

# Sren Brunak

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/7332153/soren-brunak-publications-by-year.pdf>

**Version:** 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

325 papers	71,535 citations	89 h-index	267 g-index
360 ext. papers	85,428 ext. citations	11.1 avg, IF	7.65 L-index

#	Paper	IF	Citations
325	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> , <b>2022</b> , 3, 100477	18	1
324	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	56
323	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease.. <i>Communications Biology</i> , <b>2022</b> , 5, 80	6.7	1
322	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> , <b>2022</b> , 40, 554-554	2.2	1
321	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. <i>Nature Communications</i> , <b>2022</b> , 13, 634	17.4	3
320	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> , <b>2022</b> , 105357	2.9	
319	Using Machine Learning to Identify Patients at High Risk of Inappropriate Drug Dosing in Periods with Renal Dysfunction.. <i>Clinical Epidemiology</i> , <b>2022</b> , 14, 213-223	5.9	0
318	Modeling of waning immunity after SARS-CoV-2 vaccination and influencing factors.. <i>Nature Communications</i> , <b>2022</b> , 13, 1614	17.4	4
317	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome.. <i>Nature Communications</i> , <b>2022</b> , 13, 1598	17.4	1
316	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> , <b>2022</b> , JCO2102511	2.2	3
315	Data Resource Profile: The Copenhagen Hospital Biobank (CHB). <i>International Journal of Epidemiology</i> , <b>2021</b> , 50, 719-720e	7.8	3
314	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , <b>2021</b> , 44, 511-518	14.6	6
313	Optimizing drug selection from a prescription trajectory of one patient. <i>Npj Digital Medicine</i> , <b>2021</b> , 4, 150	15.7	0
312	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> , <b>2021</b> , 9,	4.5	2
311	Artificial Intelligence and Early Detection of Pancreatic Cancer: 2020 Summative Review. <i>Pancreas</i> , <b>2021</b> , 50, 251-279	2.6	12
310	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> , <b>2021</b> , 150, 112072	4.7	3
309	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. <i>Gut</i> , <b>2021</b> ,	19.2	2

308	Impaired Vitamin D Signaling in T Cells From a Family With Hereditary Vitamin D Resistant Rickets. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 684015	8.4	3
307	Endotrophin is associated with chronic multimorbidity and all-cause mortality in a cohort of elderly women. <i>EBioMedicine</i> , <b>2021</b> , 68, 103391	8.8	3
306	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. <i>Communications Biology</i> , <b>2021</b> , 4, 655	6.7	3
305	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. <i>Scientific Reports</i> , <b>2021</b> , 11, 13153	4.9	27
304	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> , <b>2021</b> , 70, 2092-2106	0.9	4
303	Semen quality and waiting time to pregnancy explored using association mining. <i>Andrology</i> , <b>2021</b> , 9, 577-587	4.2	2
302	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , <b>2021</b> , 4, 156	6.7	11
301	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , <b>2021</b> , 42, 1959-1971	9.5	7
300	Association of Variants Near the Bradykinin Receptor B Gene With Angioedema in Patients Taking ACEInhibitors. <i>Journal of the American College of Cardiology</i> , <b>2021</b> , 78, 696-709	15.1	2
299	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> , <b>2021</b> , 100, 2226-2233	3.8	
298	Chance of live birth: a nationwide, registry-based cohort study. <i>Human Reproduction</i> , <b>2021</b> , 36, 1065-1073	3.7	11
297	Time-ordered comorbidity correlations identify patients at risk of mis- and overdiagnosis. <i>Npj Digital Medicine</i> , <b>2021</b> , 4, 12	15.7	3
296	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> , <b>2021</b> , 11, e049709	3	0
295	Disease Trajectories for Hidradenitis Suppurativa in the Danish Population. <i>JAMA Dermatology</i> , <b>2020</b> , 156, 780-786	5.1	6
294	Association between antipsychotic drug dose and length of clinical notes: a proxy of disease severity?. <i>BMC Medical Research Methodology</i> , <b>2020</b> , 20, 107	4.7	2
293	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> , <b>2020</b> , 20, 94	3.6	4
292	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> , <b>2020</b> , 17, e1003149	11.6	18
291	Immune Profiling of Human Gut-Associated Lymphoid Tissue Identifies a Role for Isolated Lymphoid Follicles in Priming of Region-Specific Immunity. <i>Immunity</i> , <b>2020</b> , 52, 557-570.e6	32.3	40

