

Johannes SÄ¶ding

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

34,898
citations

30551

56
h-index

40945

97
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118
all docs

118
docs citations

118
times ranked

53396
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale analysis of <i>Drosophila</i> core promoter function using synthetic promoters. <i>Molecular Systems Biology</i> , 2022, 18, e9816.	3.2	15
2	Cln5 represents a new type of cysteine-based S -depalmitoylase linked to neurodegeneration. <i>Science Advances</i> , 2022, 8, eabj8633.	4.7	12
3	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	6.5	46
4	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. <i>ELife</i> , 2021, 10, .	2.8	64
5	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021, 37, 3029-3031.	1.8	110
6	Bayesian Markov models improve the prediction of binding motifs beyond first order. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab026.	1.5	3
7	SpacePHARER: sensitive identification of phages from CRISPR spacers in prokaryotic hosts. <i>Bioinformatics</i> , 2021, 37, 3364-3366.	1.8	36
8	Tejaas: reverse regression increases power for detecting trans-eQTLs. <i>Genome Biology</i> , 2021, 22, 142.	3.8	4
9	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	16
10	Thermodynamic modeling reveals widespread multivalent binding by RNA-binding proteins. <i>Bioinformatics</i> , 2021, 37, i308-i316.	1.8	4
11	Mechanisms for Active Regulation of Biomolecular Condensates. <i>Trends in Cell Biology</i> , 2020, 30, 4-14.	3.6	127
12	A High-Throughput Screen for Transcription Activation Domains Reveals Their Sequence Features and Permits Prediction by Deep Learning. <i>Molecular Cell</i> , 2020, 78, 890-902.e6.	4.5	70
13	MetaEuk – sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. <i>Microbiome</i> , 2020, 8, 48.	4.9	119
14	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. <i>Current Protocols in Bioinformatics</i> , 2020, 72, e108.	25.8	458
15	Lysine/RNA-interactions drive and regulate biomolecular condensation. <i>Nature Communications</i> , 2019, 10, 2909.	5.8	164
16	HH-suite3 for fast remote homology detection and deep protein annotation. <i>BMC Bioinformatics</i> , 2019, 20, 473.	1.2	706
17	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. <i>Nature Methods</i> , 2019, 16, 603-606.	9.0	262
18	PROSST: probabilistic simulation of single-cell RNA-seq data for complex differentiation processes. <i>Bioinformatics</i> , 2019, 35, 3517-3519.	1.8	42

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19	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	1.8	321
20	A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. <i>Journal of Molecular Biology</i> , 2018, 430, 2237-2243.	2.0	1,956
21	Bayesian multiple logistic regression for case-control GWAS. <i>PLoS Genetics</i> , 2018, 14, e1007856.	1.5	28
22	Synthetic protein alignments by CCMgen quantify noise in residue-residue contact prediction. <i>PLoS Computational Biology</i> , 2018, 14, e1006526.	1.5	25
23	Clustering huge protein sequence sets in linear time. <i>Nature Communications</i> , 2018, 9, 2542.	5.8	497
24	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. <i>Scientific Reports</i> , 2018, 8, 9939.	1.6	19
25	The BaMM web server for de-novo motif discovery and regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2018, 46, W215-W220.	6.5	49
26	Big-data approaches to protein structure prediction. <i>Science</i> , 2017, 355, 248-249.	6.0	31
27	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	6.5	520
28	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. <i>Molecular Cell</i> , 2017, 66, 38-49.e6.	4.5	100
29	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. <i>Nature Biotechnology</i> , 2017, 35, 1026-1028.	9.4	1,879
30	WIsH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. <i>Bioinformatics</i> , 2017, 33, 3113-3114.	1.8	197
31	Bayesian Markov models consistently outperform PWMs at predicting motifs in nucleotide sequences. <i>Nucleic Acids Research</i> , 2016, 44, 6055-6069.	6.5	72
32	The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis. <i>Nucleic Acids Research</i> , 2016, 44, W410-W415.	6.5	369
33	Modulations of DNA Contacts by Linker Histones and Post-translational Modifications Determine the Mobility and Modifiability of Nucleosomal H3 Tails. <i>Molecular Cell</i> , 2016, 61, 247-259.	4.5	120
34	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. <i>Bioinformatics</i> , 2016, 32, 1323-1330.	1.8	131
35	Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004343.	1.5	122
36	bbcontacts: prediction of $\langle i \rangle^2 \langle j \rangle$ -strand pairing from direct coupling patterns. <i>Bioinformatics</i> , 2015, 31, 1729-1737.	1.8	34

