

Sren Brunak

List of Publications by Citations

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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	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
324	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011 , 8, 785-621	6	6866
323	Improved prediction of signal peptides: SignalP 3.0. <i>Journal of Molecular Biology</i> , 2004 , 340, 783-95	6.5	5563
322	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
321	Predicting subcellular localization of proteins based on their N-terminal amino acid sequence. <i>Journal of Molecular Biology</i> , 2000 , 300, 1005-16	6.5	3635
320	Locating proteins in the cell using TargetP, SignalP and related tools. <i>Nature Protocols</i> , 2007 , 2, 953-71	18.8	2596
319	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
318	Sequence and structure-based prediction of eukaryotic protein phosphorylation sites. <i>Journal of Molecular Biology</i> , 1999 , 294, 1351-62	6.5	2406
317	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019 , 37, 420-423	44.5	1536
316	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. <i>Proteomics</i> , 2004 , 4, 1633-49	4.8	1442
315	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
314	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
313	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
312	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
311	Mining electronic health records: towards better research applications and clinical care. <i>Nature Reviews Genetics</i> , 2012 , 13, 395-405	30.1	911
310	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003 , 12, 1652-62	6.3	880
309	Feature-based prediction of non-classical and leaderless protein secretion. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 349-56	1.9	873

308	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. <i>EMBO Journal</i> , 2013 , 32, 1478-88	13	862
307	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015 , 522, 167-72	50.4	827
306	Reliable prediction of T-cell epitopes using neural networks with novel sequence representations. <i>Protein Science</i> , 2003 , 12, 1007-17	6.3	783
305	A human phenome-interactome network of protein complexes implicated in genetic disorders. <i>Nature Biotechnology</i> , 2007 , 25, 309-16	44.5	761
304	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. <i>Glycobiology</i> , 2005 , 15, 153-64	5.8	758
303	Prediction of human mRNA donor and acceptor sites from the DNA sequence. <i>Journal of Molecular Biology</i> , 1991 , 220, 49-65	6.5	650
302	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
301	Analysis and prediction of leucine-rich nuclear export signals. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 527-36	1.9	613
300	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	50.4	581
299	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010 , 463, 757-62	50.4	567
298	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
297	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> , 1997 , 8, 581-99	6.2	552
296	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , 2011 , 334, 94-8	33.3	528
295	Non-classical protein secretion in bacteria. <i>BMC Microbiology</i> , 2005 , 5, 58	4.5	473
294	Machine learning approaches for the prediction of signal peptides and other protein sorting signals. <i>Protein Engineering, Design and Selection</i> , 1999 , 12, 3-9	1.9	461
293	NetOglyc: prediction of mucin type O-glycosylation sites based on sequence context and surface accessibility. <i>Glycoconjugate Journal</i> , 1998 , 15, 115-30	3	412
292	Prediction of twin-arginine signal peptides. <i>BMC Bioinformatics</i> , 2005 , 6, 167	3.6	408
291	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016 , 48, 510-8	36.3	404

290	Prediction of proprotein convertase cleavage sites. <i>Protein Engineering, Design and Selection</i> , 2004 , 17, 107-12	1.9	383
289	A new non-linear normalization method for reducing variability in DNA microarray experiments. <i>Genome Biology</i> , 2002 , 3, research0048	18.3	372
288	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014 , 506, 225-9	50.4	357
287	Dynamic complex formation during the yeast cell cycle. <i>Science</i> , 2005 , 307, 724-7	33.3	343
286	Linear motif atlas for phosphorylation-dependent signaling. <i>Science Signaling</i> , 2008 , 1, ra2	8.8	342
285	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
284	A scored human protein-protein interaction network to catalyze genomic interpretation. <i>Nature Methods</i> , 2017 , 14, 61-64	21.6	307
283	Early divergent strains of <i>Yersinia pestis</i> in Eurasia 5,000 years ago. <i>Cell</i> , 2015 , 163, 571-82	56.2	294
282	Prediction of human protein function from post-translational modifications and localization features. <i>Journal of Molecular Biology</i> , 2002 , 319, 1257-65	6.5	274
281	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016 , 538, 207-214	50.4	268
280	PhosphoBase, a database of phosphorylation sites: release 2.0. <i>Nucleic Acids Research</i> , 1999 , 27, 237-9	20.1	255
279	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> , 2008 , 105, 20870-5	11.5	232
278	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> , 2005 , 35, 2295-303	6.1	229
277	Sensitive quantitative predictions of peptide-MHC binding by a Query by Committee Artificial neural network approach. <i>Tissue Antigens</i> , 2003 , 62, 378-84		228
276	Definition of supertypes for HLA molecules using clustering of specificity matrices. <i>Immunogenetics</i> , 2004 , 55, 797-810	3.2	224
275	Improved prediction of MHC class I and class II epitopes using a novel Gibbs sampling approach. <i>Bioinformatics</i> , 2004 , 20, 1388-97	7.2	223
274	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> , 2002 , 76, 8757-68	6.6	223
273	Pigs in sequence space: a 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , 2005 , 6, 70	4.5	221

