Johannes Sding

List of Publications by Citations

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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.

107 papers	22,772 citations	52 h-index	118 g-index
118 ext. papers	30,103 ext. citations	12 avg, IF	7.3 L-index

#	Paper	IF	Citations
107	Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular Systems Biology*, **2011**, 7, 539	12.2	8587
106	The HHpred interactive server for protein homology detection and structure prediction. *Nucleic Acids Research*, **2005**, 33, W244-8	20.1	2558
105	Protein homology detection by HMM-HMM comparison. *Bioinformatics*, **2005**, 21, 951-60	7.2	1860
104	HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. *Nature Methods*, **2011**, 9, 173-5	21.6	1279
103	A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core. *Journal of Molecular Biology*, **2018**, 430, 2237-2243	6.5	1095
102	MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. *Nature Biotechnology*, **2017**, 35, 1026-1028	44.5	519
101	Uniform transitions of the general RNA polymerase II transcription complex. *Nature Structural and Molecular Biology*, **2010**, 17, 1272-8	17.6	341
100	Fast and accurate automatic structure prediction with HHpred. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 128-32	4.2	338
99	The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis. *Nucleic Acids Research*, **2016**, 44, W410-5	20.1	291
98	CCMpred--fast and precise prediction of protein residue-residue contacts from correlated mutations. *Bioinformatics*, **2014**, 30, 3128-30	7.2	273
97	HH-suite3 for fast remote homology detection and deep protein annotation. *BMC Bioinformatics*, **2019**, 20, 473	3.6	238
96	The MPI Bioinformatics Toolkit for protein sequence analysis. *Nucleic Acids Research*, **2006**, 34, W335-9	20.1	233
95	Clustering huge protein sequence sets in linear time. *Nature Communications*, **2018**, 9, 2542	17.4	200
94	Uniclust databases of clustered and deeply annotated protein sequences and alignments. *Nucleic Acids Research*, **2017**, 45, D170-D176	20.1	199
93	More than the sum of their parts: on the evolution of proteins from peptides. *BioEssays*, **2003**, 25, 837-46	4.1	181
92	TPRpred: a tool for prediction of TPR-, PPR- and SEL1-like repeats from protein sequences. *BMC Bioinformatics*, **2007**, 8, 2	3.6	159
91	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19748-53	11.5	158

90	The Mre11:Rad50 structure shows an ATP-dependent molecular clamp in DNA double-strand break repair. *Cell*, **2011**, 145, 54-66	56.2	157
89	Sequence context-specific profiles for homology searching. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 3770-5	11.5	136
88	Comparative analysis of coiled-coil prediction methods. *Journal of Structural Biology*, **2006**, 155, 140-5	3.4	128
87	Three-body decay of a rubidium Bose–Einstein condensate. *Applied Physics B: Lasers and Optics*, **1999**, 69, 257-261	1.9	128
86	A vocabulary of ancient peptides at the origin of folded proteins. *ELife*, **2015**, 4, e09410	8.9	124
85	RECQL5 controls transcript elongation and suppresses genome instability associated with transcription stress. *Cell*, **2014**, 157, 1037-49	56.2	122
84	Evolution of the beta-propeller fold. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 795-803	4.2	114
83	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19754-9	11.5	112
82	Protein Sequence Analysis Using the MPI Bioinformatics Toolkit. *Current Protocols in Bioinformatics*, **2020**, 72, e108	24.2	109
81	De novo identification of highly diverged protein repeats by probabilistic consistency. *Bioinformatics*, **2008**, 24, 807-14	7.2	108
80	Prediction of protein functional residues from sequence by probability density estimation. *Bioinformatics*, **2008**, 24, 613-20	7.2	104
79	Gravitational laser trap for atoms with evanescent-wave cooling. *Optics Communications*, **1995**, 119, 652-662	2	97
78	In vivo ligands of MDA5 and RIG-I in measles virus-infected cells. *PLoS Pathogens*, **2014**, 10, e1004081	7.6	96
77	WIsH: who is the host? Predicting prokaryotic hosts from metagenomic phage contigs. *Bioinformatics*, **2017**, 33, 3113-3114	7.2	92
76	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation. *Nature*, **2012**, 484, 386-9	50.4	89
75	Giant Spin Relaxation of an Ultracold Cesium Gas. *Physical Review Letters*, **1998**, 80, 1869-1872	7.4	87
74	REPPER--repeats and their periodicities in fibrous proteins. *Nucleic Acids Research*, **2005**, 33, W239-43	20.1	86
73	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold. *Nature Methods*, **2019**, 16, 603-606	21.6	84

