

Johannes SÃ¶ding

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2223474/publications.pdf>

Version: 2024-02-01

98
papers

34,898
citations

26630

56
h-index

36028

97
g-index

118
all docs

118
docs citations

118
times ranked

48385
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale analysis of <i>Drosophila</i> core promoter function using synthetic promoters. Molecular Systems Biology, 2022, 18, e9816.	7.2	15
2	Cln5 represents a new type of cysteine-based S -depalmitoylase linked to neurodegeneration. Science Advances, 2022, 8, eabj8633.	10.3	12
3	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	14.5	46
4	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. ELife, 2021, 10, .	6.0	64
5	Fast and sensitive taxonomic assignment to metagenomic contigs. Bioinformatics, 2021, 37, 3029-3031.	4.1	110
6	Bayesian Markov models improve the prediction of binding motifs beyond first order. NAR Genomics and Bioinformatics, 2021, 3, lqab026.	3.2	3
7	SpacePHARER: sensitive identification of phages from CRISPR spacers in prokaryotic hosts. Bioinformatics, 2021, 37, 3364-3366.	4.1	36
8	Tejaas: reverse regression increases power for detecting trans-eQTLs. Genome Biology, 2021, 22, 142.	8.8	4
9	Going to extremes – a metagenomic journey into the dark matter of life. FEMS Microbiology Letters, 2021, 368, .	1.8	16
10	Thermodynamic modeling reveals widespread multivalent binding by RNA-binding proteins. Bioinformatics, 2021, 37, i308-i316.	4.1	4
11	Mechanisms for Active Regulation of Biomolecular Condensates. Trends in Cell Biology, 2020, 30, 4-14.	7.9	127
12	A High-Throughput Screen for Transcription Activation Domains Reveals Their Sequence Features and Permits Prediction by Deep Learning. Molecular Cell, 2020, 78, 890-902.e6.	9.7	70
13	MetaEuk – sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. Microbiome, 2020, 8, 48.	11.1	119
14	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. Current Protocols in Bioinformatics, 2020, 72, e108.	25.8	458
15	Lysine/RNA-interactions drive and regulate biomolecular condensation. Nature Communications, 2019, 10, 2909.	12.8	164
16	HH-suite3 for fast remote homology detection and deep protein annotation. BMC Bioinformatics, 2019, 20, 473.	2.6	706
17	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. Nature Methods, 2019, 16, 603-606.	19.0	262
18	PROSSTT: probabilistic simulation of single-cell RNA-seq data for complex differentiation processes. Bioinformatics, 2019, 35, 3517-3519.	4.1	42

#	ARTICLE	IF	CITATIONS
19	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	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.	4.2	1,956
21	Bayesian multiple logistic regression for case-control GWAS. <i>PLoS Genetics</i> , 2018, 14, e1007856.	3.5	28
22	Synthetic protein alignments by CCMgen quantify noise in residue-residue contact prediction. <i>PLoS Computational Biology</i> , 2018, 14, e1006526.	3.2	25
23	Clustering huge protein sequence sets in linear time. <i>Nature Communications</i> , 2018, 9, 2542.	12.8	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.	3.3	19
25	The BaMM web server for de-novo motif discovery and regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2018, 46, W215-W220.	14.5	49
26	Big-data approaches to protein structure prediction. <i>Science</i> , 2017, 355, 248-249.	12.6	31
27	Uniclust databases of clustered and deeply annotated protein sequences and alignments. <i>Nucleic Acids Research</i> , 2017, 45, D170-D176.	14.5	520
28	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. <i>Molecular Cell</i> , 2017, 66, 38-49.e6.	9.7	100
29	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. <i>Nature Biotechnology</i> , 2017, 35, 1026-1028.	17.5	1,879
30	WIsH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. <i>Bioinformatics</i> , 2017, 33, 3113-3114.	4.1	197
31	Bayesian Markov models consistently outperform PWMs at predicting motifs in nucleotide sequences. <i>Nucleic Acids Research</i> , 2016, 44, 6055-6069.	14.5	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.	14.5	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.	9.7	120
34	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. <i>Bioinformatics</i> , 2016, 32, 1323-1330.	4.1	131
35	Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling. <i>PLoS Computational Biology</i> , 2015, 11, e1004343.	3.2	122
36	bbcontacts: prediction of $\langle i \rangle^2 \langle i \rangle$ -strand pairing from direct coupling patterns. <i>Bioinformatics</i> , 2015, 31, 1729-1737.	4.1	34

