

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	Sparse and Compositionally Robust Inference of Microbial Ecological Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004226.	3.2	1,089
2	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
3	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
4	A Validated Regulatory Network for Th17 Cell Specification. <i>Cell</i> , 2012, 151, 289-303.	28.9	1,010
5	Tweeting From Left to Right. <i>Psychological Science</i> , 2015, 26, 1531-1542.	3.3	925
6	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990.	19.0	708
7	Innate immune detection of the type III secretion apparatus through the NLRC4 inflammasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3076-3080.	7.1	680
8	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
9	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
10	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. <i>Genome Biology</i> , 2006, 7, R36.	9.6	456
11	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
12	c-MAF-dependent regulatory T cells mediate immunological tolerance to a gut pathobiont. <i>Nature</i> , 2018, 554, 373-377.	27.8	379
13	Helminth Colonization Is Associated with Increased Diversity of the Gut Microbiota. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2880.	3.0	353
14	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). <i>PLoS ONE</i> , 2013, 8, e63906.	2.5	348
15	Helminth infection promotes colonization resistance via type 2 immunity. <i>Science</i> , 2016, 352, 608-612.	12.6	347
16	Accurate de novo design of hyperstable constrained peptides. <i>Nature</i> , 2016, 538, 329-335.	27.8	327
17	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
18	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308

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19	Structure-based protein function prediction using graph convolutional networks. <i>Nature Communications</i> , 2021, 12, 3168.	12.8	300
20	Spatiotemporal dynamics of molecular pathology in amyotrophic lateral sclerosis. <i>Science</i> , 2019, 364, 89-93.	12.6	297
21	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. <i>Cell</i> , 2007, 131, 1354-1365.	28.9	284
22	Ab Initio Protein Structure Prediction: Progress and Prospects. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001, 30, 173-189.	18.3	278
23	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
24	Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234.	5.5	268
25	ICOS-based chimeric antigen receptors program bipolar TH17/TH1 cells. <i>Blood</i> , 2014, 124, 1070-1080.	1.4	268
26	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
27	Rosetta in CASP4: Progress in ab initio protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 119-126.	2.6	242
28	De Novo Prediction of Three-dimensional Structures for Major Protein Families. <i>Journal of Molecular Biology</i> , 2002, 322, 65-78.	4.2	237
29	The Critical Periphery in the Growth of Social Protests. <i>PLoS ONE</i> , 2015, 10, e0143611.	2.5	237
30	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
31	How Social Media Facilitates Political Protest: Information, Motivation, and Social Networks. <i>Political Psychology</i> , 2018, 39, 85-118.	3.6	223
32	Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. <i>BMC Bioinformatics</i> , 2006, 7, 280.	2.6	221
33	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
34	DREAM4: Combining Genetic and Dynamic Information to Identify Biological Networks and Dynamical Models. <i>PLoS ONE</i> , 2010, 5, e13397.	2.5	201
35	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	28.9	196
36	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. <i>Science of the Total Environment</i> , 2022, 805, 150121.	8.0	192

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37	Oligo(<i>N</i> -aryl glycines): A New Twist on Structured Peptoids. <i>Journal of the American Chemical Society</i> , 2008, 130, 16622-16632.	13.7	186
38	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
39	Learning representations of microbial metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	19.0	184
40	Somatodendritic microRNAs identified by laser capture and multiplex RT-PCR. <i>Rna</i> , 2007, 13, 1224-1234.	3.5	166
41	A conserved surface on Toll-like receptor 5 recognizes bacterial flagellin. <i>Journal of Experimental Medicine</i> , 2007, 204, 393-403.	8.5	157
42	deepNF: deep network fusion for protein function prediction. <i>Bioinformatics</i> , 2018, 34, 3873-3881.	4.1	155
43	DDX5 and its associated lncRNA Rmp modulate TH17 cell effector functions. <i>Nature</i> , 2015, 528, 517-522.	27.8	154
44	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
45	A physical sciences network characterization of non-tumorigenic and metastatic cells. <i>Scientific Reports</i> , 2013, 3, 1449.	3.3	146
46	Fungi stabilize connectivity in the lung and skin microbial ecosystems. <i>Microbiome</i> , 2018, 6, 12.	11.1	146
47	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
48	GABA-receptive microglia selectively sculpt developing inhibitory circuits. <i>Cell</i> , 2021, 184, 4048-4063.e32.	28.9	142
49	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
50	Lower Airway Dysbiosis Affects Lung Cancer Progression. <i>Cancer Discovery</i> , 2021, 11, 293-307.	9.4	139
51	Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. <i>Bioinformatics</i> , 2013, 29, 1060-1067.	4.1	138
52	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
53	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon <i>Halobacterium</i> NRC-1. <i>Genome Research</i> , 2004, 14, 1025-1035.	5.5	130
54	A Preliminary Survey of the Peptoid Folding Landscape. <i>Journal of the American Chemical Society</i> , 2009, 131, 16798-16807.	13.7	123

