

# Sören Brunak

## List of Publications by Year in descending order

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Version: 2024-02-01

330  
papers

94,100  
citations

2675

95  
h-index

291

293  
g-index

360  
all docs

360  
docs citations

360  
times ranked

107637  
citing authors

#	ARTICLE	IF	CITATIONS
1	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. <i>Cell Reports Medicine</i> , 2022, 3, 100477.	6.5	39
2	SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.	17.5	883
3	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. <i>Communications Biology</i> , 2022, 5, 80.	4.4	12
4	Randomized phase 2 study of nivolumab with or without ipilimumab in combination with stereotactic body radiotherapy in patients with refractory metastatic pancreatic cancer (CHECKPAC).. <i>Journal of Clinical Oncology</i> , 2022, 40, 554-554.	1.6	1
5	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	12.8	21
6	Established risk loci for systemic lupus erythematosus at NCF2, STAT4, TNPO3, IRF5 and ITGAM associate with distinct clinical manifestations: A Danish genome-wide association study. <i>Joint Bone Spine</i> , 2022, 89, 105357.	1.6	1
7	Drug interactions in hospital prescriptions in Denmark: Prevalence and associations with adverse outcomes. <i>Pharmacoepidemiology and Drug Safety</i> , 2022, 31, 632-642.	1.9	9
8	Using Machine Learning to Identify Patients at High Risk of Inappropriate Drug Dosing in Periods with Renal Dysfunction. <i>Clinical Epidemiology</i> , 2022, Volume 14, 213-223.	3.0	3
9	Modeling of waning immunity after SARS-CoV-2 vaccination and influencing factors. <i>Nature Communications</i> , 2022, 13, 1614.	12.8	117
10	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. <i>Nature Communications</i> , 2022, 13, 1598.	12.8	8
11	Multimomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1085-1095.	0.9	26
12	Randomized Phase II Study of Nivolumab With or Without Ipilimumab Combined With Stereotactic Body Radiotherapy for Refractory Metastatic Pancreatic Cancer (CheckPAC). <i>Journal of Clinical Oncology</i> , 2022, 40, 3180-3189.	1.6	29
13	Intervening on the storage time of RBC units and its effects on adverse recipient outcomes using real-world data. <i>Blood</i> , 2022, 139, 3647-3654.	1.4	12
14	Temporal patterns of multi-morbidity in 570157 ischemic heart disease patients: a nationwide cohort study. <i>Cardiovascular Diabetology</i> , 2022, 21, .	6.8	4
15	Abstract LB550: AI predicts risk of pancreatic cancer from disease trajectories using real-world electronic health records (EHRs) from Denmark and the USA. <i>Cancer Research</i> , 2022, 82, LB550-LB550.	0.9	0
16	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. <i>European Heart Journal</i> , 2022, 43, 4707-4718.	2.2	5
17	Classification of Left and Right Coronary Arteries in Coronary Angiographies Using Deep Learning. <i>Electronics (Switzerland)</i> , 2022, 11, 2087.	3.1	2
18	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). <i>International Journal of Epidemiology</i> , 2021, 50, 719-720e.	1.9	23

