Torsten F Schwede

List of Publications by Year
in descending order

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	ProMod3—A versatile homology modelling toolbox. PLoS Computational Biology, 2021, 17, e1008667.	1.5	161
2	Global Genomic Analysis of SARS-CoV-2 RNA Dependent RNA Polymerase Evolution and Antiviral Drug Resistance. Microorganisms, 2021, 9, 1094.	1.6	21
3	Continuous Automated Model EvaluatiOn (CAMEO)—Perspectives on the future of fully automated evaluation of structure prediction methods. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1977-1986.	1.5	40
4	Target highlights in <scp>CASP14</scp>: Analysis of models by structure providers. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1647-1672.	1.5	27
5	Critical assessment of methods of protein structure prediction (CASP)—Round <scp>XIV</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1607-1617.	1.5	281
6	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
7	Interactomes in the era of deep learning. Science, 2021, 374, 1319-1320.	6.0	2
8	QMEANDisCo—distance constraints applied on model quality estimation. Bioinformatics, 2020, 36, 1765-1771.	1.8	537
9	High-resolution cryo-EM structure of urease from the pathogen Yersinia enterocolitica. Nature Communications, 2020, 11, 5101.	5.8	17
10	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. International Journal of Molecular Sciences, 2020, 21, 5152.	1.8	34
11	Estimation of model accuracy in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1361-1377.	1.5	78
12	Introducing â€œbest single templateâ€•models as reference baseline for the Continuous Automated Model Evaluation (CAMEO). Proteins: Structure, Function and Bioinformatics, 2019, 87, 1378-1387.	1.5	31
13	Critical assessment of methods of protein structure prediction (CASP)—Round XIII. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1011-1020.	1.5	380
14	Target highlights in CASP13: Experimental target structures through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1037-1057.	1.5	12
15	Cover Image, Volume 87, Issue 12. Proteins: Structure, Function and Bioinformatics, 2019, 87, C4.	1.5	0
16	Modeling of Protein Tertiary and Quaternary Structures Based on Evolutionary Information. Methods in Molecular Biology, 2019, 1851, 301-316.	0.4	13
17	Assessment of protein assembly prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 247-256.	1.5	54
18	Target highlights from the first postâ€PSI CASP experiment (CASP12, Mayâ€"August 2016). Proteins: Structure, Function and Bioinformatics, 2018, 86, 27-50.	1.5	11

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19	Assessment of model accuracy estimations in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 345-360.	1.5	61
20	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
21	A tribute to Anna Tramontano (1957â€"2017). Proteins: Structure, Function and Bioinformatics, 2018, 86, 5-6.	1.5	1
22	Critical assessment of methods of protein structure prediction (CASP)â€"Round XII. Proteins: Structure, Function and Bioinformatics, 2018, 86, 7-15.	1.5	296
23	Evaluation of the templateâ€"based modeling in <scp>CASP12</scp>. Proteins: Structure, Function and Bioinformatics, 2018, 86, 321-334.	1.5	61
24	SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Research, 2018, 46, W296-W303.	6.5	8,474
25	Coordination of structural bioinformatics activities across Europe. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e231-e231.	0.0	0
26	The SWISS-MODEL Repositoryâ€"new features and functionality. Nucleic Acids Research, 2017, 45, D313-D319.	6.5	1,227
27	Drug Design Workshop: A Web-Based Educational Tool To Introduce Computer-Aided Drug Design to the General Public. Journal of Chemical Education, 2017, 94, 335-344.	1.1	39
28	A computational protocol to evaluate the effects of protein mutants in the kinase gatekeeper position on the binding of ATP substrate analogues. BMC Research Notes, 2017, 10, 104.	0.6	7
29	Anna Tramontano 1957â€"2017. Nature Structural and Molecular Biology, 2017, 24, 431-432.	3.6	2
30	Cohesive Properties of the <i>Caulobacter crescentus</i> Holdfast Adhesin Are Regulated by a Novel c-di-GMP Effector Protein. MBio, 2017, 8, .	1.8	29
31	Exome sequencing of healthy phenotypic extremes links TROVE2 to emotional memory and PTSD. Nature Human Behaviour, 2017, 1, .	6.2	8
32	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. Structure, 2017, 25, 1317-1318.	1.6	84
33	Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. Scientific Reports, 2017, 7, 10480.	1.6	608
34	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
35	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
36	Methods of model accuracy estimation can help selecting the best models from decoy sets: Assessment of model accuracy estimations in <scp>CASP</scp>11. Proteins: Structure, Function and Bioinformatics, 2016, 84, 349-369.	1.5	63

