SÃ¸ren Brunak

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7332153/publications.pdf

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	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	13.7	9,342
2	SignalP 4.0: discriminating signal peptides from transmembrane regions. Nature Methods, 2011, 8, 785-786.	9.0	8,521
3	Improved Prediction of Signal Peptides: SignalP 3.0. Journal of Molecular Biology, 2004, 340, 783-795.	2.0	6,015
4	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
5	Predicting Subcellular Localization of Proteins Based on their N-terminal Amino Acid Sequence. Journal of Molecular Biology, 2000, 300, 1005-1016.	2.0	4,166
6	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	13.7	3,641
7	SignalP 5.0 improves signal peptide predictions using deep neural networks. Nature Biotechnology, 2019, 37, 420-423.	9.4	3,317
8	Locating proteins in the cell using TargetP, SignalP and related tools. Nature Protocols, 2007, 2, 953-971.	5.5	2,940
9	Sequence and structure-based prediction of eukaryotic protein phosphorylation sites. Journal of Molecular Biology, 1999, 294, 1351-1362.	2.0	2,767
10	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. Proteomics, 2004, 4, 1633-1649.	1.3	1,784
11	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	9.4	1,664
12	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	13.7	1,627
13	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	13.7	1,506
14	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	1.6	1,319
15	Mining electronic health records: towards better research applications and clinical care. Nature Reviews Genetics, 2012, 13, 395-405.	7.7	1,226
16	Population genomics of Bronze Age Eurasia. Nature, 2015, 522, 167-172.	13.7	1,166
17	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. EMBO Journal, 2013, 32, 1478-1488.	3.5	1,130
18	Feature-based prediction of non-classical and leaderless protein secretion. Protein Engineering, Design and Selection, 2004, 17, 349-356.	1.0	1,089

#	Article	IF	Citations
19	Prediction of lipoprotein signal peptides in Gram-negative bacteria. Protein Science, 2003, 12, 1652-1662.	3.1	1,016
20	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. Protein Science, 2003, 12, 1007-1017.	3.1	1,013
21	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	9.4	909
22	SignalP 6.0 predicts all five types of signal peptides using protein language models. Nature Biotechnology, 2022, 40, 1023-1025.	9.4	883
23	A human phenome-interactome network of protein complexes implicated in genetic disorders. Nature Biotechnology, 2007, 25, 309-316.	9.4	871
24	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. Glycobiology, 2005, 15, 153-164.	1.3	825
25	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	13.7	821
26	Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature, 2010, 463, 757-762.	13.7	750
27	Prediction of human mRNA donor and acceptor sites from the DNA sequence. Journal of Molecular Biology, 1991, 220, 49-65.	2.0	749
28	Analysis and prediction of leucine-rich nuclear export signals. Protein Engineering, Design and Selection, 2004, 17, 527-536.	1.0	721
29	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	13.7	717
30	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	6.0	675
31	Non-classical protein secretion in bacteria. BMC Microbiology, 2005, 5, 58.	1.3	663
32	A Neural Network Method for Identification of Prokaryotic and Eukaryotic Signal Peptides and Prediction of their Cleavage Sites. International Journal of Neural Systems, 1997, 08, 581-599.	3.2	645
33	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
34	Machine learning approaches for the prediction of signal peptides and other protein sorting signals. Protein Engineering, Design and Selection, 1999, 12, 3-9.	1.0	546
35	A scored human proteinâ€“protein interaction network to catalyze genomic interpretation. Nature Methods, 2017, 14, 61-64.	9.0	534
36	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	13.7	500

#	Article	IF	Citations
37	Prediction of proprotein convertase cleavage sites. Protein Engineering, Design and Selection, 2004, 17, 107-112.	1.0	499
38	NetOglyc: prediction of mucin type O-glycosylation sites based on sequence context and surface accessibility. Glycoconjugate Journal, 1998, 15, 115-130.	1.4	493
39	Prediction of twin-arginine signal peptides. BMC Bioinformatics, 2005, 6, 167.	1.2	465
40	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	9.0	442
41	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	13.7	439
42	A new non-linear normalization method for reducing variability in DNA microarray experiments. Genome Biology, 2002, 3, research0048.1.	13.9	430
43	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	13.5	425
44	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	1.6	418
45	Dynamic Complex Formation During the Yeast Cell Cycle. Science, 2005, 307, 724-727.	6.0	382
46	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. Journal of Molecular Biology, 2002, 319, 1257-1265.	2.0	312
47	An integrative approach to CTL epitope prediction: A combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. European Journal of Immunology, 2005, 35, 2295-2303.	1.6	290
48	Sensitive quantitative predictions of peptide-MHC binding by a â€˜Query by Committeeâ€™ artificial neural network approach. Tissue Antigens, 2003, 62, 378-384.	1.0	289
49	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. Nature Communications, 2014, 5, 4022.	5.8	289
50	A large-scale analysis of tissue-specific pathology and gene expression of human disease genes and complexes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20870-20875.	3.3	288
51	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. BMC Genomics, 2005, 6, 70.	1.2	283
52	Prediction of glycosylation across the human proteome and the correlation to protein function. , 2001, , .		276
53	PhosphoBase, a database of phosphorylation sites: release 2.0. Nucleic Acids Research, 1999, 27, 237-239.	6.5	273
54	Pharos: Collating protein information to shed light on the druggable genome. Nucleic Acids Research, 2017, 45, D995-D1002.	6.5	271

