

Søren Brunak

List of Publications by Year in descending order

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Version: 2024-02-01

330
papers

94,100
citations

3116

95
h-index

344

292
g-index

360
all docs

360
docs citations

360
times ranked

118674
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.	3.3	39
2	SignalP 6.0 predicts all five types of signal peptides using protein language models. <i>Nature Biotechnology</i> , 2022, 40, 1023-1025.	9.4	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.	2.0	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.	0.8	1
5	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. <i>Nature Communications</i> , 2022, 13, 634.	5.8	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.	0.8	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.	0.9	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.	1.5	3
9	Modeling of waning immunity after SARS-CoV-2 vaccination and influencing factors. <i>Nature Communications</i> , 2022, 13, 1614.	5.8	117
10	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. <i>Nature Communications</i> , 2022, 13, 1598.	5.8	8
11	Multiomics 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.	0.5	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.	0.8	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.	0.6	12
14	Temporal patterns of multi-morbidity in 570157 ischemic heart disease patients: a nationwide cohort study. <i>Cardiovascular Diabetology</i> , 2022, 21, .	2.7	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.	0.4	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.	1.0	5
17	Classification of Left and Right Coronary Arteries in Coronary Angiographies Using Deep Learning. <i>Electronics (Switzerland)</i> , 2022, 11, 2087.	1.8	2
18	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). <i>International Journal of Epidemiology</i> , 2021, 50, 719-720e.	0.9	23

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19	Semen quality and waiting time to pregnancy explored using association mining. <i>Andrology</i> , 2021, 9, 577-587.	1.9	12
20	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021, 4, 156.	2.0	72
21	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021, 42, 1959-1971.	1.0	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.	1.2	7
23	Artificial Intelligence and Early Detection of Pancreatic Cancer. <i>Pancreas</i> , 2021, 50, 251-279.	0.5	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.	1.8	6
25	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. <i>Gut</i> , 2021, 70, 1538-1549.	6.1	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.	2.2	8
27	Endotrophin is associated with chronic multimorbidity and all-cause mortality in a cohort of elderly women. <i>EBioMedicine</i> , 2021, 68, 103391.	2.7	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.	2.0	12
29	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. <i>Scientific Reports</i> , 2021, 11, 13153.	1.6	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.	0.3	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.	1.2	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.	1.3	0
33	Chance of live birth: a nationwide, registry-based cohort study. <i>Human Reproduction</i> , 2021, 36, 1065-1073.	0.4	31
34	Time-ordered comorbidity correlations identify patients at risk of mis- and overdiagnosis. <i>Npj Digital Medicine</i> , 2021, 4, 12.	5.7	8
35	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	4.3	16
36	Optimizing drug selection from a prescription trajectory of one patient. <i>Npj Digital Medicine</i> , 2021, 4, 150.	5.7	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.	0.8	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.	2.3	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.	3.6	8
40	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	13.7	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.	2.7	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.	2.9	4
43	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , 2020, 517, 110923.	1.6	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.	1.0	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.	5.8	70
46	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. <i>Genome Medicine</i> , 2020, 12, 76.	3.6	15
47	Alcoholic liver disease: A registry view on comorbidities and disease prediction. <i>PLoS Computational Biology</i> , 2020, 16, e1008244.	1.5	11
48	Disease Trajectories for Hidradenitis Suppurativa in the Danish Population. <i>JAMA Dermatology</i> , 2020, 156, 780.	2.0	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.	1.4	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.	1.5	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.	3.9	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.	6.6	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.	5.9	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.	2.2	29

