

Bonnie Berger

List of Publications by Year in descending order

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Version: 2024-02-01

206
papers

20,981
citations

20817

60
h-index

13771

129
g-index

236
all docs

236
docs citations

236
times ranked

33429
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , 2020, 181, 1016-1035.e19. | 28.9 | 1,956 |
| 2 | Efficient Bayesian mixed-model analysis increases association power in large cohorts. <i>Nature Genetics</i> , 2015, 47, 284-290. | 21.4 | 1,285 |
| 3 | Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413. | 27.8 | 1,179 |
| 4 | Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797. | 12.6 | 1,124 |
| 5 | Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. <i>Nature Methods</i> , 2019, 16, 1153-1160. | 19.0 | 693 |
| 6 | MultiCoil: A program for predicting two- and three-stranded coiled coils. <i>Protein Science</i> , 1997, 6, 1179-1189. | 7.6 | 667 |
| 7 | Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. <i>Nature Biotechnology</i> , 2019, 37, 685-691. | 17.5 | 557 |
| 8 | ARACHNE: A Whole-Genome Shotgun Assembler. <i>Genome Research</i> , 2002, 12, 177-189. | 5.5 | 508 |
| 9 | Global alignment of multiple protein interaction networks with application to functional orthology detection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12763-12768. | 7.1 | 500 |
| 10 | Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660. | 28.9 | 482 |
| 11 | Inferring Admixture Histories of Human Populations Using Linkage Disequilibrium. <i>Genetics</i> , 2013, 193, 1233-1254. | 2.9 | 445 |
| 12 | Herpesviral Protein Networks and Their Interaction with the Human Proteome. <i>Science</i> , 2006, 311, 239-242. | 12.6 | 399 |
| 13 | Allergic inflammatory memory in human respiratory epithelial progenitor cells. <i>Nature</i> , 2018, 560, 649-654. | 27.8 | 368 |
| 14 | A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. <i>Cell</i> , 2014, 158, 434-448. | 28.9 | 335 |
| 15 | Protein Folding in the Hydrophobic-Hydrophilic (<i>HP</i>) Model is NP-Complete. <i>Journal of Computational Biology</i> , 1998, 5, 27-40. | 1.6 | 327 |
| 16 | IsoRankN: spectral methods for global alignment of multiple protein networks. <i>Bioinformatics</i> , 2009, 25, i253-i258. | 4.1 | 322 |
| 17 | Topaz-Denoise: general deep denoising models for cryoEM and cryoET. <i>Nature Communications</i> , 2020, 11, 5208. | 12.8 | 313 |
| 18 | Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction. <i>Genome Research</i> , 2000, 10, 950-958. | 5.5 | 303 |