#	ARTICLE	IF	CITATIONS
55	Definition of supertypes for HLA molecules using clustering of specificity matrices. Immunogenetics, 2004, 55, 797-810.	1.2	269
56	Network biology concepts in complex disease comorbidities. Nature Reviews Genetics, 2016, 17, 615-629.	7.7	269
57	Prediction of proteasome cleavage motifs by neural networks. Protein Engineering, Design and Selection, 2002, 15, 287-296.	1.0	263
58	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	21.5	263
59	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. Bioinformatics, 2004, 20, 1388-1397.	1.8	254
60	Clustering Patterns of Cytotoxic T-Lymphocyte Epitopes in Human Immunodeficiency Virus Type 1 (HIV-1) Proteins Reveal Imprints of Immune Evasion on HIV-1 Global Variation. Journal of Virology, 2002, 76, 8757-8768.	1.5	241
61	Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. PLoS Computational Biology, 2011, 7, e1002141.	1.5	236
62	Intrauterine exposure to mild analgesics is a risk factor for development of male reproductive disorders in human and rat. Human Reproduction, 2011, 26, 235-244.	0.4	234
63	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	13.7	230
64	Cleavage site analysis in picornaviral polyproteins: Discovering cellular targets by neural networks. Protein Science, 1996, 5, 2203-2216.	3.1	219
65	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. Nucleic Acids Research, 1999, 27, 370-372.	6.5	213
66	A DNA structural atlas for Escherichia coli 1 1Edited by T. Richmond. Journal of Molecular Biology, 2000, 299, 907-930.	2.0	213
67	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	13.5	209
68	The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500.	3.3	206
69	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R107.	13.9	205
70	Alternative Splicing in Colon, Bladder, and Prostate Cancer Identified by Exon Array Analysis. Molecular and Cellular Proteomics, 2008, 7, 1214-1224.	2.5	202
71	NESbase version 1.0: a database of nuclear export signals. Nucleic Acids Research, 2003, 31, 393-396.	6.5	195
72	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194

#	Article	IF	Citations
73	On the total number of genes and their length distribution in complete microbial genomes. Trends in Genetics, 2001, 17, 425-428.	2.9	193
74	Comparison of computational methods for the identification of cell cycle-regulated genes. Bioinformatics, 2005, 21, 1164-1171.	1.8	190
75	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. The Lancet Digital Health, 2020, 2, e179-e191.	5.9	187
76	The biology of eukaryotic promoter predictionâ€”a review. Computers & Chemistry, 1999, 23, 191-207.	1.2	177
77	Bacterial natural transformation by highly fragmented and damaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19860-19865.	3.3	170
78	Analysis and prediction of mammalian protein glycation. Glycobiology, 2006, 16, 844-853.	1.3	169
79	Analysis of Gene Expression Profiles of Microdissected Cell Populations Indicates that Testicular Carcinoma <i>In situ</i> Is an Arrested Gonocyte. Cancer Research, 2009, 69, 5241-5250.	0.4	169
80	Co-evolution of transcriptional and post-translational cell-cycle regulation. Nature, 2006, 443, 594-597.	13.7	168
81	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969.	5.8	164
82	Protein secondary structure and homology by neural networks The Î±-helices in rhodopsin. FEBS Letters, 1988, 241, 223-228.	1.3	158
83	A Brief History of Protein Sorting Prediction. Protein Journal, 2019, 38, 200-216.	0.7	154
84	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. Scientific Reports, 2021, 11, 13153.	1.6	147
85	Continuum Secondary Structure Captures Protein Flexibility. Structure, 2002, 10, 175-184.	1.6	135
86	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	13.7	130
87	Population-wide analysis of differences in disease progression patterns in men and women. Nature Communications, 2019, 10, 666.	5.8	128
88	Improving the Odds in Discriminating â€œDrug-likeâ€•from â€œNon Drug-likeâ€•Compounds. Journal of Chemical Information and Computer Sciences, 2000, 40, 1315-1324.	2.8	125
89	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. American Journal of Human Genetics, 2013, 93, 1072-1086.	2.6	124
90	Statistical analysis of protein kinase specificity determinants. FEBS Letters, 1998, 430, 45-50.	1.3	123