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55	Sex differences in text-mined possible adverse drug events associated with drugs for psychosis. <i>Journal of Psychopharmacology</i> , 2020, 34, 532-539.	2.0	13
56	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. <i>Diabetologia</i> , 2020, 63, 744-756.	2.9	12
57	Age-stratified longitudinal study of Alzheimer's and vascular dementia patients. <i>Alzheimer's and Dementia</i> , 2020, 16, 908-917.	0.4	25
58	Phenome-wide Analysis of Short- and Long-Run Disease Incidence Following Recurrent Pregnancy Loss Using Data From a 39-Year Period. <i>Journal of the American Heart Association</i> , 2020, 9, e015069.	1.6	20
59	Lipidomic profiles, lipid trajectories and clinical biomarkers in female elite endurance athletes. <i>Scientific Reports</i> , 2020, 10, 2349.	1.6	9
60	ARDD 2020: from aging mechanisms to interventions. <i>Aging</i> , 2020, 12, 24484-24503.	1.4	32
61	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. <i>PLoS ONE</i> , 2020, 15, e0242360.	1.1	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. <i>Npj Systems Biology and Applications</i> , 2019, 5, 27.	1.4	11
68	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, 164.	3.8	39
69	Incorporating symptom data in longitudinal disease trajectories for more detailed patient stratification. <i>International Journal of Medical Informatics</i> , 2019, 129, 107-113.	1.6	9
70	sAOP: linking chemical stressors to adverse outcomes pathway networks. <i>Bioinformatics</i> , 2019, 35, 5391-5392.	1.8	19
71	Combined Ensemble Docking and Machine Learning in Identification of Therapeutic Agents with Potential Inhibitory Effect on Human CES1. <i>Molecules</i> , 2019, 24, 2747.	1.7	6
72	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multi-enrichment Approach. <i>Journal of Infectious Diseases</i> , 2019, 220, 1312-1324.	1.9	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.	7.7	69
74	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019, 38, 200-216.	0.7	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.	5.9	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.	2.9	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.	0.8	68
78	Comorbidity landscape of the Danish patient population affected by chromosome abnormalities. <i>Genetics in Medicine</i> , 2019, 21, 2485-2495.	1.1	13
79	The use of systems biology in chemical risk assessment. <i>Current Opinion in Toxicology</i> , 2019, 15, 48-54.	2.6	10
80	Combing the Hairball: Improving Visualization of miRNA-Target Interaction Networks. <i>Methods in Molecular Biology</i> , 2019, 1970, 279-289.	0.4	0
81	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , 2019, 51, 924-930.	9.4	22
82	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , 2019, 10, 666.	5.8	128
83	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	9.4	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.	5.8	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.	1.8	13
86	A Large-Cohort, Longitudinal Study Determines Precancer Disease Routes across Different Cancer Types. <i>Cancer Research</i> , 2019, 79, 864-872.	0.4	17
87	Linking glycaemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. <i>ELife</i> , 2019, 8, .	2.8	12
88	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	21.5	263
89	Familial co-occurrence of congenital heart defects follows distinct patterns. <i>European Heart Journal</i> , 2018, 39, 1015-1022.	1.0	32
90	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	6.5	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.	2.9	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.	1.1	22
93	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. <i>Acta Veterinaria Scandinavica</i> , 2018, 60, 61.	0.5	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.	5.5	82
95	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. <i>RNA Technologies</i> , 2018, , 229-238.	0.2	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.	2.7	33
97	Retinoic Acid Signaling in Thymic Epithelial Cells Regulates Thymopoiesis. <i>Journal of Immunology</i> , 2018, 201, 524-532.	0.4	15
98	Benchmarking the HLA typing performance of Polysolver and Optitype in 50 Danish parental trios. <i>BMC Bioinformatics</i> , 2018, 19, 239.	1.2	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.	1.5	112
100	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , 2018, 13, e0189886.	1.1	9
101	The protein kinase SIK downregulates the polarity protein Par3. <i>Oncotarget</i> , 2018, 9, 5716-5735.	0.8	11
102	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. <i>Oncotarget</i> , 2018, 9, 9043-9060.	0.8	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.	0.8	10
104	Increase in clinically recorded type 2 diabetes after colectomy. <i>ELife</i> , 2018, 7, .	2.8	23
105	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017, 45, D995-D1002.	6.5	271
106	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , 2017, 60, 475-489.	2.9	31
107	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. <i>Methods in Molecular Biology</i> , 2017, 1580, 281-295.	0.4	2
108	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. <i>Reproduction</i> , 2017, 154, 145-152.	1.1	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.	1.4	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.	2.9	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.	1.3	14
112	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 3242-3256.	2.9	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 ÅYM155 in neuroblastoma via inhibition of the ABCB1 efflux transporter. <i>Scientific Reports</i> , 2017, 7, 3091.	1.6	35
115	Protein features as determinants of wild-type glycoside hydrolase thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2036-2044.	1.5	5
116	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	1.9	17
117	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017, 14, 61-64.	9.0	534
118	Pancreatic Islet Protein Complexes and Their Dysregulation in Type 2 Diabetes. <i>Frontiers in Genetics</i> , 2017, 8, 43.	1.1	19
119	The impact of the protein interactome on the syntenic structure of mammalian genomes. <i>PLoS ONE</i> , 2017, 12, e0179112.	1.1	8
120	Cutavirus in Cutaneous Malignant Melanoma. <i>Emerging Infectious Diseases</i> , 2017, 23, 363-365.	2.0	22
121	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
122	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , 2017, 13, e1006706.	1.5	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.	1.9	39
124	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , 2016, 8, 53.	1.5	11
125	ChemProt-3.0: a global chemical biology diseases mapping. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav123.	1.4	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.	0.3	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. <i>World Journal for Pediatric & Congenital Heart Surgery</i> , 2016, 7, 169-177.	0.3	5
128	Network biology concepts in complex disease comorbidities. <i>Nature Reviews Genetics</i> , 2016, 17, 615-629.	7.7	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. <i>Congenital Heart Disease</i> , 2016, 11, 283-290.	0.0	81
130	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
131	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
132	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. <i>Npj Genomic Medicine</i> , 2016, 1, 16035.	1.7	21
133	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016, 1, 16152.	5.9	56
134	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. <i>Scientific Reports</i> , 2016, 6, 36624.	1.6	66
135	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. <i>BMC Genomics</i> , 2016, 17, 396.	1.2	11
136	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. <i>Human Mutation</i> , 2016, 37, 36-42.	1.1	10
137	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	6.5	113
138	<i>Propionibacterium acnes</i> : Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016, 54, 980-987.	1.8	87
139	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016, 48, 510-518.	9.4	617
140	The hunt for fatal myocardial infarction biomarkers: predictive circulating microRNAs. <i>Annals of Translational Medicine</i> , 2016, 4, S1-S1.	0.7	0
141	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	1.6	34
142	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	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. <i>BMJ Open</i> , 2015, 5, e008702.	0.8	10
144	Traces of ATCV-1 associated with laboratory component contamination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E925-6.	3.3	24

