

Tim Hubbard

List of Publications by Year in Descending Order

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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.

170
papers

95,786
citations

85
h-index

180
g-index

180
ext. papers

109,760
ext. citations

17
avg, IF

8.49
L-index

#	Paper	IF	Citations
170	Whole genome sequencing for the diagnosis of neurological repeat expansion disorders in the UK: a retrospective diagnostic accuracy and prospective clinical validation study.. <i>Lancet Neurology, The</i> , 2022 , 21, 234-245	24.1	6
169	Transcriptional activity and strain-specific history of mouse pseudogenes. <i>Nature Communications</i> , 2020 , 11, 3695	17.4	8
168	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
167	Bi-allelic Loss-of-Function CACNA1B Mutations in Progressive Epilepsy-Dyskinesia. <i>American Journal of Human Genetics</i> , 2019 , 104, 948-956	11	17
166	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773	20.1	1140
165	The 100 000 Genomes Project: bringing whole genome sequencing to the NHS. <i>BMJ, The</i> , 2018 , 361, k1687	5.9	184
164	Scientists on the Spot: Sequencing the human genome to influence patient healthcare. <i>Cardiovascular Research</i> , 2018 , 114, e66-e67	9.9	
163	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017 , 27, 849-864	9.7	365
162	Automated PDF highlighting to support faster curation of literature for Parkinson's and Alzheimer's disease. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	1
161	Analysis of diagnoses extracted from electronic health records in a large mental health case register. <i>PLoS ONE</i> , 2017 , 12, e0171526	3.7	8
160	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016 , 8, 71	14.4	146
159	The language of mental health problems in social media 2016 ,		23
158	An interactive genome browser of association results from the UK10K cohorts project. <i>Bioinformatics</i> , 2015 , 31, 4029-31	7.2	9
157	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
156	Global implementation of genomic medicine: We are not alone. <i>Science Translational Medicine</i> , 2015 , 7, 290ps13	17.5	112
155	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
154	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3366	11.5	22

153	Characterizing genetic variants for clinical action. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2014 , 166C, 93-104	3.1	41
152	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
151	Current status and new features of the Consensus Coding Sequence database. <i>Nucleic Acids Research</i> , 2014 , 42, D865-72	20.1	122
150	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6131-8	11.5	490
149	Comparative analysis of pseudogenes across three phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13361-6	11.5	54
148	A comparison of peak callers used for DNase-Seq data. <i>PLoS ONE</i> , 2014 , 9, e96303	3.7	55
147	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013 , 10, 1177-84	21.6	477
146	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , 2013 , 10, 1185-91	21.6	371
145	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013 , 496, 498-503	50.4	2550
144	Chromatin accessibility data sets show bias due to sequence specificity of the DNase I enzyme. <i>PLoS ONE</i> , 2013 , 8, e69853	3.7	46
143	The GENCODE pseudogene resource. <i>Genome Biology</i> , 2012 , 13, R51	18.3	232
142	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
141	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012 , 22, 1760-74	9.7	3142
140	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
139	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
138	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
137	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , 2012 , 7, e28213	3.7	51
136	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. <i>Genome Research</i> , 2012 , 22, 1698-710	9.7	44

135	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
134	The GENCODE exome: sequencing the complete human exome. <i>European Journal of Human Genetics</i> , 2011 , 19, 827-31	5.3	50
133	ITFoM The IT Future of Medicine. <i>Procedia Computer Science</i> , 2011 , 7, 26-29	1.6	13
132	Developing and implementing an institute-wide data sharing policy. <i>Genome Medicine</i> , 2011 , 3, 60	14.4	27
131	Dalliance: interactive genome viewing on the web. <i>Bioinformatics</i> , 2011 , 27, 889-90	7.2	78
130	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011 , 39, D800-6	20.1	590
129	The origins, evolution, and functional potential of alternative splicing in vertebrates. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2949-59	8.3	55
128	Modernizing reference genome assemblies. <i>PLoS Biology</i> , 2011 , 9, e1001091	9.7	294
127	Shotgun proteomics aids discovery of novel protein-coding genes, alternative splicing, and "resurrected" pseudogenes in the mouse genome. <i>Genome Research</i> , 2011 , 21, 756-67	9.7	96
126	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
125	iMotifs: an integrated sequence motif visualization and analysis environment. <i>Bioinformatics</i> , 2010 , 26, 843-4	7.2	7
124	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010 , 38, D557-62	20.1	240
123	Novel candidate cancer genes identified by a large-scale cross-species comparative oncogenomics approach. <i>Cancer Research</i> , 2010 , 70, 883-95	10.1	36
122	Genome-wide end-sequenced BAC resources for the NOD/MrkTac() and NOD/ShiLtJ() mouse genomes. <i>Genomics</i> , 2010 , 95, 105-10	4.3	12
121	Metamotifs--a generative model for building families of nucleotide position weight matrices. <i>BMC Bioinformatics</i> , 2010 , 11, 348	3.6	5
120	AnnoTrack--a tracking system for genome annotation. <i>BMC Genomics</i> , 2010 , 11, 538	4.5	6
119	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. <i>Genome Research</i> , 2009 , 19, 1316-23	9.7	415
118	Ensembl 2009. <i>Nucleic Acids Research</i> , 2009 , 37, D690-7	20.1	692