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37	Context similarity scoring improves protein sequence alignments in the midnight zone. <i>Bioinformatics</i> , 2015, 31, 674-681.	1.8	12
38	A vocabulary of ancient peptides at the origin of folded proteins. <i>ELife</i> , 2015, 4, e09410.	2.8	199
39	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004081.	2.1	111
40	CCMPred—fast and precise prediction of protein residue—residue contacts from correlated mutations. <i>Bioinformatics</i> , 2014, 30, 3128-3130.	1.8	387
41	Universality of core promoter elements?. <i>Nature</i> , 2014, 511, E11-E12.	13.7	7
42	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. <i>Molecular Cell</i> , 2014, 55, 745-757.	4.5	99
43	RECQL5 Controls Transcript Elongation and Suppresses Genome Instability Associated with Transcription Stress. <i>Cell</i> , 2014, 157, 1037-1049.	13.5	162
44	kClust: fast and sensitive clustering of large protein sequence databases. <i>BMC Bioinformatics</i> , 2013, 14, 248.	1.2	83
45	<i>i>P</i>-value-based regulatory motif discovery using positional weight matrices. <i>Genome Research</i>, 2013, 23, 181-194.</i>	2.4	64
46	Recruitment of TREX to the Transcription Machinery by Its Direct Binding to the Phospho-CTD of RNA Polymerase II. <i>PLoS Genetics</i> , 2013, 9, e1003914.	1.5	58
47	Eph receptors and ephrin class B ligands are expressed at tissue boundaries in <i>Hydra vulgaris</i> . <i>International Journal of Developmental Biology</i> , 2013, 57, 759-765.	0.3	13
48	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. <i>Nucleic Acids Research</i> , 2012, 40, 1509-1522.	6.5	64
49	The XXmotif web server for eXhaustive, weight matriX-based motif discovery in nucleotide sequences. <i>Nucleic Acids Research</i> , 2012, 40, W104-W109.	6.5	40
50	Discriminative modelling of context-specific amino acid substitution probabilities. <i>Bioinformatics</i> , 2012, 28, 3240-3247.	1.8	47
51	HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. <i>Nature Methods</i> , 2012, 9, 173-175.	9.0	1,878
52	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation. <i>Nature</i> , 2012, 484, 386-389.	13.7	99
53	Fast, scalable generation of high—quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	3.2	12,778
54	The Mre11:Rad50 Structure Shows an ATP-Dependent Molecular Clamp in DNA Double-Strand Break Repair. <i>Cell</i> , 2011, 145, 54-66.	13.5	182

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55	Protein sequence comparison and fold recognition: progress and good-practice benchmarking. <i>Current Opinion in Structural Biology</i> , 2011, 21, 404-411.	2.6	73
56	Different Binding Properties and Function of CXXC Zinc Finger Domains in Dnmt1 and Tet1. <i>PLoS ONE</i> , 2011, 6, e16627.	1.1	87
57	A Conserved GA Element in TATA-Less RNA Polymerase II Promoters. <i>PLoS ONE</i> , 2011, 6, e27595.	1.1	32
58	A galaxy of folds. <i>Protein Science</i> , 2010, 19, 124-130.	3.1	71
59	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19754-19759.	3.3	122
60	Uniform transitions of the general RNA polymerase II transcription complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1272-1278.	3.6	399
61	Of Bits and Bugs – On the Use of Bioinformatics and a Bacterial Crystal Structure to Solve a Eukaryotic Repeat-Protein Structure. <i>PLoS ONE</i> , 2010, 5, e13402.	1.1	21
62	Evolution of Outer Membrane β -Barrels from an Ancestral β Hairpin. <i>Molecular Biology and Evolution</i> , 2010, 27, 1348-1358.	3.5	95
63	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	3.3	196
64	The molecular cell death machinery in the simple cnidarian Hydra includes an expanded caspase family and pro- and anti-apoptotic Bcl-2 proteins. <i>Cell Research</i> , 2010, 20, 812-825.	5.7	62
65	Sequence context-specific profiles for homology searching. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3770-3775.	3.3	155
66	Phospholipid scramblases and Tubby-like proteins belong to a new superfamily of membrane tethered transcription factors. <i>Bioinformatics</i> , 2009, 25, 159-162.	1.8	59
67	Fast and accurate automatic structure prediction with HHpred. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 128-132.	1.5	418
68	HHomp prediction and classification of outer membrane proteins. <i>Nucleic Acids Research</i> , 2009, 37, W446-W451.	6.5	86
69	PDBalert: automatic, recurrent remote homology tracking and protein structure prediction. <i>BMC Structural Biology</i> , 2008, 8, 51.	2.3	7
70	Evolution of the β propeller fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 795-803.	1.5	128
71	Prediction of protein functional residues from sequence by probability density estimation. <i>Bioinformatics</i> , 2008, 24, 613-620.	1.8	121
72	De novo identification of highly diverged protein repeats by probabilistic consistency. <i>Bioinformatics</i> , 2008, 24, 807-814.	1.8	137