290	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> , <b>2020</b> , 2, e179-e191	14.4	70
289	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> , <b>2020</b> , 22, 73	8.3	8
288	Sex differences in text-mined possible adverse drug events associated with drugs for psychosis. <i>Journal of Psychopharmacology</i> , <b>2020</b> , 34, 532-539	4.6	3
287	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. <i>Diabetologia</i> , <b>2020</b> , 63, 744-756	10.3	4
286	Age-stratified longitudinal study of Alzheimer® and vascular dementia patients. <i>Alzheimer's and Dementia</i> , <b>2020</b> , 16, 908-917	1.2	12
285	ARDD 2020: from aging mechanisms to interventions. <i>Aging</i> , <b>2020</b> , 12, 24484-24503	5.6	11
284	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. <i>PLoS ONE</i> , <b>2020</b> , 15, e0242360	3.7	2
283	Lipidomic profiles, lipid trajectories and clinical biomarkers in female elite endurance athletes. <i>Scientific Reports</i> , <b>2020</b> , 10, 2349	4.9	2
282	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , <b>2020</b> , 12, 109	14.4	3
281	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , <b>2020</b> , 588, 135-140	10.4	75
280	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. <i>EBioMedicine</i> , <b>2020</b> , 58, 102932	8.8	2
279	Complete Topological Mapping of a Cellular Protein Interactome Reveals Bow-Tie Motifs as Ubiquitous Connectors of Protein Complexes. <i>Cell Reports</i> , <b>2020</b> , 31, 107763	10.6	3
278	Effects of active farnesoid X receptor on GLUTag enteroendocrine L cells. <i>Molecular and Cellular Endocrinology</i> , <b>2020</b> , 517, 110923	4.4	3
277	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , <b>2020</b> , 41, 2618-2628	9.5	26
276	Disease trajectory browser for exploring temporal, population-wide disease progression patterns in 7.2 million Danish patients. <i>Nature Communications</i> , <b>2020</b> , 11, 4952	17.4	14
275	Systems genetics analysis identifies calcium-signaling defects as novel cause of congenital heart disease. <i>Genome Medicine</i> , <b>2020</b> , 12, 76	14.4	5
274	Alcoholic liver disease: A registry view on comorbidities and disease prediction. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008244	5	7
273	Conflicting associations between dietary patterns and changes of anthropometric traits across subgroups of middle-aged women and men. <i>Clinical Nutrition</i> , <b>2020</b> , 39, 265-275	5.9	6

272	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> , <b>2020</b> , 9, e015069	6	10
271	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
270	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
269	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
268	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
267	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
266	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , <b>2019</b> , 20, 693-701	30.1	36
265	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , <b>2019</b> , 38, 200-216	3.9	55
264	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> , <b>2019</b> , 1, e78-e89	14.4	46
263	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> , <b>2019</b> , 62, 1601-1615	10.3	14
262	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> , <b>2019</b> , 9, e028401	3	22
261	Comorbidity landscape of the Danish patient population affected by chromosome abnormalities. <i>Genetics in Medicine</i> , <b>2019</b> , 21, 2485-2495	8.1	7
260	The use of systems biology in chemical risk assessment. <i>Current Opinion in Toxicology</i> , <b>2019</b> , 15, 48-54	4.4	6
259	Combing the Hairball: Improving Visualization of miRNA-Target Interaction Networks. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1970, 279-289	1.4	
258	Roadmap for a precision-medicine initiative in the Nordic region. <i>Nature Genetics</i> , <b>2019</b> , 51, 924-930	36.3	12
257	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , <b>2019</b> , 10, 666	17.4	58
256	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. <i>Npj Systems Biology and Applications</i> , <b>2019</b> , 5, 27	5	8
255	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , <b>2019</b> , 20, 164	18.3	19

254	Incorporating symptom data in longitudinal disease trajectories for more detailed patient stratification. <i>International Journal of Medical Informatics</i> , <b>2019</b> , 129, 107-113	5.3	4
253	sAOP: linking chemical stressors to adverse outcomes pathway networks. <i>Bioinformatics</i> , <b>2019</b> , 35, 5391-5392	5.8	8
252	Combined Ensemble Docking and Machine Learning in Identification of Therapeutic Agents with Potential Inhibitory Effect on Human CES1. <i>Molecules</i> , <b>2019</b> , 24,	4.8	4
251	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multienrichment Approach. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 1312-1324	7	7
250	Linking glycemic dysregulation in diabetes to symptoms, comorbidities, and genetics through EHR data mining. <i>ELife</i> , <b>2019</b> , 8,	8.9	5
249	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 420-423	44.5	1536
248	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. <i>Nature Communications</i> , <b>2019</b> , 10, 5508	17.4	9
247	A generic deep convolutional neural network framework for prediction of receptor-ligand interactions-NetPhosPan: application to kinase phosphorylation prediction. <i>Bioinformatics</i> , <b>2019</b> , 35, 1098-1107	7.2	11
246	A Large-Cohort, Longitudinal Study Determines Precancer Disease Routes across Different Cancer Types. <i>Cancer Research</i> , <b>2019</b> , 79, 864-872	10.1	8
245	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , <b>2018</b> , 17, 317-332	64.1	156
244	Familial co-occurrence of congenital heart defects follows distinct patterns. <i>European Heart Journal</i> , <b>2018</b> , 39, 1015-1022	9.5	15
243	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D354-D359	20.1	44
242	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , <b>2018</b> , 61, 117-129	10.3	21
241	Benchmarking the HLA typing performance of Polysolver and Optitype in 50 Danish parental trios. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 239	3.6	15
240	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005962	5	70
239	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , <b>2018</b> , 13, e0189886	3.7	5
238	The protein kinase SIK downregulates the polarity protein Par3. <i>Oncotarget</i> , <b>2018</b> , 9, 5716-5735	3.3	9
237	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. <i>Oncotarget</i> , <b>2018</b> , 9, 9043-9060	3.3	606

