

# Tjelvar S G Olsson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1816741/publications.pdf>

Version: 2024-02-01

20  
papers

1,454  
citations

623188

14  
h-index

752256

20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2529  
citing authors

#	ARTICLE	IF	CITATIONS
1	dtoolAI: Reproducibility for Deep Learning. <i>Patterns</i> , 2020, 1, 100073.	3.1	23
2	Lightweight data management with dtool. <i>PeerJ</i> , 2019, 7, e6562.	0.9	5
3	Ectopic BASL Reveals Tissue Cell Polarity throughout Leaf Development in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2018, 28, 2638-2646.e4.	1.8	55
4	A calmodulin-like protein regulates plasmodesmal closure during bacterial immune responses. <i>New Phytologist</i> , 2017, 215, 77-84.	3.5	90
5	Distinct phases of Polycomb silencing to hold epigenetic memory of cold in <i>Arabidopsis</i> . <i>Science</i> , 2017, 357, 1142-1145.	6.0	167
6	Single Molecule RNA FISH in <i>Arabidopsis</i> Root Cells. <i>Bio-protocol</i> , 2017, 7, e2240.	0.2	16
7	Identifying Interactions that Determine Fragment Binding at Protein Hotspots. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4314-4325.	2.9	86
8	A method for detecting single mRNA molecules in <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2016, 12, 13.	1.9	62
9	jicbioimage: a tool for automated and reproducible bioimage analysis. <i>PeerJ</i> , 2016, 4, e2674.	0.9	6
10	Local chromatin environment of a Polycomb target gene instructs its own epigenetic inheritance. <i>ELife</i> , 2015, 4, .	2.8	92
11	Assessment of a Cambridge Structural Database-Driven Overlay Program. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 3091-3098.	2.5	11
12	Subpocket Analysis Method for Fragment-Based Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 131-141.	2.5	23
13	Evaluation of molecular crystal structures using Full Interaction Maps. <i>CrystEngComm</i> , 2013, 15, 65-72.	1.3	109
14	Computational design of a Diels-Alderase from a thermophilic esterase: the importance of dynamics. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 1079-1095.	1.3	12
15	Validating and Understanding Ring Conformations Using Small Molecule Crystallographic Data. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 956-962.	2.5	40
16	The Hydrogen Bond Environments of 1 <i>H</i> -Tetrazole and Tetrazolate Rings: The Structural Basis for Tetrazole-Carboxylic Acid Bioisosterism. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 857-866.	2.5	65
17	Potential and Limitations of Ensemble Docking. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 1262-1274.	2.5	149
18	Designing a New Diels-Alderase: A Combinatorial, Semirational Approach Including Dynamic Optimization.. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 1906-1917.	2.5	11

#	ARTICLE	IF	CITATIONS
19	Extent of enthalpy-entropy compensation in protein-ligand interactions. <i>Protein Science</i> , 2011, 20, 1607-1618.	3.1	143
20	The Thermodynamics of Protein-Ligand Interaction and Solvation: Insights for Ligand Design. <i>Journal of Molecular Biology</i> , 2008, 384, 1002-1017.	2.0	281