

Alfonso Valencia

List of Articles by Year in descending order

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Version: 2025-02-01

425

PR articles

43,575

PR citations

2239

93

PR h-index

2021

202

g-index

489

documents

56176

doc citations

1594

108

h-index

101568

citing authors

#	ARTICLE	IF	CITATIONS
1	Translocations can drive expression changes of multiple genes in regulons covering entire chromosome arms. <i>Nucleic Acids Research</i> , 2025, 53, .	15.5	0
2	Assessing the impact of interregional mobility on COVID19 spread in Spain using transfer entropy. <i>Scientific Reports</i> , 2025, 15, .	3.4	0
3	Patient stratification reveals the molecular basis of disease co-occurrences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2025, 122, .	7.5	4
4	UNCAN.eu: Toward a European Federated Cancer Research Data Hub. <i>Cancer Discovery</i> , 2024, 14, 30-35.	25.1	4
5	DIRECTEUR: transcriptome-based prediction of small molecules that replace transcription factors for direct cell conversion. <i>Bioinformatics</i> , 2024, 40, .	4.7	0
6	Drug-target identification in COVID-19 disease mechanisms using computational systems biology approaches. <i>Frontiers in Immunology</i> , 2024, 14, .	4.9	14
7	Rare disease research workflow using multilayer networks elucidates the molecular determinants of severity in Congenital Myasthenic Syndromes. <i>Nature Communications</i> , 2024, 15, .	13.7	14
8	Immunization with V987H-stabilized Spike glycoprotein protects K18-hACE2 mice and golden Syrian hamsters upon SARS-CoV-2 infection. <i>Nature Communications</i> , 2024, 15, .	13.7	1
9	Frustraevo: a web server to localize and quantify the conservation of local energetic frustration in protein families. <i>Nucleic Acids Research</i> , 2024, 52, W233-W237.	15.5	6
10	p53 rapidly restructures 3D chromatin organization to trigger a transcriptional response. <i>Nature Communications</i> , 2024, 15, .	13.7	25
11	3Dmapper: a command line tool for BioBank-scale mapping of variants to protein structures. <i>Bioinformatics</i> , 2024, 40, .	4.7	0
12	Lung Tissue Multilayer Network Analysis Uncovers the Molecular Heterogeneity of Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2024, 210, 1219-1229.	8.9	14
13	Prevalence and differences in the co-administration of drugs known to interact: an analysis of three distinct and large populations. <i>BMC Medicine</i> , 2024, 22, .	7.1	13
14	Gene set proximity analysis: expanding gene set enrichment analysis through learned geometric embeddings, with drug-repurposing applications in COVID-19. <i>Bioinformatics</i> , 2023, 39, .	4.7	10
15	CanMethdb: a database for genome-wide DNA methylation annotation in cancers. <i>Bioinformatics</i> , 2023, 39, .	4.7	5
16	Efficient querying of genomic reference databases with gget. <i>Bioinformatics</i> , 2023, 39, .	4.7	31
17	CATHe: detection of remote homologues for CATH superfamilies using embeddings from protein language models. <i>Bioinformatics</i> , 2023, 39, .	4.7	36
18	Low input capture Hi-C (liChi-C) identifies promoter-enhancer interactions at high-resolution. <i>Nature Communications</i> , 2023, 14, .	13.7	17