236	Identifying the druggable interactome of EWS-FLI1 reveals MCL-1 dependent differential sensitivities of Ewing sarcoma cells to apoptosis inducers. <i>Oncotarget</i> , <b>2018</b> , 9, 31018-31031	3.3	3
235	Increase in clinically recorded type 2 diabetes after colectomy. <i>ELife</i> , <b>2018</b> , 7,	8.9	11
234	Analysis of Time-Series Gene Expression Data to Explore Mechanisms of Chemical-Induced Hepatic Steatosis Toxicity. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 396	4.5	10
233	Protective role of the vulture facial skin and gut microbiomes aid adaptation to scavenging. <i>Acta Veterinaria Scandinavica</i> , <b>2018</b> , 60, 61	2	21
232	A computational framework to integrate high-throughput Omics Datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , <b>2018</b> , 13, 2781-2800	18.8	44
231	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. <i>RNA Technologies</i> , <b>2018</b> , 229-238	0.2	
230	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> , <b>2018</b> , 9, 586	9.8	17
229	Retinoic Acid Signaling in Thymic Epithelial Cells Regulates Thymopoiesis. <i>Journal of Immunology</i> , <b>2018</b> , 201, 524-532	5.3	10
228	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D995-D1002	20.1	146
227	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , <b>2017</b> , 60, 475-489	10.3	24
226	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1580, 281-295	1.4	1
225	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. <i>Reproduction</i> , <b>2017</b> , 154, 145-152	3.8	32
224	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 1219-1229	5.6	51
223	Chromosome-wise Protein Interaction Patterns and Their Impact on Functional Implications of Large-Scale Genomic Aberrations. <i>Cell Systems</i> , <b>2017</b> , 4, 357-364.e3	10.6	7
222	Comparison of global gene expression profiles of microdissected human foetal Leydig cells with their normal and hyperplastic adult equivalents. <i>Molecular Human Reproduction</i> , <b>2017</b> , 23, 339-354	4.4	9
221	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , <b>2017</b> , 18, 3242-3256	10.6	59
220	TEMPORAL ORDER OF DISEASE PAIRS AFFECTS SUBSEQUENT DISEASE TRAJECTORIES: THE CASE OF DIABETES AND SLEEP APNEA. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , <b>2017</b> , 22, 380-389	1.3	8
219	The impact of the protein interactome on the syntenic structure of mammalian genomes. <i>PLoS ONE</i> , <b>2017</b> , 12, e0179112	3.7	6



218	Cutavirus in Cutaneous Malignant Melanoma. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 363-365	10.2	14
217	Lapatinib potentiates cytotoxicity of LYM155 in neuroblastoma via inhibition of the ABCB1 efflux transporter. <i>Scientific Reports</i> , <b>2017</b> , 7, 3091	4.9	19
216	Protein features as determinants of wild-type glycoside hydrolase thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2017</b> , 85, 2036-2044	4.2	4
215	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , <b>2017</b> , 16, 88-101	6.1	13
214	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , <b>2017</b> , 14, 61-64	21.6	307
213	Pancreatic Islet Protein Complexes and Their Dysregulation in Type 2 Diabetes. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 43	4.5	12
212	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006706	6	102
211	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , <b>2017</b> , 548, 87-91	50.4	87
210	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268
209	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , <b>2016</b> , 535, 376-81	50.4	977
208	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. <i>Npj Genomic Medicine</i> , <b>2016</b> , 1, 16035	6.2	14
207	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16152	26.6	38
206	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. <i>Scientific Reports</i> , <b>2016</b> , 6, 36624	4.9	48
205	KinMutRF: a random forest classifier of sequence variants in the human protein kinase superfamily. <i>BMC Genomics</i> , <b>2016</b> , 17 Suppl 2, 396	4.5	7
204	wKinMut-2: Identification and Interpretation of Pathogenic Variants in Human Protein Kinases. <i>Human Mutation</i> , <b>2016</b> , 37, 36-42	4.7	7
203	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D38-47	20.1	81
202	Propionibacterium acnes: Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , <b>2016</b> , 54, 980-7	9.7	57
201	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , <b>2016</b> , 48, 510-8	36.3	404