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19	Semen quality and waiting time to pregnancy explored using association mining. <i>Andrology</i> , 2021, 9, 577-587.	3.5	12
20	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021, 4, 156.	4.4	72
21	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021, 42, 1959-1971.	2.2	27
22	Predictive utilities of lipid traits, lipoprotein subfractions and other risk factors for incident diabetes: a machine learning approach in the Diabetes Prevention Program. <i>BMJ Open Diabetes Research and Care</i> , 2021, 9, e001953.	2.8	7
23	Artificial Intelligence and Early Detection of Pancreatic Cancer. <i>Pancreas</i> , 2021, 50, 251-279.	1.1	71
24	The burden of disease of three food-associated heavy metals in clusters in the Danish population – Towards targeted public health strategies. <i>Food and Chemical Toxicology</i> , 2021, 150, 112072.	3.6	6
25	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. <i>Gut</i> , 2021, 70, 1538-1549.	12.1	21
26	Impaired Vitamin D Signaling in T Cells From a Family With Hereditary Vitamin D Resistant Rickets. <i>Frontiers in Immunology</i> , 2021, 12, 684015.	4.8	8
27	Endotrophin is associated with chronic multimorbidity and all-cause mortality in a cohort of elderly women. <i>EBioMedicine</i> , 2021, 68, 103391.	6.1	20
28	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. <i>Communications Biology</i> , 2021, 4, 655.	4.4	12
29	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 13153.	3.3	147
30	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. <i>Diabetes</i> , 2021, 70, 2092-2106.	0.6	17
31	Association of Variants Near the Bradykinin Receptor B2 Gene With Angioedema in Patients Taking ACE-Inhibitors. <i>Journal of the American College of Cardiology</i> , 2021, 78, 696-709.	2.8	10
32	The impact of early pregnancy complications on completed family size – A nationwide, registry-based cohort study with 40 years of data. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2021, 100, 2226-2233.	2.8	0
33	Chance of live birth: a nationwide, registry-based cohort study. <i>Human Reproduction</i> , 2021, 36, 1065-1073.	0.9	31
34	Time-ordered comorbidity correlations identify patients at risk of mis- and overdiagnosis. <i>Npj Digital Medicine</i> , 2021, 4, 12.	10.9	8
35	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	8.6	16
36	Optimizing drug selection from a prescription trajectory of one patient. <i>Npj Digital Medicine</i> , 2021, 4, 150.	10.9	8

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37	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. <i>BMJ Open</i> , 2021, 11, e049709.	1.9	7
38	Conflicting associations between dietary patterns and changes of anthropometric traits across subgroups of middle-aged women and men. <i>Clinical Nutrition</i> , 2020, 39, 265-275.	5.0	8
39	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020, 12, 109.	8.2	8
40	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	27.8	230
41	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. <i>EBioMedicine</i> , 2020, 58, 102932.	6.1	3
42	Complete Topological Mapping of a Cellular Protein Interactome Reveals Bow-Tie Motifs as Ubiquitous Connectors of Protein Complexes. <i>Cell Reports</i> , 2020, 31, 107763.	6.4	4
43	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , 2020, 517, 110923.	3.2	5
44	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020, 41, 2618-2628.	2.2	61
45	Disease trajectory browser for exploring temporal, population-wide disease progression patterns in 7.2 million Danish patients. <i>Nature Communications</i> , 2020, 11, 4952.	12.8	70
46	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. <i>Genome Medicine</i> , 2020, 12, 76.	8.2	15
47	Alcoholic liver disease: A registry view on comorbidities and disease prediction. <i>PLoS Computational Biology</i> , 2020, 16, e1008244.	3.2	11
48	Disease Trajectories for Hidradenitis Suppurativa in the Danish Population. <i>JAMA Dermatology</i> , 2020, 156, 780.	4.1	17
49	Association between antipsychotic drug dose and length of clinical notes: a proxy of disease severity?. <i>BMC Medical Research Methodology</i> , 2020, 20, 107.	3.1	3
50	Implementation and comparison of two text mining methods with a standard pharmacovigilance method for signal detection of medication errors. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 94.	3.0	5
51	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. <i>PLoS Medicine</i> , 2020, 17, e1003149.	8.4	47
52	Immune Profiling of Human Gut-Associated Lymphoid Tissue Identifies a Role for Isolated Lymphoid Follicles in Priming of Region-Specific Immunity. <i>Immunity</i> , 2020, 52, 557-570.e6.	14.3	90
53	Dynamic and explainable machine learning prediction of mortality in patients in the intensive care unit: a retrospective study of high-frequency data in electronic patient records. <i>The Lancet Digital Health</i> , 2020, 2, e179-e191.	12.3	187
54	Secreted breast tumor interstitial fluid microRNAs and their target genes are associated with triple-negative breast cancer, tumor grade, and immune infiltration. <i>Breast Cancer Research</i> , 2020, 22, 73.	5.0	29