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55	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
56	Learning biological networks: from modules to dynamics. <i>Nature Chemical Biology</i> , 2008, 4, 658-664.	8.0	117
57	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
58	Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>ELife</i> , 2020, 9, .	6.0	116
59	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
60	Detecting Bots on Russian Political Twitter. <i>Big Data</i> , 2017, 5, 310-324.	3.4	107
61	General transcription factor specified global gene regulation in archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4630-4635.	7.1	105
62	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
63	UniPep—a database for human N-linked glycosites: a resource for biomarker discovery. <i>Genome Biology</i> , 2006, 7, R73.	9.6	101
64	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
65	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
66	Contact order and ab initio protein structure prediction. <i>Protein Science</i> , 2002, 11, 1937-1944.	7.6	95
67	DREAM3: Network Inference Using Dynamic Context Likelihood of Relatedness and the Inferelator. <i>PLoS ONE</i> , 2010, 5, e9803.	2.5	95
68	FIREWACH: high-throughput functional detection of transcriptional regulatory modules in mammalian cells. <i>Nature Methods</i> , 2014, 11, 559-565.	19.0	95
69	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
70	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
71	Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. <i>Genome Research</i> , 2019, 29, 449-463.	5.5	87
72	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

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73	Dynamic MicroRNA Gene Transcription and Processing during T Cell Development. <i>Journal of Immunology</i> , 2012, 188, 3257-3267.	0.8	80
74	Improving the performance of rosetta using multiple sequence alignment information and global measures of hydrophobic core formation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 1-11.	2.6	79
75	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
76	Engineered Coiled-Coil Protein Microfibers. <i>Biomacromolecules</i> , 2014, 15, 3503-3510.	5.4	70
77	Distributions of beta sheets in proteins with application to structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 85-97.	2.6	69
78	Multi-study inference of regulatory networks for more accurate models of gene regulation. <i>PLoS Computational Biology</i> , 2019, 15, e1006591.	3.2	67
79	Design of Peptoid-peptide Macrocycles to Inhibit the β -catenin TCF Interaction in Prostate Cancer. <i>Nature Communications</i> , 2018, 9, 4396.	12.8	66
80	The coat morphogenetic protein SpoVID is necessary for spore encasement in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009, 74, 634-649.	2.5	64
81	Peptoid Atropisomers. <i>Journal of the American Chemical Society</i> , 2011, 133, 10910-10919.	13.7	61
82	Diurnally Entrained Anticipatory Behavior in Archaea. <i>PLoS ONE</i> , 2009, 4, e5485.	2.5	59
83	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. <i>PLoS ONE</i> , 2013, 8, e67051.	2.5	59
84	NSD2 overexpression drives clustered chromatin and transcriptional changes in a subset of insulated domains. <i>Nature Communications</i> , 2019, 10, 4843.	12.8	57
85	Genetic and epigenetic coordination of cortical interneuron development. <i>Nature</i> , 2021, 597, 693-697.	27.8	56
86	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
87	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
88	Breaking TADs: insights into hierarchical genome organization. <i>Epigenomics</i> , 2015, 7, 523-526.	2.1	50
89	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
90	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. <i>PLoS Biology</i> , 2007, 5, e76.	5.6	48

