List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	27.8	9,342
2	SignalP 4.0: discriminating signal peptides from transmembrane regions. Nature Methods, 2011, 8, 785-786.	19.0	8,521
3	Improved Prediction of Signal Peptides: SignalP 3.0. Journal of Molecular Biology, 2004, 340, 783-795.	4.2	6,015
4	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	27.8	5,800
5	Predicting Subcellular Localization of Proteins Based on their N-terminal Amino Acid Sequence. Journal of Molecular Biology, 2000, 300, 1005-1016.	4.2	4,166
6	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
7	SignalP 5.0 improves signal peptide predictions using deep neural networks. Nature Biotechnology, 2019, 37, 420-423.	17.5	3,317
8	Locating proteins in the cell using TargetP, SignalP and related tools. Nature Protocols, 2007, 2, 953-971.	12.0	2,940
9	Sequence and structure-based prediction of eukaryotic protein phosphorylation sites. Journal of Molecular Biology, 1999, 294, 1351-1362.	4.2	2,767
10	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. Proteomics, 2004, 4, 1633-1649.	2.2	1,784
11	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
12	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
13	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
14	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	3.6	1,319
15	Mining electronic health records: towards better research applications and clinical care. Nature Reviews Genetics, 2012, 13, 395-405.	16.3	1,226
16	Population genomics of Bronze Age Eurasia. Nature, 2015, 522, 167-172.	27.8	1,166
17	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. EMBO Journal, 2013, 32, 1478-1488.	7.8	1,130
18	Feature-based prediction of non-classical and leaderless protein secretion. Protein Engineering, Design and Selection, 2004, 17, 349-356.	2.1	1,089

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19	Prediction of lipoprotein signal peptides in Gram-negative bacteria. Protein Science, 2003, 12, 1652-1662.	7.6	1,016
20	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. Protein Science, 2003, 12, 1007-1017.	7.6	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.	17.5	909
22	SignalP 6.0 predicts all five types of signal peptides using protein language models. Nature Biotechnology, 2022, 40, 1023-1025.	17.5	883
23	A human phenome-interactome network of protein complexes implicated in genetic disorders. Nature Biotechnology, 2007, 25, 309-316.	17.5	871
24	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. Glycobiology, 2005, 15, 153-164.	2.5	825
25	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. Nature, 2014, 505, 87-91.	27.8	821
26	Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature, 2010, 463, 757-762.	27.8	750
27	Prediction of human mRNA donor and acceptor sites from the DNA sequence. Journal of Molecular Biology, 1991, 220, 49-65.	4.2	749
28	Analysis and prediction of leucine-rich nuclear export signals. Protein Engineering, Design and Selection, 2004, 17, 527-536.	2.1	721
29	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. Nature, 2013, 499, 74-78.	27.8	717
30	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. Science, 2011, 334, 94-98.	12.6	675
31	Non-classical protein secretion in bacteria. BMC Microbiology, 2005, 5, 58.	3.3	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.	5.2	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.	21.4	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.	2.1	546
35	A scored human protein–protein interaction network to catalyze genomic interpretation. Nature Methods, 2017, 14, 61-64.	19.0	534
36	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. Nature, 2014, 506, 225-229.	27.8	500

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37	Prediction of proprotein convertase cleavage sites. Protein Engineering, Design and Selection, 2004, 17, 107-112.	2.1	499
38	NetOglyc: prediction of mucin type O-glycosylation sites based on sequence context and surface accessibility. Glycoconjugate Journal, 1998, 15, 115-130.	2.7	493
39	Prediction of twin-arginine signal peptides. BMC Bioinformatics, 2005, 6, 167.	2.6	465
40	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	19.0	442
41	A genomic history of Aboriginal Australia. Nature, 2016, 538, 207-214.	27.8	439
42	A new non-linear normalization method for reducing variability in DNA microarray experiments. Genome Biology, 2002, 3, research0048.	9.6	430
43	Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago. Cell, 2015, 163, 571-582.	28.9	425
44	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	3.6	418
45	Dynamic Complex Formation During the Yeast Cell Cycle. Science, 2005, 307, 724-727.	12.6	382
46	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. Journal of Molecular Biology, 2002, 319, 1257-1265.	4.2	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.	2.9	290
48	Sensitive quantitative predictions of peptide-MHC binding by a â€~Query by Committee' 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.	12.8	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.	7.1	288
51	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. BMC Genomics, 2005, 6, 70.	2.8	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.	14.5	273
54	Pharos: Collating protein information to shed light on the druggable genome. Nucleic Acids Research, 2017, 45, D995-D1002.	14.5	271

