Johannes SÃ¶ding

List of Publications by Year
in descending order

98	34,898	26630	36028
papers	citations	56	97
		h-index	g-index

118	118	118	48385
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Fast, scalable generation of high‐quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology, 2011, 7, 539.	7.2	12,778
2	The HHpred interactive server for protein homology detection and structure prediction. Nucleic Acids Research, 2005, 33, W244-W248.	14.5	3,246
3	Protein homology detection by HMM–HMM comparison. Bioinformatics, 2005, 21, 951-960.	4.1	2,193
4	A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. Journal of Molecular Biology, 2018, 430, 2237-2243.	4.2	1,956
5	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. Nature Biotechnology, 2017, 35, 1026-1028.	17.5	1,879
6	HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. Nature Methods, 2012, 9, 173-175.	19.0	1,878
7	HH-suite3 for fast remote homology detection and deep protein annotation. BMC Bioinformatics, 2019, 20, 473.	2.6	706
8	Uniclust databases of clustered and deeply annotated protein sequences and alignments. Nucleic Acids Research, 2017, 45, D170-D176.	14.5	520
9	Clustering huge protein sequence sets in linear time. Nature Communications, 2018, 9, 2542.	12.8	497
10	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. Current Protocols in Bioinformatics, 2020, 72, e108.	25.8	458
11	Fast and accurate automatic structure prediction with HHpred. Proteins: Structure, Function and Bioinformatics, 2009, 77, 128-132.	2.6	418
12	Uniform transitions of the general RNA polymerase II transcription complex. Nature Structural and Molecular Biology, 2010, 17, 1272-1278.	8.2	399
13	CCMpred—fast and precise prediction of protein residue–residue contacts from correlated mutations. Bioinformatics, 2014, 30, 3128-3130.	4.1	387
14	The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis. Nucleic Acids Research, 2016, 44, W410-W415.	14.5	369
15	MMseqs2 desktop and local web server app for fast, interactive sequence searches. Bioinformatics, 2019, 35, 2856-2858.	4.1	321
16	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. Nature Methods, 2019, 16, 603-606.	19.0	262
17	The MPI Bioinformatics Toolkit for protein sequence analysis. Nucleic Acids Research, 2006, 34, W335-W339.	14.5	247
18	More than the sum of their parts: On the evolution of proteins from peptides. BioEssays, 2003, 25, 837-846.	2.5	229

#	ARTICLE	IF	CITATIONS
19	A vocabulary of ancient peptides at the origin of folded proteins. ELife, 2015, 4, e09410.	6.0	199
20	WIsH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. Bioinformatics, 2017, 33, 3113-3114.	4.1	197
21	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-â„« resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19748-19753.	7.1	196
22	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. BMC Bioinformatics, 2007, 8, 2.	2.6	194
23	The Mre11:Rad50 Structure Shows an ATP-Dependent Molecular Clamp in DNA Double-Strand Break Repair. Cell, 2011, 145, 54-66.	28.9	182
24	Lysine/RNA-interactions drive and regulate biomolecular condensation. Nature Communications, 2019, 10, 2909.	12.8	164
25	RECQL5 Controls Transcript Elongation and Suppresses Genome Instability Associated with Transcription Stress. Cell, 2014, 157, 1037-1049.	28.9	162
26	Sequence context-specific profiles for homology searching. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3770-3775.	7.1	155
27	Comparative analysis of coiled-coil prediction methods. Journal of Structural Biology, 2006, 155, 140-145.	2.8	150
28	Three-body decay of a rubidium Bose–Einstein condensate. Applied Physics B: Lasers and Optics, 1999, 69, 257-261.	2.2	147
29	<i>De novo</i> identification of highly diverged protein repeats by probabilistic consistency. Bioinformatics, 2008, 24, 807-814.	4.1	137
30	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. Bioinformatics, 2016, 32, 1323-1330.	4.1	131
31	Evolution of the Î²â€propeller fold. Proteins: Structure, Function and Bioinformatics, 2008, 71, 795-803.	2.6	128
32	Mechanisms for Active Regulation of Biomolecular Condensates. Trends in Cell Biology, 2020, 30, 4-14.	7.9	127
33	Localization of eukaryote-specific ribosomal proteins in a 5.5-â„« cryo-EM map of the 80S eukaryotic ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19754-19759.	7.1	122
34	Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling. PLoS Computational Biology, 2015, 11, e1004343.	3.2	122
35	Prediction of protein functional residues from sequence by probability density estimation. Bioinformatics, 2008, 24, 613-620.	4.1	121
36	Modulations of DNA Contacts by Linker Histones and Post-translational Modifications Determine the Mobility and Modifiability of Nucleosomal H3 Tails. Molecular Cell, 2016, 61, 247-259.	9.7	120