#	ARTICLE	IF	CITATIONS
91	Prediction of N-terminal protein sorting signals. Current Opinion in Structural Biology, 1997, 7, 394-398.	2.6	122
92	Genetic and environmental risk factors in congenital heart disease functionally converge in protein networks driving heart development. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14035-14040.	3.3	117
93	Modeling of waning immunity after SARS-CoV-2 vaccination and influencing factors. Nature Communications, 2022, 13, 1614.	5.8	117
94	Modeling the adaptive immune system: predictions and simulations. Bioinformatics, 2007, 23, 3265-3275.	1.8	115
95	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113
96	Prediction of protein secondary structure at 80% accuracy. Proteins: Structure, Function and Bioinformatics, 2000, 41, 17-20.	1.5	112
97	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. PLoS Computational Biology, 2018, 14, e1005962.	1.5	112
98	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	2.9	110
99	A novel approach to prediction of the 3-dimensional structures of protein backbones by neural networks. FEBS Letters, 1990, 261, 43-46.	1.3	107
100	Scanning the available Dictyostelium discoideum proteome for O-linked GlcNAc glycosylation sites using neural networks. Glycobiology, 1999, 9, 1009-1022.	1.3	99
101	Prediction methods and databases within chemoinformatics: emphasis on drugs and drug candidates. Bioinformatics, 2005, 21, 2145-2160.	1.8	98
102	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. Journal of Medical Genetics, 2012, 49, 58-65.	1.5	96
103	Dose-Specific Adverse Drug Reaction Identification in Electronic Patient Records: Temporal Data Mining in an Inpatient Psychiatric Population. Drug Safety, 2014, 37, 237-247.	1.4	96
104	A Systematic Study of Site-specific GalNAc-type O-Glycosylation Modulating Proprotein Convertase Processing. Journal of Biological Chemistry, 2011, 286, 40122-40132.	1.6	93
105	hERG Classification Model Based on a Combination of Support Vector Machine Method and GRIND Descriptors. Molecular Pharmaceutics, 2008, 5, 117-127.	2.3	91
106	Immune Profiling of Human Gut-Associated Lymphoid Tissue Identifies a Role for Isolated Lymphoid Follicles in Priming of Region-Specific Immunity. Immunity, 2020, 52, 557-570.e6.	6.6	90
107	Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology. BMC Bioinformatics, 2004, 5, 72.	1.2	88
108	Identification of Phosphorylation Sites in Protein Kinase A Substrates Using Artificial Neural Networks and Mass Spectrometry. Journal of Proteome Research, 2004, 3, 426-433.	1.8	88

#	ARTICLE	IF	CITATIONS
109	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.	1.8	87
110	Predicting proteasomal cleavage sites: a comparison of available methods. International Immunology, 2003, 15, 781-787.	1.8	86
111	Many Putative Endocrine Disruptors Inhibit Prostaglandin Synthesis. Environmental Health Perspectives, 2011, 119, 534-541.	2.8	85
112	Prediction of pH-Dependent Aqueous Solubility of Druglike Molecules. Journal of Chemical Information and Modeling, 2006, 46, 2601-2609.	2.5	84
113	A computational framework to integrate high-throughput â€˜-omicsâ€™ datasets for the identification of potential mechanistic links. Nature Protocols, 2018, 13, 2781-2800.	5.5	82
114	DNA structure in human RNA polymerase II promoters 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 281, 663-673.	2.0	81
115	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.	0.0	81
116	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. Cell Reports, 2017, 18, 3242-3256.	2.9	81
117	Dissecting spatioâ€•temporal protein networks driving human heart development and related disorders. Molecular Systems Biology, 2010, 6, 381.	3.2	80
118	Genome organisation and chromatin structure in Escherichia coli. Biochimie, 2001, 83, 201-212.	1.3	79
119	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. The Lancet Digital Health, 2019, 1, e78-e89.	5.9	76
120	Defining a similarity threshold for a functional protein sequence pattern: The signal peptide cleavage site. , 1996, 24, 165-177.		75
121	ChemProt-3.0: a global chemical biology diseases mapping. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav123.	1.4	75
122	Blood cell gene expression profiling in rheumatoid arthritis. Immunology Letters, 2004, 93, 217-226.	1.1	73
123	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	1.8	73
124	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. Human Molecular Genetics, 2017, 26, 1219-1229.	1.4	73
125	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
126	ChemProt: a disease chemical biology database. Nucleic Acids Research, 2011, 39, D367-D372.	6.5	71

#	Article	IF	Citations
127	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 947-953.	2.2	71
128	Artificial Intelligence and Early Detection of Pancreatic Cancer. Pancreas, 2021, 50, 251-279.	0.5	71
129	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	9.0	70
130	Disease trajectory browser for exploring temporal, population-wide disease progression patterns in 7.2 million Danish patients. Nature Communications, 2020, 11, 4952.	5.8	70
131	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	7.7	69
132	Sigma A recognition sites in the Bacillus subtilis genome. Microbiology (United Kingdom), 2001, 147, 2417-2424.	0.7	69
133	Naturally Occurring Nucleosome Positioning Signals in Human Exons and Introns. Journal of Molecular Biology, 1996, 263, 503-510.	2.0	68
134	Cyclebase.org a comprehensive multi-organism online database of cell-cycle experiments. Nucleic Acids Research, 2007, 36, D854-D859.	6.5	68
135	DBDS Genomic Cohort, a prospective and comprehensive resource for integrative and temporal analysis of genetic, environmental and lifestyle factors affecting health of blood donors. BMJ Open, 2019, 9, e028401.	0.8	68
136	Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. Genome Biology, 2007, 8, R45.	13.9	67
137	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. Scientific Reports, 2016, 6, 36624.	1.6	66
138	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	6.5	61
139	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
140	Multiple alignment using simulated annealing: branch point definition in human mRNA splicing. Nucleic Acids Research, 1992, 20, 2511-2516.	6.5	60
141	A Wiring of the Human Nucleolus. Molecular Cell, 2006, 22, 285-295.	4.5	56
142	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. Nature Microbiology, 2016, 1, 16152.	5.9	56
143	Huntingtin-interacting protein 14 is a type 1 diabetes candidate protein regulating insulin secretion and Î²-cell apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E681-8.	3.3	55
144	Protein Interaction-Based Genome-Wide Analysis of Incident Coronary Heart Disease. Circulation: Cardiovascular Genetics, 2011, 4, 549-556.	5.1	55