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145	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	5.8	164
146	Individualization of treatments with drugs metabolized by CES1: combining genetics and metabolomics. <i>Pharmacogenomics</i> , 2015, 16, 649-665.	0.6	19
147	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	13.5	425
148	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
149	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. <i>Journal of Research in Pharmacy Practice</i> , 2015, 4, 64.	0.2	6
150	REACH and Environmental Chemicals. <i>QSAR in Environmental and Health Sciences</i> , 2015, , 23-36.	0.3	1
151	Finding Cervical Cancer Symptoms in Swedish Clinical Text using a Machine Learning Approach and NegEx. <i>AMIA ... Annual Symposium proceedings</i> , 2015, 2015, 1296-305.	0.2	5
152	Identification of Odorant-Receptor Interactions by Global Mapping of the Human Odorome. <i>PLoS ONE</i> , 2014, 9, e93037.	1.1	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. <i>Frontiers in Physiology</i> , 2014, 5, 332.	1.3	15
155	Discrepancies in listed adverse drug reactions in pharmaceutical product information supplied by the regulatory authorities in Denmark and the USA. <i>Pharmacology Research and Perspectives</i> , 2014, 2, e00038.	1.1	17
156	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	13.7	500
157	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1819-1828.	1.5	36
158	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.	13.7	821
159	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. <i>Briefings in Bioinformatics</i> , 2014, 15, 942-952.	3.2	16
160	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.	1.8	73
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