200	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> , <b>2016</b> , 22, 322-328	6.2	28
199	Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers. <i>Viruses</i> , <b>2016</b> , 8,	6.2	9
198	ChemProt-3.0: a global chemical biology diseases mapping. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	53
197	Investigating the impact of missense mutations in hCES1 by in silico structure-based approaches. <i>Drug Metabolism and Personalized Therapy</i> , <b>2016</b> ,	2	5
196	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 &amp; Congenital Heart Surgery</i> , <b>2016</b> , 7, 169-77	1.1	4
195	Network biology concepts in complex disease comorbidities. <i>Nature Reviews Genetics</i> , <b>2016</b> , 17, 615-29	30.1	183
194	Familial Atrial Septal Defect and Sudden Cardiac Death: Identification of a Novel NKX2-5 Mutation and a Review of the Literature. <i>Congenital Heart Disease</i> , <b>2016</b> , 11, 283-90	3.1	58
193	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , <b>2015</b> , 6, 5969	17.4	119
192	Individualization of treatments with drugs metabolized by CES1: combining genetics and metabolomics. <i>Pharmacogenomics</i> , <b>2015</b> , 16, 649-65	2.6	18
191	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , <b>2015</b> , 163, 571-82	56.2	294
190	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , <b>2015</b> , 528, 262-266	50.4	1107
189	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , <b>2015</b> , 5, 13201	4.9	30
188	Population genomics of Bronze Age Eurasia. <i>Nature</i> , <b>2015</b> , 522, 167-72	50.4	827
187	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> , <b>2015</b> , 5, e008702	3	8
186	Traces of ATCV-1 associated with laboratory component contamination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E925-6	11.5	20
185	Finding Cervical Cancer Symptoms in Swedish Clinical Text using a Machine Learning Approach and NegEx <b>2015</b> , 2015, 1296-305	0.7	4
184	Identification of possible adverse drug reactions in clinical notes: The case of glucose-lowering medicines. <i>Journal of Research in Pharmacy Practice</i> , <b>2015</b> , 4, 64-72	1.3	6
183	REACH and Environmental Chemicals <b>2015</b> , 23-36		1

182	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , <b>2014</b> , 506, 225-9	50.4	357
181	Cofactory: sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2014</b> , 82, 1819-28	4.2	27
180	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 479	11	78
179	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , <b>2014</b> , 505, 87-91	50.4	581
178	Facilitating the use of large-scale biological data and tools in the era of translational bioinformatics. <i>Briefings in Bioinformatics</i> , <b>2014</b> , 15, 942-52	13.4	16
177	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , <b>2014</b> , 24, R1035-7	6.3	62
176	Polychlorinated dibenzo-p-dioxins, furans, and biphenyls (PCDDs/PCDFs and PCBs) in breast milk and early childhood growth and IGF1. <i>Reproduction</i> , <b>2014</b> , 147, 391-9	3.8	31
175	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <i>Nature Methods</i> , <b>2014</b> , 11, 868-74	21.6	50
174	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. <i>Diabetologia</i> , <b>2014</b> , 57, 1132-42	10.3	39
173	Bacterial diversity in snow on North Pole ice floes. <i>Extremophiles</i> , <b>2014</b> , 18, 945-51	3	19
172	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 822-8	44.5	624
171	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 834-41	44.5	1088
170	Dose-specific adverse drug reaction identification in electronic patient records: temporal data mining in an inpatient psychiatric population. <i>Drug Safety</i> , <b>2014</b> , 37, 237-47	5.1	48
169	Lineage-specific interface proteins match up the cell cycle and differentiation in embryo stem cells. <i>Stem Cell Research</i> , <b>2014</b> , 13, 316-28	1.6	8
168	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. <i>Nature Communications</i> , <b>2014</b> , 5, 4022	17.4	186
167	Identification of odorant-receptor interactions by global mapping of the human odorome. <i>PLoS ONE</i> , <b>2014</b> , 9, e93037	3.7	32
166	Patient stratification and identification of adverse event correlations in the space of 1190 drug related adverse events. <i>Frontiers in Physiology</i> , <b>2014</b> , 5, 332	4.6	10
165	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> , <b>2014</b> , 2, e00038	3.1	14

164	Transcriptome profiling of mice testes following low dose irradiation. <i>Reproductive Biology and Endocrinology</i> , <b>2013</b> , 11, 50	5	8
163	Reply to Mining electronic health records: an additional perspective <i>ONature Reviews Genetics</i> , <b>2013</b> , 14, 75	30.1	1
162	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , <b>2013</b> , 500, 541-6	50.4	2584
161	A nondegenerate code of deleterious variants in Mendelian loci contributes to complex disease risk. <i>Cell</i> , <b>2013</b> , 155, 70-80	56.2	160
160	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , <b>2013</b> , 10, 1196-9	21.6	340
159	Whole-exome sequencing of 2,000 Danish individuals and the role of rare coding variants in type 2 diabetes. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 1072-86	11	109
158	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. <i>EMBO Journal</i> , <b>2013</b> , 32, 1478-88	13	862
157	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 19860-5	11.5	111
156	The SH2 domain interaction landscape. <i>Cell Reports</i> , <b>2013</b> , 3, 1293-305	10.6	89
155	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , <b>2013</b> , 499, 74-8	50.4	563
154	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2013</b> , 20, 947-53	8.6	50
153	Genome-wide assessment of the association of rare and common copy number variations to testicular germ cell cancer. <i>Frontiers in Endocrinology</i> , <b>2013</b> , 4, 2	5.7	13
152	Concordance of gene expression in human protein complexes reveals tissue specificity and pathology. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e171	20.1	19
151	MetaRanker 2.0: a web server for prioritization of genetic variation data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W104-8	20.1	24
150	A computational approach to chemical etiologies of diabetes. <i>Scientific Reports</i> , <b>2013</b> , 3, 2712	4.9	25
149	Prediction of disease causing non-synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. <i>PLoS ONE</i> , <b>2013</b> , 8, e68370	3.7	17
148	ChemProt-2.0: visual navigation in a disease chemical biology database. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D464-9	20.1	46
147	Complete genes may pass from food to human blood. <i>PLoS ONE</i> , <b>2013</b> , 8, e69805	3.7	31

