

# Torsten F Schwede

## List of Publications by Year in descending order

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113  
papers

42,033  
citations

28736

57  
h-index

31191

106  
g-index

123  
all docs

123  
docs citations

123  
times ranked

57168  
citing authors

#	ARTICLE	IF	CITATIONS
1	SWISS-MODEL: homology modelling of protein structures and complexes. <i>Nucleic Acids Research</i> , 2018, 46, W296-W303.	6.5	8,474
2	The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. <i>Bioinformatics</i> , 2006, 22, 195-201.	1.8	6,515
3	SWISS-MODEL: an automated protein homology-modeling server. <i>Nucleic Acids Research</i> , 2003, 31, 3381-3385.	6.5	4,722
4	SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. <i>Nucleic Acids Research</i> , 2014, 42, W252-W258.	6.5	4,247
5	Toward the estimation of the absolute quality of individual protein structure models. <i>Bioinformatics</i> , 2011, 27, 343-350.	1.8	1,855
6	The SWISS-MODEL Repository and associated resources. <i>Nucleic Acids Research</i> , 2009, 37, D387-D392.	6.5	1,789
7	Automated comparative protein structure modeling with SWISS-MODEL and SwissPdbViewer: A historical perspective. <i>Electrophoresis</i> , 2009, 30, S162-73.	1.3	1,574
8	The SWISS-MODEL Repository's new features and functionality. <i>Nucleic Acids Research</i> , 2017, 45, D313-D319.	6.5	1,227
9	Protein structure homology modeling using SWISS-MODEL workspace. <i>Nature Protocols</i> , 2009, 4, 1-13.	5.5	1,092
10	QMEAN server for protein model quality estimation. <i>Nucleic Acids Research</i> , 2009, 37, W510-W514.	6.5	716
11	lDDT: a local superposition-free score for comparing protein structures and models using distance difference tests. <i>Bioinformatics</i> , 2013, 29, 2722-2728.	1.8	634
12	Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. <i>Scientific Reports</i> , 2017, 7, 10480.	1.6	608
13	QMEANDisCo's distance constraints applied on model quality estimation. <i>Bioinformatics</i> , 2020, 36, 1765-1771.	1.8	537
14	The SWISS-MODEL Repository: new features and functionalities. <i>Nucleic Acids Research</i> , 2006, 34, D315-D318.	6.5	454
15	Critical assessment of methods of protein structure prediction (CASP) Round XIII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1011-1020.	1.5	380
16	Critical assessment of methods of protein structure prediction (CASP) round x. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1-6.	1.5	366
17	Critical assessment of methods of protein structure prediction (CASP) Round XII. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 7-15.	1.5	296
18	The SWISS-MODEL Repository of annotated three-dimensional protein structure homology models. <i>Nucleic Acids Research</i> , 2004, 32, 230D-234.	6.5	294

#	ARTICLE	IF	CITATIONS
19	Critical assessment of methods of protein structure prediction (CASP)â€”Round <sc>XIV</sc>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1607-1617.	1.5	281
20	Second messenger-mediated spatiotemporal control of protein degradation regulates bacterial cell cycle progression. Genes and Development, 2009, 23, 93-104.	2.7	272
21	The Protein Model Portalâ€”a comprehensive resource for protein structure and model information. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat031.	1.4	254
22	Crystal Structure of Histidine Ammonia-Lyase Revealing a Novel Polypeptide Modification as the Catalytic Electrophileâ€”â€¦. Biochemistry, 1999, 38, 5355-5361.	1.2	221
23	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. Acta Crystallographica Section D: Structural Biology, 2017, 73, 710-728.	1.1	205
24	Critical assessment of methods of protein structure prediction: Progress and new directions in round XI. Proteins: Structure, Function and Bioinformatics, 2016, 84, 4-14.	1.5	198
25	ProMod3â€”A versatile homology modelling toolbox. PLoS Computational Biology, 2021, 17, e1008667.	1.5	161
26	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
27	Assessment of template based protein structure predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 37-58.	1.5	152
28	Assessment of CASP7 predictions for template-based modeling targets. Proteins: Structure, Function and Bioinformatics, 2007, 69, 38-56.	1.5	146
29	Modelling three-dimensional protein structures for applications in drug design. Drug Discovery Today, 2014, 19, 890-897.	3.2	134
30	QMEANclust: estimation of protein model quality by combining a composite scoring function with structural density information. BMC Structural Biology, 2009, 9, 35.	2.3	131
31	The Protein Model Portal. Journal of Structural and Functional Genomics, 2009, 10, 1-8.	1.2	130
32	Assessing the local structural quality of transmembrane protein models using statistical potentials (QMEANBrane). Bioinformatics, 2014, 30, i505-i511.	1.8	129
33	Continuous Automated Model EvaluatiOn (CAMEO) complementing the critical assessment of structure prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 387-398.	1.5	127
34	Automated Protein Structure Modeling with SWISS-MODEL Workspace and the Protein Model Portal. Methods in Molecular Biology, 2011, 857, 107-136.	0.4	124
35	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	1.5	114
36	Protein structure computing in the genomic era. Research in Microbiology, 2000, 151, 107-112.	1.0	111