72	Short-Distance Atomic Beam Deceleration with a Stimulated Light Force. *Physical Review Letters*, **1997**, 78, 1420-1423	7.4	81
71	Modulations of DNA Contacts by Linker Histones and Post-translational Modifications Determine the Mobility and Modifiability of Nucleosomal H3 Tails. *Molecular Cell*, **2016**, 61, 247-59	17.6	80
70	Lysine/RNA-interactions drive and regulate biomolecular condensation. *Nature Communications*, **2019**, 10, 2909	17.4	80
69	Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling. *PLoS Computational Biology*, **2015**, 11, e1004343	5	78
68	HHomp--prediction and classification of outer membrane proteins. *Nucleic Acids Research*, **2009**, 37, W446-51	20.1	78
67	Evolution of outer membrane beta-barrels from an ancestral beta beta hairpin. *Molecular Biology and Evolution*, **2010**, 27, 1348-58	8.3	76
66	AbrB-like transcription factors assume a swapped hairpin fold that is evolutionarily related to double-psi beta barrels. *Structure*, **2005**, 13, 919-28	5.2	73
65	Different binding properties and function of CXXC zinc finger domains in Dnmt1 and Tet1. *PLoS ONE*, **2011**, 6, e16627	3.7	73
64	MMseqs2 desktop and local web server app for fast, interactive sequence searches. *Bioinformatics*, **2019**, 35, 2856-2858	7.2	73
63	Transcriptome maps of mRNP biogenesis factors define pre-mRNA recognition. *Molecular Cell*, **2014**, 55, 745-57	17.6	72
62	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. *Molecular Cell*, **2017**, 66, 38-49.e6	17.6	68
61	HHsenser: exhaustive transitive profile search using HMM-HMM comparison. *Nucleic Acids Research*, **2006**, 34, W374-8	20.1	64
60	Mechanisms for Active Regulation of Biomolecular Condensates. *Trends in Cell Biology*, **2020**, 30, 4-14	18.3	60
59	HHrep: de novo protein repeat detection and the origin of TIM barrels. *Nucleic Acids Research*, **2006**, 34, W137-42	20.1	56
58	kClust: fast and sensitive clustering of large protein sequence databases. *BMC Bioinformatics*, **2013**, 14, 248	3.6	55
57	Protein sequence comparison and fold recognition: progress and good-practice benchmarking. *Current Opinion in Structural Biology*, **2011**, 21, 404-11	8.1	55
56	A galaxy of folds. *Protein Science*, **2010**, 19, 124-30	6.3	53
55	MMseqs software suite for fast and deep clustering and searching of large protein sequence sets. *Bioinformatics*, **2016**, 32, 1323-30	7.2	52

54	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. *Nucleic Acids Research*, **2012**, 40, 1509-22	20.1	52
53	P-value-based regulatory motif discovery using positional weight matrices. *Genome Research*, **2013**, 23, 181-94	9.7	51
52	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, 812-25	24.7	49
51	Coherent beam splitter for atoms based on a bichromatic standing light wave. *Optics Letters*, **1994**, 19, 658-60	3	49
50	Bayesian Markov models consistently outperform PWMs at predicting motifs in nucleotide sequences. *Nucleic Acids Research*, **2016**, 44, 6055-69	20.1	48
49	ScbA from Streptomyces coelicolor A3(2) has homology to fatty acid synthases and is able to synthesize gamma-butyrolactones. *Microbiology (United Kingdom)*, **2007**, 153, 1394-1404	2.9	47
48	Recruitment of TREX to the transcription machinery by its direct binding to the phospho-CTD of RNA polymerase II. *PLoS Genetics*, **2013**, 9, e1003914	6	46
47	Phospholipid scramblases and Tubby-like proteins belong to a new superfamily of membrane tethered transcription factors. *Bioinformatics*, **2009**, 25, 159-62	7.2	45
46	Strong evaporative cooling of a trapped cesium gas. *Optics Express*, **1998**, 2, 323-9	3.3	41
45	Discriminative modelling of context-specific amino acid substitution probabilities. *Bioinformatics*, **2012**, 28, 3240-7	7.2	39
44	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, 1056-63	2.9	38
43	Is Bose-Einstein condensation of atomic cesium possible?. *Europhysics Letters*, **1998**, 44, 25-30	1.6	38
42	The XXmotif web server for eXhaustive, weight matriX-based motif discovery in nucleotide sequences. *Nucleic Acids Research*, **2012**, 40, W104-9	20.1	36
41	Genome-associated RNA polymerase II includes the dissociable Rpb4/7 subcomplex. *Journal of Biological Chemistry*, **2008**, 283, 26423-7	5.4	36
40	On the origin of the histone fold. *BMC Structural Biology*, **2007**, 7, 17	2.7	34
39	MetaEuk-sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. *Microbiome*, **2020**, 8, 48	16.6	29
38	bbcontacts: prediction of β-strand pairing from direct coupling patterns. *Bioinformatics*, **2015**, 31, 1729-37	7.2	28
37	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, 415-8		28