146	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. <i>Journal of Medical Genetics</i> , <b>2012</b> , 49, 58-65	5.8	86
145	Uncovering the molecular machinery of the human spindle--an integration of wet and dry systems biology. <i>PLoS ONE</i> , <b>2012</b> , 7, e31813	3.7	11
144	Mining electronic health records: towards better research applications and clinical care. <i>Nature Reviews Genetics</i> , <b>2012</b> , 13, 395-405	30.1	911
143	Knowledge engineering for health: a new discipline required to bridge the "ICT gap" between research and healthcare. <i>Human Mutation</i> , <b>2012</b> , 33, 797-802	4.7	20
142	Cometin is a novel neurotrophic factor that promotes neurite outgrowth and neuroblast migration in vitro and supports survival of spiral ganglion neurons in vivo. <i>Experimental Neurology</i> , <b>2012</b> , 233, 172-81	5.7	30
141	Genetic and environmental risk factors in congenital heart disease functionally converge in protein networks driving heart development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 14035-40	11.5	90
140	The cancer exome generated by alternative mRNA splicing dilutes predicted HLA class I epitope density. <i>PLoS ONE</i> , <b>2012</b> , 7, e38670	3.7	13
139	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , <b>2011</b> , 8, 785-621.6	6866	
138	Bioinformatics-driven identification and examination of candidate genes for non-alcoholic fatty liver disease. <i>PLoS ONE</i> , <b>2011</b> , 6, e16542	3.7	19
137	Enterotypes of the human gut microbiome. <i>Nature</i> , <b>2011</b> , 473, 174-80	50.4	4240
136	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , <b>2011</b> , 334, 94-8	33.3	528
135	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 310	3.6	2
134	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , <b>2011</b> , 35, 318-32	2.6	28
133	ChemProt: a disease chemical biology database. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D367-72	20.1	58
132	Huntingtin-interacting protein 14 is a type 1 diabetes candidate protein regulating insulin secretion and beta-cell apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, E681-8	11.5	50
131	A systematic study of site-specific GalNAc-type O-glycosylation modulating proprotein convertase processing. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 40122-32	5.4	80
130	Protein interaction-based genome-wide analysis of incident coronary heart disease. <i>Circulation: Cardiovascular Genetics</i> , <b>2011</b> , 4, 549-56		53
129	Intrauterine exposure to mild analgesics is a risk factor for development of male reproductive disorders in human and rat. <i>Human Reproduction</i> , <b>2011</b> , 26, 235-44	5.7	194

128	Using electronic patient records to discover disease correlations and stratify patient cohorts. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002141	5	193
127	Many putative endocrine disruptors inhibit prostaglandin synthesis. <i>Environmental Health Perspectives</i> , <b>2011</b> , 119, 534-41	8.4	73
126	The strength of intron donor splice sites in human genes displays a bell-shaped pattern. <i>Bioinformatics</i> , <b>2011</b> , 27, 3079-84	7.2	
125	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , <b>2010</b> , 464, 59-65	50.4	7044
124	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , <b>2010</b> , 463, 757-62	50.4	567
123	The type 1 diabetes - HLA susceptibility interactome--identification of HLA genotype-specific disease genes for type 1 diabetes. <i>PLoS ONE</i> , <b>2010</b> , 5, e9576	3.7	20
122	OCT4 and downstream factors are expressed in human somatic urogenital epithelia and in culture of epididymal spheres. <i>Molecular Human Reproduction</i> , <b>2010</b> , 16, 835-45	4.4	21
121	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D699-702	20.1	45
120	Deciphering diseases and biological targets for environmental chemicals using toxicogenomics networks. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000788	5	40
119	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , <b>2010</b> , 3, ra3	8.8	1106
118	Dissecting spatio-temporal protein networks driving human heart development and related disorders. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 381	12.2	72
117	ImmunoGrid: towards agent-based simulations of the human immune system at a natural scale. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , <b>2010</b> , 368, 2799-815 <sup>3</sup>		35
116	Protein annotation in the era of personal genomics. <i>Current Opinion in Structural Biology</i> , <b>2010</b> , 20, 335-41	4.1	1
115	Analysis of gene expression profiles of microdissected cell populations indicates that testicular carcinoma in situ is an arrested gonocyte. <i>Cancer Research</i> , <b>2009</b> , 69, 5241-50	10.1	154
114	Analysis and prediction of gene splice sites in four <i>Aspergillus</i> genomes. <i>Fungal Genetics and Biology</i> , <b>2009</b> , 46 Suppl 1, S14-8	3.9	24
113	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , <b>2009</b> , 10, 206	18.3	48
112	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. <i>Briefings in Bioinformatics</i> , <b>2009</b> , 10, 330-40	13.4	29
111	Expression profiling of human genetic and protein interaction networks in type 1 diabetes. <i>PLoS ONE</i> , <b>2009</b> , 4, e6250	3.7	14