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55	Sex differences in text-mined possible adverse drug events associated with drugs for psychosis. Journal of Psychopharmacology, 2020, 34, 532-539.	4.0	13
56	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. Diabetologia, 2020, 63, 744-756.	6.3	12
57	Age-stratified longitudinal study of Alzheimer's and vascular dementia patients. Alzheimer's and Dementia, 2020, 16, 908-917.	0.8	25
58	Phenome-Wide Analysis of Short- and Long-Run Disease Incidence Following Recurrent Pregnancy Loss Using Data From a 39-Year Period. Journal of the American Heart Association, 2020, 9, e015069.	3.7	20
59	Lipidomic profiles, lipid trajectories and clinical biomarkers in female elite endurance athletes. Scientific Reports, 2020, 10, 2349.	3.3	9
60	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	3.1	32
61	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. PLoS ONE, 2020, 15, e0242360.	2.5	7
62	Title is missing!. , 2020, 17, e1003149.		0
63	Title is missing!. , 2020, 17, e1003149.		0
64	Title is missing!. , 2020, 17, e1003149.		0
65	Title is missing!. , 2020, 17, e1003149.		0
66	Title is missing!. , 2020, 17, e1003149.		0
67	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. Npj Systems Biology and Applications, 2019, 5, 27.	3.0	11
68	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
69	Incorporating symptom data in longitudinal disease trajectories for more detailed patient stratification. International Journal of Medical Informatics, 2019, 129, 107-113.	3.3	9
70	sAOP: linking chemical stressors to adverse outcomes pathway networks. Bioinformatics, 2019, 35, 5391-5392.	4.1	19
71	Combined Ensemble Docking and Machine Learning in Identification of Therapeutic Agents with Potential Inhibitory Effect on Human CES1. Molecules, 2019, 24, 2747.	3.8	6
72	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324.	4.0	13

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73	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
74	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	1.6	154
75	Survival prediction in intensive-care units based on aggregation of long-term disease history and acute physiology: a retrospective study of the Danish National Patient Registry and electronic patient records. <i>The Lancet Digital Health</i> , 2019, 1, e78-e89.	12.3	76
76	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. <i>Diabetologia</i> , 2019, 62, 1601-1615.	6.3	22
77	DBDS Genomic Cohort, a prospective and comprehensive resource for integrative and temporal analysis of genetic, environmental and lifestyle factors affecting health of blood donors. <i>BMJ Open</i> , 2019, 9, e028401.	1.9	68
78	Comorbidity landscape of the Danish patient population affected by chromosome abnormalities. <i>Genetics in Medicine</i> , 2019, 21, 2485-2495.	2.4	13
79	The use of systems biology in chemical risk assessment. <i>Current Opinion in Toxicology</i> , 2019, 15, 48-54.	5.0	10
80	Combing the Hairball: Improving Visualization of miRNA-Target Interaction Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 279-289.	0.9	0
81	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , 2019, 51, 924-930.	21.4	22
82	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , 2019, 10, 666.	12.8	128
83	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	17.5	3,317
84	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. <i>Nature Communications</i> , 2019, 10, 5508.	12.8	17
85	A generic deep convolutional neural network framework for prediction of receptor-ligand interactions-NetPhosPan: application to kinase phosphorylation prediction. <i>Bioinformatics</i> , 2019, 35, 1098-1107.	4.1	13
86	A Large-Cohort, Longitudinal Study Determines Precancer Disease Routes across Different Cancer Types. <i>Cancer Research</i> , 2019, 79, 864-872.	0.9	17
87	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. <i>ELife</i> , 2019, 8, .	6.0	12
88	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	46.4	263
89	Familial co-occurrence of congenital heart defects follows distinct patterns. <i>European Heart Journal</i> , 2018, 39, 1015-1022.	2.2	32
90	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	14.5	61