#	ARTICLE	IF	CITATIONS
145	Protein structure and the sequential structure of mRNA: Î±â€helix and Î²â€sheet signals at the nucleotide level. Proteins: Structure, Function and Bioinformatics, 1996, 25, 237-252.	1.5	54
146	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	13.9	53
147	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. Nucleic Acids Research, 2010, 38, D699-D702.	6.5	53
148	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. Genome Biology, 2007, 8, R253.	13.9	52
149	Cometin is a novel neurotrophic factor that promotes neurite outgrowth and neuroblast migration in vitro and supports survival of spiral ganglion neurons in vivo. Experimental Neurology, 2012, 233, 172-181.	2.0	52
150	Complete Genes May Pass from Food to Human Blood. PLoS ONE, 2013, 8, e69805.	1.1	52
151	ChemProt-2.0: visual navigation in a disease chemical biology database. Nucleic Acids Research, 2012, 41, D464-D469.	6.5	50
152	Protein Structures from Distance Inequalities. Journal of Molecular Biology, 1993, 231, 861-869.	2.0	49
153	Immunological Bioinformatics. , 2005, , .		49
154	New weakly expressed cell cycle-regulated genes in yeast. Yeast, 2005, 22, 1191-1201.	0.8	48
155	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.	2.9	48
156	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. PLoS Medicine, 2020, 17, e1003149.	3.9	47
157	Deciphering Diseases and Biological Targets for Environmental Chemicals using Toxicogenomics Networks. PLoS Computational Biology, 2010, 6, e1000788.	1.5	43
158	Identification of Odorant-Receptor Interactions by Global Mapping of the Human Odorome. PLoS ONE, 2014, 9, e93037.	1.1	42
159	Computational analyses and annotations of theArabidopsisperoxidase gene family. FEBS Letters, 1998, 433, 98-102.	1.3	41
160	Optimization and immune recognition of multiple novel conserved HLA-A2, human immunodeficiency virus type 1-specific CTL epitopes. Journal of General Virology, 2003, 84, 2409-2421.	1.3	40
161	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. Acta Veterinaria Scandinavica, 2018, 60, 61.	0.5	40
162	G + C-rich tract in 5â€² end of human introns. Journal of Molecular Biology, 1992, 227, 108-113.	2.0	39

#	Article	IF	Citations
163	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale <sup />. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2799-2815.	1.6	39
164	Integration of Known DNA, RNA and Protein Biomarkers Provides Prediction of Anti-TNF Response in Rheumatoid Arthritis: Results from the COMBINE Study. Molecular Medicine, 2016, 22, 322-328.	1.9	39
165	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	3.8	39
166	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study. Cell Reports Medicine, 2022, 3, 100477.	3.3	39
167	Cleaning up gene databases. Nature, 1990, 343, 123-123.	13.7	37
168	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. Reproduction, 2017, 154, 145-152.	1.1	37
169	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. Briefings in Bioinformatics, 2008, 10, 330-340.	3.2	36
170	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1819-1828.	1.5	36
171	Prediction of the secondary structure of HIV-1 gp120. , 1996, 25, 1-11.		35
172	Functionality of System Components: Conservation of Protein Function in Protein Feature Space. Genome Research, 2003, 13, 2444-2449.	2.4	35
173	Lapatinib potentiates cytotoxicity of ÂYM155 in neuroblastoma via inhibition of the ABCB1 efflux transporter. Scientific Reports, 2017, 7, 3091.	1.6	35
174	Protein structure and the sequential structure of mRNA: Î±-Helix and Î²-sheet signals at the nucleotide level. Proteins: Structure, Function and Bioinformatics, 1996, 25, 237-252.	1.5	34
175	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. Scientific Reports, 2015, 5, 13201.	1.6	34
176	Benchmarking the HLA typing performance of Polysolver and Optitype in 50 Danish parental trios. BMC Bioinformatics, 2018, 19, 239.	1.2	34
177	Relationship between protein structure and geometrical constraints. Protein Science, 1996, 5, 2217-2225.	3.1	33
178	Prediction of novel archaeal enzymes from sequence-derived features. Protein Science, 2009, 11, 2894-2898.	3.1	33
179	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.	1.1	33
180	Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells. Cell Death and Disease, 2018, 9, 586.	2.7	33