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|----|---|------|-----------|
| 19 | CryoDRGN: reconstruction of heterogeneous cryo-EM structures using neural networks. <i>Nature Methods</i> , 2021, 18, 176-185. | 19.0 | 299 |
| 20 | Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346. | 16.3 | 288 |
| 21 | Ancient west Eurasian ancestry in southern and eastern Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2632-2637. | 7.1 | 246 |
| 22 | Genetic Evidence for Recent Population Mixture in India. <i>American Journal of Human Genetics</i> , 2013, 93, 422-438. | 6.2 | 234 |
| 23 | Compact Integration of Multi-Network Topology for Functional Analysis of Genes. <i>Cell Systems</i> , 2016, 3, 540-548.e5. | 6.2 | 207 |
| 24 | Learning the protein language: Evolution, structure, and function. <i>Cell Systems</i> , 2021, 12, 654-669.e3. | 6.2 | 194 |
| 25 | Pertactin beta-helix folding mechanism suggests common themes for the secretion and folding of autotransporter proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4918-4923. | 7.1 | 187 |
| 26 | Matt: Local Flexibility Aids Protein Multiple Structure Alignment. <i>PLoS Computational Biology</i> , 2008, 4, e10. | 3.2 | 185 |
| 27 | Learning the language of viral evolution and escape. <i>Science</i> , 2021, 371, 284-288. | 12.6 | 184 |
| 28 | Opposing Effects of Glutamine and Asparagine Govern Prion Formation by Intrinsically Disordered Proteins. <i>Molecular Cell</i> , 2011, 43, 72-84. | 9.7 | 174 |
| 29 | Reconstructing Austronesian population history in Island Southeast Asia. <i>Nature Communications</i> , 2014, 5, 4689. | 12.8 | 158 |
| 30 | Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly. <i>Biophysical Journal</i> , 1998, 75, 2626-2636. | 0.5 | 148 |
| 31 | Conserved microRNA targeting in <i>Drosophila</i> is as widespread in coding regions as in 3'UTRs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15751-15756. | 7.1 | 146 |
| 32 | LearnCoil-VMF: computational evidence for coiled-coil-like motifs in many viral membrane-fusion proteins. <i>Journal of Molecular Biology</i> , 1999, 290, 1031-1041. | 4.2 | 144 |
| 33 | Large-scale identification of genetic design strategies using local search. <i>Molecular Systems Biology</i> , 2009, 5, 296. | 7.2 | 143 |
| 34 | Secure genome-wide association analysis using multiparty computation. <i>Nature Biotechnology</i> , 2018, 36, 547-551. | 17.5 | 139 |
| 35 | Structured States of Disordered Proteins from Genomic Sequences. <i>Cell</i> , 2016, 167, 158-170.e12. | 28.9 | 127 |
| 36 | Unusually effective microRNA targeting within repeat-rich coding regions of mammalian mRNAs. <i>Genome Research</i> , 2011, 21, 1395-1403. | 5.5 | 123 |

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|----|--|------|-----------|
| 37 | Struct2Net: a web service to predict protein-protein interactions using a structure-based approach. <i>Nucleic Acids Research</i> , 2010, 38, W508-W515. | 14.5 | 121 |
| 38 | Efficient Moment-Based Inference of Admixture Parameters and Sources of Gene Flow. <i>Molecular Biology and Evolution</i> , 2013, 30, 1788-1802. | 8.9 | 121 |
| 39 | Genome-Scale Networks Link Neurodegenerative Disease Genes to α -Synuclein through Specific Molecular Pathways. <i>Cell Systems</i> , 2017, 4, 157-170.e14. | 6.2 | 102 |
| 40 | Predicting the mutational drivers of future SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2022, 14, eabk3445. | 12.4 | 101 |
| 41 | Integrated single-cell analysis of multicellular immune dynamics during hyperacute HIV-1 infection. <i>Nature Medicine</i> , 2020, 26, 511-518. | 30.7 | 100 |
| 42 | Compressive genomics. <i>Nature Biotechnology</i> , 2012, 30, 627-630. | 17.5 | 99 |
| 43 | Comprehensive Dissection of PDGF-PDGFR Signaling Pathways in PDGFR Genetically Defined Cells. <i>PLoS ONE</i> , 2008, 3, e3794. | 2.5 | 99 |
| 44 | Exploiting ontology graph for predicting sparsely annotated gene function. <i>Bioinformatics</i> , 2015, 31, i357-i364. | 4.1 | 97 |
| 45 | Enhancing Evolutionary Couplings with Deep Convolutional Neural Networks. <i>Cell Systems</i> , 2018, 6, 65-74.e3. | 6.2 | 97 |
| 46 | Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape. <i>Cell Systems</i> , 2019, 8, 483-493.e7. | 6.2 | 95 |
| 47 | Leveraging Uncertainty in Machine Learning Accelerates Biological Discovery and Design. <i>Cell Systems</i> , 2020, 11, 461-477.e9. | 6.2 | 92 |
| 48 | Multimodal profiling of lung granulomas in macaques reveals cellular correlates of tuberculosis control. <i>Immunity</i> , 2022, 55, 827-846.e10. | 14.3 | 92 |
| 49 | BETASCAN: Probable β -amyloids Identified by Pairwise Probabilistic Analysis. <i>PLoS Computational Biology</i> , 2009, 5, e1000333. | 3.2 | 91 |
| 50 | IsoBase: a database of functionally related proteins across PPI networks. <i>Nucleic Acids Research</i> , 2011, 39, D295-D300. | 14.5 | 90 |
| 51 | Methods in Comparative Genomics: Genome Correspondence, Gene Identification and Regulatory Motif Discovery. <i>Journal of Computational Biology</i> , 2004, 11, 319-355. | 1.6 | 88 |
| 52 | Proteomic and Functional Genomic Landscape of Receptor Tyrosine Kinase and Ras to Extracellular Signal-Regulated Kinase Signaling. <i>Science Signaling</i> , 2011, 4, rs10. | 3.6 | 87 |
| 53 | Visualization of clustered protocadherin neuronal self-recognition complexes. <i>Nature</i> , 2019, 569, 280-283. | 27.8 | 86 |
| 54 | Computational Methods for Single-Cell RNA Sequencing. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 339-364. | 6.5 | 81 |

