEAUTY: sequence comparison on the net. <i>Trends in Genetics</i> , 1995 , 11, 330-1 | 8.5 | 12 |
| 46 | 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, 1539-55 | 7.6 | 12 |
| 45 | Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAG15 challenge. <i>Human Mutation</i> , 2019 , 40, 1392-1399 | 4.7 | 11 |
| 44 | 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, 1884-94 | 5.8 | 11 |
| 43 | Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2186-202 | 7.6 | 10 |
| 42 | A quantitative methodology for the de novo design of proteins. <i>Protein Science</i> , 1994 , 3, 1871-82 | 6.3 | 10 |
| 41 | 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 | 11 | 10 |
| 40 | Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017 , 38, 1042-1050 | 4.7 | 9 |
| 39 | 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 | 4.7 | 9 |

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| 38 | A novel plant enzyme with dual activity: an atypical Nudix hydrolase and a dipeptidyl peptidase III. <i>Biological Chemistry</i> , 2017 , 398, 101-112 | 4.5 | 9 |
| 37 | An SF1 affinity model to identify branch point sequences in human introns. <i>Nucleic Acids Research</i> , 2011 , 39, 2344-56 | 20.1 | 9 |
| 36 | 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 | 4.2 | 8 |
| 35 | Structural genomics and structural biology: compare and contrast. <i>Genome Biology</i> , 2004 , 5, 343 | 18.3 | 8 |
| 34 | Phylogenetic molecular function annotation. <i>Journal of Physics: Conference Series</i> , 2009 , 180, 12024 | 0.3 | 7 |
| 33 | The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens | | 7 |
| 32 | Alignment-free local structural search by writhe decomposition. <i>Bioinformatics</i> , 2010 , 26, 1176-84 | 7.2 | 6 |
| 31 | Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2019 , 40, 1314-1320 | 4.7 | 5 |
| 30 | 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 | 4.7 | 5 |
| 29 | Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5. <i>Human Mutation</i> , 2019 , 40, 1474-1485 | 4.7 | 5 |
| 28 | Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: recurrence of tyrosine aminotransferase activity in the β subfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1593-609 | 4.2 | 5 |
| 27 | StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants | | 5 |
| 26 | A novel 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, | 2.8 | 5 |
| 25 | 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 | 4.7 | 4 |
| 24 | Assessment of patient clinical descriptions and pathogenic variants from gene panel sequences in the CAGI-5 intellectual disability challenge. <i>Human Mutation</i> , 2019 , 40, 1330-1345 | 4.7 | 4 |
| 23 | Assessment of predicted enzymatic activity of EN-acetylglucosaminidase variants of unknown significance for CAGI 2016. <i>Human Mutation</i> , 2019 , 40, 1519-1529 | 4.7 | 4 |
| 22 | Automated particle correspondence and accurate tilt-axis detection in tilted-image pairs. <i>Journal of Structural Biology</i> , 2014 , 187, 66-75 | 3.4 | 4 |
| 21 | PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE 2014 , | | 4 |

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| 20 | StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants.. <i>American Journal of Human Genetics</i> , 2022 , | 11 | 4 |
| 19 | Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. <i>Human Mutation</i> , 2019 , 40, 1530-1545 | 4.7 | 3 |
| 18 | A continuous fluorescence assay for the characterization of Nudix hydrolases. <i>Analytical Biochemistry</i> , 2013 , 437, 178-84 | 3.1 | 3 |
| 17 | A graphical model for predicting protein molecular function 2006 , | | 3 |
| 16 | PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016 , 21, 243-8 | 1.3 | 3 |
| 15 | Revealing molecular pathways for cancer cell fitness through a genetic screen of the cancer translome. <i>Cell Reports</i> , 2021 , 35, 109321 | 10.6 | 3 |
| 14 | PRECISION MEDICINE: FROM DILOTYPES TO DISPARITIES TOWARDS IMPROVED HEALTH AND THERAPIES 2018 , | | 2 |
| 13 | PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY 2016 , | | 2 |
| 12 | DNA from dried blood spots yields high quality sequences for exome analysis | | 2 |
| 11 | Perturbation robustness analyses reveal important parameters in variant interpretation pipelines | | 2 |
| 10 | FDA oversight of NSIGHT genomic research: the need for an integrated systems approach to regulation. <i>Npj Genomic Medicine</i> , 2019 , 4, 32 | 6.2 | 2 |
| 9 | Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. <i>Human Mutation</i> , 2017 , 38, 460-463 | 4.7 | 1 |
| 8 | 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, | 2.6 | 1 |
| 7 | Optimal and fast rotational alignment of volumes with missing data in Fourier space. <i>Journal of Structural Biology</i> , 2013 , 184, 345-7 | 3.4 | 1 |
| 6 | Personalized medicine: from genotypes and molecular phenotypes towards therapy- session introduction. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014 , 19, 224-8 | 1.3 | 1 |
| 5 | ANDY: a general, fault-tolerant tool for database searching on computer clusters. <i>Bioinformatics</i> , 2006 , 22, 618-20 | 7.2 | 1 |
| 4 | Networks of Splice Factor Regulation by Unproductive Splicing Coupled With Nonsense Mediated mRNA Decay | | 1 |
| 3 | Polysome fractionation analysis reveals features important for human nonsense-mediated mRNA decay | | 1 |

- 2 The evolving roles of alternative splicing. *Current Opinion in Structural Biology*, **2004**, 14, 273-273 8.1 ○
- 1 Application of full-genome analysis to diagnose rare monogenic disorders. *Npj Genomic Medicine*, **2021**, 6, 77 6.2 ○