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91	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
92	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
93	Thermoresponsive Protein-Engineered Coiled-Coil Hydrogel for Sustained Small Molecule Release. <i>Biomacromolecules</i> , 2019, 20, 3340-3351.	5.4	45
94	Multiple abiotic stimuli are integrated in the regulation of rice gene expression under field conditions. <i>ELife</i> , 2015, 4, .	6.0	43
95	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
96	Lung microbiome and host immune tone in subjects with idiopathic pulmonary fibrosis treated with inhaled interferon- β . <i>ERJ Open Research</i> , 2017, 3, 00008-2017.	2.6	42
97	Temporal probabilistic modeling of bacterial compositions derived from 16S rRNA sequencing. <i>Bioinformatics</i> , 2018, 34, 372-380.	4.1	42
98	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
99	Computationally designed peptide macrocycle inhibitors of New Delhi metallo- β -lactamase 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	41
100	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
101	Fused Regression for Multi-source Gene Regulatory Network Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1005157.	3.2	40
102	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
103	The inferelator 2.0: A scalable framework for reconstruction of dynamic regulatory network models. <i>PLoS Computational Biology</i> , 2009, 2009, 5448-51.		38
104	Multi-species integrative biclustering. <i>Genome Biology</i> , 2010, 11, R96.	9.6	38
105	Analysis of 3D genomic interactions identifies candidate host genes that transposable elements potentially regulate. <i>Genome Biology</i> , 2018, 19, 216.	8.8	38
106	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
107	Side-Chain Conformational Preferences Govern Protein-Protein Interactions. <i>Journal of the American Chemical Society</i> , 2016, 138, 10386-10389.	13.7	36
108	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

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109	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
110	Negative Example Selection for Protein Function Prediction: The NoGO Database. <i>PLoS Computational Biology</i> , 2014, 10, e1003644.	3.2	32
111	Masked graph modeling for molecule generation. <i>Nature Communications</i> , 2021, 12, 3156.	12.8	32
112	Maternal cecal microbiota transfer rescues early-life antibiotic-induced enhancement of type 1 diabetes in mice. <i>Cell Host and Microbe</i> , 2021, 29, 1249-1265.e9.	11.0	32
113	High-performance single-cell gene regulatory network inference at scale: the Inferelator 3.0. <i>Bioinformatics</i> , 2022, 38, 2519-2528.	4.1	32
114	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
115	Mocap: large-scale inference of transcription factor binding sites from chromatin accessibility. <i>Nucleic Acids Research</i> , 2017, 45, 4315-4329.	14.5	30
116	Biophysically Motivated Regulatory Network Inference: Progress and Prospects. <i>Human Heredity</i> , 2016, 81, 62-77.	0.8	29
117	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
118	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
119	Better together: Elements of successful scientific software development in a distributed collaborative community. <i>PLoS Computational Biology</i> , 2020, 16, e1007507.	3.2	27
120	Computing structure-based lipid accessibility of membrane proteins with mp_lipid_acc in RosettaMP. <i>BMC Bioinformatics</i> , 2017, 18, 115.	2.6	26
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	Integrative Protein Modeling in RosettaNMR from Sparse Paramagnetic Restraints. <i>Structure</i> , 2019, 27, 1721-1734.e5.	3.3	25
123	News credibility labels have limited average effects on news diet quality and fail to reduce misperceptions. <i>Science Advances</i> , 2022, 8, eabl3844.	10.3	24
124	Condition-Specific Modeling of Biophysical Parameters Advances Inference of Regulatory Networks. <i>Cell Reports</i> , 2018, 23, 376-388.	6.4	23
125	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
126	Extending RosettaDock with water, sugar, and pH for prediction of complex structures and affinities for CAPRI rounds 20-27. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2201-2209.	2.6	22