#	ARTICLE	IF	CITATIONS
37	Context similarity scoring improves protein sequence alignments in the midnight zone. <i>Bioinformatics</i> , 2015, 31, 674-681.	4.1	12
38	A vocabulary of ancient peptides at the origin of folded proteins. <i>ELife</i> , 2015, 4, e09410.	6.0	199
39	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004081.	4.7	111
40	CCMPredâ€”fast and precise prediction of protein residueâ€”residue contacts from correlated mutations. <i>Bioinformatics</i> , 2014, 30, 3128-3130.	4.1	387
41	Universality of core promoter elements?. <i>Nature</i> , 2014, 511, E11-E12.	27.8	7
42	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. <i>Molecular Cell</i> , 2014, 55, 745-757.	9.7	99
43	RECQL5 Controls Transcript Elongation and Suppresses Genome Instability Associated with Transcription Stress. <i>Cell</i> , 2014, 157, 1037-1049.	28.9	162
44	kClust: fast and sensitive clustering of large protein sequence databases. <i>BMC Bioinformatics</i> , 2013, 14, 248.	2.6	83
45	<i>i>P</i>-value-based regulatory motif discovery using positional weight matrices. <i>Genome Research</i>, 2013, 23, 181-194.</i>	5.5	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.	3.5	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.	0.6	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.	14.5	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.	14.5	40
50	Discriminative modelling of context-specific amino acid substitution probabilities. <i>Bioinformatics</i> , 2012, 28, 3240-3247.	4.1	47
51	HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. <i>Nature Methods</i> , 2012, 9, 173-175.	19.0	1,878
52	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation. <i>Nature</i> , 2012, 484, 386-389.	27.8	99
53	Fast, scalable generation of highâ€”quality protein multiple sequence alignments using Clustal Omega. <i>Molecular Systems Biology</i> , 2011, 7, 539.	7.2	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.	28.9	182

#	ARTICLE	IF	CITATIONS
55	Protein sequence comparison and fold recognition: progress and good-practice benchmarking. <i>Current Opinion in Structural Biology</i> , 2011, 21, 404-411.	5.7	73
56	Different Binding Properties and Function of CXXC Zinc Finger Domains in Dnmt1 and Tet1. <i>PLoS ONE</i> , 2011, 6, e16627.	2.5	87
57	A Conserved GA Element in TATA-Less RNA Polymerase II Promoters. <i>PLoS ONE</i> , 2011, 6, e27595.	2.5	32
58	A galaxy of folds. <i>Protein Science</i> , 2010, 19, 124-130.	7.6	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.	7.1	122
60	Uniform transitions of the general RNA polymerase II transcription complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1272-1278.	8.2	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.	2.5	21
62	Evolution of Outer Membrane β -Barrels from an Ancestral β Hairpin. <i>Molecular Biology and Evolution</i> , 2010, 27, 1348-1358.	8.9	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.	7.1	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.	12.0	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.	7.1	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.	4.1	59
67	Fast and accurate automatic structure prediction with HHpred. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 128-132.	2.6	418
68	HHomp – prediction and classification of outer membrane proteins. <i>Nucleic Acids Research</i> , 2009, 37, W446-W451.	14.5	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.	2.6	128
71	Prediction of protein functional residues from sequence by probability density estimation. <i>Bioinformatics</i> , 2008, 24, 613-620.	4.1	121
72	De novo identification of highly diverged protein repeats by probabilistic consistency. <i>Bioinformatics</i> , 2008, 24, 807-814.	4.1	137