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91	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , 2018, 61, 117-129.	6.3	32
92	Analysis of Time-Series Gene Expression Data to Explore Mechanisms of Chemical-Induced Hepatic Steatosis Toxicity. <i>Frontiers in Genetics</i> , 2018, 9, 396.	2.3	22
93	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. <i>Acta Veterinaria Scandinavica</i> , 2018, 60, 61.	1.6	40
94	A computational framework to integrate high-throughput omics datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , 2018, 13, 2781-2800.	12.0	82
95	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. <i>RNA Technologies</i> , 2018, , 229-238.	0.3	0
96	Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells. <i>Cell Death and Disease</i> , 2018, 9, 586.	6.3	33
97	Retinoic Acid Signaling in Thymic Epithelial Cells Regulates Thymopoiesis. <i>Journal of Immunology</i> , 2018, 201, 524-532.	0.8	15
98	Benchmarking the HLA typing performance of Polysolver and Optitype in 50 Danish parental trios. <i>BMC Bioinformatics</i> , 2018, 19, 239.	2.6	34
99	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. <i>PLoS Computational Biology</i> , 2018, 14, e1005962.	3.2	112
100	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , 2018, 13, e0189886.	2.5	9
101	The protein kinase SIK downregulates the polarity protein Par3. <i>Oncotarget</i> , 2018, 9, 5716-5735.	1.8	11
102	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. <i>Oncotarget</i> , 2018, 9, 9043-9060.	1.8	8
103	Identifying the druggable interactome of EWS-FLI1 reveals MCL-1 dependent differential sensitivities of Ewing sarcoma cells to apoptosis inducers. <i>Oncotarget</i> , 2018, 9, 31018-31031.	1.8	10
104	Increase in clinically recorded type 2 diabetes after colectomy. <i>ELife</i> , 2018, 7, .	6.0	23
105	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002.	14.5	271
106	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , 2017, 60, 475-489.	6.3	31
107	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. <i>Methods in Molecular Biology</i> , 2017, 1580, 281-295.	0.9	2
108	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. <i>Reproduction</i> , 2017, 154, 145-152.	2.6	37

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109	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. <i>Human Molecular Genetics</i> , 2017, 26, 1219-1229.	2.9	73
110	Chromosome-wise Protein Interaction Patterns and Their Impact on Functional Implications of Large-Scale Genomic Aberrations. <i>Cell Systems</i> , 2017, 4, 357-364.e3.	6.2	9
111	Comparison of global gene expression profiles of microdissected human foetal Leydig cells with their normal and hyperplastic adult equivalents. <i>Molecular Human Reproduction</i> , 2017, 23, 339-354.	2.8	14
112	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	6.4	81
113	TEMPORAL ORDER OF DISEASE PAIRS AFFECTS SUBSEQUENT DISEASE TRAJECTORIES: THE CASE OF DIABETES AND SLEEP APNEA. , 2017, 22, 380-389.		12
114	Lapatinib potentiates cytotoxicity of ÂYM155 in neuroblastoma via inhibition of the ABCB1 efflux transporter. <i>Scientific Reports</i> , 2017, 7, 3091.	3.3	35
115	Protein features as determinants of wildâ€type glycoside hydrolase thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2036-2044.	2.6	5
116	Combinatorial Drug Screening Identifies Ewing Sarcomaâ€specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	4.1	17
117	A scored human proteinâ€protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017, 14, 61-64.	19.0	534
118	Pancreatic Islet Protein Complexes and Their Dysregulation in Type 2 Diabetes. <i>Frontiers in Genetics</i> , 2017, 8, 43.	2.3	19
119	The impact of the protein interactome on the syntenic structure of mammalian genomes. <i>PLoS ONE</i> , 2017, 12, e0179112.	2.5	8
120	Cutavirus in Cutaneous Malignant Melanoma. <i>Emerging Infectious Diseases</i> , 2017, 23, 363-365.	4.3	22
121	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	27.8	130
122	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , 2017, 13, e1006706.	3.5	194
123	Integration of Known DNA, RNA and Protein Biomarkers Provides Prediction of Anti-TNF Response in Rheumatoid Arthritis: Results from the COMBINE Study. <i>Molecular Medicine</i> , 2016, 22, 322-328.	4.4	39
124	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , 2016, 8, 53.	3.3	11
125	ChemProt-3.0: a global chemical biology diseases mapping. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav123.	3.0	75
126	Investigating the impact of missense mutations in hCES1 by <i>in silico</i> structure-based approaches. <i>Drug Metabolism and Personalized Therapy</i> , 2016, 31, 97-106.	0.6	8