272	Prediction of proteasome cleavage motifs by neural networks. <i>Protein Engineering, Design and Selection</i> , 2002 , 15, 287-96	1.9	202
271	Intrauterine exposure to mild analgesics is a risk factor for development of male reproductive disorders in human and rat. <i>Human Reproduction</i> , 2011 , 26, 235-44	5.7	194
270	A DNA structural atlas for Escherichia coli. <i>Journal of Molecular Biology</i> , 2000 , 299, 907-30	6.5	194
269	Using electronic patient records to discover disease correlations and stratify patient cohorts. <i>PLoS Computational Biology</i> , 2011 , 7, e1002141	5	193
268	Cleavage site analysis in picornaviral polyproteins: discovering cellular targets by neural networks. <i>Protein Science</i> , 1996 , 5, 2203-16	6.3	192
267	Temporal disease trajectories condensed from population-wide registry data covering 6.2 million patients. <i>Nature Communications</i> , 2014 , 5, 4022	17.4	186
266	Network biology concepts in complex disease comorbidities. <i>Nature Reviews Genetics</i> , 2016 , 17, 615-29	30.1	183
265	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> , 2007 , 104, 5495-500	11.5	177
264	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006 , 7, R107	18.3	177
263	NESbase version 1.0: a database of nuclear export signals. <i>Nucleic Acids Research</i> , 2003 , 31, 393-6	20.1	176
262	Alternative splicing in colon, bladder, and prostate cancer identified by exon array analysis. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1214-24	7.6	174
261	On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , 2001 , 17, 425-8	8.5	170
260	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. <i>Nucleic Acids Research</i> , 1999 , 27, 370-2	20.1	163
259	A nondegenerate code of deleterious variants in Mendelian loci contributes to complex disease risk. <i>Cell</i> , 2013 , 155, 70-80	56.2	160
258	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018 , 17, 317-332	64.1	156
257	Analysis of gene expression profiles of microdissected cell populations indicates that testicular carcinoma in situ is an arrested gonocyte. <i>Cancer Research</i> , 2009 , 69, 5241-50	10.1	154
256	Co-evolution of transcriptional and post-translational cell-cycle regulation. <i>Nature</i> , 2006 , 443, 594-7	50.4	153
255	Comparison of computational methods for the identification of cell cycle-regulated genes. <i>Bioinformatics</i> , 2005 , 21, 1164-71	7.2	150

254	Analysis and prediction of mammalian protein glycation. <i>Glycobiology</i> , 2006 , 16, 844-53	5.8	147
253	Pharos: Collating protein information to shed light on the druggable genome. <i>Nucleic Acids Research</i> , 2017 , 45, D995-D1002	20.1	146
252	The biology of eukaryotic promoter prediction--a review. <i>Computers & Chemistry</i> , 1999 , 23, 191-207		146
251	Protein secondary structure and homology by neural networks. The alpha-helices in rhodopsin. <i>FEBS Letters</i> , 1988 , 241, 223-8	3.8	135
250	Continuum secondary structure captures protein flexibility. <i>Structure</i> , 2002 , 10, 175-84	5.2	122
249	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015 , 6, 5969	17.4	119
248	Prediction of N-terminal protein sorting signals. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 394-8	8.1	115
247	Bacterial natural transformation by highly fragmented and damaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19860-5	11.5	111
246	Improving the odds in discriminating "drug-like" from "non drug-like" compounds. <i>Journal of Chemical Information and Computer Sciences</i> , 2000 , 40, 1315-24		110
245	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> , 2013 , 93, 1072-86	11	109
244	Statistical analysis of protein kinase specificity determinants. <i>FEBS Letters</i> , 1998 , 430, 45-50	3.8	108
243	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , 2017 , 13, e1006706	6	102
242	Modeling the adaptive immune system: predictions and simulations. <i>Bioinformatics</i> , 2007 , 23, 3265-75	7.2	101
241	Prediction of protein secondary structure at 80% accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 17-20	4.2	96
240	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> , 2012 , 109, 14035-40	11.5	90
239	Scanning the available Dictyostelium discoideum proteome for O-linked GlcNAc glycosylation sites using neural networks. <i>Glycobiology</i> , 1999 , 9, 1009-22	5.8	90
238	A novel approach to prediction of the 3-dimensional structures of protein backbones by neural networks. <i>FEBS Letters</i> , 1990 , 261, 43-6	3.8	90
237	The SH2 domain interaction landscape. <i>Cell Reports</i> , 2013 , 3, 1293-305	10.6	89

