

Richard A Bonneau

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

22,702
citations

10389

72
h-index

10734

138
g-index

215
all docs

215
docs citations

215
times ranked

32575
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Short of Suspension: How Suspension Warnings Can Reduce Hate Speech on Twitter. Perspectives on Politics, 2023, 21, 651-663. | 0.3 | 3 |
| 2 | SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. Science of the Total Environment, 2022, 805, 150121. | 8.0 | 192 |
| 3 | Whatâ€™s Not to Like? Facebook Page Likes Reveal Limited Polarization in Lifestyle Preferences. Political Communication, 2022, 39, 311-338. | 3.9 | 9 |
| 4 | High-performance single-cell gene regulatory network inference at scale: the Inferelator 3.0. Bioinformatics, 2022, 38, 2519-2528. | 4.1 | 32 |
| 5 | Engineered protein-iron oxide hybrid biomaterial for MRI-traceable drug encapsulation. Molecular Systems Design and Engineering, 2022, 7, 915-932. | 3.4 | 4 |
| 6 | News credibility labels have limited average effects on news diet quality and fail to reduce misperceptions. Science Advances, 2022, 8, eabl3844. | 10.3 | 24 |
| 7 | Evaluating the Conformations and Dynamics of Peptoid Macrocycles. Journal of Physical Chemistry B, 2022, 126, 5161-5174. | 2.6 | 5 |
| 8 | Lower Airway Dysbiosis Affects Lung Cancer Progression. Cancer Discovery, 2021, 11, 293-307. | 9.4 | 139 |
| 9 | Reply to: Examining microbe-metabolite correlations by linear methods. Nature Methods, 2021, 18, 40-41. | 19.0 | 6 |
| 10 | Computationally designed peptide macrocycle inhibitors of New Delhi metallo- β -lactamase 1. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 41 |
| 11 | Masked graph modeling for molecule generation. Nature Communications, 2021, 12, 3156. | 12.8 | 32 |
| 12 | Structure-based protein function prediction using graph convolutional networks. Nature Communications, 2021, 12, 3168. | 12.8 | 300 |
| 13 | Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. PLoS Computational Biology, 2021, 17, e1009056. | 3.2 | 2 |
| 14 | A convolutional neural network for common coordinate registration of high-resolution histology images. Bioinformatics, 2021, 37, 4216-4226. | 4.1 | 6 |
| 15 | GABA-receptive microglia selectively sculpt developing inhibitory circuits. Cell, 2021, 184, 4048-4063.e32. | 28.9 | 142 |
| 16 | Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. Cell Host and Microbe, 2021, 29, 1249-1265.e9. | 11.0 | 32 |
| 17 | Genetic and epigenetic coordination of cortical interneuron development. Nature, 2021, 597, 693-697. | 27.8 | 56 |
| 18 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. PLoS Computational Biology, 2021, 17, e1008569. | 3.2 | 19 |

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|----|--|------|-----------|
| 19 | Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947. | 12.8 | 16 |
| 20 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 21 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 22 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 23 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 24 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 25 | Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. , 2021, 17, e1008569. | | 0 |
| 26 | CDK7 Inhibition Potentiates Genome Instability Triggering Anti-tumor Immunity in Small Cell Lung Cancer. <i>Cancer Cell</i> , 2020, 37, 37-54.e9. | 16.8 | 138 |
| 27 | Alternative Activation of Macrophages Is Accompanied by Chromatin Remodeling Associated with Lineage-Dependent DNA Shape Features Flanking PU.1 Motifs. <i>Journal of Immunology</i> , 2020, 205, 1070-1083. | 0.8 | 7 |
| 28 | Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020, 16, e1007507. | 3.2 | 27 |
| 29 | Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>ELife</i> , 2020, 9, . | 6.0 | 116 |
| 30 | Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680. | 19.0 | 513 |
| 31 | Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. <i>MSystems</i> , 2020, 5, . | 3.8 | 14 |
| 32 | Characterization of antibiotic resistance and host-microbiome interactions in the human upper respiratory tract during influenza infection. <i>Microbiome</i> , 2020, 8, 39. | 11.1 | 41 |
| 33 | Characterizing chromatin landscape from aggregate and single-cell genomic assays using flexible duration modeling. <i>Nature Communications</i> , 2020, 11, 747. | 12.8 | 11 |
| 34 | A Comprehensive Map of the Monocyte-Derived Dendritic Cell Transcriptional Network Engaged upon Innate Sensing of HIV. <i>Cell Reports</i> , 2020, 30, 914-931.e9. | 6.4 | 15 |
| 35 | Classification of the Molecular Defects Associated with Pathogenic Variants of the <i>SLC6A8</i> Creatine Transporter. <i>Biochemistry</i> , 2020, 59, 1367-1377. | 2.5 | 17 |
| 36 | OutPredict: multiple datasets can improve prediction of expression and inference of causality. <i>Scientific Reports</i> , 2020, 10, 6804. | 3.3 | 13 |