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37	MetaEuk—sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. Microbiome, 2020, 8, 48.	11.1	119
38	REPPER--repeats and their periodicities in fibrous proteins. Nucleic Acids Research, 2005, 33, W239-W243.	14.5	118
39	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. PLoS Pathogens, 2014, 10, e1004081.	4.7	111
40	Fast and sensitive taxonomic assignment to metagenomic contigs. Bioinformatics, 2021, 37, 3029-3031.	4.1	110
41	Gravitational laser trap for atoms with evanescent-wave cooling. Optics Communications, 1995, 119, 652-662.	2.1	103
42	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. Molecular Cell, 2017, 66, 38-49.e6.	9.7	100
43	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation. Nature, 2012, 484, 386-389.	27.8	99
44	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. Molecular Cell, 2014, 55, 745-757.	9.7	99
45	Short-Distance Atomic Beam Deceleration with a Stimulated Light Force. Physical Review Letters, 1997, 78, 1420-1423.	7.8	96
46	Evolution of Outer Membrane β-Barrels from an Ancestral $\beta\beta$ Hairpin. Molecular Biology and Evolution, 2010, 27, 1348-1358.	8.9	95
47	Giant Spin Relaxation of an Ultracold Cesium Gas. Physical Review Letters, 1998, 80, 1869-1872.	7.8	94
48	Different Binding Properties and Function of CXXC Zinc Finger Domains in Dnmt1 and Tet1. PLoS ONE, 2011, 6, e16627.	2.5	87
49	HHomp—prediction and classification of outer membrane proteins. Nucleic Acids Research, 2009, 37, W446-W451.	14.5	86
50	kClust: fast and sensitive clustering of large protein sequence databases. BMC Bioinformatics, 2013, 14, 248.	2.6	83
51	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
52	Protein sequence comparison and fold recognition: progress and good-practice benchmarking. Current Opinion in Structural Biology, 2011, 21, 404-411.	5.7	73
53	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. Nucleic Acids Research, 2006, 34, W374-W378.	14.5	72
54	Bayesian Markov models consistently outperform PWMs at predicting motifs in nucleotide sequences. Nucleic Acids Research, 2016, 44, 6055-6069.	14.5	72

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55	A galaxy of folds. Protein Science, 2010, 19, 124-130.	7.6	71
56	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
57	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. Nucleic Acids Research, 2012, 40, 1509-1522.	14.5	64
58	P-value-based regulatory motif discovery using positional weight matrices. Genome Research, 2013, 23, 181-194.	5.5	64
59	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. ELife, 2021, 10, .	6.0	64
60	HHrep: de novo protein repeat detection and the origin of TIM barrels. Nucleic Acids Research, 2006, 34, W137-W142.	14.5	63
61	The molecular cell death machinery in the simple cnidarian Hydra includes an expanded caspase family and pro- and anti-apoptotic Bcl-2 proteins. Cell Research, 2010, 20, 812-825.	12.0	62
62	ScbA from Streptomyces coelicolor A3(2) has homology to fatty acid synthases and is able to synthesize Î³-butyrolactones. Microbiology (United Kingdom), 2007, 153, 1394-1404.	1.8	61
63	Phospholipid scramblases and Tubby-like proteins belong to a new superfamily of membrane tethered transcription factors. Bioinformatics, 2009, 25, 159-162.	4.1	59
64	Recruitment of TREX to the Transcription Machinery by Its Direct Binding to the Phospho-CTD of RNA Polymerase II. PLoS Genetics, 2013, 9, e1003914.	3.5	58
65	Coherent beam splitter for atoms based on a bichromatic standing light wave. Optics Letters, 1994, 19, 658.	3.3	52
66	The BaMM web server for de-novo motif discovery and regulatory sequence analysis. Nucleic Acids Research, 2018, 46, W215-W220.	14.5	49
67	Discriminative modelling of context-specific amino acid substitution probabilities. Bioinformatics, 2012, 28, 3240-3247.	4.1	47
68	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	14.5	46
69	On the origin of the histone fold. BMC Structural Biology, 2007, 7, 17.	2.3	45
70	Retroactive, a membrane-anchored extracellular protein related to vertebrate snake neurotoxin-like proteins, is required for cuticle organization in the larva ofDrosophila melanogaster. Developmental Dynamics, 2005, 233, 1056-1063.	1.8	43
71	Strong evaporative cooling of a trapped cesium gas. Optics Express, 1998, 2, 323.	3.4	42
72	Is Bose-Einstein condensation of atomic cesium possible?. Europhysics Letters, 1998, 44, 25-30.	2.0	42

