

Liisa Holm

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.

94
papers

19,436
citations

44
h-index

97
g-index

97
ext. papers

22,637
ext. citations

9.2
avg, IF

7.47
L-index

#	Paper	IF	Citations
94	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets 2022 , 2, 49-62		1
93	Metatranscriptomic assessment of burn wound infection clearance. <i>Clinical Microbiology and Infection</i> , 2021 , 27, 144-146	9.5	0
92	PANNZER-A practical tool for protein function prediction. <i>Protein Science</i> , 2021 ,	6.3	4
91	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. <i>Bioscience Reports</i> , 2020 , 40,	4.1	5
90	Novel NGS pipeline for virus discovery from a wide spectrum of hosts and sample types. <i>Virus Evolution</i> , 2020 , 6, veaa091	3.7	10
89	DALI and the persistence of protein shape. <i>Protein Science</i> , 2020 , 29, 128-140	6.3	243
88	Using Dali for Protein Structure Comparison. <i>Methods in Molecular Biology</i> , 2020 , 2112, 29-42	1.4	93
87	Benchmarking fold detection by DaliLite v.5. <i>Bioinformatics</i> , 2019 , 35, 5326-5327	7.2	205
86	Novel comparison of evaluation metrics for gene ontology classifiers reveals drastic performance differences. <i>PLoS Computational Biology</i> , 2019 , 15, e1007419	5	6
85	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
84	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. <i>Carcinogenesis</i> , 2018 , 39, 788-797	4.6	10
83	PANNZER2: a rapid functional annotation web server. <i>Nucleic Acids Research</i> , 2018 , 46, W84-W88	20.1	143
82	TOPAZ: asymmetric suffix array neighbourhood search for massive protein databases. <i>BMC Bioinformatics</i> , 2018 , 19, 278	3.6	2
81	Bracketing phenogenotypic limits of mammalian hybridization. <i>Royal Society Open Science</i> , 2018 , 5, 180903	9.3	16
80	AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination. <i>Nucleic Acids Research</i> , 2018 , 46, W479-W485	20.1	66
79	Robust multi-group gene set analysis with few replicates. <i>BMC Bioinformatics</i> , 2016 , 17, 526	3.6	3
78	Dali server update. <i>Nucleic Acids Research</i> , 2016 , 44, W351-5	20.1	652

77	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
76	SANSPARALLEL: interactive homology search against Uniprot. <i>Nucleic Acids Research</i> , 2015 , 43, W24-9	20.1	26
75	Flight-induced changes in gene expression in the Glanville fritillary butterfly. <i>Molecular Ecology</i> , 2015 , 24, 4886-900	5.7	25
74	BluB/CobT2 fusion enzyme activity reveals mechanisms responsible for production of active form of vitamin B12 by <i>Propionibacterium freudenreichii</i> . <i>Microbial Cell Factories</i> , 2015 , 14, 186	6.4	27
73	PANNZER: high-throughput functional annotation of uncharacterized proteins in an error-prone environment. <i>Bioinformatics</i> , 2015 , 31, 1544-52	7.2	89
72	Genomics and Proteomics Provide New Insight into the Commensal and Pathogenic Lifestyles of Bovine- and Human-Associated <i>Staphylococcus epidermidis</i> Strains. <i>Journal of Proteome Research</i> , 2014 , 13, 3748-3762	5.6	14
71	Atlas of nonribosomal peptide and polyketide biosynthetic pathways reveals common occurrence of nonmodular enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9259-64	11.5	212
70	Gene set analysis: limitations in popular existing methods and proposed improvements. <i>Bioinformatics</i> , 2014 , 30, 2747-56	7.2	11
69	Transcriptome analysis reveals signature of adaptation to landscape fragmentation. <i>PLoS ONE</i> , 2014 , 9, e101467	3.7	20
68	Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. <i>PLoS Computational Biology</i> , 2014 , 10, e1003465	5	59
67	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014 , 5, 4737	17.4	151
66	Reply to Sasso et al.: Distribution and phylogeny of nonribosomal peptide and polyketide biosynthetic pathways in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3947	11.5	2
65	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014 , 42, D222-30	20.1	3975
64	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
63	Automated Sequence-Based Approaches for Identifying Domain Families 2013 , 1-24		1
62	Genome Sequence of <i>Dickeya solani</i> , a New soft Rot Pathogen of Potato, Suggests its Emergence May Be Related to a Novel Combination of Non-Ribosomal Peptide/Polyketide Synthetase Clusters. <i>Diversity</i> , 2013 , 5, 824-842	2.5	22
61	Defense-related transcription factors WRKY70 and WRKY54 modulate osmotic stress tolerance by regulating stomatal aperture in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2013 , 200, 457-472	9.8	156
60	Mutational analysis of positively charged amino acid residues of Uukuniemi phlebovirus nucleocapsid protein. <i>Virus Research</i> , 2012 , 167, 118-23	6.4	1