236	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017 , 548, 87-91	50.4	87
235	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. <i>Journal of Medical Genetics</i> , 2012 , 49, 58-65	5.8	86
234	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016 , 44, D38-47	20.1	81
233	A systematic study of site-specific GalNAc-type O-glycosylation modulating proprotein convertase processing. <i>Journal of Biological Chemistry</i> , 2011 , 286, 40122-32	5.4	80
232	hERG classification model based on a combination of support vector machine method and GRIND descriptors. <i>Molecular Pharmaceutics</i> , 2008 , 5, 117-27	5.6	80
231	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> , 2014 , 94, 479	11	78
230	Prediction methods and databases within chemoinformatics: emphasis on drugs and drug candidates. <i>Bioinformatics</i> , 2005 , 21, 2145-60	7.2	78
229	Predicting proteasomal cleavage sites: a comparison of available methods. <i>International Immunology</i> , 2003 , 15, 781-7	4.9	76
228	Prediction of pH-dependent aqueous solubility of druglike molecules. <i>Journal of Chemical Information and Modeling</i> , 2006 , 46, 2601-9	6.1	75
227	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020 , 588, 135-140	50.4	75
226	Many putative endocrine disruptors inhibit prostaglandin synthesis. <i>Environmental Health Perspectives</i> , 2011 , 119, 534-41	8.4	73
225	DNA structure in human RNA polymerase II promoters. <i>Journal of Molecular Biology</i> , 1998 , 281, 663-73	6.5	73
224	Dissecting spatio-temporal protein networks driving human heart development and related disorders. <i>Molecular Systems Biology</i> , 2010 , 6, 381	12.2	72
223	Genome organisation and chromatin structure in Escherichia coli. <i>Biochimie</i> , 2001 , 83, 201-12	4.6	71
222	Dynamic and explainable machine learning prediction of mortality in patients in the intensive care unit: a retrospective study of high-frequency data in electronic patient records. <i>The Lancet Digital Health</i> , 2020 , 2, e179-e191	14.4	70
221	A comprehensive and quantitative comparison of text-mining in 15 million full-text articles versus their corresponding abstracts. <i>PLoS Computational Biology</i> , 2018 , 14, e1005962	5	70
220	Coronavirus 3CLpro proteinase cleavage sites: possible relevance to SARS virus pathology. <i>BMC Bioinformatics</i> , 2004 , 5, 72	3.6	68
219	Blood cell gene expression profiling in rheumatoid arthritis. Discriminative genes and effect of rheumatoid factor. <i>Immunology Letters</i> , 2004 , 93, 217-26	4.1	67