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|----|---|------|-----------|
| 37 | Political psycholinguistics: A comprehensive analysis of the language habits of liberal and conservative social media users.. <i>Journal of Personality and Social Psychology</i> , 2020, 118, 805-834. | 2.8 | 39 |
| 38 | Shrinkage improves estimation of microbial associations under different normalization methods. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa100. | 3.2 | 22 |
| 39 | Who Leads? Who Follows? Measuring Issue Attention and Agenda Setting by Legislators and the Mass Public Using Social Media Data. <i>American Political Science Review</i> , 2019, 113, 883-901. | 3.7 | 209 |
| 40 | Thermoresponsive Protein-Engineered Coiled-Coil Hydrogel for Sustained Small Molecule Release. <i>Biomacromolecules</i> , 2019, 20, 3340-3351. | 5.4 | 45 |
| 41 | Characterization of Transcriptional Regulatory Networks that Promote and Restrict Identities and Functions of Intestinal Innate Lymphoid Cells. <i>Immunity</i> , 2019, 51, 185-197.e6. | 14.3 | 72 |
| 42 | The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7. | 11.0 | 274 |
| 43 | Learning representations of microbeâ€“metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314. | 19.0 | 184 |
| 44 | Distinct Polysaccharide Utilization Profiles of Human Intestinal <i>Prevotella copri</i> Isolates. <i>Cell Host and Microbe</i> , 2019, 26, 680-690.e5. | 11.0 | 115 |
| 45 | Pre-detection history of extensively drug-resistant tuberculosis in KwaZulu-Natal, South Africa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23284-23291. | 7.1 | 23 |
| 46 | High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990. | 19.0 | 708 |
| 47 | Integrative Protein Modeling in RosettaNMR from Sparse Paramagnetic Restraints. <i>Structure</i> , 2019, 27, 1721-1734.e5. | 3.3 | 25 |
| 48 | Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. <i>Genome Research</i> , 2019, 29, 449-463. | 5.5 | 87 |
| 49 | Multi-study inference of regulatory networks for more accurate models of gene regulation. <i>PLoS Computational Biology</i> , 2019, 15, e1006591. | 3.2 | 67 |
| 50 | For Whom the Bot Tolls: A Neural Networks Approach to Measuring Political Orientation of Twitter Bots in Russia. <i>SAGE Open</i> , 2019, 9, 215824401982771. | 1.7 | 28 |
| 51 | Spatiotemporal dynamics of molecular pathology in amyotrophic lateral sclerosis. <i>Science</i> , 2019, 364, 89-93. | 12.6 | 297 |
| 52 | The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244. | 8.8 | 261 |
| 53 | NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. <i>Nature Communications</i> , 2019, 10, 4843. | 12.8 | 57 |
| 54 | Towards region-specific propagation of protein functions. <i>Bioinformatics</i> , 2019, 35, 1737-1744. | 4.1 | 7 |