#	ARTICLE	IF	CITATIONS
181	Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands. PLoS ONE, 2009, 4, e7448.	1.1	33
182	Bias of purine stretches in sequenced chromosomes. Computers & Chemistry, 2002, 26, 531-541.	1.2	32
183	Familial co-occurrence of congenital heart defects follows distinct patterns. European Heart Journal, 2018, 39, 1015-1022.	1.0	32
184	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. Diabetologia, 2018, 61, 117-129.	2.9	32
185	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	1.4	32
186	Evolution of Cell Cycle Control: Same Molecular Machines, Different Regulation. Cell Cycle, 2007, 6, 1819-1825.	1.3	31
187	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. Genetic Epidemiology, 2011, 35, 318-332.	0.6	31
188	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. Diabetologia, 2017, 60, 475-489.	2.9	31
189	Chance of live birth: a nationwide, registry-based cohort study. Human Reproduction, 2021, 36, 1065-1073.	0.4	31
190	Analysis of eukaryotic promoter sequences reveals a systematically occurring CT-signal. Nucleic Acids Research, 1995, 23, 1223-1230.	6.5	30
191	SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. Bioinformatics, 2007, 23, i387-i391.	1.8	29
192	Integration of Clinical Chemistry, Expression, and Metabolite Data Leads to Better Toxicological Class Separation. Toxicological Sciences, 2008, 102, 444-454.	1.4	29
193	OCT4 and downstream factors are expressed in human somatic urogenital epithelia and in culture of epididymal spheres. Molecular Human Reproduction, 2010, 16, 835-845.	1.3	29
194	A computational approach to chemical etiologies of diabetes. Scientific Reports, 2013, 3, 2712.	1.6	29
195	Secreted breast tumor interstitial fluid microRNAs and their target genes are associated with triple-negative breast cancer, tumor grade, and immune infiltration. Breast Cancer Research, 2020, 22, 73.	2.2	29
196	Randomized Phase II Study of Nivolumab With or Without Ipilimumab Combined With Stereotactic Body Radiotherapy for Refractory Metastatic Pancreatic Cancer (CheckPAC). Journal of Clinical Oncology, 2022, 40, 3180-3189.	0.8	29
197	Protein Feature Based Identification of Cell Cycle Regulated Proteins in Yeast. Journal of Molecular Biology, 2003, 329, 663-674.	2.0	28
198	Knowledge engineering for health: A new discipline required to bridge the â€œICT gapâ€•between research and healthcare. Human Mutation, 2012, 33, 797-802.	1.1	27

#	ARTICLE	IF	CITATIONS
199	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
200	Bacterial diversity in snow on North Pole ice floes. Extremophiles, 2014, 18, 945-951.	0.9	26
201	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.5	26
202	Analysis and prediction of gene splice sites in four Aspergillus genomes. Fungal Genetics and Biology, 2009, 46, S14-S18.	0.9	25
203	Ageâ€stratified longitudinal study of Alzheimer's and vascular dementia patients. Alzheimer's and Dementia, 2020, 16, 908-917.	0.4	25
204	Concordance of gene expression in human protein complexes reveals tissue specificity and pathology. Nucleic Acids Research, 2013, 41, e171-e171.	6.5	24
205	MetaRanker 2.0: a web server for prioritization of genetic variation data. Nucleic Acids Research, 2013, 41, W104-W108.	6.5	24
206	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.	3.3	24
207	Protein secondary structure: category assignment and predictability. FEBS Letters, 2001, 507, 6-10.	1.3	23
208	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). International Journal of Epidemiology, 2021, 50, 719-720e.	0.9	23
209	Increase in clinically recorded type 2 diabetes after colectomy. ELife, 2018, 7, .	2.8	23
210	Identification of a new hTERT-derived HLA-A*0201 restricted, naturally processed CTL epitope. Cancer Immunology, Immunotherapy, 2007, 56, 1755-1763.	2.0	22
211	Cutavirus in Cutaneous Malignant Melanoma. Emerging Infectious Diseases, 2017, 23, 363-365.	2.0	22
212	Analysis of Time-Series Gene Expression Data to Explore Mechanisms of Chemical-Induced Hepatic Steatosis Toxicity. Frontiers in Genetics, 2018, 9, 396.	1.1	22
213	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. Diabetologia, 2019, 62, 1601-1615.	2.9	22
214	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	9.4	22
215	The Type 1 Diabetes - HLA Susceptibility Interactome - Identification of HLA Genotype-Specific Disease Genes for Type 1 Diabetes. PLoS ONE, 2010, 5, e9576.	1.1	21
216	Bioinformatics-Driven Identification and Examination of Candidate Genes for Non-Alcoholic Fatty Liver Disease. PLoS ONE, 2011, 6, e16542.	1.1	21