110	Systematic characterisation of cellular localisation and expression profiles of proteins containing MHC ligands. <i>PLoS ONE</i> , <b>2009</b> , 4, e7448	3.7	25
109	Circular reasoning rather than cyclic expression. <i>Genome Biology</i> , <b>2008</b> , 9, 403	18.3	4
108	Motif decomposition of the phosphotyrosine proteome reveals a new N-terminal binding motif for SHIP2. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 181-92	7.6	13
107	A large-scale analysis of tissue-specific pathology and gene expression of human disease genes and complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 20870-5	11.5	232
106	Integration of clinical chemistry, expression, and metabolite data leads to better toxicological class separation. <i>Toxicological Sciences</i> , <b>2008</b> , 102, 444-54	4.4	22
105	Alternative splicing in colon, bladder, and prostate cancer identified by exon array analysis. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 1214-24	7.6	174
104	hERG classification model based on a combination of support vector machine method and GRIND descriptors. <i>Molecular Pharmaceutics</i> , <b>2008</b> , 5, 117-27	5.6	80
103	Linear motif atlas for phosphorylation-dependent signaling. <i>Science Signaling</i> , <b>2008</b> , 1, ra2	8.8	342
102	Cyclebase.org--a comprehensive multi-organism online database of cell-cycle experiments. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D854-9	20.1	55
101	A human phenome-interactome network of protein complexes implicated in genetic disorders. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 309-16	44.5	761
100	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , <b>2007</b> , 2, 953-71	18.8	2596
99	Analysis of cell death inducing compounds. <i>Archives of Toxicology</i> , <b>2007</b> , 81, 803-11	5.8	6
98	Identification of a new hTERT-derived HLA-A*0201 restricted, naturally processed CTL epitope. <i>Cancer Immunology, Immunotherapy</i> , <b>2007</b> , 56, 1755-63	7.4	19
97	Modeling the adaptive immune system: predictions and simulations. <i>Bioinformatics</i> , <b>2007</b> , 23, 3265-75	7.2	101
96	SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. <i>Bioinformatics</i> , <b>2007</b> , 23, i387-91	7.2	26
95	Evolution of cell cycle control: same molecular machines, different regulation. <i>Cell Cycle</i> , <b>2007</b> , 6, 1819-25	7.7	26
94	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 5495-500	11.5	177
93	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. <i>Genome Biology</i> , <b>2007</b> , 8, R253	18.3	45

92	Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. <i>Genome Biology</i> , <b>2007</b> , 8, R45	18.3	63
91	Analysis and prediction of mammalian protein glycation. <i>Glycobiology</i> , <b>2006</b> , 16, 844-53	5.8	147
90	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , <b>2006</b> , 7, R107	18.3	177
89	A wiring of the human nucleolus. <i>Molecular Cell</i> , <b>2006</b> , 22, 285-95	17.6	52
88	Co-evolution of transcriptional and post-translational cell-cycle regulation. <i>Nature</i> , <b>2006</b> , 443, 594-7	50.4	153
87	Prediction of pH-dependent aqueous solubility of druglike molecules. <i>Journal of Chemical Information and Modeling</i> , <b>2006</b> , 46, 2601-9	6.1	75
86	Modelling the human immune system by combining bioinformatics and systems biology approaches. <i>Journal of Biological Physics</i> , <b>2006</b> , 32, 335-53	1.6	15
85	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. <i>Glycobiology</i> , <b>2005</b> , 15, 153-64	5.8	758
84	Dynamic complex formation during the yeast cell cycle. <i>Science</i> , <b>2005</b> , 307, 724-7	33.3	343
83	DNA Bendability and Nucleosome Positioning in Transcriptional Regulation <b>2005</b> , 189-202		1
82	Prediction of twin-arginine signal peptides. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 167	3.6	408
81	Pigs in sequence space: a 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , <b>2005</b> , 6, 70	4.5	221
80	Non-classical protein secretion in bacteria. <i>BMC Microbiology</i> , <b>2005</b> , 5, 58	4.5	473
79	An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. <i>European Journal of Immunology</i> , <b>2005</b> , 35, 2295-303	6.1	229
78	New weakly expressed cell cycle-regulated genes in yeast. <i>Yeast</i> , <b>2005</b> , 22, 1191-201	3.4	45
77	Comparison of computational methods for the identification of cell cycle-regulated genes. <i>Bioinformatics</i> , <b>2005</b> , 21, 1164-71	7.2	150
76	Prediction methods and databases within chemoinformatics: emphasis on drugs and drug candidates. <i>Bioinformatics</i> , <b>2005</b> , 21, 2145-60	7.2	78
75	Immunological Bioinformatics <b>2005</b> ,		44