#	ARTICLE	IF	CITATIONS
73	Genome-associated RNA Polymerase II Includes the Dissociable Rpb4/7 Subcomplex. Journal of Biological Chemistry, 2008, 283, 26423-26427.	3.4	40
74	ScbA from Streptomyces coelicolor A3(2) has homology to fatty acid synthases and is able to synthesize β -butyrolactones. Microbiology (United Kingdom), 2007, 153, 1394-1404.	1.8	61
75	On the origin of the histone fold. BMC Structural Biology, 2007, 7, 17.	2.3	45
76	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. BMC Bioinformatics, 2007, 8, 2.	2.6	194
77	Comparative analysis of coiled-coil prediction methods. Journal of Structural Biology, 2006, 155, 140-145.	2.8	150
78	Expression, crystallization and preliminary X-ray crystallographic studies of the outer membrane protein OmpW from Escherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 415-418.	0.7	33
79	HHrep: de novo protein repeat detection and the origin of TIM barrels. Nucleic Acids Research, 2006, 34, W137-W142.	14.5	63
80	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. Nucleic Acids Research, 2006, 34, W374-W378.	14.5	72
81	The MPI Bioinformatics Toolkit for protein sequence analysis. Nucleic Acids Research, 2006, 34, W335-W339.	14.5	247
82	AbrB-like Transcription Factors Assume a Swapped Hairpin Fold that Is Evolutionarily Related to Double-Psi β Barrels. Structure, 2005, 13, 919-928.	3.3	78
83	Retroactive, a membrane-anchored extracellular protein related to vertebrate snake neurotoxin-like proteins, is required for cuticle organization in the larva of Drosophila melanogaster. Developmental Dynamics, 2005, 233, 1056-1063.	1.8	43
84	The HHpred interactive server for protein homology detection and structure prediction. Nucleic Acids Research, 2005, 33, W244-W248.	14.5	3,246
85	Protein homology detection by HMM-HMM comparison. Bioinformatics, 2005, 21, 951-960.	4.1	2,193
86	REPPER-repeats and their periodicities in fibrous proteins. Nucleic Acids Research, 2005, 33, W239-W243.	14.5	118
87	More than the sum of their parts: On the evolution of proteins from peptides. BioEssays, 2003, 25, 837-846.	2.5	229
88	Three-body decay of a rubidium Bose-Einstein condensate. Applied Physics B: Lasers and Optics, 1999, 69, 257-261.	2.2	147
89	Strong evaporative cooling of a trapped cesium gas. Optics Express, 1998, 2, 323.	3.4	42
90	Giant Spin Relaxation of an Ultracold Cesium Gas. Physical Review Letters, 1998, 80, 1869-1872.	7.8	94

#	ARTICLE	IF	CITATIONS
91	Is Bose-Einstein condensation of atomic cesium possible?. Europhysics Letters, 1998, 44, 25-30.	2.0	42
92	Short-Distance Atomic Beam Deceleration with a Stimulated Light Force. Physical Review Letters, 1997, 78, 1420-1423.	7.8	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.	2.1	103
95	Stimulated magneto-optical force in the dressed-atom picture. Physical Review A, 1994, 50, 2517-2527.	2.5	6
96	Coherent beam splitter for atoms based on a bichromatic standing light wave. Optics Letters, 1994, 19, 658.	3.3	52
97	Sub-Doppler manifestation of the magneto-optical radiation force. Optics Communications, 1993, 98, 54-60.	2.1	5
98	Observation of the Magneto-Optical Radiation Force by Laser Spectroscopy. Europhysics Letters, 1992, 20, 101-106.	2.0	12