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37	Protein Modeling: What Happened to the "Protein Structure Gap"? Structure, 2013, 21, 1531-1540.	1.6	111
38	Automated protein structure homology modeling: a progress report. Pharmacogenomics, 2004, 5, 405-416.	0.6	105
39	Automated server predictions in CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 68-82.	1.5	105
40	Assessment of disorder predictions in CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 129-136.	1.5	102
41	The protein structure initiative structural genomics knowledgebase. Nucleic Acids Research, 2009, 37, D365-D368.	6.5	94
42	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
43	OpenStructure: an integrated software framework for computational structural biology. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 701-709.	2.5	93
44	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. Structure, 2017, 25, 1317-1318.	1.6	84
45	The Mouse Eugenol Odorant Receptor: Structural and Functional Plasticity of a Broadly Tuned Odorant Binding Pocket. Biochemistry, 2011, 50, 843-853.	1.2	81
46	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
47	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. Structure, 2013, 21, 875-881.	1.6	77
48	Novel missense mutations of TMPRSS3 in two consanguineous Tunisian families with non-syndromic autosomal recessive deafness. Human Mutation, 2001, 18, 101-108.	1.1	76
49	Novel Inhibitors of Dengue Virus Methyltransferase: Discovery by in Vitro-Driven Virtual Screening on a Desktop Computer Grid. Journal of Medicinal Chemistry, 2010, 53, 1483-1495.	2.9	76
50	The Plug Domain of Yeast Sec61p Is Important for Efficient Protein Translocation, but Is Not Essential for Cell Viability. Molecular Biology of the Cell, 2006, 17, 4063-4068.	0.9	74
51	Assessment of ligand-binding residue predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 126-136.	1.5	72
52	Mutations in the Sec61p Channel Affecting Signal Sequence Recognition and Membrane Protein Topology. Journal of Biological Chemistry, 2007, 282, 33201-33209.	1.6	66
53	Mutations in the TMPRSS3 gene are a rare cause of childhood nonsyndromic deafness in Caucasian patients. Journal of Molecular Medicine, 2002, 80, 124-131.	1.7	65
54	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. Journal of Structural and Functional Genomics, 2011, 12, 45-54.	1.2	65

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55	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
56	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <sc>CASP</sc> 11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 349-369.	1.5	63
57	CASP9 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 21-36.	1.5	61
58	Assessment of model accuracy estimations in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 345-360.	1.5	61
59	Evaluation of the templateâ€based modeling in <sc>CASP12</sc>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 321-334.	1.5	61
60	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	1.6	60
61	Increased efficiency of <i>Campylobacter jejuni N</i>-oligosaccharyltransferase PglB by structure-guided engineering. <i>Open Biology</i> , 2015, 5, 140227.	1.5	59
62	Novel cargo-binding site in the $\hat{I}^2$ and $\hat{I}^1$ subunits of coatamer. <i>Journal of Cell Biology</i> , 2007, 179, 209-217.	2.3	57
63	Global and local model quality estimation at CASP8 using the scoring functions QMEAN and QMEANclust. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 173-180.	1.5	56
64	Assessment of protein assembly prediction in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 247-256.	1.5	54
65	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 26-42.	1.5	53
66	Automated protein modelling - the proteome in 3D. <i>Pharmacogenomics</i> , 2000, 1, 257-266.	0.6	49
67	Sulfonylureas and Glinides Exhibit Peroxisome Proliferator-Activated Receptor $\hat{I}^3$ Activity: A Combined Virtual Screening and Biological Assay Approach. <i>Molecular Pharmacology</i> , 2007, 71, 398-406.	1.0	49
68	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017, 9, 113.	3.6	47
69	Asp1424Asn MYH9 mutation results in an unstable protein responsible for the phenotypes in May-Hegglin anomaly/Fechtner syndrome. <i>Blood</i> , 2003, 102, 529-534.	0.6	43
70	Continuous Automated Model EvaluatiOn (CAMEO)â€™Perspectives on the future of fully automated evaluation of structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1977-1986.	1.5	40
71	Drug Design Workshop: A Web-Based Educational Tool To Introduce Computer-Aided Drug Design to the General Public. <i>Journal of Chemical Education</i> , 2017, 94, 335-344.	1.1	39
72	Assessment of ligand binding site predictions in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 154-163.	1.5	37