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|----|--|------|-----------|
| 55 | Structures of radial spokes and associated complexes important for ciliary motility. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 29-37. | 8.2 | 81 |
| 56 | Near-Linear Time Construction of Sparse Neighborhood Covers. <i>SIAM Journal on Computing</i> , 1998, 28, 263-277. | 1.0 | 79 |
| 57 | Human airway mast cells proliferate and acquire distinct inflammation-driven phenotypes during type 2 inflammation. <i>Science Immunology</i> , 2021, 6, . | 11.9 | 79 |
| 58 | D-SCRIPT translates genome to phenome with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions. <i>Cell Systems</i> , 2021, 12, 969-982.e6. | 6.2 | 78 |
| 59 | MSARI: Multiple sequence alignments for statistical detection of RNA secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12102-12107. | 7.1 | 77 |
| 60 | HapTree: A Novel Bayesian Framework for Single Individual Polyplotyping Using NGS Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003502. | 3.2 | 75 |
| 61 | Assessing single-cell transcriptomic variability through density-preserving data visualization. <i>Nature Biotechnology</i> , 2021, 39, 765-774. | 17.5 | 74 |
| 62 | Fast and accurate algorithms for protein side-chain packing. <i>Journal of the ACM</i> , 2006, 53, 533-557. | 2.2 | 73 |
| 63 | Conserved piRNA Expression from a Distinct Set of piRNA Cluster Loci in Eutherian Mammals. <i>PLoS Genetics</i> , 2015, 11, e1005652. | 3.5 | 73 |
| 64 | Multicoil2: Predicting Coiled Coils and Their Oligomerization States from Sequence in the Twilight Zone. <i>PLoS ONE</i> , 2011, 6, e23519. | 2.5 | 72 |
| 65 | Identification of protein complexes by integrating multiple alignment of protein interaction networks. <i>Bioinformatics</i> , 2017, 33, 1681-1688. | 4.1 | 72 |
| 66 | A gene expression profile of stem cell pluripotentiality and differentiation is conserved across diverse solid and hematopoietic cancers. <i>Genome Biology</i> , 2012, 13, R71. | 9.6 | 69 |
| 67 | Efficient NC algorithms for set cover with applications to learning and geometry. <i>Journal of Computer and System Sciences</i> , 1994, 49, 454-477. | 1.2 | 68 |
| 68 | Local topology of silica networks. <i>Philosophical Magazine A: Physics of Condensed Matter, Structure, Defects and Mechanical Properties</i> , 1998, 78, 679-711. | 0.6 | 68 |
| 69 | RCK: accurate and efficient inference of sequence- and structure-based protein-RNA binding models from RNAcompete data. <i>Bioinformatics</i> , 2016, 32, i351-i359. | 4.1 | 67 |
| 70 | Allelic decomposition and exact genotyping of highly polymorphic and structurally variant genes. <i>Nature Communications</i> , 2018, 9, 828. | 12.8 | 67 |
| 71 | Simulating $(\log c n)$ -wise independence in NC. <i>Journal of the ACM</i> , 1991, 38, 1026-1046. | 2.2 | 65 |
| 72 | Entropy-Scaling Search of Massive Biological Data. <i>Cell Systems</i> , 2015, 1, 130-140. | 6.2 | 64 |