74	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. <i>Bioinformatics</i> , <b>2004</b> , 20, 1388-97	7.2	223
73	Prediction of proprotein convertase cleavage sites. <i>Protein Engineering, Design and Selection</i> , <b>2004</b> , 17, 107-12	1.9	383
72	Analysis and prediction of leucine-rich nuclear export signals. <i>Protein Engineering, Design and Selection</i> , <b>2004</b> , 17, 527-36	1.9	613
71	Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 72	3.6	68
70	Definition of supertypes for HLA molecules using clustering of specificity matrices. <i>Immunogenetics</i> , <b>2004</b> , 55, 797-810	3.2	224
69	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. <i>Proteomics</i> , <b>2004</b> , 4, 1633-49	4.8	1442
68	Blood cell gene expression profiling in rheumatoid arthritis. Discriminative genes and effect of rheumatoid factor. <i>Immunology Letters</i> , <b>2004</b> , 93, 217-26	4.1	67
67	Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , <b>2004</b> , 17, 349-56	1.9	873
66	Identification of phosphorylation sites in protein kinase A substrates using artificial neural networks and mass spectrometry. <i>Journal of Proteome Research</i> , <b>2004</b> , 3, 426-33	5.6	67
65	Improved prediction of signal peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , <b>2004</b> , 340, 783-95	6.5	5563
64	MHC Class I Epitope Binding Prediction Trained on Small Data Sets. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 217-225	0.9	2
63	Functionality of system components: conservation of protein function in protein feature space. <i>Genome Research</i> , <b>2003</b> , 13, 2444-9	9.7	31
62	NESbase version 1.0: a database of nuclear export signals. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 393-6	20.1	176
61	Selecting informative data for developing peptide-MHC binding predictors using a query by committee approach. <i>Neural Computation</i> , <b>2003</b> , 15, 2931-42	2.9	13
60	Sensitive quantitative predictions of peptide-MHC binding by a Query by Committee Artificial neural network approach. <i>Tissue Antigens</i> , <b>2003</b> , 62, 378-84		228
59	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. <i>Protein Science</i> , <b>2003</b> , 12, 1007-17	6.3	783
58	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , <b>2003</b> , 12, 1652-62	6.3	880
57	Protein feature based identification of cell cycle regulated proteins in yeast. <i>Journal of Molecular Biology</i> , <b>2003</b> , 329, 663-74	6.5	24

56	Optimization and immune recognition of multiple novel conserved HLA-A2, human immunodeficiency virus type 1-specific CTL epitopes. <i>Journal of General Virology</i> , <b>2003</b> , 84, 2409-2421	4.9	37
55	Predicting proteasomal cleavage sites: a comparison of available methods. <i>International Immunology</i> , <b>2003</b> , 15, 781-7	4.9	76
54	Prediction of Protein Secondary Structure at High Accuracy Using a Combination of Many Neural Networks. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 117-122	0.9	1
53	Prediction of novel archaeal enzymes from sequence-derived features. <i>Protein Science</i> , <b>2002</b> , 11, 2894-86.3	6.3	25
52	Continuum secondary structure captures protein flexibility. <i>Structure</i> , <b>2002</b> , 10, 175-84	5.2	122
51	Bias of purine stretches in sequenced chromosomes. <i>Computers &amp; Chemistry</i> , <b>2002</b> , 26, 531-41		31
50	Prediction of proteasome cleavage motifs by neural networks. <i>Protein Engineering, Design and Selection</i> , <b>2002</b> , 15, 287-96	1.9	202
49	The Atlas visualization of genomewide information. <i>Methods in Microbiology</i> , <b>2002</b> , 49-63	2.8	9
48	A new non-linear normalization method for reducing variability in DNA microarray experiments. <i>Genome Biology</i> , <b>2002</b> , 3, research0048	18.3	372
47	RNA secondary structure and squence conservation in C1 region of human immunodeficiency virus type 1 env gene. <i>AIDS Research and Human Retroviruses</i> , <b>2002</b> , 18, 867-78	1.6	13
46	Prediction of human protein function from post-translational modifications and localization features. <i>Journal of Molecular Biology</i> , <b>2002</b> , 319, 1257-65	6.5	274
45	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. <i>Journal of Virology</i> , <b>2002</b> , 76, 8757-68	6.6	223
44	Recognition of environmental and genetic effects on barley phenolic fingerprints by neural networks. <i>Computers &amp; Chemistry</i> , <b>2001</b> , 25, 301-7		6
43	On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , <b>2001</b> , 17, 425-8	8.5	170
42	Genome organisation and chromatin structure in Escherichia coli. <i>Biochimie</i> , <b>2001</b> , 83, 201-12	4.6	71
41	Protein secondary structure: category assignment and predictability. <i>FEBS Letters</i> , <b>2001</b> , 507, 6-10	3.8	17
40	Prediction of glycosylation across the human proteome and the correlation to protein function <b>2001</b> ,		33
39	Sigma A recognition sites in the Bacillus subtilis genome. <i>Microbiology (United Kingdom)</i> , <b>2001</b> , 147, 2417-2424	24.24	56