59	Mismatch repair analysis of inherited MSH2 and/or MSH6 variation pairs found in cancer patients. <i>Human Mutation</i> , 2012 , 33, 1294-301	4.7	8
58	Revised phylogeny and novel horizontally acquired virulence determinants of the model soft rot phytopathogen <i>Pectobacterium wasabiae</i> SCC3193. <i>PLoS Pathogens</i> , 2012 , 8, e1003013	7.6	81
57	SANS: high-throughput retrieval of protein sequences allowing 50% mismatches. <i>Bioinformatics</i> , 2012 , 28, i438-i443	7.2	14
56	Genome sequence of <i>Pectobacterium</i> sp. strain SCC3193. <i>Journal of Bacteriology</i> , 2012 , 194, 6004	3.5	14
55	The wiring of protein networks: Computational approaches for predicting protein interaction networks. <i>Biochemist</i> , 2011 , 33, 8-11	0.5	
54	Genome sequence of <i>Lactobacillus crispatus</i> ST1. <i>Journal of Bacteriology</i> , 2010 , 192, 3547-8	3.5	31
53	Oligomerization of Uukuniemi virus nucleocapsid protein. <i>Virology Journal</i> , 2010 , 7, 187	6.1	17
52	Dali server: conservation mapping in 3D. <i>Nucleic Acids Research</i> , 2010 , 38, W545-9	20.1	3027
51	Advances and pitfalls of protein structural alignment. <i>Current Opinion in Structural Biology</i> , 2009 , 19, 341-8	8.1	290
50	Evaluation of different domain-based methods in protein interaction prediction. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 390, 357-62	3.4	22
49	PairsDB atlas of protein sequence space. <i>Nucleic Acids Research</i> , 2008 , 36, D276-80	20.1	12
48	The RPSP: Web server for prediction of signal peptides. <i>Polymer</i> , 2007 , 48, 5493-5496	3.9	16
47	The global trace graph, a novel paradigm for searching protein sequence databases. <i>Bioinformatics</i> , 2007 , 23, 2361-7	7.2	19
46	Loss of neurturin in frog--comparative genomics study of GDNF family ligand-receptor pairs. <i>Molecular and Cellular Neurosciences</i> , 2007 , 34, 155-67	4.8	26
45	Identifying functional gene sets from hierarchically clustered expression data: map of abiotic stress regulated genes in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2006 , 34, e124	20.1	11
44	POXO: a web-enabled tool series to discover transcription factor binding sites. <i>Nucleic Acids Research</i> , 2006 , 34, W534-40	20.1	10
43	Oligomerization of hantavirus nucleocapsid protein: analysis of the N-terminal coiled-coil domain. <i>Journal of Virology</i> , 2006 , 80, 9073-81	6.6	22
42	Bayesian search of functionally divergent protein subgroups and their function specific residues. <i>Bioinformatics</i> , 2006 , 22, 2466-74	7.2	40