36	A conserved GA element in TATA-less RNA polymerase II promoters. *PLoS ONE*, **2011**, 6, e27595	3.7	27
35	Big-data approaches to protein structure prediction. *Science*, **2017**, 355, 248-249	33.3	26
34	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	17.6	23
33	PROSSTT: probabilistic simulation of single-cell RNA-seq data for complex differentiation processes. *Bioinformatics*, **2019**, 35, 3517-3519	7.2	22
32	Of bits and bugs--on the use of bioinformatics and a bacterial crystal structure to solve a eukaryotic repeat-protein structure. *PLoS ONE*, **2010**, 5, e13402	3.7	19
31	Fast and sensitive taxonomic assignment to metagenomic contigs. *Bioinformatics*, **2021**,	7.2	17
30	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. *Scientific Reports*, **2018**, 8, 9939	4.9	16
29	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. *ELife*, **2021**, 10,	8.9	16
28	The BaMM web server for de-novo motif discovery and regulatory sequence analysis. *Nucleic Acids Research*, **2018**, 46, W215-W220	20.1	15
27	Bayesian multiple logistic regression for case-control GWAS. *PLoS Genetics*, **2018**, 14, e1007856	6	13
26	Synthetic protein alignments by CCMgen quantify noise in residue-residue contact prediction. *PLoS Computational Biology*, **2018**, 14, e1006526	5	12
25	Observation of the Magneto-Optical Radiation Force by Laser Spectroscopy. *Europhysics Letters*, **1992**, 20, 101-106	1.6	11
24	DescribePROT: database of amino acid-level protein structure and function predictions. *Nucleic Acids Research*, **2021**, 49, D298-D308	20.1	11
23	Context similarity scoring improves protein sequence alignments in the midnight zone. *Bioinformatics*, **2015**, 31, 674-81	7.2	10
22	Eph receptors and ephrin class B ligands are expressed at tissue boundaries in Hydra vulgaris. *International Journal of Developmental Biology*, **2013**, 57, 759-65	1.9	10
21	HH-suite3 for fast remote homology detection and deep protein annotation		10
20	MMseqs2: sensitive protein sequence searching for the analysis of massive data sets		9
19	SpacePHARER: Sensitive identification of phages from CRISPR spacers in prokaryotic hosts. *Bioinformatics*, **2021**,	7.2	8

18	Universality of core promoter elements?. *Nature*, **2014**, 511, E11-2	50.4	7
17	Foldseek: fast and accurate protein structure search		7
16	Going to extremes - a metagenomic journey into the dark matter of life. *FEMS Microbiology Letters*, **2021**, 368,	2.9	7
15	Stimulated magneto-optical force in the dressed-atom picture. *Physical Review A*, **1994**, 50, 2517-2527	2.6	6
14	PDBalert: automatic, recurrent remote homology tracking and protein structure prediction. *BMC Structural Biology*, **2008**, 8, 51	2.7	5
13	Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold		5
12	Sub-Doppler manifestation of the magneto-optical radiation force. *Optics Communications*, **1993**, 98, 54-60	2	4
11	Fast and sensitive taxonomic assignment to metagenomic contigs		4
10	Mechanisms of active regulation of biomolecular condensates		1
9	Clustering huge protein sequence sets in linear time		1
8	SpacePHARER: Sensitive identification of phages from CRISPR spacers in prokaryotic hosts		1
7	MetaEuk □sensitive, high-throughput gene discovery and annotation for large-scale eukaryotic metagenomics		1
6	Tejaas: reverse regression increases power for detecting trans-eQTLs. *Genome Biology*, **2021**, 22, 142	18.3	1
5	Thermodynamic modeling reveals widespread multivalent binding by RNA-binding proteins. *Bioinformatics*, **2021**, 37, i308-i316	7.2	1
4	Large-scale analysis of Drosophila core promoter function using synthetic promoters.. *Molecular Systems Biology*, **2022**, 18, e9816	12.2	1
3	Bayesian Markov models improve the prediction of binding motifs beyond first order. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab026	3.7	0
2	Cln5 represents a new type of cysteine-based -depalmitoylase linked to neurodegeneration.. *Science Advances*, **2022**, 8, eabj8633	14.3	0
1	In silico-Funktions- und Strukturvorhersagen bei Proteinen. *BioSpektrum*, **2014**, 20, 158-161	0.1	