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19	PANACEA: network-based methods for pharmacotherapy prioritization in personalized oncology. <i>Bioinformatics</i> , 2023, 39, .	4.7	3
20	Predicting protein stability changes upon mutation using a simple orientational potential. <i>Bioinformatics</i> , 2023, 39, .	4.7	24
21	LEGO-CSM: a tool for functional characterization of proteins. <i>Bioinformatics</i> , 2023, 39, .	4.7	2
22	Molecular bases of comorbidities: present and future perspectives. <i>Trends in Genetics</i> , 2023, 39, 773-786.	9.8	15
23	PC_ali: a tool for improved multiple alignments and evolutionary inference based on a hybrid protein sequence and structure similarity score. <i>Bioinformatics</i> , 2023, 39, .	4.7	5
24	PhysiBoSS 2.0: a sustainable integration of stochastic Boolean and agent-based modelling frameworks. <i>Npj Systems Biology and Applications</i> , 2023, 9, .	2.9	33
25	Overview of DrugProt task at BioCreative VII: data and methods for large-scale text mining and knowledge graph generation of heterogeneous chemical-protein relations. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	2.7	22
26	The PENGUIN approach to reconstruct protein interactions at enhancer-promoter regions and its application to prostate cancer. <i>Nature Communications</i> , 2023, 14, .	13.7	1
27	Local energetic frustration conservation in protein families and superfamilies. <i>Nature Communications</i> , 2023, 14, .	13.7	39
28	Limits and potential of combined folding and docking. <i>Bioinformatics</i> , 2022, 38, 954-961.	4.7	20
29	The structural coverage of the human proteome before and after AlphaFold. <i>PLoS Computational Biology</i> , 2022, 18, e1009818.	3.1	121
30	Plotgardener: cultivating precise multi-panel figures in R. <i>Bioinformatics</i> , 2022, 38, 2042-2045.	4.7	116
31	ExTRI: Extraction of transcription regulation interactions from literature. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194778.	2.4	14
32	Parallel model exploration for tumor treatment simulations. <i>Computational Intelligence</i> , 2022, 38, 1379-1401.	1.9	12
33	Optimizing Dosage-Specific Treatments in a Multi-Scale Model of a Tumor Growth. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	3.5	10
34	Mortality in Persons With Autism Spectrum Disorder or Attention-Deficit/Hyperactivity Disorder. <i>JAMA Pediatrics</i> , 2022, 176, e216401.	8.6	114
35	Detection of oncogenic and clinically actionable mutations in cancer genomes critically depends on variant calling tools. <i>Bioinformatics</i> , 2022, 38, 3181-3191.	4.7	22
36	Design and methodological characteristics of studies using observational routinely collected health data for investigating the link between cancer and neurodegenerative diseases: protocol for a meta-research study. <i>BMJ Open</i> , 2022, 12, e058738.	1.9	1

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37	Evaluating the policy of closing bars and restaurants in Cataluña and its effects on mobility and COVID19 incidence. <i>Scientific Reports</i> , 2022, 12, .	3.4	10
38	TVAR: assessing tissue-specific functional effects of non-coding variants with deep learning. <i>Bioinformatics</i> , 2022, 38, 4697-4704.	4.7	5
39	A structural biology community assessment of AlphaFold2 applications. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 1056-1067.	8.8	562
40	3D chromatin connectivity underlies replication origin efficiency in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2022, 50, 12149-12165.	15.5	15
41	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. <i>Bioinformatics</i> , 2021, 37, 650-658.	4.7	1
42	Classification in biological networks with hypergraphlet kernels. <i>Bioinformatics</i> , 2021, 37, 1000-1007.	4.7	24
43	STAG2 loss-of-function affects short-range genomic contacts and modulates the basal-luminal transcriptional program of bladder cancer cells. <i>Nucleic Acids Research</i> , 2021, 49, 11005-11021.	15.5	29
44	Simulating SARS-CoV-2 epidemics by region-specific variables and modeling contact tracing app containment. <i>Npj Digital Medicine</i> , 2021, 4, .	10.4	31
45	Unraveling the molecular basis of host cell receptor usage in SARS-CoV-2 and other human pathogenic Î²-CoVs. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 759-766.	3.9	5
46	Artificial intelligence in cancer research: learning at different levels of data granularity. <i>Molecular Oncology</i> , 2021, 15, 817-829.	4.1	32
47	The eTRANSafe Project on Translational Safety Assessment through Integrative Knowledge Management: Achievements and Perspectives. <i>Pharmaceuticals</i> , 2021, 14, 237.	4.2	29
48	Protein contact map refinement for improving structure prediction using generative adversarial networks. <i>Bioinformatics</i> , 2021, 37, 3168-3174.	4.7	12
49	The multilayer community structure of medulloblastoma. <i>IScience</i> , 2021, 24, 102365.	3.6	9
50	Visual exploration of large metabolic models. <i>Bioinformatics</i> , 2021, 37, 4460-4468.	4.7	9
51	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.7	52
52	Transcriptomic and Genetic Associations between Alzheimer's Disease, Parkinson's Disease, and Cancer. <i>Cancers</i> , 2021, 13, 2990.	3.8	34
53	Computational analysis of sense-antisense chimeric transcripts reveals their potential regulatory features and the landscape of expression in human cells. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, .	2.2	19
54	Co-evolutionary distance predictions contain flexibility information. <i>Bioinformatics</i> , 2021, 38, 65-72.	4.7	18