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|----|---|------|-----------|
| 55 | Elites Tweet to Get Feet Off the Streets: Measuring Regime Social Media Strategies During Protest. <i>Political Science Research and Methods</i> , 2019, 7, 815-834. | 2.3 | 36 |
| 56 | Condition-Specific Modeling of Biophysical Parameters Advances Inference of Regulatory Networks. <i>Cell Reports</i> , 2018, 23, 376-388. | 6.4 | 23 |
| 57 | How Social Media Facilitates Political Protest: Information, Motivation, and Social Networks. <i>Political Psychology</i> , 2018, 39, 85-118. | 3.6 | 223 |
| 58 | Temporal probabilistic modeling of bacterial compositions derived from 16S rRNA sequencing. <i>Bioinformatics</i> , 2018, 34, 372-380. | 4.1 | 42 |
| 59 | c-MAF-dependent regulatory T cells mediate immunological tolerance to a gut pathobiont. <i>Nature</i> , 2018, 554, 373-377. | 27.8 | 379 |
| 60 | Statistically derived asymmetric membrane potentials from $\hat{1}\pm$ -helical and $\hat{1}^2$ -barrel membrane proteins. <i>Scientific Reports</i> , 2018, 8, 4446. | 3.3 | 12 |
| 61 | Why are there hotspot mutations in the TP53 gene in human cancers?. <i>Cell Death and Differentiation</i> , 2018, 25, 154-160. | 11.2 | 393 |
| 62 | A Novel Domain Assembly Routine for Creating Full-Length Models of Membrane Proteins from Known Domain Structures. <i>Biochemistry</i> , 2018, 57, 1939-1944. | 2.5 | 10 |
| 63 | Computational-guided determination of the functional role of 447-52D long CDRH3. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 479-487. | 2.1 | 0 |
| 64 | An adaptive geometric search algorithm for macromolecular scaffold selection. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 345-354. | 2.1 | 0 |
| 65 | Analysis of 3D genomic interactions identifies candidate host genes that transposable elements potentially regulate. <i>Genome Biology</i> , 2018, 19, 216. | 8.8 | 38 |
| 66 | Design of Peptoid-peptide Macrocyces to Inhibit the $\hat{1}^2$ -catenin TCF Interaction in Prostate Cancer. <i>Nature Communications</i> , 2018, 9, 4396. | 12.8 | 66 |
| 67 | deepNF: deep network fusion for protein function prediction. <i>Bioinformatics</i> , 2018, 34, 3873-3881. | 4.1 | 155 |
| 68 | Generative Models for Quantification of DNA Modifications. <i>Methods in Molecular Biology</i> , 2018, 1807, 37-50. | 0.9 | 1 |
| 69 | Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , 2018, 6, 12. | 11.1 | 146 |
| 70 | Airway Microbiota Is Associated with Upregulation of the PI3K Pathway in Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1188-1198. | 5.6 | 232 |
| 71 | Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. <i>Nature Immunology</i> , 2017, 18, 412-421. | 14.5 | 103 |
| 72 | The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3031-3048. | 5.3 | 1,032 |

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|----|--|------|-----------|
| 73 | Mocap: large-scale inference of transcription factor binding sites from chromatin accessibility. <i>Nucleic Acids Research</i> , 2017, 45, 4315-4329. | 14.5 | 30 |
| 74 | Low-Grade Astrocytoma Mutations in IDH1, P53, and ATRX Cooperate to Block Differentiation of Human Neural Stem Cells via Repression of SOX2. <i>Cell Reports</i> , 2017, 21, 1267-1280. | 6.4 | 95 |
| 75 | Rotamer Libraries for the High-Resolution Design of Î ² -Amino Acid Foldamers. <i>Structure</i> , 2017, 25, 1771-1780.e3. | 3.3 | 13 |
| 76 | A single early-in-life macrolide course has lasting effects on murine microbial network topology and immunity. <i>Nature Communications</i> , 2017, 8, 518. | 12.8 | 119 |
| 77 | Discovery of peptide ligands through docking and virtual screening at nicotinic acetylcholine receptor homology models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8100-E8109. | 7.1 | 51 |
| 78 | Lung microbiome and host immune tone in subjects with idiopathic pulmonary fibrosis treated with inhaled interferon-Î ³ . <i>ERJ Open Research</i> , 2017, 3, 00008-2017. | 2.6 | 42 |
| 79 | Integrated Analysis of Biopsies from Inflammatory Bowel Disease Patients Identifies SAA1 as a Link Between Mucosal Microbes with TH17 and TH22 Cells. <i>Inflammatory Bowel Diseases</i> , 2017, 23, 1544-1554. | 1.9 | 31 |
| 80 | Efficient Dual siRNA and Drug Delivery Using Engineered Lipoproteoplexes. <i>Biomacromolecules</i> , 2017, 18, 2688-2698. | 5.4 | 14 |
| 81 | Computing structure-based lipid accessibility of membrane proteins with mp_lipid_acc in RosettaMP. <i>BMC Bioinformatics</i> , 2017, 18, 115. | 2.6 | 26 |
| 82 | Detecting Bots on Russian Political Twitter. <i>Big Data</i> , 2017, 5, 310-324. | 3.4 | 107 |
| 83 | Modeling and Design of Peptidomimetics to Modulate Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2017, 1561, 291-307. | 0.9 | 4 |
| 84 | Identifying direct contacts between protein complex subunits from their conditional dependence in proteomics datasets. <i>PLoS Computational Biology</i> , 2017, 13, e1005625. | 3.2 | 22 |
| 85 | Biophysically Motivated Regulatory Network Inference: Progress and Prospects. <i>Human Heredity</i> , 2016, 81, 62-77. | 0.8 | 29 |
| 86 | 4C-ker: A Method to Reproducibly Identify Genome-Wide Interactions Captured by 4C-Seq Experiments. <i>PLoS Computational Biology</i> , 2016, 12, e1004780. | 3.2 | 84 |
| 87 | Fused Regression for Multi-source Gene Regulatory Network Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1005157. | 3.2 | 40 |
| 88 | Toward rational thermostabilization of <i>Aspergillus oryzae</i> cutinase: Insights into catalytic and structural stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 60-72. | 2.6 | 42 |
| 89 | Helminth infection promotes colonization resistance via type 2 immunity. <i>Science</i> , 2016, 352, 608-612. | 12.6 | 347 |
| 90 | Antibiotic perturbation of the murine gut microbiome enhances the adiposity, insulin resistance, and liver disease associated with high-fat diet. <i>Genome Medicine</i> , 2016, 8, 48. | 8.2 | 153 |