218	Identification of phosphorylation sites in protein kinase A substrates using artificial neural networks and mass spectrometry. <i>Journal of Proteome Research</i> , 2004 , 3, 426-33	5.6	67
217	Porcine transcriptome analysis based on 97 non-normalized cDNA libraries and assembly of 1,021,891 expressed sequence tags. <i>Genome Biology</i> , 2007 , 8, R45	18.3	63
216	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014 , 24, R1035-7	6.3	62
215	Naturally occurring nucleosome positioning signals in human exons and introns. <i>Journal of Molecular Biology</i> , 1996 , 263, 503-10	6.5	62
214	Defining a similarity threshold for a functional protein sequence pattern: the signal peptide cleavage site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 165-77	4.2	61
213	Phosphoproteomics of Primary Cells Reveals Druggable Kinase Signatures in Ovarian Cancer. <i>Cell Reports</i> , 2017 , 18, 3242-3256	10.6	59
212	Population-wide analysis of differences in disease progression patterns in men and women. <i>Nature Communications</i> , 2019 , 10, 666	17.4	58
211	ChemProt: a disease chemical biology database. <i>Nucleic Acids Research</i> , 2011 , 39, D367-72	20.1	58
210	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> , 2016 , 11, 283-90	3.1	58
209	Propionibacterium acnes: Disease-Causing Agent or Common Contaminant? Detection in Diverse Patient Samples by Next-Generation Sequencing. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 980-7	9.7	57
208	SignalP 6.0 predicts all five types of signal peptides using protein language models.. <i>Nature Biotechnology</i> , 2022 ,	44.5	56
207	Sigma A recognition sites in the Bacillus subtilis genome. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 2417-2424	24.2	56
206	A Brief History of Protein Sorting Prediction. <i>Protein Journal</i> , 2019 , 38, 200-216	3.9	55
205	Cyclebase.org--a comprehensive multi-organism online database of cell-cycle experiments. <i>Nucleic Acids Research</i> , 2008 , 36, D854-9	20.1	55
204	Protein interaction-based genome-wide analysis of incident coronary heart disease. <i>Circulation: Cardiovascular Genetics</i> , 2011 , 4, 549-56		53
203	ChemProt-3.0: a global chemical biology diseases mapping. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	53
202	A wiring of the human nucleolus. <i>Molecular Cell</i> , 2006 , 22, 285-95	17.6	52
201	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. <i>Human Molecular Genetics</i> , 2017 , 26, 1219-1229	5.6	51

200	Protein structure and the sequential structure of mRNA: Helix and Sheet signals at the nucleotide level. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 237-252	4.2	51
199	Annotation of loci from genome-wide association studies using tissue-specific quantitative interaction proteomics. <i>Nature Methods</i> , 2014 , 11, 868-74	21.6	50
198	Dictionary construction and identification of possible adverse drug events in Danish clinical narrative text. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013 , 20, 947-53	8.6	50
197	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> , 2011 , 108, E681-8	11.5	50
196	Diagnosis trajectories of prior multi-morbidity predict sepsis mortality. <i>Scientific Reports</i> , 2016 , 6, 36624	4.9	48
195	Dose-specific adverse drug reaction identification in electronic patient records: temporal data mining in an inpatient psychiatric population. <i>Drug Safety</i> , 2014 , 37, 237-47	5.1	48
194	Sequence-based feature prediction and annotation of proteins. <i>Genome Biology</i> , 2009 , 10, 206	18.3	48
193	Multiple alignment using simulated annealing: branch point definition in human mRNA splicing. <i>Nucleic Acids Research</i> , 1992 , 20, 2511-6	20.1	47
192	Survival prediction in intensive-care units based on aggregation of long-term disease history and acute physiology: a retrospective study of the Danish National Patient Registry and electronic patient records. <i>The Lancet Digital Health</i> , 2019 , 1, e78-e89	14.4	46
191	ChemProt-2.0: visual navigation in a disease chemical biology database. <i>Nucleic Acids Research</i> , 2013 , 41, D464-9	20.1	46
190	Protein structures from distance inequalities. <i>Journal of Molecular Biology</i> , 1993 , 231, 861-9	6.5	46
189	Cyclebase.org: version 2.0, an updated comprehensive, multi-species repository of cell cycle experiments and derived analysis results. <i>Nucleic Acids Research</i> , 2010 , 38, D699-702	20.1	45
188	Integrative analysis for finding genes and networks involved in diabetes and other complex diseases. <i>Genome Biology</i> , 2007 , 8, R253	18.3	45
187	New weakly expressed cell cycle-regulated genes in yeast. <i>Yeast</i> , 2005 , 22, 1191-201	3.4	45
186	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018 , 46, D354-D359	20.1	44
185	Immunological Bioinformatics 2005 ,		44
184	A computational framework to integrate high-throughput Omics Datasets for the identification of potential mechanistic links. <i>Nature Protocols</i> , 2018 , 13, 2781-2800	18.8	44
183	Immune Profiling of Human Gut-Associated Lymphoid Tissue Identifies a Role for Isolated Lymphoid Follicles in Priming of Region-Specific Immunity. <i>Immunity</i> , 2020 , 52, 557-570.e6	32.3	40