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55	Systems biology at the giga-scale: Large multiscale models of complex, heterogeneous multicellular systems. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100385.	1.4	40
56	MAX mutant small-cell lung cancers exhibit impaired activities of MGA-dependent noncanonical polycomb repressive complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.5	12
57	Assessing the accuracy of contact and distance predictions in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1888-1900.	2.6	20
58	A catalogue of 863 Rett-syndrome-causing MECP2 mutations and lessons learned from data integration. <i>Scientific Data</i> , 2021, 8, .	5.7	29
59	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, .	6.7	77
60	VINYL: Variant prioritization by survival analysis. <i>Bioinformatics</i> , 2021, 36, 5590-5599.	4.7	5
61	COVID-19 Flow-Maps an open geographic information system on COVID-19 and human mobility for Spain. <i>Scientific Data</i> , 2021, 8, .	5.7	25
62	iScore: a novel graph kernel-based function for scoring protein-protein docking models. <i>Bioinformatics</i> , 2020, 36, 112-121.	4.7	75
63	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	15.5	127
64	On the inconsistent treatment of gene-protein-reaction rules in context-specific metabolic models. <i>Bioinformatics</i> , 2020, 36, 1986-1988.	4.7	7
65	cd2sbgmml: bidirectional conversion between CellDesigner and SBGN formats. <i>Bioinformatics</i> , 2020, 36, 2620-2622.	4.7	10
66	Towards FAIR principles for research software. <i>Data Science</i> , 2020, 3, 37-59.	1.2	233
67	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	37.9	2,189
68	Formal axioms in biomedical ontologies improve analysis and interpretation of associated data. <i>Bioinformatics</i> , 2020, 36, 2229-2236.	4.7	16
69	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, .	13.7	44
70	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, .	13.7	86
71	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. <i>Nature Communications</i> , 2020, 11, .	13.7	31
72	Sex and gender differences and biases in artificial intelligence for biomedicine and healthcare. <i>Npj Digital Medicine</i> , 2020, 3, .	10.4	420

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73	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, .	13.7	33
74	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	4.7	66
75	Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig. Nature Communications, 2020, 11, .	13.7	45
76	iPAC: a genome-guided assembler of isoforms via phasing and combing paths. Bioinformatics, 2020, 36, 2712-2717.	4.7	5
77	Heterogeneous networks integration for disease gene prioritization with node kernels. Bioinformatics, 2020, 36, 2649-2656.	4.7	23
78	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, .	13.7	118
79	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. Nature Communications, 2020, 11, .	13.7	195
80	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. Nature Communications, 2020, 11, .	13.7	68
81	Combined burden and functional impact tests for cancer driver discovery using DriverPower. Nature Communications, 2020, 11, .	13.7	55
82	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, .	13.7	209
83	Divergent mutational processes distinguish hypoxic and normoxic tumours. Nature Communications, 2020, 11, .	13.7	129
84	Inferring structural variant cancer cell fraction. Nature Communications, 2020, 11, .	13.7	45
85	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, .	13.7	99
86	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	37.9	978
87	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	37.9	797
88	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	37.9	3,137
89	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	37.9	570
90	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	37.9	2,826