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|-----|---|------|-----------|
| 91 | An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184. | 8.8 | 308 |
| 92 | A Damage-Independent Role for 53BP1 that Impacts Break Order and Igh Architecture during Class Switch Recombination. <i>Cell Reports</i> , 2016, 16, 48-55. | 6.4 | 29 |
| 93 | Side-Chain Conformational Preferences Govern Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2016, 138, 10386-10389. | 13.7 | 36 |
| 94 | PPII Helical Peptidomimetics Templated by Cation- π Interactions. <i>ChemBioChem</i> , 2016, 17, 1824-1828. | 2.6 | 10 |
| 95 | Accurate de novo design of hyperstable constrained peptides. <i>Nature</i> , 2016, 538, 329-335. | 27.8 | 327 |
| 96 | EGRINs (Environmental Gene Regulatory Influence Networks) in Rice That Function in the Response to Water Deficit, High Temperature, and Agricultural Environments. <i>Plant Cell</i> , 2016, 28, 2365-2384. | 6.6 | 139 |
| 97 | Racemization barriers of atropisomeric 3,3'-bipyrroles: an experimental study with theoretical verification. <i>RSC Advances</i> , 2016, 6, 71245-71249. | 3.6 | 3 |
| 98 | Identification of multi-loci hubs from 4C-seq demonstrates the functional importance of simultaneous interactions. <i>Nucleic Acids Research</i> , 2016, 44, 8714-8725. | 14.5 | 47 |
| 99 | Active and Inactive Enhancers Cooperate to Exert Localized and Long-Range Control of Gene Regulation. <i>Cell Reports</i> , 2016, 15, 2159-2169. | 6.4 | 35 |
| 100 | A Miniature Protein Stabilized by a Cation- π Interaction Network. <i>Journal of the American Chemical Society</i> , 2016, 138, 1543-1550. | 13.7 | 45 |
| 101 | Robust classification of protein variation using structural modelling and large-scale data integration. <i>Nucleic Acids Research</i> , 2016, 44, 2501-2513. | 14.5 | 52 |
| 102 | Mediator facilitates transcriptional activation and dynamic long-range contacts at the IgH locus during class switch recombination. <i>Journal of Experimental Medicine</i> , 2016, 213, 303-312. | 8.5 | 37 |
| 103 | An experimentally supported model of the <i>Bacillus subtilis</i> global transcriptional regulatory network. <i>Molecular Systems Biology</i> , 2015, 11, 839. | 7.2 | 186 |
| 104 | Multiple abiotic stimuli are integrated in the regulation of rice gene expression under field conditions. <i>ELife</i> , 2015, 4, . | 6.0 | 43 |
| 105 | Inter-species pathway perturbation prediction via data-driven detection of functional homology. <i>Bioinformatics</i> , 2015, 31, 501-508. | 4.1 | 6 |
| 106 | DDX5 and its associated lncRNA Rmrp modulate TH17 cell effector functions. <i>Nature</i> , 2015, 528, 517-522. | 27.8 | 154 |
| 107 | Breaking TADs: insights into hierarchical genome organization. <i>Epigenomics</i> , 2015, 7, 523-526. | 2.1 | 50 |
| 108 | Sparse and Compositionally Robust Inference of Microbial Ecological Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004226. | 3.2 | 1,089 |