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127	How Suitable Are Registry Data for Recurrence Risk Calculations? Validation of Diagnoses on 1,593 Families With Congenital Heart Disease. World Journal for Pediatric & Congenital Heart Surgery, 2016, 7, 169-177.	0.8	5
128	Network biology concepts in complex disease comorbidities. Nature Reviews Genetics, 2016, 17, 615-629.	16.3	269
129	Familial Atrial Septal Defect and Sudden Cardiac Death: Identification of a Novel<i>NKX2-5</i>Mutation and a Review of the Literature. Congenital Heart Disease, 2016, 11, 283-290.	0.2	81
130	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
131	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
132	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. Npj Genomic Medicine, 2016, 1, 16035.	3.8	21
133	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. Nature Microbiology, 2016, 1, 16152.	13.3	56
134	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. Scientific Reports, 2016, 6, 36624.	3.3	66
135	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. BMC Genomics, 2016, 17, 396.	2.8	11
136	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. Human Mutation, 2016, 37, 36-42.	2.5	10
137	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
138	Propionibacterium acnes: Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. Journal of Clinical Microbiology, 2016, 54, 980-987.	3.9	87
139	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	21.4	617
140	The hunt for fatal myocardial infarction biomarkers: predictive circulating microRNAs. Annals of Translational Medicine, 2016, 4, S1-S1.	1.7	0
141	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. Scientific Reports, 2015, 5, 13201.	3.3	34
142	Population genomics of Bronze Age Eurasia. Nature, 2015, 522, 167-172.	27.8	1,166
143	Long-term risk of cardiovascular and cerebrovascular disease after removal of the colonic microbiota by colectomy: a cohort study based on the Danish National Patient Register from 1996 to 2014. BMJ Open, 2015, 5, e008702.	1.9	10
144	Traces of ATCV-1 associated with laboratory component contamination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E925-6.	7.1	24

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145	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969.	12.8	164
146	Individualization of treatments with drugs metabolized by CES1: combining genetics and metabolomics. Pharmacogenomics, 2015, 16, 649-665.	1.3	19
147	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	28.9	425
148	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
149	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. Journal of Research in Pharmacy Practice, 2015, 4, 64.	0.7	6
150	REACH and Environmental Chemicals. QSAR in Environmental and Health Sciences, 2015, , 23-36.	0.3	1
151	Finding Cervical Cancer Symptoms in Swedish Clinical Text using a Machine Learning Approach and NegEx. AMIA ... Annual Symposium proceedings, 2015, 2015, 1296-305.	0.2	5
152	Identification of Odorant-Receptor Interactions by Global Mapping of the Human Odorome. PLoS ONE, 2014, 9, e93037.	2.5	42
153	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT "OMICS" DATA. , 2014, , .		0
154	Patient stratification and identification of adverse event correlations in the space of 1190 drug related adverse events. Frontiers in Physiology, 2014, 5, 332.	2.8	15
155	Discrepancies in listed adverse drug reactions in pharmaceutical product information supplied by the regulatory authorities in Denmark and the USA. Pharmacology Research and Perspectives, 2014, 2, e00038.	2.4	17
156	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	27.8	500
157	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1819-1828.	2.6	36
158	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	27.8	821
159	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. Briefings in Bioinformatics, 2014, 15, 942-952.	6.5	16
160	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	3.9	73
161	Polychlorinated dibenzo-p-dioxins, furans, and biphenyls (PCDDs/PCDFs and PCBs) in breast milk and early childhood growth and IGF1. Reproduction, 2014, 147, 391-399.	2.6	33
162	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70

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163	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: rationale and design of the epidemiological studies within the IMI DIRECT Consortium. Diabetologia, 2014, 57, 1132-1142.	6.3	48
164	Bacterial diversity in snow on North Pole ice floes. Extremophiles, 2014, 18, 945-951.	2.3	26
165	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
166	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
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