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37	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
38	Some of the most interesting <scp>CASP</scp>11 targets through the eyes of their authors. Proteins: Structure, Function and Bioinformatics, 2016, 84, 34-50.	1.5	16
39	Plasmid-mediated colistin resistance in a patient infected with Klebsiella pneumoniae. Lancet Infectious Diseases, The, 2016, 16, 998-999.	4.6	15
40	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
41	Data to knowledge: how to get meaning from your result. IUCrJ, 2015, 2, 45-58.	1.0	12
42	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	1.6	159
43	Increased efficiency of <i>Campylobacter jejuni N</i> -oligosaccharyltransferase PglB by structure-guided engineering. Open Biology, 2015, 5, 140227.	1.5	59
44	Assessing the local structural quality of transmembrane protein models using statistical potentials (QMEANBrane). Bioinformatics, 2014, 30, i505-i511.	1.8	129
45	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13
46	Critical assessment of methods of protein structure prediction (CASP) â€" round x. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1-6.	1.5	366
47	Assessment of the assessment: Evaluation of the model quality estimates in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 112-126.	1.5	114
48	Zinc-selective inhibition of the promiscuous bacterial amide-hydrolase DapE: implications of metal heterogeneity for evolution and antibioticdrug design. Metallomics, 2014, 6, 88-95.	1.0	21
49	Modelling three-dimensional protein structures for applications in drug design. Drug Discovery Today, 2014, 19, 890-897.	3.2	134
50	Computational Analysis of Methyl Transfer Reactions in Dengue Virus Methyltransferase. Journal of Physical Chemistry B, 2014, 118, 5882-5890.	1.2	11
51	Assessment of ligand binding site predictions in CASP10. Proteins: Structure, Function and Bioinformatics, 2014, 82, 154-163.	1.5	37
52	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. Proteins: Structure, Function and Bioinformatics, 2014, 82, 26-42.	1.5	53
53	SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. Nucleic Acids Research, 2014, 42, W252-W258.	6.5	4,247
54	Protein Modeling: What Happened to the â€œProtein Structure Gapâ€?. Structure, 2013, 21, 1531-1540.	1.6	111

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55	Homology Modeling of Protein Structures. , 2013, , 992-998.		2
56	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
57	lDDT: a local superposition-free score for comparing protein structures and models using distance difference tests. Bioinformatics, 2013, 29, 2722-2728.	1.8	634
58	*OpenStructure*: an integrated software framework for computational structural biology. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 701-709.	2.5	93
59	The Protein Model Portal—a comprehensive resource for protein structure and model information. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat031.	1.4	254
60	ECCB 2012: The 11th European Conference on Computational Biology. Bioinformatics, 2012, 28, i303-i305.	1.8	3
61	Improving your target-template alignment with MODalign. Bioinformatics, 2012, 28, 1038-1039.	1.8	10
62	Structural Biology Knowledgebase: a biologists resource for protein structure and sample information. FASEB Journal, 2012, 26, lb194.	0.2	0
63	The Structural Biology Knowledgebase - search Online for Protein Sequences, Structures, Functions, Methods and More. Biophysical Journal, 2011, 100, 319a.	0.2	0
64	Automated Protein Structure Modeling with SWISS-MODEL Workspace and the Protein Model Portal. Methods in Molecular Biology, 2011, 857, 107-136.	0.4	124
65	The Mouse Eugenol Odorant Receptor: Structural and Functional Plasticity of a Broadly Tuned Odorant Binding Pocket. Biochemistry, 2011, 50, 843-853.	1.2	81
66	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
67	Assessment of ligand–binding residue predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 126-136.	1.5	72
68	Assessment of template based protein structure predictions in CASP9. Proteins: Structure, Function and Bioinformatics, 2011, 79, 37-58.	1.5	152
69	CASP9 target classification. Proteins: Structure, Function and Bioinformatics, 2011, 79, 21-36.	1.5	61
70	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	1.5	19
71	Toward the estimation of the absolute quality of individual protein structure models. Bioinformatics, 2011, 27, 343-350.	1.8	1,855
72	OpenStructure: a flexible software framework for computational structural biology. Bioinformatics, 2010, 26, 2626-2628.	1.8	34