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73	Covalent and three-dimensional structure of the cyclodextrinase from <i>Flavobacterium</i> sp. no. 92. <i>FEBS Journal</i> , 2003, 270, 2332-2341.	0.2	36
74	OpenStructure: a flexible software framework for computational structural biology. <i>Bioinformatics</i> , 2010, 26, 2626-2628.	1.8	34
75	A Comprehensive Mapping of the Druggable Cavities within the SARS-CoV-2 Therapeutically Relevant Proteins by Combining Pocket and Docking Searches as Implemented in Pockets 2.0. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5152.	1.8	34
76	Introducing "best single template" models as reference baseline for the Continuous Automated Model Evaluation (CAMEO). <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1378-1387.	1.5	31
77	Cohesive Properties of the <i>Caulobacter crescentus</i> Holdfast Adhesin Are Regulated by a Novel c-di-GMP Effector Protein. <i>MBio</i> , 2017, 8, .	1.8	29
78	How inaccuracies in protein structure models affect estimates of protein-ligand interactions: Computational analysis of HIV-1 protease inhibitor binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 407-423.	1.5	28
79	Target highlights in <i>CASP14</i> : Analysis of models by structure providers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1647-1672.	1.5	27
80	Homogenization and crystallization of histidine ammonia-lyase by exchange of a surface cysteine residue. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 151-153.	1.0	26
81	Domain definition and target classification for <i>CASP7</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 10-18.	1.5	21
82	Dual Activities of Odorants on Olfactory and Nuclear Hormone Receptors. <i>Journal of Biological Chemistry</i> , 2009, 284, 30547-30555.	1.6	21
83	Zinc-selective inhibition of the promiscuous bacterial amide-hydrolase DapE: implications of metal heterogeneity for evolution and antibiotic drug design. <i>Metallomics</i> , 2014, 6, 88-95.	1.0	21
84	Global Genomic Analysis of SARS-CoV-2 RNA Dependent RNA Polymerase Evolution and Antiviral Drug Resistance. <i>Microorganisms</i> , 2021, 9, 1094.	1.6	21
85	Target highlights in <i>CASP9</i> : Experimental target structures for the critical assessment of techniques for protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 6-20.	1.5	19
86	Computational Structural Biology. , 2008, , .		18
87	High-resolution cryo-EM structure of urease from the pathogen <i>Yersinia enterocolitica</i> . <i>Nature Communications</i> , 2020, 11, 5101.	5.8	17
88	Some of the most interesting <i>CASP11</i> targets through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 34-50.	1.5	16
89	Plasmid-mediated colistin resistance in a patient infected with <i>Klebsiella pneumoniae</i> . <i>Lancet Infectious Diseases</i> , The, 2016, 16, 998-999.	4.6	15
90	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	6.5	13

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91	Modeling of Protein Tertiary and Quaternary Structures Based on Evolutionary Information. <i>Methods in Molecular Biology</i> , 2019, 1851, 301-316.	0.4	13
92	Data to knowledge: how to get meaning from your result. <i>IUCr</i> , 2015, 2, 45-58.	1.0	12
93	Target highlights in CASP13: Experimental target structures through the eyes of their authors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1037-1057.	1.5	12
94	Computational Analysis of Methyl Transfer Reactions in Dengue Virus Methyltransferase. <i>Journal of Physical Chemistry B</i> , 2014, 118, 5882-5890.	1.2	11
95	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
96	Improving your target-template alignment with MODalign. <i>Bioinformatics</i> , 2012, 28, 1038-1039.	1.8	10
97	Exome sequencing of healthy phenotypic extremes links TROVE2 to emotional memory and PTSD. <i>Nature Human Behaviour</i> , 2017, 1, .	6.2	8
98	A computational protocol to evaluate the effects of protein mutants in the kinase gatekeeper position on the binding of ATP substrate analogues. <i>BMC Research Notes</i> , 2017, 10, 104.	0.6	7
99	Protein Tertiary Structure Modeling. <i>Current Protocols in Protein Science</i> , 2001, 23, Unit2.8.	2.8	3
100	ECCB 2012: The 11th European Conference on Computational Biology. <i>Bioinformatics</i> , 2012, 28, i303-i305.	1.8	3
101	Homology Modeling of Protein Structures. , 2013, , 992-998.		2
102	Anna Tramontano 1957-2017. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 431-432.	3.6	2
103	Interactomes in the era of deep learning. <i>Science</i> , 2021, 374, 1319-1320.	6.0	2
104	SWISS-TANDEM: A Web-Based Workspace for MS/MS Protein Identification on PC Grids. <i>Proceedings of the IEEE Symposium on Computer-Based Medical Systems</i> , 2007, , .	0.0	1
105	A tribute to Anna Tramontano (1957-2017). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 5-6.	1.5	1
106	Novel missense mutations of TMPRSS3 in two consanguineous Tunisian families with non-syndromic autosomal recessive deafness. <i>Human Mutation</i> , 2002, 19, 183-183.	1.1	0
107	Dual activities of odorants on olfactory and nuclear hormone receptors.. <i>Journal of Biological Chemistry</i> , 2009, 284, 36720.	1.6	0
108	Protein Structure Modeling and Docking at the Swiss Institute of Bioinformatics. , 2009, , 219-246.		0

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109	How to use the PSI Structural Genomics Knowledgebase to Enable Research. Biophysical Journal, 2010, 98, 250a.	0.2	0
110	The Structural Biology Knowledgebase - search Online for Protein Sequences, Structures, Functions, Methods and More. Biophysical Journal, 2011, 100, 319a.	0.2	0
111	Cover Image, Volume 87, Issue 12. Proteins: Structure, Function and Bioinformatics, 2019, 87, C4.	1.5	0
112	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. FASEB Journal, 2012, 26, lb194.	0.2	0
113	Coordination of structural bioinformatics activities across Europe. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e231-e231.	0.0	0