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91	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	37.9	385
92	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , 2020, 52, 320-330.	25.2	349
93	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	25.2	422
94	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	25.2	262
95	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	25.2	640
96	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. <i>Communications Biology</i> , 2020, 3, .	4.4	172
97	Understanding oncogenicity of cancer driver genes and mutations in the cancer genomics era. <i>FEBS Letters</i> , 2020, 594, 4233-4246.	2.7	46
98	Unveiling new disease, pathway, and gene associations via multi-scale neural network. <i>PLoS ONE</i> , 2020, 15, e0231059.	2.3	21
99	PathExt: a general framework for path-based mining of omics-integrated biological networks. <i>Bioinformatics</i> , 2020, 37, 1254-1262.	4.7	18
100	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020, 38, 288-292.	29.8	13
101	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.	25.2	398
102	CoMeBack: DNA methylation array data analysis for co-methylated regions. <i>Bioinformatics</i> , 2020, 36, 2675-2683.	4.7	60
103	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. <i>F1000Research</i> , 2020, 9, 1229.	0.5	6
104	COVID-19 and beyond: A call for action and audacious solidarity to all the citizens and nations, it is humanity's fight. <i>F1000Research</i> , 2020, 9, 1130.	0.5	3
105	ECCB2020: the 19th European Conference on Computational Biology. <i>Bioinformatics</i> , 2020, 36, i569-i572.	4.7	1
106	BIPSPI: a method for the prediction of partner-specific protein-protein interfaces. <i>Bioinformatics</i> , 2019, 35, 470-477.	4.7	94
107	Random walk with restart on multiplex and heterogeneous biological networks. <i>Bioinformatics</i> , 2019, 35, 497-505.	4.7	287
108	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, .	8.1	62

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109	Next generation community assessment of biomedical entity recognition web servers: metrics, performance, interoperability aspects of BeCalm. <i>Journal of Cheminformatics</i> , 2019, 11, .	5.4	4
110	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	47.0	83
111	Intronic CNVs and gene expression variation in human populations. <i>PLoS Genetics</i> , 2019, 15, e1007902.	3.2	85
112	Large-scale analysis of human gene expression variability associates highly variable drug targets with lower drug effectiveness and safety. <i>Bioinformatics</i> , 2019, 35, 3028-3037.	4.7	32
113	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3114.	4.4	15
114	Association of Anorexia Nervosa With Risk of Cancer. <i>JAMA Network Open</i> , 2019, 2, e195313.	6.6	19
115	vulcanSpot: a tool to prioritize therapeutic vulnerabilities in cancer. <i>Bioinformatics</i> , 2019, 35, 4846-4848.	4.7	10
116	Interactive Extreme-Scale Analytics: Towards Battling Cancer. <i>IEEE Technology and Society Magazine</i> , 2019, 38, 54-61.	0.3	5
117	AlphaFold at CASP13. <i>Bioinformatics</i> , 2019, 35, 4862-4865.	4.7	300
118	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. <i>Bioinformatics</i> , 2019, 35, 4647-4655.	4.7	164
119	Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. <i>Molecular Autism</i> , 2019, 10, .	4.4	43
120	Big data analytics for personalized medicine. <i>Current Opinion in Biotechnology</i> , 2019, 58, 161-167.	6.8	226
121	Protein multiple alignments: sequence-based versus structure-based programs. <i>Bioinformatics</i> , 2019, 35, 3970-3980.	4.7	41
122	PhenoPro: a novel toolkit for assisting in the diagnosis of Mendelian disease. <i>Bioinformatics</i> , 2019, 35, 3559-3566.	4.7	31
123	Gene expression models based on transcription factor binding events confer insight into functional cis-regulatory variants. <i>Bioinformatics</i> , 2019, 35, 2610-2617.	4.7	19
124	Protein-protein interaction sites prediction by ensemble random forests with synthetic minority oversampling technique. <i>Bioinformatics</i> , 2019, 35, 2395-2402.	4.7	157
125	Characterization and identification of long non-coding RNAs based on feature relationship. <i>Bioinformatics</i> , 2019, 35, 2949-2956.	4.7	114
126	The EVcouplings Python framework for coevolutionary sequence analysis. <i>Bioinformatics</i> , 2019, 35, 1582-1584.	4.7	286