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55	Definition of supertypes for HLA molecules using clustering of specificity matrices. Immunogenetics, 2004, 55, 797-810.	2.4	269
56	Network biology concepts in complex disease comorbidities. Nature Reviews Genetics, 2016, 17, 615-629.	16.3	269
57	Prediction of proteasome cleavage motifs by neural networks. Protein Engineering, Design and Selection, 2002, 15, 287-296.	2.1	263
58	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	46.4	263
59	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. Bioinformatics, 2004, 20, 1388-1397.	4.1	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.	3.4	241
61	Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. PLoS Computational Biology, 2011, 7, e1002141.	3.2	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.	0.9	234
63	A reference map of potential determinants for the human serum metabolome. Nature, 2020, 588, 135-140.	27.8	230
64	Cleavage site analysis in picornaviral polyproteins: Discovering cellular targets by neural networks. Protein Science, 1996, 5, 2203-2216.	7.6	219
65	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. Nucleic Acids Research, 1999, 27, 370-372.	14.5	213
66	A DNA structural atlas for Escherichia coli 1 1Edited by T. Richmond. Journal of Molecular Biology, 2000, 299, 907-930.	4.2	213
67	A Nondegenerate Code of Deleterious Variants in Mendelian Loci Contributes to Complex Disease Risk. Cell, 2013, 155, 70-80.	28.9	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.	7.1	206
69	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in Saccharomyces cerevisiae. Genome Biology, 2006, 7, R107.	9.6	205
70	Alternative Splicing in Colon, Bladder, and Prostate Cancer Identified by Exon Array Analysis. Molecular and Cellular Proteomics, 2008, 7, 1214-1224.	3.8	202
71	NESbase version 1.0: a database of nuclear export signals. Nucleic Acids Research, 2003, 31, 393-396.	14.5	195
72	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	3.5	194

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73	On the total number of genes and their length distribution in complete microbial genomes. Trends in Genetics, 2001, 17, 425-428.	6.7	193
74	Comparison of computational methods for the identification of cell cycle-regulated genes. Bioinformatics, 2005, 21, 1164-1171.	4.1	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.	12.3	187
76	The biology of eukaryotic promoter prediction—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.	7.1	170
78	Analysis and prediction of mammalian protein glycation. Glycobiology, 2006, 16, 844-853.	2.5	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.	0.9	169
80	Co-evolution of transcriptional and post-translational cell-cycle regulation. Nature, 2006, 443, 594-597.	27.8	168
81	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. Nature Communications, 2015, 6, 5969.	12.8	164
82	Protein secondary structure and homology by neural networks The α-helices in rhodopsin. FEBS Letters, 1988, 241, 223-228.	2.8	158
83	A Brief History of Protein Sorting Prediction. Protein Journal, 2019, 38, 200-216.	1.6	154
84	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. Scientific Reports, 2021, 11, 13153.	3.3	147
85	Continuum Secondary Structure Captures Protein Flexibility. Structure, 2002, 10, 175-184.	3.3	135
86	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	27.8	130
87	Population-wide analysis of differences in disease progression patterns in men and women. Nature Communications, 2019, 10, 666.	12.8	128
88	Improving the Odds in Discriminating "Drug-like―from "Non Drug-like―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.	6.2	124
90	Statistical analysis of protein kinase specificity determinants. FEBS Letters, 1998, 430, 45-50.	2.8	123