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127	Shrinkage improves estimation of microbial associations under different normalization methods. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa100.	3.2	22
128	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
129	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
130	Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. <i>PLoS Computational Biology</i> , 2021, 17, e1008569.	3.2	19
131	Rational Design of Temperature-Sensitive Alleles Using Computational Structure Prediction. <i>PLoS ONE</i> , 2011, 6, e23947.	2.5	17
132	Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements. <i>Methods in Cell Biology</i> , 2012, 110, 19-56.	1.1	17
133	<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
134	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
135	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	12.8	16
136	Ab Initio Methods. <i>Methods of Biochemical Analysis</i> , 2005, 44, 547-557.	0.2	15
137	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
138	Efficient Dual siRNA and Drug Delivery Using Engineered Lipoproteoplexes. <i>Biomacromolecules</i> , 2017, 18, 2688-2698.	5.4	14
139	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. <i>MSystems</i> , 2020, 5, .	3.8	14
140	Rotamer Libraries for the High-Resolution Design of β -Amino Acid Foldamers. <i>Structure</i> , 2017, 25, 1771-1780.e3.	3.3	13
141	OutPredict: multiple datasets can improve prediction of expression and inference of causality. <i>Scientific Reports</i> , 2020, 10, 6804.	3.3	13
142	Statistically derived asymmetric membrane potentials from α -helical and β -barrel membrane proteins. <i>Scientific Reports</i> , 2018, 8, 4446.	3.3	12
143	Learning Global Models of Transcriptional Regulatory Networks from Data. <i>Methods in Molecular Biology</i> , 2009, 541, 181-210.	0.9	12
144	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

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145	Characterizing chromatin landscape from aggregate and single-cell genomic assays using flexible duration modeling. <i>Nature Communications</i> , 2020, 11, 747.	12.8	11
146	PPII Helical Peptidomimetics Templated by Cation- π Interactions. <i>ChemBioChem</i> , 2016, 17, 1824-1828.	2.6	10
147	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
148	Conformational preferences of peptide-peptoid hybrid oligomers. <i>Biopolymers</i> , 2014, 102, 369-378.	2.4	9
149	What's Not to Like? Facebook Page Likes Reveal Limited Polarization in Lifestyle Preferences. <i>Political Communication</i> , 2022, 39, 311-338.	3.9	9
150	Comparative Microbial Modules Resource: Generation and Visualization of Multi-species Biclusters. <i>PLoS Computational Biology</i> , 2011, 7, e1002228.	3.2	7
151	Towards region-specific propagation of protein functions. <i>Bioinformatics</i> , 2019, 35, 1737-1744.	4.1	7
152	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
153	The 2010 Rosetta Developers Meeting: Macromolecular Prediction and Design Meets Reproducible Publishing. <i>PLoS ONE</i> , 2011, 6, e22431.	2.5	7
154	Inter-species pathway perturbation prediction via data-driven detection of functional homology. <i>Bioinformatics</i> , 2015, 31, 501-508.	4.1	6
155	Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.0	6
156	A convolutional neural network for common coordinate registration of high-resolution histology images. <i>Bioinformatics</i> , 2021, 37, 4216-4226.	4.1	6
157	Evaluating the Conformations and Dynamics of Peptoid Macrocycles. <i>Journal of Physical Chemistry B</i> , 2022, 126, 5161-5174.	2.6	5
158	Modeling and Design of Peptidomimetics to Modulate Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2017, 1561, 291-307.	0.9	4
159	Engineered protein-iron oxide hybrid biomaterial for MRI-traceable drug encapsulation. <i>Molecular Systems Design and Engineering</i> , 2022, 7, 915-932.	3.4	4
160	Racemization barriers of atropisomeric 3,3'-bipyrrroles: an experimental study with theoretical verification. <i>RSC Advances</i> , 2016, 6, 71245-71249.	3.6	3
161	Short of Suspension: How Suspension Warnings Can Reduce Hate Speech on Twitter. <i>Perspectives on Politics</i> , 2023, 21, 651-663.	0.3	3
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