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|----|---|------|-----------|
| 73 | Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. <i>Nature Communications</i> , 2021, 12, 5910. | 12.8 | 64 |
| 74 | Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks. <i>Lecture Notes in Computer Science</i> , 2015, 9029, 62-64. | 1.3 | 63 |
| 75 | Enabling Privacy-Preserving GWASs in Heterogeneous Human Populations. <i>Cell Systems</i> , 2016, 3, 54-61. | 6.2 | 62 |
| 76 | Reconstructing Roma History from Genome-Wide Data. <i>PLoS ONE</i> , 2013, 8, e58633. | 2.5 | 61 |
| 77 | Improving the Power of GWAS and Avoiding Confounding from Population Stratification with PC-Select. <i>Genetics</i> , 2014, 197, 1045-1049. | 2.9 | 59 |
| 78 | Revealing the spatial distribution of a disease while preserving privacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17608-17613. | 7.1 | 58 |
| 79 | A method for probing the mutational landscape of amyloid structure. <i>Bioinformatics</i> , 2011, 27, i34-i42. | 4.1 | 58 |
| 80 | Quality score compression improves genotyping accuracy. <i>Nature Biotechnology</i> , 2015, 33, 240-243. | 17.5 | 57 |
| 81 | Deep learning guided optimization of human antibody against SARS-CoV-2 variants with broad neutralization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122954119. | 7.1 | 57 |
| 82 | iWRAP: An Interface Threading Approach with Application to Prediction of Cancer-Related Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2011, 405, 1295-1310. | 4.2 | 56 |
| 83 | Computational biology in the 21st century. <i>Communications of the ACM</i> , 2016, 59, 72-80. | 4.5 | 56 |
| 84 | Fast characterization of segmental duplications in genome assemblies. <i>Bioinformatics</i> , 2018, 34, i706-i714. | 4.1 | 55 |
| 85 | Compressive genomics for protein databases. <i>Bioinformatics</i> , 2013, 29, i283-i290. | 4.1 | 53 |
| 86 | Optimizing a global alignment of protein interaction networks. <i>Bioinformatics</i> , 2013, 29, 2765-2773. | 4.1 | 53 |
| 87 | Realizing private and practical pharmacological collaboration. <i>Science</i> , 2018, 362, 347-350. | 12.6 | 52 |
| 88 | Fast genotyping of known SNPs through approximate k -mer matching. <i>Bioinformatics</i> , 2016, 32, i538-i544. | 4.1 | 51 |
| 89 | Levenshtein Distance, Sequence Comparison and Biological Database Search. <i>IEEE Transactions on Information Theory</i> , 2021, 67, 3287-3294. | 2.4 | 51 |
| 90 | Minimizer-space de Bruijn graphs: Whole-genome assembly of long reads in minutes on a personal computer. <i>Cell Systems</i> , 2021, 12, 958-968.e6. | 6.2 | 51 |