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73	PROSSTT: probabilistic simulation of single-cell RNA-seq data for complex differentiation processes. Bioinformatics, 2019, 35, 3517-3519.	4.1	42
74	Genome-associated RNA Polymerase II Includes the Dissociable Rpb4/7 Subcomplex. Journal of Biological Chemistry, 2008, 283, 26423-26427.	3.4	40
75	The XXmotif web server for eXhaustive, weight matriX-based motif discovery in nucleotide sequences. Nucleic Acids Research, 2012, 40, W104-W109.	14.5	40
76	SpacePHARER: sensitive identification of phages from CRISPR spacers in prokaryotic hosts. Bioinformatics, 2021, 37, 3364-3366.	4.1	36
77	bbcontacts: prediction of β -strand pairing from direct coupling patterns. Bioinformatics, 2015, 31, 1729-1737.	4.1	34
78	Expression, crystallization and preliminary X-ray crystallographic studies of the outer membrane protein OmpW fromEscherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 415-418.	0.7	33
79	A Conserved GA Element in TATA-Less RNA Polymerase II Promoters. PLoS ONE, 2011, 6, e27595.	2.5	32
80	Big-data approaches to protein structure prediction. Science, 2017, 355, 248-249.	12.6	31
81	Bayesian multiple logistic regression for case-control GWAS. PLoS Genetics, 2018, 14, e1007856.	3.5	28
82	Synthetic protein alignments by CCMgen quantify noise in residue-residue contact prediction. PLoS Computational Biology, 2018, 14, e1006526.	3.2	25
83	Of Bits and Bugs â€" On the Use of Bioinformatics and a Bacterial Crystal Structure to Solve a Eukaryotic Repeat-Protein Structure. PLoS ONE, 2010, 5, e13402.	2.5	21
84	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
85	Going to extremes â€" a metagenomic journey into the dark matter of life. FEMS Microbiology Letters, 2021, 368, .	1.8	16
86	Largeâ€scale analysis of *Drosophila* core promoter function using synthetic promoters. Molecular Systems Biology, 2022, 18, e9816.	7.2	15
87	Eph receptors and ephrin class B ligands are expressed at tissue boundaries in Hydra vulgaris. International Journal of Developmental Biology, 2013, 57, 759-765.	0.6	13
88	Observation of the Magneto-Optical Radiation Force by Laser Spectroscopy. Europhysics Letters, 1992, 20, 101-106.	2.0	12
89	Context similarity scoring improves protein sequence alignments in the midnight zone. Bioinformatics, 2015, 31, 674-681.	4.1	12
90	Cln5 represents a new type of cysteine-based *S* -depalmitoylase linked to neurodegeneration. Science Advances, 2022, 8, eabj8633.	10.3	12

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91	PDBalert: automatic, recurrent remote homology tracking and protein structure prediction. BMC Structural Biology, 2008, 8, 51.	2.3	7
92	Universality of core promoter elements?. Nature, 2014, 511, E11-E12.	27.8	7
93	Stimulated magneto-optical force in the dressed-atom picture. Physical Review A, 1994, 50, 2517-2527.	2.5	6
94	Sub-Doppler manifestation of the magneto-optical radiation force. Optics Communications, 1993, 98, 54-60.	2.1	5
95	Tejaas: reverse regression increases power for detecting trans-eQTLs. Genome Biology, 2021, 22, 142.	8.8	4
96	Thermodynamic modeling reveals widespread multivalent binding by RNA-binding proteins. Bioinformatics, 2021, 37, i308-i316.	4.1	4
97	Bayesian Markov models improve the prediction of binding motifs beyond first order. NAR Genomics and Bioinformatics, 2021, 3, lqab026.	3.2	3
98	<title>Cooling atoms in dark gravitational laser traps</title>. , 1996, , .		0