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|-----|--|------|-----------|
| 109 | An IL-23R/IL-22 Circuit Regulates Epithelial Serum Amyloid A to Promote Local Effector Th17 Responses. <i>Cell</i> , 2015, 163, 381-393. | 28.9 | 474 |
| 110 | Cohesin loss alters adult hematopoietic stem cell homeostasis, leading to myeloproliferative neoplasms. <i>Journal of Experimental Medicine</i> , 2015, 212, 1833-1850. | 8.5 | 145 |
| 111 | Tweeting From Left to Right. <i>Psychological Science</i> , 2015, 26, 1531-1542. | 3.3 | 925 |
| 112 | The Critical Periphery in the Growth of Social Protests. <i>PLoS ONE</i> , 2015, 10, e0143611. | 2.5 | 237 |
| 113 | ICOS-based chimeric antigen receptors program bipolar TH17/TH1 cells. <i>Blood</i> , 2014, 124, 1070-1080. | 1.4 | 268 |
| 114 | Helminth Colonization Is Associated with Increased Diversity of the Gut Microbiota. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2880. | 3.0 | 353 |
| 115 | Negative Example Selection for Protein Function Prediction: The NoGO Database. <i>PLoS Computational Biology</i> , 2014, 10, e1003644. | 3.2 | 32 |
| 116 | Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014, 20, 1903-1912. | 4.4 | 11 |
| 117 | Collier/OLF/EBF-Dependent Transcriptional Dynamics Control Pharyngeal Muscle Specification from Primed Cardiopharyngeal Progenitors. <i>Developmental Cell</i> , 2014, 29, 263-276. | 7.0 | 96 |
| 118 | FIREWACH: high-throughput functional detection of transcriptional regulatory modules in mammalian cells. <i>Nature Methods</i> , 2014, 11, 559-565. | 19.0 | 95 |
| 119 | Rational Design of Topographical Helix Mimics as Potent Inhibitors of Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2014, 136, 7877-7888. | 13.7 | 116 |
| 120 | Conformational preferences of peptide-peptoid hybrid oligomers. <i>Biopolymers</i> , 2014, 102, 369-378. | 2.4 | 9 |
| 121 | One third of dynamic protein expression profiles can be predicted by a simple rate equation. <i>Molecular BioSystems</i> , 2014, 10, 2850-2862. | 2.9 | 25 |
| 122 | Engineered Coiled-Coil Protein Microfibers. <i>Biomacromolecules</i> , 2014, 15, 3503-3510. | 5.4 | 70 |
| 123 | CX3CR1+ mononuclear phagocytes support colitis-associated innate lymphoid cell production of IL-22. <i>Journal of Experimental Medicine</i> , 2014, 211, 1571-1583. | 8.5 | 320 |
| 124 | A Rotamer Library to Enable Modeling and Design of Peptoid Foldamers. <i>Journal of the American Chemical Society</i> , 2014, 136, 8772-8782. | 13.7 | 40 |
| 125 | <i>Bacillus subtilis</i> Systems Biology: Applications of -Omics Techniques to the Study of Endospore Formation. <i>Microbiology Spectrum</i> , 2014, 2, . | 3.0 | 17 |
| 126 | Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. <i>Bioinformatics</i> , 2013, 29, 1060-1067. | 4.1 | 138 |