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|-----|---|------|-----------|
| 91 | A better performance guarantee for approximate graph coloring. <i>Algorithmica</i> , 1990, 5, 459-466. | 1.3 | 49 |
| 92 | Calibrating the Human Mutation Rate via Ancestral Recombination Density in Diploid Genomes. <i>PLoS Genetics</i> , 2015, 11, e1005550. | 3.5 | 49 |
| 93 | Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. <i>Cell Systems</i> , 2018, 7, 185-191.e4. | 6.2 | 49 |
| 94 | Integrative analysis of genetic data sets reveals a shared innate immune component in autism spectrum disorder and its co-morbidities. <i>Genome Biology</i> , 2016, 17, 228. | 8.8 | 46 |
| 95 | Fast Distributed Network Decompositions and Covers. <i>Journal of Parallel and Distributed Computing</i> , 1996, 39, 105-114. | 4.1 | 45 |
| 96 | Emerging technologies towards enhancing privacy in genomic data sharing. <i>Genome Biology</i> , 2019, 20, 128. | 8.8 | 45 |
| 97 | “Local Rules” Theory Applied to Polyomavirus Polymorphic Capsid Assemblies. <i>Virology</i> , 2000, 268, 461-470. | 2.4 | 44 |
| 98 | A computational framework for boosting confidence in high-throughput protein-protein interaction datasets. <i>Genome Biology</i> , 2012, 13, R76. | 9.6 | 44 |
| 99 | Realizing privacy preserving genome-wide association studies. <i>Bioinformatics</i> , 2016, 32, 1293-1300. | 4.1 | 44 |
| 100 | Efficient Algorithms for Probing the RNA Mutation Landscape. <i>PLoS Computational Biology</i> , 2008, 4, e1000124. | 3.2 | 38 |
| 101 | Predicting the Beta-Helix Fold from Protein Sequence Data. <i>Journal of Computational Biology</i> , 2002, 9, 261-276. | 1.6 | 37 |
| 102 | Structure-based prediction reveals capping motifs that inhibit \hat{A} -helix aggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11099-11104. | 7.1 | 37 |
| 103 | An exact arithmetic toolbox for a consistent and reproducible structural analysis of metabolic network models. <i>Nature Communications</i> , 2014, 5, 4893. | 12.8 | 37 |
| 104 | Predicting transmembrane \hat{I}^2 -barrels and interstrand residue interactions from sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 61-74. | 2.6 | 36 |
| 105 | Large mosaic copy number variations confer autism risk. <i>Nature Neuroscience</i> , 2021, 24, 197-203. | 14.8 | 36 |
| 106 | Making sense out of massive data by going beyond differential expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5594-5599. | 7.1 | 35 |
| 107 | transFold: a web server for predicting the structure and residue contacts of transmembrane beta-barrels. <i>Nucleic Acids Research</i> , 2006, 34, W189-W193. | 14.5 | 34 |
| 108 | Compressive mapping for next-generation sequencing. <i>Nature Biotechnology</i> , 2016, 34, 374-376. | 17.5 | 33 |