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91	Prediction of N-terminal protein sorting signals. Current Opinion in Structural Biology, 1997, 7, 394-398.	5.7	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.	7.1	117
93	Modeling of waning immunity after SARS-CoV-2 vaccination and influencing factors. Nature Communications, 2022, 13, 1614.	12.8	117
94	Modeling the adaptive immune system: predictions and simulations. Bioinformatics, 2007, 23, 3265-3275.	4.1	115
95	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
96	Prediction of protein secondary structure at 80% accuracy. Proteins: Structure, Function and Bioinformatics, 2000, 41, 17-20.	2.6	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.	3.2	112
98	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	6.4	110
99	A novel approach to prediction of the 3-dimensional structures of protein backbones by neural networks. FEBS Letters, 1990, 261, 43-46.	2.8	107
100	Scanning the available Dictyostelium discoideum proteome for O-linked GlcNAc glycosylation sites using neural networks. Glycobiology, 1999, 9, 1009-1022.	2.5	99
101	Prediction methods and databases within chemoinformatics: emphasis on drugs and drug candidates. Bioinformatics, 2005, 21, 2145-2160.	4.1	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.	3.2	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.	3.2	96
104	A Systematic Study of Site-specific GalNAc-type O-Glycosylation Modulating Proprotein Convertase Processing. Journal of Biological Chemistry, 2011, 286, 40122-40132.	3.4	93
105	hERG Classification Model Based on a Combination of Support Vector Machine Method and GRIND Descriptors. Molecular Pharmaceutics, 2008, 5, 117-127.	4.6	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.	14.3	90
107	Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology. BMC Bioinformatics, 2004, 5, 72.	2.6	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.	3.7	88

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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.	3.9	87
110	Predicting proteasomal cleavage sites: a comparison of available methods. International Immunology, 2003, 15, 781-787.	4.0	86
111	Many Putative Endocrine Disruptors Inhibit Prostaglandin Synthesis. Environmental Health Perspectives, 2011, 119, 534-541.	6.0	85
112	Prediction of pH-Dependent Aqueous Solubility of Druglike Molecules. Journal of Chemical Information and Modeling, 2006, 46, 2601-2609.	5.4	84
113	A computational framework to integrate high-throughput â€~-omics' datasets for the identification of potential mechanistic links. Nature Protocols, 2018, 13, 2781-2800.	12.0	82
114	DNA structure in human RNA polymerase II promoters 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 281, 663-673.	4.2	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.	0.2	81
116	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. Cell Reports, 2017, 18, 3242-3256.	6.4	81
117	Dissecting spatioâ€ŧemporal protein networks driving human heart development and related disorders. Molecular Systems Biology, 2010, 6, 381.	7.2	80
118	Genome organisation and chromatin structure in Escherichia coli. Biochimie, 2001, 83, 201-212.	2.6	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.	12.3	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.	3.0	75
122	Blood cell gene expression profiling in rheumatoid arthritis. Immunology Letters, 2004, 93, 217-226.	2.5	73
123	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	3.9	73
124	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. Human Molecular Genetics, 2017, 26, 1219-1229.	2.9	73
125	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	4.4	72
126	ChemProt: a disease chemical biology database. Nucleic Acids Research, 2011, 39, D367-D372.	14.5	71

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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.	4.4	71
128	Artificial Intelligence and Early Detection of Pancreatic Cancer. Pancreas, 2021, 50, 251-279.	1.1	71
129	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. Nature Methods, 2014, 11, 868-874.	19.0	70
130	Disease trajectory browser for exploring temporal, population-wide disease progression patterns in 7.2 million Danish patients. Nature Communications, 2020, 11, 4952.	12.8	70
131	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
132	Sigma A recognition sites in the Bacillus subtilis genome. Microbiology (United Kingdom), 2001, 147, 2417-2424.	1.8	69
133	Naturally Occurring Nucleosome Positioning Signals in Human Exons and Introns. Journal of Molecular Biology, 1996, 263, 503-510.	4.2	68
134	Cyclebase.org a comprehensive multi-organism online database of cell-cycle experiments. Nucleic Acids Research, 2007, 36, D854-D859.	14.5	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.	1.9	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.	9.6	67
137	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. Scientific Reports, 2016, 6, 36624.	3.3	66
138	miRandola 2017: a curated knowledge base of non-invasive biomarkers. Nucleic Acids Research, 2018, 46, D354-D359.	14.5	61
139	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	2.2	61
140	Multiple alignment using simulated annealing: branch point definition in human mRNA splicing. Nucleic Acids Research, 1992, 20, 2511-2516.	14.5	60
141	A Wiring of the Human Nucleolus. Molecular Cell, 2006, 22, 285-295.	9.7	56
142	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. Nature Microbiology, 2016, 1, 16152.	13.3	56
143	Huntingtin-interacting protein 14 is a type 1 diabetes candidate protein regulating insulin secretion and β-cell apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E681-8.	7.1	55
144	Protein Interaction-Based Genome-Wide Analysis of Incident Coronary Heart Disease. Circulation: Cardiovascular Genetics, 2011, 4, 549-556.	5.1	55

