

Liisa Holm

List of Publications by Year in descending order

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93
papers

24,751
citations

71004

43
h-index

60403

85
g-index

97
all docs

97
docs citations

97
times ranked

36054
citing authors

#	ARTICLE	IF	CITATIONS
1	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
2	Protein Structure Comparison by Alignment of Distance Matrices. <i>Journal of Molecular Biology</i> , 1993, 233, 123-138.	2.0	3,851
3	Dali server: conservation mapping in 3D. <i>Nucleic Acids Research</i> , 2010, 38, W545-W549.	6.5	3,433
4	Dali: a network tool for protein structure comparison. <i>Trends in Biochemical Sciences</i> , 1995, 20, 478-480.	3.7	1,390
5	Dali server update. <i>Nucleic Acids Research</i> , 2016, 44, W351-W355.	6.5	872
6	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
7	DALI and the persistence of protein shape. <i>Protein Science</i> , 2020, 29, 128-140.	3.1	537
8	Using Dali for Protein Structure Comparison. <i>Methods in Molecular Biology</i> , 2020, 2112, 29-42.	0.4	451
9	An evolutionary treasure: unification of a broad set of amidohydrolases related to urease. , 1997, 28, 72-82.		441
10	Dali/FSSP classification of three-dimensional protein folds. <i>Nucleic Acids Research</i> , 1997, 25, 231-234.	6.5	413
11	Dali server: structural unification of protein families. <i>Nucleic Acids Research</i> , 2022, 50, W210-W215.	6.5	409
12	Advances and pitfalls of protein structural alignment. <i>Current Opinion in Structural Biology</i> , 2009, 19, 341-348.	2.6	332
13	PANNZER2: a rapid functional annotation web server. <i>Nucleic Acids Research</i> , 2018, 46, W84-W88.	6.5	328
14	Database algorithm for generating protein backbone and side-chain co-ordinates from a C α trace. <i>Journal of Molecular Biology</i> , 1991, 218, 183-194.	2.0	326
15	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, 9259-9264.	3.3	310
16	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	3.8	308
17	Rapid automatic detection and alignment of repeats in protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 224-237.	1.5	296
18	Benchmarking fold detection by DaliLite v.5. <i>Bioinformatics</i> , 2019, 35, 5326-5327.	1.8	285

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19	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.	3.8	261
20	Searching protein structure databases has come of age. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 165-173.	1.5	243
21	Parser for protein folding units. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 19, 256-268.	1.5	223
22	Defense-related transcription factors <i>WRKY70</i> and <i>WRKY54</i> modulate osmotic stress tolerance by regulating stomatal aperture in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2013, 200, 457-472.	3.5	223
23	Evaluation of protein models by atomic solvation preference. <i>Journal of Molecular Biology</i> , 1992, 225, 93-105.	2.0	201
24	Protein folds and families: sequence and structure alignments. <i>Nucleic Acids Research</i> , 1999, 27, 244-247.	6.5	196
25	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in <i>Lepidoptera</i> . <i>Nature Communications</i> , 2014, 5, 4737.	5.8	196
26	A database of protein structure families with common folding motifs. <i>Protein Science</i> , 1992, 1, 1691-1698.	3.1	193
27	Dictionary of recurrent domains in protein structures. , 1998, 33, 88-96.		162
28	Codon usage and gene expression. <i>Nucleic Acids Research</i> , 1986, 14, 3075-3087.	6.5	136
29	The happy family of cytochrome oxidases. <i>Biochemical Society Transactions</i> , 1991, 19, 608-612.	1.6	129
30	PANNZER: high-throughput functional annotation of uncharacterized proteins in an error-prone environment. <i>Bioinformatics</i> , 2015, 31, 1544-1552.	1.8	123
31	AAI-profiler: fast proteome-wide exploratory analysis reveals taxonomic identity, misclassification and contamination. <i>Nucleic Acids Research</i> , 2018, 46, W479-W485.	6.5	119
32	Exhaustive Enumeration of Protein Domain Families. <i>Journal of Molecular Biology</i> , 2003, 328, 749-767.	2.0	118
33	Identification of homology in protein structure classification. , 2001, 8, 953-957.		117
34	Using Dali for Structural Comparison of Proteins. , 2006, Chapter 5, Unit 5.5.		116
35	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.	2.1	93
36	The cytidyltransferase superfamily: Identification of the nucleotide-binding site and fold prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 259-266.	1.5	89