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73	How to use the PSI Structural Genomics Knowledgebase to Enable Research. Biophysical Journal, 2010, 98, 250a.	0.2	0
74	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
75	Dual activities of odorants on olfactory and nuclear hormone receptors.. Journal of Biological Chemistry, 2009, 284, 36720.	1.6	0
76	Dual Activities of Odorants on Olfactory and Nuclear Hormone Receptors. Journal of Biological Chemistry, 2009, 284, 30547-30555.	1.6	21
77	Protein Structure Modeling and Docking at the Swiss Institute of Bioinformatics. , 2009, , 219-246.		0
78	The protein structure initiative structural genomics knowledgebase. Nucleic Acids Research, 2009, 37, D365-D368.	6.5	94
79	Automated comparative protein structure modeling with SWISSâ€MODEL and Swissâ€PdbViewer: A historical perspective. Electrophoresis, 2009, 30, S162-73.	1.3	1,574
80	The Protein Model Portal. Journal of Structural and Functional Genomics, 2009, 10, 1-8.	1.2	130
81	Global and local model quality estimation at CASP8 using the scoring functions QMEAN and QMEANclust. Proteins: Structure, Function and Bioinformatics, 2009, 77, 173-180.	1.5	56
82	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
83	Protein structure homology modeling using SWISS-MODEL workspace. Nature Protocols, 2009, 4, 1-13.	5.5	1,092
84	Second messenger-mediated spatiotemporal control of protein degradation regulates bacterial cell cycle progression. Genes and Development, 2009, 23, 93-104.	2.7	272
85	The SWISS-MODEL Repository and associated resources. Nucleic Acids Research, 2009, 37, D387-D392.	6.5	1,789
86	QMEAN server for protein model quality estimation. Nucleic Acids Research, 2009, 37, W510-W514.	6.5	716
87	Computational Structural Biology. , 2008, , .		18
88	SWISS-TANDEM: A Web-Based Workspace for MS/MS Protein Identification on PC Grids. Proceedings of the IEEE Symposium on Computer-Based Medical Systems, 2007, , .	0.0	1
89	Novel cargo-binding site in the Î² and Î´ subunits of coatomer. Journal of Cell Biology, 2007, 179, 209-217.	2.3	57
90	Mutations in the Sec61p Channel Affecting Signal Sequence Recognition and Membrane Protein Topology. Journal of Biological Chemistry, 2007, 282, 33201-33209.	1.6	66

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91	Sulfonylureas and Glinides Exhibit Peroxisome Proliferator-Activated Receptor Î³ Activity: A Combined Virtual Screening and Biological Assay Approach. Molecular Pharmacology, 2007, 71, 398-406.	1.0	49
92	Assessment of disorder predictions in CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 129-136.	1.5	102
93	Domain definition and target classification for CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 10-18.	1.5	21
94	Assessment of CASP7 predictions for template-based modeling targets. Proteins: Structure, Function and Bioinformatics, 2007, 69, 38-56.	1.5	146
95	Automated server predictions in CASP7. Proteins: Structure, Function and Bioinformatics, 2007, 69, 68-82.	1.5	105
96	The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. Bioinformatics, 2006, 22, 195-201.	1.8	6,515
97	How inaccuracies in protein structure models affect estimates of protein-ligand interactions: Computational analysis of HIV-I protease inhibitor binding. Proteins: Structure, Function and Bioinformatics, 2006, 65, 407-423.	1.5	28
98	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	1.6	60
99	The SWISS-MODEL Repository: new features and functionalities. Nucleic Acids Research, 2006, 34, D315-D318.	6.5	454
100	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
101	The SWISS-MODEL Repository of annotated three-dimensional protein structure homology models. Nucleic Acids Research, 2004, 32, 230D-234.	6.5	294
102	Automated protein structure homology modeling: a progress report. Pharmacogenomics, 2004, 5, 405-416.	0.6	105
103	Covalent and three-dimensional structure of the cyclodextrinase from Flavobacterium sp. no. 92. FEBS Journal, 2003, 270, 2332-2341.	0.2	36
104	SWISS-MODEL: an automated protein homology-modeling server. Nucleic Acids Research, 2003, 31, 3381-3385.	6.5	4,722
105	Asp1424Asn MYH9 mutation results in an unstable protein responsible for the phenotypes in May-Hegglin anomaly/Fechtner syndrome. Blood, 2003, 102, 529-534.	0.6	43
106	Novel missense mutations of TMPRSS3 in two consanguineous Tunisian families with non-syndromic autosomal recessive deafness. Human Mutation, 2002, 19, 183-183.	1.1	0
107	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
108	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

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109	Protein Tertiary Structure Modeling. Current Protocols in Protein Science, 2001, 23, Unit2.8.	2.8	3
110	Automated protein modelling - the proteome in 3D. Pharmacogenomics, 2000, 1, 257-266.	0.6	49
111	Protein structure computing in the genomic era. Research in Microbiology, 2000, 151, 107-112.	1.0	111
112	Homogenization and crystallization of histidine ammonia-lyase by exchange of a surface cysteine residue. Protein Engineering, Design and Selection, 1999, 12, 151-153.	1.0	26
113	Crystal Structure of Histidine Ammonia-Lyase Revealing a Novel Polypeptide Modification as the Catalytic Electrophileâ€,â€¡. Biochemistry, 1999, 38, 5355-5361.	1.2	221