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145	Protein structure and the sequential structure of mRNA: αâ€helix and βâ€sheet signals at the nucleotide level. Proteins: Structure, Function and Bioinformatics, 1996, 25, 237-252.	2.6	54
146	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	9.6	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.	14.5	53
148	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. Genome Biology, 2007, 8, R253.	9.6	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.	4.1	52
150	Complete Genes May Pass from Food to Human Blood. PLoS ONE, 2013, 8, e69805.	2.5	52
151	ChemProt-2.0: visual navigation in a disease chemical biology database. Nucleic Acids Research, 2012, 41, D464-D469.	14.5	50
152	Protein Structures from Distance Inequalities. Journal of Molecular Biology, 1993, 231, 861-869.	4.2	49
153	Immunological Bioinformatics. , 2005, , .		49
154	New weakly expressed cell cycle-regulated genes in yeast. Yeast, 2005, 22, 1191-1201.	1.7	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.	6.3	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.	8.4	47
157	Deciphering Diseases and Biological Targets for Environmental Chemicals using Toxicogenomics Networks. PLoS Computational Biology, 2010, 6, e1000788.	3.2	43
158	Identification of Odorant-Receptor Interactions by Global Mapping of the Human Odorome. PLoS ONE, 2014, 9, e93037.	2.5	42
159	Computational analyses and annotations of theArabidopsisperoxidase gene family. FEBS Letters, 1998, 433, 98-102.	2.8	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.	2.9	40
161	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. Acta Veterinaria Scandinavica, 2018, 60, 61.	1.6	40
162	G + C-rich tract in 5′ end of human introns. Journal of Molecular Biology, 1992, 227, 108-113.	4.2	39

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163	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale . Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2010, 368, 2799-2815.	3.4	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.	4.4	39
165	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	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.	6.5	39
167	Cleaning up gene databases. Nature, 1990, 343, 123-123.	27.8	37
168	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. Reproduction, 2017, 154, 145-152.	2.6	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.	6.5	36
170	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1819-1828.	2.6	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.	5.5	35
173	Lapatinib potentiates cytotoxicity of ÂYM155 in neuroblastoma via inhibition of the ABCB1 efflux transporter. Scientific Reports, 2017, 7, 3091.	3.3	35
174	Protein structure and the sequential structure of mRNA: α-Helix and β-sheet signals at the nucleotide level. Proteins: Structure, Function and Bioinformatics, 1996, 25, 237-252.	2.6	34
175	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. Scientific Reports, 2015, 5, 13201.	3.3	34
176	Benchmarking the HLA typing performance of Polysolver and Optitype in 50 Danish parental trios. BMC Bioinformatics, 2018, 19, 239.	2.6	34
177	Relationship between protein structure and geometrical constraints. Protein Science, 1996, 5, 2217-2225.	7.6	33
178	Prediction of novel archaeal enzymes from sequence-derived features. Protein Science, 2009, 11, 2894-2898.	7.6	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.	2.6	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.	6.3	33

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181	Systematic Characterisation of Cellular Localisation and Expression Profiles of Proteins Containing MHC Ligands. PLoS ONE, 2009, 4, e7448.	2.5	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.	2.2	32
184	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. Diabetologia, 2018, 61, 117-129.	6.3	32
185	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	3.1	32
186	Evolution of Cell Cycle Control: Same Molecular Machines, Different Regulation. Cell Cycle, 2007, 6, 1819-1825.	2.6	31
187	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. Genetic Epidemiology, 2011, 35, 318-332.	1.3	31
188	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. Diabetologia, 2017, 60, 475-489.	6.3	31
189	Chance of live birth: a nationwide, registry-based cohort study. Human Reproduction, 2021, 36, 1065-1073.	0.9	31
190	Analysis of eukaryotic promoter sequences reveals a systematically occurring CT-signal. Nucleic Acids Research, 1995, 23, 1223-1230.	14.5	30
191	SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. Bioinformatics, 2007, 23, i387-i391.	4.1	29
192	Integration of Clinical Chemistry, Expression, and Metabolite Data Leads to Better Toxicological Class Separation. Toxicological Sciences, 2008, 102, 444-454.	3.1	29
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194	A computational approach to chemical etiologies of diabetes. Scientific Reports, 2013, 3, 2712.	3.3	29
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