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|-----|---|------|-----------|
| 109 | A global sampling approach to designing and reengineering RNA secondary structures. <i>Nucleic Acids Research</i> , 2012, 40, 10041-10052. | 14.5 | 32 |
| 110 | The Fourth Moment Method. <i>SIAM Journal on Computing</i> , 1997, 26, 1188-1207. | 1.0 | 30 |
| 111 | An Iterative Method for Improved Protein Structural Motif Recognition. <i>Journal of Computational Biology</i> , 1997, 4, 261-273. | 1.6 | 29 |
| 112 | Algorithms for Protein Structural Motif Recognition. <i>Journal of Computational Biology</i> , 1995, 2, 125-138. | 1.6 | 28 |
| 113 | Topsy-Turvy: integrating a global view into sequence-based PPI prediction. <i>Bioinformatics</i> , 2022, 38, i264-i272. | 4.1 | 28 |
| 114 | Markov random fields reveal an N-terminal double beta-propeller motif as part of a bacterial hybrid two-component sensor system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4069-4074. | 7.1 | 27 |
| 115 | Modeling ensembles of transmembrane β -barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1097-1112. | 2.6 | 26 |
| 116 | Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690. | 6.2 | 26 |
| 117 | Sequencing a Genome by Walking with Clone-End Sequences: A Mathematical Analysis. <i>Genome Research</i> , 1999, 9, 1163-1174. | 5.5 | 25 |
| 118 | LOCAL OPTIMIZATION FOR GLOBAL ALIGNMENT OF PROTEIN INTERACTION NETWORKS. , 2009, , 123-132. | | 25 |
| 119 | Fold recognition and accurate sequence-structure alignment of sequences directing β -sheet proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 976-985. | 2.6 | 24 |
| 120 | Optimal contact map alignment of protein-protein interfaces. <i>Bioinformatics</i> , 2008, 24, 2324-2328. | 4.1 | 24 |
| 121 | An engineered protein-phosphorylation toggle network with implications for endogenous network discovery. <i>Science</i> , 2021, 373, . | 12.6 | 24 |
| 122 | Struct2net: integrating structure into protein-protein interaction prediction. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 403-14. | 0.7 | 24 |
| 123 | A Dictionary-Based Approach for Gene Annotation. <i>Journal of Computational Biology</i> , 1999, 6, 419-430. | 1.6 | 23 |
| 124 | GLOBAL ALIGNMENT OF MULTIPLE PROTEIN INTERACTION NETWORKS. , 2007, , . | | 23 |
| 125 | Genome-wide mapping of somatic mutation rates uncovers drivers of cancer. <i>Nature Biotechnology</i> , 2022, 40, 1634-1643. | 17.5 | 23 |
| 126 | Schema: metric learning enables interpretable synthesis of heterogeneous single-cell modalities. <i>Genome Biology</i> , 2021, 22, 131. | 8.8 | 22 |

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|-----|--|------|-----------|
| 127 | Metagenomic binning through low-density hashing. <i>Bioinformatics</i> , 2019, 35, 219-226. | 4.1 | 21 |
| 128 | CryoDRGN2: Ab initio neural reconstruction of 3D protein structures from real cryo-EM images. , 2021, , . | | 21 |
| 129 | Traversing the k-mer Landscape of NGS Read Datasets for Quality Score Sparsification. <i>Lecture Notes in Computer Science</i> , 2014, 8394, 385-399. | 1.3 | 20 |
| 130 | RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. <i>Nucleic Acids Research</i> , 2009, 37, W281-W286. | 14.5 | 19 |
| 131 | STITCHER: Dynamic assembly of likely amyloid and prion β -structures from secondary structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 410-420. | 2.6 | 19 |
| 132 | Tight Bounds for the Maximum Acyclic Subgraph Problem. <i>Journal of Algorithms</i> , 1997, 25, 1-18. | 0.9 | 18 |
| 133 | Statistical Binning for Barcoded Reads Improves Downstream Analyses. <i>Cell Systems</i> , 2018, 7, 219-226.e5. | 6.2 | 18 |
| 134 | STRUCT2NET: INTEGRATING STRUCTURE INTO PROTEIN-PROTEIN INTERACTION PREDICTION. , 2005, , . | | 16 |
| 135 | Phenotype Prediction Using Regularized Regression on Genetic Data in the DREAM5 Systems Genetics B Challenge. <i>PLoS ONE</i> , 2011, 6, e29095. | 2.5 | 16 |
| 136 | A Randomized Parallel Algorithm for Efficiently Finding Near-Optimal Universal Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2020, , 37-53. | 1.3 | 16 |
| 137 | Topological modeling of cascade amorphization in network structures using local rules. <i>Materials Science & Engineering A: Structural Materials: Properties, Microstructure and Processing</i> , 1998, 253, 16-29. | 5.6 | 14 |
| 138 | TOPAZ: A Positive-Unlabeled Convolutional Neural Network CryoEM Particle Picker that can Pick Any Size and Shape Particle. <i>Microscopy and Microanalysis</i> , 2019, 25, 986-987. | 0.4 | 14 |
| 139 | Improved haplotype inference by exploiting long-range linking and allelic imbalance in RNA-seq datasets. <i>Nature Communications</i> , 2020, 11, 4662. | 12.8 | 14 |
| 140 | Hopper: a mathematically optimal algorithm for sketching biological data. <i>Bioinformatics</i> , 2020, 36, i236-i241. | 4.1 | 14 |
| 141 | Privacy-Preserving Biomedical Database Queries with Optimal Privacy-Utility Trade-Offs. <i>Cell Systems</i> , 2020, 10, 408-416.e9. | 6.2 | 14 |
| 142 | Carnelian uncovers hidden functional patterns across diverse study populations from whole metagenome sequencing reads. <i>Genome Biology</i> , 2020, 21, 47. | 8.8 | 14 |
| 143 | An Evaluation Framework for Lossy Compression of Genome Sequencing Quality Values. , 2016, 2016, 221-230. | | 13 |
| 144 | Reconstructing Causal Biological Networks through Active Learning. <i>PLoS ONE</i> , 2016, 11, e0150611. | 2.5 | 13 |