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127	A natural upper bound to the accuracy of predicting protein stability changes upon mutations. <i>Bioinformatics</i> , 2019, 35, 1513-1517.	4.7	41
128	ConDo: protein domain boundary prediction using coevolutionary information. <i>Bioinformatics</i> , 2019, 35, 2411-2417.	4.7	22
129	<i>De novo</i> pattern discovery enables robust assessment of functional consequences of non-coding variants. <i>Bioinformatics</i> , 2019, 35, 1453-1460.	4.7	21
130	Precision medicine needs pioneering clinical bioinformaticians. <i>Briefings in Bioinformatics</i> , 2019, 20, 752-766.	6.6	51
131	Enhancing protein fold determination by exploring the complementary information of chemical cross-linking and coevolutionary signals. <i>Bioinformatics</i> , 2018, 34, 2201-2208.	4.7	18
132	Co-complex protein membership evaluation using Maximum Entropy on GO ontology and InterPro annotation. <i>Bioinformatics</i> , 2018, 34, 1884-1892.	4.7	21
133	DeepSF: deep convolutional neural network for mapping protein sequences to folds. <i>Bioinformatics</i> , 2018, 34, 1295-1303.	4.7	167
134	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, .	2.1	93
135	Phenotypic stability and plasticity in GMP-derived cells as determined by their underlying regulatory network. <i>Bioinformatics</i> , 2018, 34, 1174-1182.	4.7	14
136	MemBrain-contact 2.0: a new two-stage machine learning model for the prediction enhancement of transmembrane protein residue contacts in the full chain. <i>Bioinformatics</i> , 2018, 34, 230-238.	4.7	17
137	DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. <i>Bioinformatics</i> , 2018, 34, 1466-1472.	4.7	160
138	High precision in protein contact prediction using fully convolutional neural networks and minimal sequence features. <i>Bioinformatics</i> , 2018, 34, 3308-3315.	4.7	179
139	On the mechanisms of protein interactions: predicting their affinity from unbound tertiary structures. <i>Bioinformatics</i> , 2018, 34, 592-598.	4.7	12
140	Proteinâ€™protein interaction specificity is captured by contact preferences and interface composition. <i>Bioinformatics</i> , 2018, 34, 459-468.	4.7	35
141	APPRIS 2017: principal isoforms for multiple gene sets. <i>Nucleic Acids Research</i> , 2018, 46, D213-D217.	15.5	155
142	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. <i>Gastroenterology</i> , 2018, 154, 181-194.e20.	0.9	33
143	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.3	134
144	Bio-knowledge-based filters improve residueâ€™residue contact prediction accuracy. <i>Bioinformatics</i> , 2018, 34, 3675-3683.	4.7	1