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|-----|---|------|-----------|
| 127 | Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20â€“27. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2201-2209. | 2.6 | 22 |
| 128 | A physical sciences network characterization of non-tumorigenic and metastatic cells. <i>Scientific Reports</i> , 2013, 3, 1449. | 3.3 | 146 |
| 129 | sbv IMPROVER Diagnostic Signature Challenge. <i>Systems Biomedicine (Austin, Tex)</i> , 2013, 1, 208-216. | 0.7 | 2 |
| 130 | Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. <i>PLoS ONE</i> , 2013, 8, e67051. | 2.5 | 59 |
| 131 | Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). <i>PLoS ONE</i> , 2013, 8, e63906. | 2.5 | 348 |
| 132 | A Validated Regulatory Network for Th17 Cell Specification. <i>Cell</i> , 2012, 151, 289-303. | 28.9 | 1,010 |
| 133 | Androgen Receptor Antagonism by Divalent Ethisterone Conjugates in Castrate-Resistant Prostate Cancer Cells. <i>ACS Chemical Biology</i> , 2012, 7, 1693-1701. | 3.4 | 20 |
| 134 | De novo structure prediction and experimental characterization of folded peptoid oligomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14320-14325. | 7.1 | 88 |
| 135 | Dynamic MicroRNA Gene Transcription and Processing during T Cell Development. <i>Journal of Immunology</i> , 2012, 188, 3257-3267. | 0.8 | 80 |
| 136 | The mRNA-Bound Proteome and Its Global Occupancy Profile on Protein-Coding Transcripts. <i>Molecular Cell</i> , 2012, 46, 674-690. | 9.7 | 1,077 |
| 137 | Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements. <i>Methods in Cell Biology</i> , 2012, 110, 19-56. | 1.1 | 17 |
| 138 | Incorporation of Noncanonical Amino Acids into Rosetta and Use in Computational Protein-Peptide Interface Design. <i>PLoS ONE</i> , 2012, 7, e32637. | 2.5 | 98 |
| 139 | SlrA/SinR/SlrR inhibits motility gene expression upstream of a hypersensitive and hysteretic switch at the level of σ^D in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2012, 83, 1210-1228. | 2.5 | 49 |
| 140 | Peptoid Atropisomers. <i>Journal of the American Chemical Society</i> , 2011, 133, 10910-10919. | 13.7 | 61 |
| 141 | Rational Design of Temperature-Sensitive Alleles Using Computational Structure Prediction. <i>PLoS ONE</i> , 2011, 6, e23947. | 2.5 | 17 |
| 142 | MODELING HOST-PATHOGEN INTERACTIONS: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS FOR INFECTIOUS DISEASE RESEARCH. , 2011, , . | | 0 |
| 143 | Comparative Microbial Modules Resource: Generation and Visualization of Multi-species Biclusters. <i>PLoS Computational Biology</i> , 2011, 7, e1002228. | 3.2 | 7 |
| 144 | The 2010 Rosetta Developers Meeting: Macromolecular Prediction and Design Meets Reproducible Publishing. <i>PLoS ONE</i> , 2011, 6, e22431. | 2.5 | 7 |

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|-----|--|------|-----------|
| 145 | DREAM3: Network Inference Using Dynamic Context Likelihood of Relatedness and the Inferelator. PLoS ONE, 2010, 5, e9803. | 2.5 | 95 |
| 146 | DREAM4: Combining Genetic and Dynamic Information to Identify Biological Networks and Dynamical Models. PLoS ONE, 2010, 5, e13397. | 2.5 | 201 |
| 147 | Innate immune detection of the type III secretion apparatus through the NLRC4 inflammasome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3076-3080. | 7.1 | 680 |
| 148 | Multi-species integrative biclustering. Genome Biology, 2010, 11, R96. | 9.6 | 38 |
| 149 | Diurnally Entrained Anticipatory Behavior in Archaea. PLoS ONE, 2009, 4, e5485. | 2.5 | 59 |
| 150 | The inferelator 2.0: A scalable framework for reconstruction of dynamic regulatory network models. , 2009, 2009, 5448-51. | | 38 |
| 151 | The coat morphogenetic protein SpoVID is necessary for spore encasement in <i>Bacillus subtilis</i> . Molecular Microbiology, 2009, 74, 634-649. | 2.5 | 64 |
| 152 | A Preliminary Survey of the Peptoid Folding Landscape. Journal of the American Chemical Society, 2009, 131, 16798-16807. | 13.7 | 123 |
| 153 | Learning Global Models of Transcriptional Regulatory Networks from Data. Methods in Molecular Biology, 2009, 541, 181-210. | 0.9 | 12 |
| 154 | Learning biological networks: from modules to dynamics. Nature Chemical Biology, 2008, 4, 658-664. | 8.0 | 117 |
| 155 | Oligo(<i>N</i> -aryl glycines): A New Twist on Structured Peptoids. Journal of the American Chemical Society, 2008, 130, 16622-16632. | 13.7 | 186 |
| 156 | A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. Cell, 2008, 134, 534-545. | 28.9 | 196 |
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