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37	Structural similarity of plant chitinase and lysozymes from animals and phage. FEBS Letters, 1994, 340, 129-132.	1.3	84
38	Comparative Genome-Scale Reconstruction of Gapless Metabolic Networks for Present and Ancestral Species. PLoS Computational Biology, 2014, 10, e1003465.	1.5	84
39	Evolution of the GDNF Family Ligands and Receptors. Brain, Behavior and Evolution, 2006, 68, 181-190.	0.9	80
40	Random mutagenesis used to probe the structure and function of Bacillus stearothermophilus alpha-amylase. Protein Engineering, Design and Selection, 1990, 3, 181-191.	1.0	79
41	Structural alignment of globins, phycocyanins and colicin A. FEBS Letters, 1993, 315, 301-306.	1.3	77
42	Unraveling protein interaction networks with near-optimal efficiency. Nature Biotechnology, 2004, 22, 98-103.	9.4	77
43	[39] Alignment of three-dimensional protein structures: Network server for database searching. Methods in Enzymology, 1996, 266, 653-662.	0.4	76
44	New structure "A novel fold?. Structure, 1997, 5, 165-171.	1.6	65
45	<scp>PANNZER</scp>"A practical tool for protein function prediction. Protein Science, 2022, 31, 118-128.	3.1	55
46	Genome Sequence of Dickeya solani, a New soft Rot Pathogen of Potato, Suggests its Emergence May Be Related to a Novel Combination of Non-Ribosomal Peptide/Polyketide Synthetase Clusters. Diversity, 2013, 5, 824-842.	0.7	54
47	POBO, transcription factor binding site verification with bootstrapping. Nucleic Acids Research, 2004, 32, W222-W229.	6.5	49
48	Towards a covering set of protein family profiles. Progress in Biophysics and Molecular Biology, 2000, 73, 321-337.	1.4	46
49	Bayesian search of functionally divergent protein subgroups and their function specific residues. Bioinformatics, 2006, 22, 2466-2474.	1.8	40
50	BluB/CobT2 fusion enzyme activity reveals mechanisms responsible for production of active form of vitamin B12 by Propionibacterium freudenreichii. Microbial Cell Factories, 2015, 14, 186.	1.9	40
51	Genome Sequence of Lactobacillus crispatus ST1. Journal of Bacteriology, 2010, 192, 3547-3548.	1.0	38
52	SANSparallel: interactive homology search against Uniprot. Nucleic Acids Research, 2015, 43, W24-W29.	6.5	38
53	Globin fold in a bacterial toxin. Nature, 1993, 361, 309-309.	13.7	36
54	LexA repressor and iron uptake regulator from Escherichia coli: new members of the CAP-like DNA binding domain superfamily. Protein Engineering, Design and Selection, 1994, 7, 1449-1453.	1.0	36