#	ARTICLE	IF	CITATIONS
217	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. Npj Genomic Medicine, 2016, 1, 16035.	1.7	21
218	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. Gut, 2021, 70, 1538-1549.	6.1	21
219	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
220	Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. PLoS ONE, 2013, 8, e68370.	1.1	20
221	Phenomeâ€•Wide Analysis of Shortâ€•and Longâ€•Run Disease Incidence Following Recurrent Pregnancy Loss Using Data From a 39â€•Year Period. Journal of the American Heart Association, 2020, 9, e015069.	1.6	20
222	Endotrophin is associated with chronic multimorbidity and all-cause mortality in a cohort of elderly women. EBioMedicine, 2021, 68, 103391.	2.7	20
223	Modelling the Human Immune System by Combining Bioinformatics and Systems Biology Approaches. Journal of Biological Physics, 2006, 32, 335-353.	0.7	19
224	Individualization of treatments with drugs metabolized by CES1: combining genetics and metabolomics. Pharmacogenomics, 2015, 16, 649-665.	0.6	19
225	Pancreatic Islet Protein Complexes and Their Dysregulation in Type 2 Diabetes. Frontiers in Genetics, 2017, 8, 43.	1.1	19
226	sAOP: linking chemical stressors to adverse outcomes pathway networks. Bioinformatics, 2019, 35, 5391-5392.	1.8	19
227	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.	1.1	17
228	Combinatorial Drug Screening Identifies Ewing Sarcomaâ€“specific Sensitivities. Molecular Cancer Therapeutics, 2017, 16, 88-101.	1.9	17
229	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. Nature Communications, 2019, 10, 5508.	5.8	17
230	A Large-Cohort, Longitudinal Study Determines Precancer Disease Routes across Different Cancer Types. Cancer Research, 2019, 79, 864-872.	0.4	17
231	Disease Trajectories for Hidradenitis Suppurativa in the Danish Population. JAMA Dermatology, 2020, 156, 780.	2.0	17
232	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. Diabetes, 2021, 70, 2092-2106.	0.3	17
233	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. Briefings in Bioinformatics, 2014, 15, 942-952.	3.2	16
234	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	4.3	16

#	ARTICLE	IF	CITATIONS
235	Motif Decomposition of the Phosphotyrosine Proteome Reveals a New N-terminal Binding Motif for SHIP2. Molecular and Cellular Proteomics, 2008, 7, 181-192.	2.5	15
236	Patient stratification and identification of adverse event correlations in the space of 1190 drug related adverse events. Frontiers in Physiology, 2014, 5, 332.	1.3	15
237	Retinoic Acid Signaling in Thymic Epithelial Cells Regulates Thymopoiesis. Journal of Immunology, 2018, 201, 524-532.	0.4	15
238	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. Genome Medicine, 2020, 12, 76.	3.6	15
239	Expression Profiling of Human Genetic and Protein Interaction Networks in Type 1 Diabetes. PLoS ONE, 2009, 4, e6250.	1.1	15
240	Selecting Informative Data for Developing Peptide-MHC Binding Predictors Using a Query by Committee Approach. Neural Computation, 2003, 15, 2931-2942.	1.3	14
241	Uncovering the Molecular Machinery of the Human Spindleâ€"An Integration of Wet and Dry Systems Biology. PLoS ONE, 2012, 7, e31813.	1.1	14
242	Genome-Wide Assessment of the Association of Rare and Common Copy Number Variations to Testicular Germ Cell Cancer. Frontiers in Endocrinology, 2013, 4, 2.	1.5	14
243	Comparison of global gene expression profiles of microdissected human foetal Leydig cells with their normal and hyperplastic adult equivalents. Molecular Human Reproduction, 2017, 23, 339-354.	1.3	14
244	The Cancer Exome Generated by Alternative mRNA Splicing Dilutes Predicted HLA Class I Epitope Density. PLoS ONE, 2012, 7, e38670.	1.1	14
245	RNA Secondary Structure and Sequence Conservation in C1 Region of Human Immunodeficiency Virus Type 1envGene. AIDS Research and Human Retroviruses, 2002, 18, 867-878.	0.5	13
246	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. Journal of Infectious Diseases, 2019, 220, 1312-1324.	1.9	13
247	Comorbidity landscape of the Danish patient population affected by chromosome abnormalities. Genetics in Medicine, 2019, 21, 2485-2495.	1.1	13
248	A generic deep convolutional neural network framework for prediction of receptorâ€"ligand interactionsâ€"NetPhosPan: application to kinase phosphorylation prediction. Bioinformatics, 2019, 35, 1098-1107.	1.8	13
249	Sex differences in text-mined possible adverse drug events associated with drugs for psychosis. Journal of Psychopharmacology, 2020, 34, 532-539.	2.0	13
250	TEMPORAL ORDER OF DISEASE PAIRS AFFECTS SUBSEQUENT DISEASE TRAJECTORIES: THE CASE OF DIABETES AND SLEEP APNEA. , 2017, 22, 380-389.		12
251	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.	2.9	12
252	Semen quality and waiting time to pregnancy explored using association mining. Andrology, 2021, 9, 577-587.	1.9	12