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|-----|--|------|-----------|
| 145 | Seq: a high-performance language for bioinformatics. , 2019, 3, 1-29. | | 12 |
| 146 | Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. , 2018, 10812, 245-247. | | 12 |
| 147 | Low-diameter graph decomposition is in NC. Random Structures and Algorithms, 1994, 5, 441-452. | 1.1 | 9 |
| 148 | Reconstruction of phyletic trees by global alignment of multiple metabolic networks. BMC Bioinformatics, 2013, 14, S12. | 2.6 | 9 |
| 149 | Discovering What Dimensionality Reduction Really Tells Us About RNA-Seq Data. Journal of Computational Biology, 2015, 22, 715-728. | 1.6 | 9 |
| 150 | A Python-based programming language for high-performance computational genomics. Nature Biotechnology, 2021, 39, 1062-1064. | 17.5 | 9 |
| 151 | Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils. Journal of Computational Biology, 2005, 12, 777-795. | 1.6 | 8 |
| 152 | LTHREADER: Prediction of extracellular ligand-receptor interactions in cytokines using localized threading. Protein Science, 2008, 17, 279-292. | 7.6 | 8 |
| 153 | One Size Doesn't Fit All: Measuring Individual Privacy in Aggregate Genomic Data. , 2015, 2015, 41-49. | | 8 |
| 154 | HapTree-X: An Integrative Bayesian Framework for Haplotype Reconstruction from Transcriptome and Genome Sequencing Data. Lecture Notes in Computer Science, 2015, 9029, 28-29. | 1.3 | 8 |
| 155 | An iterative method for improved protein structural motif recognition. , 1997, , . | | 7 |
| 156 | On the Structure of the Scaffolding Core of Bacteriophage T4 and Its Role in Head Length Determination. Journal of Structural Biology, 1998, 121, 285-294. | 2.8 | 7 |
| 157 | Predicting the $\hat{\alpha}$ -helix fold from protein sequence data. , 2001, , . | | 7 |
| 158 | Finding RNA structure in the unstructured RBPome. BMC Genomics, 2018, 19, 154. | 2.8 | 7 |
| 159 | HIV infection drives interferon signaling within intestinal SARS-CoV-2 target cells. JCI Insight, 2021, 6, . | 5.0 | 7 |
| 160 | Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models. Journal of Computational Biology, 2011, 18, 1635-1647. | 1.6 | 6 |
| 161 | Meta-analysis of <i>Caenorhabditis elegans</i> single-cell developmental data reveals multi-frequency oscillation in gene activation. Bioinformatics, 2020, 36, 4047-4057. | 4.1 | 6 |
| 162 | Efficient Design of Compact Unstructured RNA Libraries Covering All <i>k</i> -mers. Journal of Computational Biology, 2016, 23, 67-79. | 1.6 | 5 |

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|-----|---|-----|-----------|
| 163 | CHAINTWEAK: SAMPLING FROM THE NEIGHBOURHOOD OF A PROTEIN CONFORMATION. , 2004, , . | | 5 |
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