117	Discovery of candidate disease genes in ENU-induced mouse mutants by large-scale sequencing, including a splice-site mutation in nucleoredoxin. <i>PLoS Genetics</i> , 2009 , 5, e1000759	6	37
116	Petabyte-scale innovations at the European Nucleotide Archive. <i>Nucleic Acids Research</i> , 2009 , 37, D19-25	20.1	72
115	Cancer gene discovery in mouse and man. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2009 , 1796, 140-61	11.2	8
114	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
113	Post-publication sharing of data and tools. <i>Nature</i> , 2009 , 461, 171-3	50.4	109
112	Accurate and sensitive peptide identification with Mascot Percolator. <i>Journal of Proteome Research</i> , 2009 , 8, 3176-81	5.6	323
111	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008 , 26, 779-85	44.5	533
110	NestedMICA as an ab initio protein motif discovery tool. <i>BMC Bioinformatics</i> , 2008 , 9, 19	3.6	23
109	Integrating biological data--the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 8, S3	3.6	77
108	Large-scale mutagenesis in p19(ARF)- and p53-deficient mice identifies cancer genes and their collaborative networks. <i>Cell</i> , 2008 , 133, 727-41	56.2	149
107	The Protein Feature Ontology: a tool for the unification of protein feature annotations. <i>Bioinformatics</i> , 2008 , 24, 2767-72	7.2	16
106	Comparison of Mascot and X!Tandem performance for low and high accuracy mass spectrometry and the development of an adjusted Mascot threshold. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 962-70	7.6	55
105	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008 , 18, 1518-29	9.7	304
104	The vertebrate genome annotation (Vega) database. <i>Nucleic Acids Research</i> , 2008 , 36, D753-60	20.1	187
103	Data growth and its impact on the SCOP database: new developments. <i>Nucleic Acids Research</i> , 2008 , 36, D419-25	20.1	768
102	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2008 , 36, D5-12	20.1	39
101	Ensembl 2008. <i>Nucleic Acids Research</i> , 2008 , 36, D707-14	20.1	408
100	New tools and expanded data analysis capabilities at the Protein Structure Prediction Center. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 19-26	4.2	29

99	Critical assessment of methods of protein structure prediction-Round VII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 3-9	4.2	189
98	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
97	Integrating sequence and structural biology with DAS. <i>BMC Bioinformatics</i> , 2007 , 8, 333	3.6	57
96	SISYPHUS--structural alignments for proteins with non-trivial relationships. <i>Nucleic Acids Research</i> , 2007 , 35, D253-9	20.1	61
95	Large-scale discovery of promoter motifs in <i>Drosophila melanogaster</i> . <i>PLoS Computational Biology</i> , 2007 , 3, e7	5	56
94	Prominent use of distal 5Ntranscription start sites and discovery of a large number of additional exons in ENCODE regions. <i>Genome Research</i> , 2007 , 17, 746-59	9.7	156
93	Ensembl 2007. <i>Nucleic Acids Research</i> , 2007 , 35, D610-7	20.1	669
92	Lessons learned from the initial sequencing of the pig genome: comparative analysis of an 8 Mb region of pig chromosome 17. <i>Genome Biology</i> , 2007 , 8, R168	18.3	33
91	A machine learning strategy to identify candidate binding sites in human protein-coding sequence. <i>BMC Bioinformatics</i> , 2006 , 7, 419	3.6	12
90	Ensembl 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D556-61	20.1	324
89	Genomic anatomy of the Tyrp1 (brown) deletion complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3704-9	11.5	28
88	GENCODE: producing a reference annotation for ENCODE. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S4.1-9	18.3	434
87	EGASP: the human ENCODE Genome Annotation Assessment Project. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S2.1-31	18.3	187
86	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. <i>Nature</i> , 2006 , 440, 1045-9	50.4	114
85	The DNA sequence and biological annotation of human chromosome 1. <i>Nature</i> , 2006 , 441, 315-21	50.4	169
84	NestedMICA: sensitive inference of over-represented motifs in nucleic acid sequence. <i>Nucleic Acids Research</i> , 2005 , 33, 1445-53	20.1	87
83	The Vertebrate Genome Annotation (Vega) database. <i>Nucleic Acids Research</i> , 2005 , 33, D459-65	20.1	118
82	Ensembl 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D447-53	20.1	363