#	ARTICLE	IF	CITATIONS
253	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. Communications Biology, 2021, 4, 655.	2.0	12
254	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. ELife, 2019, 8, .	2.8	12
255	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease. Communications Biology, 2022, 5, 80.	2.0	12
256	Intervening on the storage time of RBC units and its effects on adverse recipient outcomes using real-world data. Blood, 2022, 139, 3647-3654.	0.6	12
257	Transcriptome profiling of mice testes following low dose irradiation. Reproductive Biology and Endocrinology, 2013, 11, 50.	1.4	11
258	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. Viruses, 2016, 8, 53.	1.5	11
259	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. BMC Genomics, 2016, 17, 396.	1.2	11
260	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. Npj Systems Biology and Applications, 2019, 5, 27.	1.4	11
261	Alcoholic liver disease: A registry view on comorbidities and disease prediction. PLoS Computational Biology, 2020, 16, e1008244.	1.5	11
262	The protein kinase SIK downregulates the polarity protein Par3. Oncotarget, 2018, 9, 5716-5735.	0.8	11
263	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.	0.8	10
264	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. Human Mutation, 2016, 37, 36-42.	1.1	10
265	The use of systems biology in chemical risk assessment. Current Opinion in Toxicology, 2019, 15, 48-54.	2.6	10
266	Association of Variants Near the Bradykinin Receptor B2 Gene With Angioedema in Patients Taking ACEÂInhibitors. Journal of the American College of Cardiology, 2021, 78, 696-709.	1.2	10
267	Identifying the druggable interactome of EWS-FLI1 reveals MCL-1 dependent differential sensitivities of Ewing sarcoma cells to apoptosis inducers. Oncotarget, 2018, 9, 31018-31031.	0.8	10
268	The Atlas visualization of genomewide information. Methods in Microbiology, 2002, , 49-63.	0.4	9
269	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. Stem Cell Research, 2014, 13, 316-328.	0.3	9
270	Chromosome-wise Protein Interaction Patterns and Their Impact on Functional Implications of Large-Scale Genomic Aberrations. Cell Systems, 2017, 4, 357-364.e3.	2.9	9

#	ARTICLE	IF	CITATIONS
271	Incorporating symptom data in longitudinal disease trajectories for more detailed patient stratification. International Journal of Medical Informatics, 2019, 129, 107-113.	1.6	9
272	Lipidomic profiles, lipid trajectories and clinical biomarkers in female elite endurance athletes. Scientific Reports, 2020, 10, 2349.	1.6	9
273	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. PLoS ONE, 2018, 13, e0189886.	1.1	9
274	Drug interactions in hospital prescriptions in Denmark: Prevalence and associations with adverse outcomes. Pharmacoepidemiology and Drug Safety, 2022, 31, 632-642.	0.9	9
275	Recognition of environmental and genetic effects on barley phenolic fingerprints by neural networks. Computers & Chemistry, 2001, 25, 301-307.	1.2	8
276	Analysis of cell death inducing compounds. Archives of Toxicology, 2007, 81, 803-811.	1.9	8
277	Investigating the impact of missense mutations in hCES1 by <i>in silico</i> structure-based approaches. Drug Metabolism and Personalized Therapy, 2016, 31, 97-106.	0.3	8
278	The impact of the protein interactome on the syntenic structure of mammalian genomes. PLoS ONE, 2017, 12, e0179112.	1.1	8
279	Conflicting associations between dietary patterns and changes of anthropometric traits across subgroups of middle-aged women and men. Clinical Nutrition, 2020, 39, 265-275.	2.3	8
280	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. Genome Medicine, 2020, 12, 109.	3.6	8
281	Impaired Vitamin D Signaling in T Cells From a Family With Hereditary Vitamin D Resistant Rickets. Frontiers in Immunology, 2021, 12, 684015.	2.2	8
282	Time-ordered comorbidity correlations identify patients at risk of mis- and overdiagnosis. Npj Digital Medicine, 2021, 4, 12.	5.7	8
283	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. Oncotarget, 2018, 9, 9043-9060.	0.8	8
284	Optimizing drug selection from a prescription trajectory of one patient. Npj Digital Medicine, 2021, 4, 150.	5.7	8
285	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
286	Predictive utilities of lipid traits, lipoprotein subfractions and other risk factors for incident diabetes: a machine learning approach in the Diabetes Prevention Program. BMJ Open Diabetes Research and Care, 2021, 9, e001953.	1.2	7
287	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. PLoS ONE, 2020, 15, e0242360.	1.1	7
288	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. BMJ Open, 2021, 11, e049709.	0.8	7

