

# Tilman Flock

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

1,913  
citations

471509

17  
h-index

752698

20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

3091  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Elements Directing G Proteins and $\beta$ -Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. <i>ACS Pharmacology and Translational Science</i> , 2022, 5, 89-101.	4.9	2
2	Molecular determinants underlying functional innovations of TBP and their impact on transcription initiation. <i>Nature Communications</i> , 2020, 11, 2384.	12.8	17
3	An online resource for GPCR structure determination and analysis. <i>Nature Methods</i> , 2019, 16, 151-162.	19.0	108
4	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. <i>Nature Communications</i> , 2019, 10, 1261.	12.8	86
5	Cryo-EM structure of the rhodopsin-G $\beta$ - $\gamma$ complex reveals binding of the rhodopsin C-terminal tail to the $\gamma$ subunit. <i>ELife</i> , 2019, 8, .	6.0	52
6	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 279-288.	8.2	43
7	Visualization and analysis of non-covalent contacts using the Protein Contacts Atlas. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 185-194.	8.2	103
8	Crystal structure of rhodopsin in complex with a mini-G $\alpha$ sheds light on the principles of G protein selectivity. <i>Science Advances</i> , 2018, 4, eaat7052.	10.3	65
9	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6201-6206.	7.1	19
10	Molecular mechanism of modulating arrestin conformation by GPCR phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 538-545.	8.2	87
11	Selectivity determinants of GPCR-G-protein binding. <i>Nature</i> , 2017, 545, 317-322.	27.8	297
12	Exploiting sequence and stability information for directing nanobody stability engineering. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2196-2205.	2.4	38
13	Molecular Principles of Gene Fusion Mediated Rewiring of Protein Interaction Networks in Cancer. <i>Molecular Cell</i> , 2016, 63, 579-592.	9.7	63
14	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , 2016, 536, 484-487.	27.8	245
15	Universal allosteric mechanism for G $\beta$ activation by GPCRs. <i>Nature</i> , 2015, 524, 173-179.	27.8	291
16	How do disordered regions achieve comparable functions to structured domains?. <i>Protein Science</i> , 2015, 24, 909-922.	7.6	41
17	Probing G $\beta$ 1 protein activation at single amino acid resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 686-694.	8.2	58
18	Controlling entropy to tune the functions of intrinsically disordered regions. <i>Current Opinion in Structural Biology</i> , 2014, 26, 62-72.	5.7	127

#	ARTICLE	IF	CITATIONS
19	Structured and disordered facets of the GPCR fold. <i>Current Opinion in Structural Biology</i> , 2014, 27, 129-137.	5.7	68
20	General approach to reversing ketol-acid reductoisomerase cofactor dependence from NADPH to NADH. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10946-10951.	7.1	102