38	Prediction of protein secondary structure at 80% accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2000</b> , 41, 17-20	4.2	96
37	A DNA structural atlas for Escherichia coli. <i>Journal of Molecular Biology</i> , <b>2000</b> , 299, 907-30	6.5	194
36	Predicting subcellular localization of proteins based on their N-terminal amino acid sequence. <i>Journal of Molecular Biology</i> , <b>2000</b> , 300, 1005-16	6.5	3635
35	Improving the odds in discriminating "drug-like" from "non drug-like" compounds. <i>Journal of Chemical Information and Computer Sciences</i> , <b>2000</b> , 40, 1315-24		110
34	Scanning the available Dictyostelium discoideum proteome for O-linked GlcNAc glycosylation sites using neural networks. <i>Glycobiology</i> , <b>1999</b> , 9, 1009-22	5.8	90
33	Machine learning approaches for the prediction of signal peptides and other protein sorting signals. <i>Protein Engineering, Design and Selection</i> , <b>1999</b> , 12, 3-9	1.9	461
32	PhosphoBase, a database of phosphorylation sites: release 2.0. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 237-9	20.1	255
31	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 370-2	20.1	163
30	The biology of eukaryotic promoter prediction--a review. <i>Computers &amp; Chemistry</i> , <b>1999</b> , 23, 191-207		146
29	Sequence and structure-based prediction of eukaryotic protein phosphorylation sites. <i>Journal of Molecular Biology</i> , <b>1999</b> , 294, 1351-62	6.5	2406
28	NetOglyc: prediction of mucin type O-glycosylation sites based on sequence context and surface accessibility. <i>Glycoconjugate Journal</i> , <b>1998</b> , 15, 115-30	3	412
27	Statistical analysis of protein kinase specificity determinants. <i>FEBS Letters</i> , <b>1998</b> , 430, 45-50	3.8	108
26	Computational analyses and annotations of the Arabidopsis peroxidase gene family. <i>FEBS Letters</i> , <b>1998</b> , 433, 98-102	3.8	32
25	DNA structure in human RNA polymerase II promoters. <i>Journal of Molecular Biology</i> , <b>1998</b> , 281, 663-73	6.5	73
24	A neural network method for identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. <i>International Journal of Neural Systems</i> , <b>1997</b> , 8, 581-99	6.2	552
23	Prediction of N-terminal protein sorting signals. <i>Current Opinion in Structural Biology</i> , <b>1997</b> , 7, 394-8	8.1	115
22	Hidden Markov Models for Human Genes <b>1997</b> , 15-32		
21	Naturally occurring nucleosome positioning signals in human exons and introns. <i>Journal of Molecular Biology</i> , <b>1996</b> , 263, 503-10	6.5	62

20	Defining a similarity threshold for a functional protein sequence pattern: the signal peptide cleavage site. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 24, 165-77	4.2	61
19	Prediction of the secondary structure of HIV-1 gp120. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 25, 1-11	4.2	28
18	Protein structure and the sequential structure of mRNA: alpha-helix and beta-sheet signals at the nucleotide level. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 25, 237-52	4.2	24
17	Cleavage site analysis in picornaviral polyproteins: discovering cellular targets by neural networks. <i>Protein Science</i> , <b>1996</b> , 5, 2203-16	6.3	192
16	Relationship between protein structure and geometrical constraints. <i>Protein Science</i> , <b>1996</b> , 5, 2217-25	6.3	31
15	Protein structure and the sequential structure of mRNA: helix and sheet signals at the nucleotide level. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>1996</b> , 25, 237-252	4.2	51
14	Analysis of eukaryotic promoter sequences reveals a systematically occurring CT-signal. <i>Nucleic Acids Research</i> , <b>1995</b> , 23, 1223-30	20.1	27
13	Protein structures from distance inequalities. <i>Journal of Molecular Biology</i> , <b>1993</b> , 231, 861-9	6.5	46
12	Multiple alignment using simulated annealing: branch point definition in human mRNA splicing. <i>Nucleic Acids Research</i> , <b>1992</b> , 20, 2511-6	20.1	47
11	G+C-rich tract in 5' end of human introns. <i>Journal of Molecular Biology</i> , <b>1992</b> , 227, 108-13	6.5	37
10	Prediction of human mRNA donor and acceptor sites from the DNA sequence. <i>Journal of Molecular Biology</i> , <b>1991</b> , 220, 49-65	6.5	650
9	Cleaning up gene databases. <i>Nature</i> , <b>1990</b> , 343, 123	50.4	32
8	A novel approach to prediction of the 3-dimensional structures of protein backbones by neural networks. <i>FEBS Letters</i> , <b>1990</b> , 261, 43-6	3.8	90
7	Protein secondary structure and homology by neural networks. The alpha-helices in rhodopsin. <i>FEBS Letters</i> , <b>1988</b> , 241, 223-8	3.8	135
6	Prediction of Glycosylation Sites in Proteins		163-192
5	Text mining of 15 million full-text scientific articles		5
4	Pathway and network analysis of more than 2,500 whole cancer genomes		4
3	Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study		1

2	Pancreatic cancer risk predicted from disease trajectories using deep learning	1
1	Drug interactions in hospital prescriptions in Denmark: Prevalence and associations with adverse outcomes	1