41	Evolution of the GDNF family ligands and receptors. <i>Brain, Behavior and Evolution</i> , 2006 , 68, 181-90	1.5	68
40	Using Dali for structural comparison of proteins. <i>Current Protocols in Bioinformatics</i> , 2006 , Chapter 5, Unit 5.5	24.2	88
39	From sequences to a functional unit. <i>Physiological Genomics</i> , 2006 , 25, 1-8	3.6	1
38	POCO: discovery of regulatory patterns from promoters of oppositely expressed gene sets. <i>Nucleic Acids Research</i> , 2005 , 33, W427-31	20.1	16
37	POBO, transcription factor binding site verification with bootstrapping. <i>Nucleic Acids Research</i> , 2004 , 32, W222-9	20.1	45
36	Accurate detection of very sparse sequence motifs. <i>Journal of Computational Biology</i> , 2004 , 11, 843-57	1.7	15
35	Unraveling protein interaction networks with near-optimal efficiency. <i>Nature Biotechnology</i> , 2004 , 22, 98-103	44.5	72
34	Exhaustive enumeration of protein domain families. <i>Journal of Molecular Biology</i> , 2003 , 328, 749-67	6.5	107
33	A theoretical model for the regulation of Sex-lethal, a gene that controls sex determination and dosage compensation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2003 , 165, 1355-84	4	16
32	Identification of homology in protein structure classification. <i>Nature Structural Biology</i> , 2001 , 8, 953-7		99
31	Rapid automatic detection and alignment of repeats in protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 224-37	4.2	235
30	Towards a covering set of protein family profiles. <i>Progress in Biophysics and Molecular Biology</i> , 2000 , 73, 321-37	4.7	38
29	Protein folds and families: sequence and structure alignments. <i>Nucleic Acids Research</i> , 1999 , 27, 244-7	20.1	182
28	Dictionary of recurrent domains in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 33, 88-96	4.2	142
27	Dali/FSSP classification of three-dimensional protein folds. <i>Nucleic Acids Research</i> , 1997 , 25, 231-4	20.1	381
26	Enzyme HIT. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 116-7	10.3	20
25	New structure--novel fold?. <i>Structure</i> , 1997 , 5, 165-71	5.2	54
24	An evolutionary treasure: unification of a broad set of amidohydrolases related to urease 1997 , 28, 72-82		370

23	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 29, 134-139	4.2	7
22	An evolutionary treasure: unification of a broad set of amidohydrolases related to urease 1997 , 28, 72		6
21	Alignment of three-dimensional protein structures: network server for database searching. <i>Methods in Enzymology</i> , 1996 , 266, 653-62	1.7	70
20	The cytidyltransferase superfamily: identification of the nucleotide-binding site and fold prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 22, 259-66	4.2	81
19	Dali: a network tool for protein structure comparison. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 478-80	10.3	1275
18	LexA repressor and iron uptake regulator from Escherichia coli: new members of the CAP-like DNA binding domain superfamily. <i>Protein Engineering, Design and Selection</i> , 1994 , 7, 1449-53	1.9	31
17	Searching protein structure databases has come of age. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 165-73	4.2	220
16	Parser for protein folding units. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994 , 19, 256-68	4.2	182
15	Three sisters, different names. <i>Nature Structural Biology</i> , 1994 , 1, 146-7		28
14	Structural similarity of plant chitinase and lysozymes from animals and phage. An evolutionary connection. <i>FEBS Letters</i> , 1994 , 340, 129-32	3.8	76
13	Protein structure comparison by alignment of distance matrices. <i>Journal of Molecular Biology</i> , 1993 , 233, 123-38	6.5	3573
12	Globin fold in a bacterial toxin. <i>Nature</i> , 1993 , 361, 309	50.4	28
11	Structural alignment of globins, phycocyanins and colicin A. <i>FEBS Letters</i> , 1993 , 315, 301-6	3.8	68
10	Molecular dynamics simulations of hapten binding to structural models of 2-phenyloxazolone antibodies. <i>ImmunoMethods</i> , 1992 , 1, 80-90		4
9	Evaluation of protein models by atomic solvation preference. <i>Journal of Molecular Biology</i> , 1992 , 225, 93-105	6.5	186
8	A database of protein structure families with common folding motifs. <i>Protein Science</i> , 1992 , 1, 1691-8	6.3	171
7	The happy family of cytochrome oxidases. <i>Biochemical Society Transactions</i> , 1991 , 19, 608-12	5.1	116
6	Database algorithm for generating protein backbone and side-chain co-ordinates from a C alpha trace application to model building and detection of co-ordinate errors. <i>Journal of Molecular Biology</i> , 1991 , 218, 183-94	6.5	301

5	Molecular modelling study of antigen binding to oxazolone-specific antibodies: the Ox1 idiotypic IgG and its mature variant with increased affinity to 2-phenyloxazolone. <i>Protein Engineering, Design and Selection</i> , 1990 , 3, 403-9	1.9	16
4	Random mutagenesis used to probe the structure and function of <i>Bacillus stearothermophilus</i> alpha-amylase. <i>Protein Engineering, Design and Selection</i> , 1990 , 3, 181-91	1.9	70
3	Codon usage and gene expression. <i>Nucleic Acids Research</i> , 1986 , 14, 3075-87	20.1	125
2	Novel Comparison of Evaluation Metrics for Gene Ontology Classifiers Reveals Drastic Performance Differences		
1	Novel NGS Pipeline for Virus Discovery from a Wide Spectrum of Hosts and Sample Types		2