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55	Three sisters, different names. <i>Nature Structural Biology</i> , 1994, 1, 146-147.	9.7	32
56	Loss of neurturin in frog – Comparative genomics study of GDNF family ligand-receptor pairs. <i>Molecular and Cellular Neurosciences</i> , 2007, 34, 155-167.	1.0	29
57	Flight-induced changes in gene expression in the Glanville fritillary butterfly. <i>Molecular Ecology</i> , 2015, 24, 4886-4900.	2.0	28
58	Novel NGS pipeline for virus discovery from a wide spectrum of hosts and sample types. <i>Virus Evolution</i> , 2020, 6, veaa091.	2.2	28
59	Oligomerization of Hantavirus Nucleocapsid Protein: Analysis of the N-Terminal Coiled-Coil Domain. <i>Journal of Virology</i> , 2006, 80, 9073-9081.	1.5	27
60	Evaluation of different domain-based methods in protein interaction prediction. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 357-362.	1.0	24
61	Transcriptome Analysis Reveals Signature of Adaptation to Landscape Fragmentation. <i>PLoS ONE</i> , 2014, 9, e101467.	1.1	24
62	Bracketing phenogenotypic limits of mammalian hybridization. <i>Royal Society Open Science</i> , 2018, 5, 180903.	1.1	24
63	SANS: high-throughput retrieval of protein sequences allowing 50% mismatches. <i>Bioinformatics</i> , 2012, 28, i438-i443.	1.8	22
64	Enzyme HIT. <i>Trends in Biochemical Sciences</i> , 1997, 22, 116-117.	3.7	21
65	A Theoretical Model for the Regulation of <i>Sex-lethal</i> , a Gene That Controls Sex Determination and Dosage Compensation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2003, 165, 1355-1384.	1.2	21
66	The global trace graph, a novel paradigm for searching protein sequence databases. <i>Bioinformatics</i> , 2007, 23, 2361-2367.	1.8	20
67	Accurate Detection of Very Sparse Sequence Motifs. <i>Journal of Computational Biology</i> , 2004, 11, 843-857.	0.8	18
68	The RPSP: Web server for prediction of signal peptides. <i>Polymer</i> , 2007, 48, 5493-5496.	1.8	18
69	Oligomerization of Uukuniemi virus nucleocapsid protein. <i>Virology Journal</i> , 2010, 7, 187.	1.4	18
70	Mlh1 deficiency in normal mouse colon mucosa associates with chromosomally unstable colon cancer. <i>Carcinogenesis</i> , 2018, 39, 788-797.	1.3	18
71	POCO: discovery of regulatory patterns from promoters of oppositely expressed gene sets. <i>Nucleic Acids Research</i> , 2005, 33, W427-W431.	6.5	17
72	Genome Sequence of <i>Pectobacterium</i> sp. Strain SCC3193. <i>Journal of Bacteriology</i> , 2012, 194, 6004-6004.	1.0	17

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73	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, 403-409.	1.0	16
74	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.	1.8	16
75	Gene set analysis: limitations in popular existing methods and proposed improvements. <i>Bioinformatics</i> , 2014, 30, 2747-2756.	1.8	15
76	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-e124.	6.5	13
77	PairsDB atlas of protein sequence space. <i>Nucleic Acids Research</i> , 2008, 36, D276-D280.	6.5	13
78	Mismatch repair analysis of inherited MSH2 and/or MSH6 variation pairs found in cancer patients. <i>Human Mutation</i> , 2012, 33, 1294-1301.	1.1	13
79	Novel comparison of evaluation metrics for gene ontology classifiers reveals drastic performance differences. <i>PLoS Computational Biology</i> , 2019, 15, e1007419.	1.5	12
80	POXO: a web-enabled tool series to discover transcription factor binding sites. <i>Nucleic Acids Research</i> , 2006, 34, W534-W540.	6.5	10
81	Predicting protein structure using hidden Markov models. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 134-139.	1.5	8
82	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. <i>Bioscience Reports</i> , 2020, 40, .	1.1	8
83	An evolutionary treasure: unification of a broad set of amidohydrolases related to urease. , 1997, 28, 72.		6
84	Molecular dynamics simulations of hapten binding to structural models of 2-phenyloxazolone antibodies. <i>ImmunoMethods</i> , 1992, 1, 80-90.	0.8	4
85	Robust multi-group gene set analysis with few replicates. <i>BMC Bioinformatics</i> , 2016, 17, 526.	1.2	4
86	TOPAZ: asymmetric suffix array neighbourhood search for massive protein databases. <i>BMC Bioinformatics</i> , 2018, 19, 278.	1.2	4
87	Metatranscriptomic assessment of burn wound infection clearance. <i>Clinical Microbiology and Infection</i> , 2021, 27, 144-146.	2.8	4
88	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-E3947.	3.3	2
89	Novel split quality measures for stratified multilabel cross validation with application to large and sparse gene ontology datasets. , 2022, 2, 49-62.		2
90	From sequences to a functional unit. <i>Physiological Genomics</i> , 2006, 25, 1-8.	1.0	1

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91	Mutational analysis of positively charged amino acid residues of Uukuniemi phlebovirus nucleocapsid protein. <i>Virus Research</i> , 2012, 167, 118-123.	1.1	1
92	Evaluation of Novel Protein Structure Comparison Algorithms Based on Objective Function Rankings. , 2009, , .		0
93	The wiring of protein networks: Computational approaches for predicting protein interaction networks. <i>Biochemist</i> , 2011, 33, 8-11.	0.2	0