81	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005 , 434, 325-37	50.4	822
80	Critical assessment of methods of protein structure prediction (CASP)--round 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61 Suppl 7, 3-7	4.2	148
79	Adding some SPICE to DAS. <i>Bioinformatics</i> , 2005 , 21 Suppl 2, ii40-1	7.2	40
78	An overview of Ensembl. <i>Genome Research</i> , 2004 , 14, 925-8	9.7	316
77	Ensembl 2004. <i>Nucleic Acids Research</i> , 2004 , 32, D468-70	20.1	142
76	A new trade framework for global healthcare R&D. <i>PLoS Biology</i> , 2004 , 2, E52	9.7	56
75	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004 , 4, 177-83	31.3	2424
74	The DNA sequence and analysis of human chromosome 13. <i>Nature</i> , 2004 , 428, 522-8	50.4	71
73	The DNA sequence and comparative analysis of human chromosome 10. <i>Nature</i> , 2004 , 429, 375-81	50.4	62
72	DNA sequence and analysis of human chromosome 9. <i>Nature</i> , 2004 , 429, 369-74	50.4	102
71	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004 , 431, 931-45	50.4	3444
70	What can we learn from noncoding regions of similarity between genomes?. <i>BMC Bioinformatics</i> , 2004 , 5, 131	3.6	6
69	SCOP database in 2004: refinements integrate structure and sequence family data. <i>Nucleic Acids Research</i> , 2004 , 32, D226-9	20.1	733
68	Domain insertions in protein structures. <i>Journal of Molecular Biology</i> , 2004 , 338, 633-41	6.5	59
67	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004 , 306, 636-40	33.3	1692
66	CASP5 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 340-51	4.2	20
65	Critical assessment of methods of protein structure prediction (CASP)-round V. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53 Suppl 6, 334-9	4.2	206
64	The DNA sequence and analysis of human chromosome 6. <i>Nature</i> , 2003 , 425, 805-11	50.4	243

63	ddbRNA: detection of conserved secondary structures in multiple alignments. <i>Bioinformatics</i> , 2003 , 19, 1606-11	7.2	50
62	Ensembl 2002: accommodating comparative genomics. <i>Nucleic Acids Research</i> , 2003 , 31, 38-42	20.1	180
61	The significance of performance ranking in CASP--response to Marti-Renom et al. <i>Structure</i> , 2002 , 10, 291-2; discussion 292-3	5.2	5
60	A physical map of the mouse genome. <i>Nature</i> , 2002 , 418, 743-50	50.4	282
59	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
58	Computational detection and location of transcription start sites in mammalian genomic DNA. <i>Genome Research</i> , 2002 , 12, 458-61	9.7	205
57	Databases and tools for browsing genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2002 , 3, 293-310	9.7	17
56	SCOP database in 2002: refinements accommodate structural genomics. <i>Nucleic Acids Research</i> , 2002 , 30, 264-7	20.1	348
55	MaxBench: evaluation of sequence and structure comparison methods. <i>Bioinformatics</i> , 2002 , 18, 494-5	7.2	12
54	Biological information: making it accessible and integrated (and trying to make sense of it). <i>Bioinformatics</i> , 2002 , 18 Suppl 2, S140	7.2	14
53	The Ensembl genome database project. <i>Nucleic Acids Research</i> , 2002 , 30, 38-41	20.1	1084
52	Critical assessment of methods of protein structure prediction (CASP): Round IV. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 2-7	4.2	119
51	Prediction targets of CASP4. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 8-12	4.2	9
50	Assessment of novel fold targets in CASP4: predictions of three-dimensional structures, secondary structures, and interresidue contacts. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , Suppl 5, 98-113	4.2	66
49	Peter Andrew Kollman. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 2-3	4.2	40
48	The DNA sequence and comparative analysis of human chromosome 20. <i>Nature</i> , 2001 , 414, 865-71	50.4	177
47	Mining the draft human genome. <i>Nature</i> , 2001 , 409, 827-8	50.4	51
46	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366