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145	LncRNAnet: long non-coding RNA identification using deep learning. <i>Bioinformatics</i> , 2018, 34, 3889-3897.	4.7	98
146	Sequential search leads to faster, more efficient fragment-based de novo protein structure prediction. <i>Bioinformatics</i> , 2018, 34, 1132-1140.	4.7	12
147	ProteomeVis: a web app for exploration of protein properties from structure to sequence evolution across organisms's proteomes. <i>Bioinformatics</i> , 2018, 34, 3557-3565.	4.7	7
148	CommWalker: correctly evaluating modules in molecular networks in light of annotation bias. <i>Bioinformatics</i> , 2018, 34, 994-1000.	4.7	10
149	Germline variation in the oxidative DNA repair genes NUDT1 and OGG1 is not associated with hereditary colorectal cancer or polyposis. <i>Human Mutation</i> , 2018, 39, 1214-1225.	4.5	12
150	Prioritizing predictive biomarkers for gene essentiality in cancer cells with mRNA expression data and DNA copy number profile. <i>Bioinformatics</i> , 2018, 34, 3975-3982.	4.7	4
151	Deep convolutional networks for quality assessment of protein folds. <i>Bioinformatics</i> , 2018, 34, 4046-4053.	4.7	96
152	Increasing the accuracy of protein loop structure prediction with evolutionary constraints. <i>Bioinformatics</i> , 2018, 35, 2585-2592.	4.7	9
153	A pipeline for local assembly of minisatellite alleles from single-molecule sequencing data. <i>Bioinformatics</i> , 2017, 33, 650-653.	4.7	2
154	ISCB's initial reaction to <i>New England Journal of Medicine</i> editorial on data sharing. <i>Bioinformatics</i> , 2017, 33, 2968-2968.	4.7	1
155	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, .	8.1	113
156	EigenTHREADER: analogous protein fold recognition by efficient contact map threading. <i>Bioinformatics</i> , 2017, 33, 2684-2690.	4.7	65
157	Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. <i>Bioinformatics</i> , 2017, 33, 2842-2849.	4.7	349
158	Reliability of algorithmic somatic copy number alteration detection from targeted capture data. <i>Bioinformatics</i> , 2017, 33, 2791-2798.	4.7	15
159	Most Alternative Isoforms Are Not Functionally Important. <i>Trends in Biochemical Sciences</i> , 2017, 42, 408-410.	6.7	85
160	A deep learning framework for improving long-range residue-residue contact prediction using a hierarchical strategy. <i>Bioinformatics</i> , 2017, 33, 2675-2683.	4.7	41
161	Annotating function to differentially expressed lincRNAs in myelodysplastic syndrome using a network-based method. <i>Bioinformatics</i> , 2017, 33, 2622-2630.	4.7	14
162	Information Retrieval and Text Mining Technologies for Chemistry. <i>Chemical Reviews</i> , 2017, 117, 7673-7761.	52.6	258

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163	HiPred: an integrative approach to predicting haploinsufficient genes. <i>Bioinformatics</i> , 2017, 33, 1751-1757.	4.7	42
164	Predicting accurate contacts in thousands of Pfam domain families using PconsC3. <i>Bioinformatics</i> , 2017, 33, 2859-2866.	4.7	42
165	LimTox: a web tool for applied text mining of adverse event and toxicity associations of compounds, drugs and genes. <i>Nucleic Acids Research</i> , 2017, 45, W484-W489.	15.5	49
166	ChiPPI: a novel method for mapping chimeric protein-protein interactions uncovers selection principles of protein fusion events in cancer. <i>Nucleic Acids Research</i> , 2017, 45, 7094-7105.	15.5	35
167	Elucidating the molecular basis of MSH2-deficient tumors by combined germline and somatic analysis. <i>International Journal of Cancer</i> , 2017, 141, 1365-1380.	4.3	28
168	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017, 14, 782-788.	24.6	77
169	Correlated mutations select misfolded from properly folded proteins. <i>Bioinformatics</i> , 2017, 33, 1497-1504.	4.7	3
170	Epigenomic annotation-based interpretation of genomic data: from enrichment analysis to machine learning. <i>Bioinformatics</i> , 2017, 33, 3323-3330.	4.7	36
171	A molecular hypothesis to explain direct and inverse co-morbidities between Alzheimer's Disease, Glioblastoma and Lung cancer. <i>Scientific Reports</i> , 2017, 7, .	3.4	101
172	Forecasting residue-residue contact prediction accuracy. <i>Bioinformatics</i> , 2017, 33, 3405-3414.	4.7	4
173	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. <i>Nucleic Acids Research</i> , 2017, 45, 9244-9259.	15.5	22
174	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, .	8.1	173
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