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73	Genome-associated RNA Polymerase II Includes the Dissociable Rpb4/7 Subcomplex. <i>Journal of Biological Chemistry</i> , 2008, 283, 26423-26427.	1.6	40
74	ScbA from <i>Streptomyces coelicolor</i> A3(2) has homology to fatty acid synthases and is able to synthesize β -butyrolactones. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1394-1404.	0.7	61
75	On the origin of the histone fold. <i>BMC Structural Biology</i> , 2007, 7, 17.	2.3	45
76	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. <i>BMC Bioinformatics</i> , 2007, 8, 2.	1.2	194
77	Comparative analysis of coiled-coil prediction methods. <i>Journal of Structural Biology</i> , 2006, 155, 140-145.	1.3	150
78	Expression, crystallization and preliminary X-ray crystallographic studies of the outer membrane protein OmpW from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 415-418.	0.7	33
79	HHrep: de novo protein repeat detection and the origin of TIM barrels. <i>Nucleic Acids Research</i> , 2006, 34, W137-W142.	6.5	63
80	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. <i>Nucleic Acids Research</i> , 2006, 34, W374-W378.	6.5	72
81	The MPI Bioinformatics Toolkit for protein sequence analysis. <i>Nucleic Acids Research</i> , 2006, 34, W335-W339.	6.5	247
82	AbrB-like Transcription Factors Assume a Swapped Hairpin Fold that Is Evolutionarily Related to Double-Psi β Barrels. <i>Structure</i> , 2005, 13, 919-928.	1.6	78
83	Retroactive, a membrane-anchored extracellular protein related to vertebrate snake neurotoxin-like proteins, is required for cuticle organization in the larva of <i>Drosophila melanogaster</i> . <i>Developmental Dynamics</i> , 2005, 233, 1056-1063.	0.8	43
84	The HHpred interactive server for protein homology detection and structure prediction. <i>Nucleic Acids Research</i> , 2005, 33, W244-W248.	6.5	3,246
85	Protein homology detection by HMM-HMM comparison. <i>Bioinformatics</i> , 2005, 21, 951-960.	1.8	2,193
86	REPPER-repeats and their periodicities in fibrous proteins. <i>Nucleic Acids Research</i> , 2005, 33, W239-W243.	6.5	118
87	More than the sum of their parts: On the evolution of proteins from peptides. <i>BioEssays</i> , 2003, 25, 837-846.	1.2	229
88	Three-body decay of a rubidium Bose-Einstein condensate. <i>Applied Physics B: Lasers and Optics</i> , 1999, 69, 257-261.	1.1	147
89	Strong evaporative cooling of a trapped cesium gas. <i>Optics Express</i> , 1998, 2, 323.	1.7	42
90	Giant Spin Relaxation of an Ultracold Cesium Gas. <i>Physical Review Letters</i> , 1998, 80, 1869-1872.	2.9	94

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91	Is Bose-Einstein condensation of atomic cesium possible?. Europhysics Letters, 1998, 44, 25-30.	0.7	42
92	Short-Distance Atomic Beam Deceleration with a Stimulated Light Force. Physical Review Letters, 1997, 78, 1420-1423.	2.9	96
93	<title>Cooling atoms in dark gravitational laser traps</title>. , 1996, , .		0
94	Gravitational laser trap for atoms with evanescent-wave cooling. Optics Communications, 1995, 119, 652-662.	1.0	103
95	Stimulated magneto-optical force in the dressed-atom picture. Physical Review A, 1994, 50, 2517-2527.	1.0	6
96	Coherent beam splitter for atoms based on a bichromatic standing light wave. Optics Letters, 1994, 19, 658.	1.7	52
97	Sub-Doppler manifestation of the magneto-optical radiation force. Optics Communications, 1993, 98, 54-60.	1.0	5
98	Observation of the Magneto-Optical Radiation Force by Laser Spectroscopy. Europhysics Letters, 1992, 20, 101-106.	0.7	12