45	Quality control in databanks for molecular biology. <i>BioEssays</i> , 2000 , 22, 1024-34	4.1	10
44	Open annotation offers a democratic solution to genome sequencing. <i>Nature</i> , 2000 , 403, 825	50.4	26
43	A browser for expression data. <i>Bioinformatics</i> , 2000 , 16, 402-3	7.2	2
42	SCOP: a structural classification of proteins database. <i>Nucleic Acids Research</i> , 2000 , 28, 257-9	20.1	468
41	BioJava. <i>ACM SIGBIO Newsletter</i> , 2000 , 20, 10-12		24
40	SCOP: a Structural Classification of Proteins database. <i>Nucleic Acids Research</i> , 1999 , 27, 254-6	20.1	191
39	The DNA sequence of human chromosome 22. <i>Nature</i> , 1999 , 402, 489-95	50.4	917
38	RMS/Coverage graphs: A qualitative method for comparing three-dimensional protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 15-21	4.2	36
37	Critical assessment of methods of protein structure prediction (CASP): Round III. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 2-6	4.2	134
36	Critical assessment of methods of protein structure prediction (CASP): Round III. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 2-6	4.2	23
35	Analysis and assessment of ab initio three-dimensional prediction, secondary structure, and contacts prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , Suppl 3, 149-70	4.2	35
34	Critical assessment of methods of protein structure prediction (CASP): Round III 1999 , 37, 2		6
33	RMS/coverage graphs: a qualitative method for comparing three-dimensional protein structure predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , Suppl 3, 15-21	4.2	11
32	GLASS: a tool to visualize protein structure prediction data in three dimensions and evaluate their consistency. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 30, 339-51	4.2	1
31	SCOP, Structural Classification of Proteins database: applications to evaluation of the effectiveness of sequence alignment methods and statistics of protein structural data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1147-54		26
30	Sequence comparisons using multiple sequences detect three times as many remote homologues as pairwise methods. <i>Journal of Molecular Biology</i> , 1998 , 284, 1201-10	6.5	449
29	SPEM: a parser for EMBL style flat file database entries. <i>Bioinformatics</i> , 1998 , 14, 823-4	7.2	2
28	Using neural networks for prediction of the subcellular location of proteins. <i>Nucleic Acids Research</i> , 1998 , 26, 2230-6	20.1	429

27	Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 6073-8	11.5	438
26	SCOP: a structural classification of proteins database. <i>Nucleic Acids Research</i> , 1997 , 25, 236-9	20.1	228
25	Protein folds in the all-beta and all-alpha classes. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997 , 26, 597-627		93
24	Intermediate sequences increase the detection of homology between sequences. <i>Journal of Molecular Biology</i> , 1997 , 273, 349-54	6.5	203
23	New horizons in sequence analysis. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 190-3	8.1	5
22	Population statistics of protein structures: lessons from structural classifications. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 369-76	8.1	158
21	The solution structure of the S1 RNA binding domain: a member of an ancient nucleic acid-binding fold. <i>Cell</i> , 1997 , 88, 235-42	56.2	350
20	Critical assessment of methods of protein structure prediction (CASP): Round II 1997 , 29, 2-6		107
19	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 140-150	4.2	1
18	Critical assessment of methods of protein structure prediction (CASP): Round II. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 2-6	4.2	19
17	Critical assessment of methods of protein structure prediction (CASP): Round II 1997 , 29, 2		3
16	Numerical criteria for the evaluation of ab initio predictions of protein structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , Suppl 1, 140-50	4.2	5
15	Understanding protein structure: using scop for fold interpretation. <i>Methods in Enzymology</i> , 1996 , 266, 635-43	1.7	69
14	Protein structure prediction: playing the fold. <i>Trends in Biochemical Sciences</i> , 1996 , 21, 279-281	10.3	
13	Protein structure prediction: playing the fold. <i>Trends in Biochemical Sciences</i> , 1996 , 21, 279-281	10.3	5
12	Prediction of the structure of GroES and its interaction with GroEL. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 22, 199-209	4.2	13
11	Fold recognition and ab initio structure predictions using hidden Markov models and beta-strand pair potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 23, 398-402	4.2	62
10	Gene duplications in <i>H. influenzae</i> . <i>Nature</i> , 1995 , 378, 140	50.4	71

9	SCOP: A structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995 , 247, 536-540	6.5	2645
8	SCOP: a structural classification of proteins database for the investigation of sequences and structures. <i>Journal of Molecular Biology</i> , 1995 , 247, 536-40	6.5	5115
7	Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 12, 105-10	4.2	25
6	The role of heat-shock and chaperone proteins in protein folding: possible molecular mechanisms. <i>Protein Engineering, Design and Selection</i> , 1991 , 4, 711-7	1.9	67
5	18th Sir Hans Krebs lecture. Knowledge-based protein modelling and design. <i>FEBS Journal</i> , 1988 , 172, 513-20		211
4	Comparison of solvent-inaccessible cores of homologous proteins: definitions useful for protein modelling. <i>Protein Engineering, Design and Selection</i> , 1987 , 1, 159-71	1.9	161
3	Heat-shock proteins during growth and sporulation of <i>Bacillus subtilis</i> . <i>FEBS Letters</i> , 1985 , 188, 209-14	3.8	29
2	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly		13
1	Pseudogenes in the mouse lineage: transcriptional activity and strain-specific history		1