#	ARTICLE	IF	CITATIONS
289	Combined Ensemble Docking and Machine Learning in Identification of Therapeutic Agents with Potential Inhibitory Effect on Human CES1. Molecules, 2019, 24, 2747.	1.7	6
290	The burden of disease of three food-associated heavy metals in clusters in the Danish population â€“ Towards targeted public health strategies. Food and Chemical Toxicology, 2021, 150, 112072.	1.8	6
291	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. Journal of Research in Pharmacy Practice, 2015, 4, 64.	0.2	6
292	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.	0.3	5
293	Protein features as determinants of wildâ€type glycoside hydrolase thermostability. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2036-2044.	1.5	5
294	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. Molecular and Cellular Endocrinology, 2020, 517, 110923.	1.6	5
295	Implementation and comparison of two text mining methods with a standard pharmacovigilance method for signal detection of medication errors. BMC Medical Informatics and Decision Making, 2020, 20, 94.	1.5	5
296	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
297	Polygenic risk score for ACE-inhibitor-associated cough based on the discovery of new genetic loci. European Heart Journal, 2022, 43, 4707-4718.	1.0	5
298	Circular reasoning rather than cyclic expression. Genome Biology, 2008, 9, 403.	13.9	4
299	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. BMC Bioinformatics, 2011, 12, 310.	1.2	4
300	Complete Topological Mapping of a Cellular Protein Interactome Reveals Bow-Tie Motifs as Ubiquitous Connectors of Protein Complexes. Cell Reports, 2020, 31, 107763.	2.9	4
301	Temporal patterns of multi-morbidity in 570157 ischemic heart disease patients: a nationwide cohort study. Cardiovascular Diabetology, 2022, 21, .	2.7	4
302	DNA Bendability and Nucleosome Positioning in Transcriptional Regulation. , 2005, , 189-202.		3
303	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. EBioMedicine, 2020, 58, 102932.	2.7	3
304	Association between antipsychotic drug dose and length of clinical notes: a proxy of disease severity?. BMC Medical Research Methodology, 2020, 20, 107.	1.4	3
305	Using Machine Learning to Identify Patients at High Risk of Inappropriate Drug Dosing in Periods with Renal Dysfunction. Clinical Epidemiology, 2022, Volume 14, 213-223.	1.5	3
306	MHC Class I Epitope Binding Prediction Trained on Small Data Sets. Lecture Notes in Computer Science, 2004, , 217-225.	1.0	2

#	Article	IF	Citations
307	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. Methods in Molecular Biology, 2017, 1580, 281-295.	0.4	2
308	Classification of Left and Right Coronary Arteries in Coronary Angiographies Using Deep Learning. Electronics (Switzerland), 2022, 11, 2087.	1.8	2
309	Protein annotation in the era of personal genomics. Current Opinion in Structural Biology, 2010, 20, 335-341.	2.6	1
310	Reply to 'Mining electronic health records: an additional perspective'. Nature Reviews Genetics, 2013, 14, 75-75.	7.7	1
311	Prediction of Protein Secondary Structure at High Accuracy Using a Combination of Many Neural Networks. Lecture Notes in Computer Science, 2003, , 117-122.	1.0	1
312	REACH and Environmental Chemicals. QSAR in Environmental and Health Sciences, 2015, , 23-36.	0.3	1
313	Randomized phase 2 study of nivolumab with or without ipilimumab in combination with stereotactic body radiotherapy in patients with refractory metastatic pancreatic cancer (CHECKPAC).. Journal of Clinical Oncology, 2022, 40, 554-554.	0.8	1
314	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. Joint Bone Spine, 2022, 89, 105357.	0.8	1
315	Just-in-time assembly of cell-cycle protein complexes. Nature Precedings, 2008, , .	0.1	0
316	The strength of intron donor splice sites in human genes displays a bell-shaped pattern. Bioinformatics, 2011, 27, 3079-3084.	1.8	0
317	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT â€œOMICSâ€•DATA. , 2014, , .		0
318	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. RNA Technologies, 2018, , 229-238.	0.2	0
319	Combing the Hairball: Improving Visualization of miRNAâ€“Target Interaction Networks. Methods in Molecular Biology, 2019, 1970, 279-289.	0.4	0
320	The impact of early pregnancy complications on completed family sizeâ€”A nationwide, registryâ€•based cohort study with 40 years of data. Acta Obstetricia Et Gynecologica Scandinavica, 2021, 100, 2226-2233.	1.3	0
321	CANCER PANOMICS: COMPUTATIONAL METHODS AND INFRASTRUCTURE FOR INTEGRATIVE ANALYSIS OF CANCER HIGH-THROUGHPUT â€œOMICSâ€•DATA- SESSION INTRODUCTION. , 2013, , .		0
322	Hidden Markov Models for Human Genes. , 1997, , 15-32.		0
323	The hunt for fatal myocardial infarction biomarkers: predictive circulating microRNAs. Annals of Translational Medicine, 2016, 4, S1-S1.	0.7	0
324	Title is missing!. , 2020, 17, e1003149.		0

#	ARTICLE	IF	CITATIONS
325	Title is missing!. , 2020, 17, e1003149.		0
326	Title is missing!. , 2020, 17, e1003149.		0
327	Title is missing!. , 2020, 17, e1003149.		0
328	Title is missing!. , 2020, 17, e1003149.		0
329	Abstract LB550: AI predicts risk of pancreatic cancer from disease trajectories using real-world electronic health records (EHRs) from Denmark and the USA. Cancer Research, 2022, 82, LB550-LB550.	0.4	0
330	Machine Learning to Identify Patients at Risk of Inappropriate Dosing for Renal Risk Medications: A Critical Comment on Kaas-Hansen et al [Response to Letter]. Clinical Epidemiology, 0, Volume 14, 765-766.	1.5	0