182	Deciphering diseases and biological targets for environmental chemicals using toxicogenomics networks. <i>PLoS Computational Biology</i> , 2010 , 6, e1000788	5	40
181	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> , 2014 , 57, 1132-42	10.3	39
180	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016 , 1, 16152	26.6	38
179	Optimization and immune recognition of multiple novel conserved HLA-A2, human immunodeficiency virus type 1-specific CTL epitopes. <i>Journal of General Virology</i> , 2003 , 84, 2409-2421	4.9	37
178	G+C-rich tract in 5' end of human introns. <i>Journal of Molecular Biology</i> , 1992 , 227, 108-13	6.5	37
177	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019 , 20, 693-701	30.1	36
176	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> , 2010 , 368, 2799-815 ³		35
175	Prediction of glycosylation across the human proteome and the correlation to protein function 2001 ,		33
174	Prenatal exposure to paracetamol/acetaminophen and precursor aniline impairs masculinisation of male brain and behaviour. <i>Reproduction</i> , 2017 , 154, 145-152	3.8	32
173	Identification of odorant-receptor interactions by global mapping of the human odorome. <i>PLoS ONE</i> , 2014 , 9, e93037	3.7	32
172	Computational analyses and annotations of the Arabidopsis peroxidase gene family. <i>FEBS Letters</i> , 1998 , 433, 98-102	3.8	32
171	Cleaning up gene databases. <i>Nature</i> , 1990 , 343, 123	50.4	32
170	Polychlorinated dibenzo-p-dioxins, furans, and biphenyls (PCDDs/PCDFs and PCBs) in breast milk and early childhood growth and IGF1. <i>Reproduction</i> , 2014 , 147, 391-9	3.8	31
169	Functionality of system components: conservation of protein function in protein feature space. <i>Genome Research</i> , 2003 , 13, 2444-9	9.7	31
168	Bias of purine stretches in sequenced chromosomes. <i>Computers & Chemistry</i> , 2002 , 26, 531-41		31
167	Relationship between protein structure and geometrical constraints. <i>Protein Science</i> , 1996 , 5, 2217-25	6.3	31
166	Complete genes may pass from food to human blood. <i>PLoS ONE</i> , 2013 , 8, e69805	3.7	31
165	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015 , 5, 13201	4.9	30

164	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> , 2012 , 233, 172-81	5.7	30
163	ImmunoGrid, an integrative environment for large-scale simulation of the immune system for vaccine discovery, design and optimization. <i>Briefings in Bioinformatics</i> , 2009 , 10, 330-40	13.4	29
162	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , 2011 , 35, 318-32	2.6	28
161	Prediction of the secondary structure of HIV-1 gp120. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 1-11	4.2	28
160	Integration of known DNA, RNA and protein biomarkers provides prediction of anti-TNF response in rheumatoid arthritis: results from the COMBINE study. <i>Molecular Medicine</i> , 2016 , 22, 322-328	6.2	28
159	Cofactory: sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 1819-28	4.2	27
158	Analysis of eukaryotic promoter sequences reveals a systematically occurring CT-signal. <i>Nucleic Acids Research</i> , 1995 , 23, 1223-30	20.1	27
157	Acute and persistent symptoms in non-hospitalized PCR-confirmed COVID-19 patients. <i>Scientific Reports</i> , 2021 , 11, 13153	4.9	27
156	SNP mining porcine ESTs with MAVIANT, a novel tool for SNP evaluation and annotation. <i>Bioinformatics</i> , 2007 , 23, i387-91	7.2	26
155	Evolution of cell cycle control: same molecular machines, different regulation. <i>Cell Cycle</i> , 2007 , 6, 1819-25	5.7	26
154	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020 , 41, 2618-2628	9.5	26
153	A computational approach to chemical etiologies of diabetes. <i>Scientific Reports</i> , 2013 , 3, 2712	4.9	25
152	Prediction of novel archaeal enzymes from sequence-derived features. <i>Protein Science</i> , 2002 , 11, 2894-86	3	25
151	Systematic characterisation of cellular localisation and expression profiles of proteins containing MHC ligands. <i>PLoS ONE</i> , 2009 , 4, e7448	3.7	25
150	Early differences in islets from prediabetic NOD mice: combined microarray and proteomic analysis. <i>Diabetologia</i> , 2017 , 60, 475-489	10.3	24
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