

Christoph Thomas

List of Publications by Year in descending order

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22
papers

2,020
citations

394286

19
h-index

677027

22
g-index

23
all docs

23
docs citations

23
times ranked

2809
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for IL-12 and IL-23 receptor sharing reveals a gateway for shaping actions on T versus NK cells. <i>Cell</i> , 2021, 184, 983-999.e24.	13.5	78
2	MHC I assembly and peptide editing – chaperones, clients, and molecular plasticity in immunity. <i>Current Opinion in Immunology</i> , 2021, 70, 48-56.	2.4	30
3	Structural and functional diversity calls for a new classification of ABC transporters. <i>FEBS Letters</i> , 2020, 594, 3767-3775.	1.3	169
4	Structural and Mechanistic Principles of ABC Transporters. <i>Annual Review of Biochemistry</i> , 2020, 89, 605-636.	5.0	252
5	A loop structure allows TAPBPR to exert its dual function as MHC I chaperone and peptide editor. <i>ELife</i> , 2020, 9, .	2.8	33
6	Conformation space of a heterodimeric ABC exporter under turnover conditions. <i>Nature</i> , 2019, 571, 580-583.	13.7	185
7	MHC I chaperone complexes shaping immunity. <i>Current Opinion in Immunology</i> , 2019, 58, 9-15.	2.4	41
8	Multifaceted structures and mechanisms of ABC transport systems in health and disease. <i>Current Opinion in Structural Biology</i> , 2018, 51, 116-128.	2.6	74
9	Crystal structure and mechanistic basis of a functional homolog of the antigen transporter TAP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E438-E447.	3.3	67
10	Structure of the TAPBPR–MHC I complex defines the mechanism of peptide loading and editing. <i>Science</i> , 2017, 358, 1060-1064.	6.0	115
11	Proofreading of Peptide–MHC Complexes through Dynamic Multivalent Interactions. <i>Frontiers in Immunology</i> , 2017, 8, 65.	2.2	58
12	Instructive roles for cytokine-receptor binding parameters in determining signaling and functional potency. <i>Science Signaling</i> , 2015, 8, ra114.	1.6	57
13	Mechanistic Basis for Epitope Proofreading in the Peptide-Loading Complex. <i>Journal of Immunology</i> , 2015, 195, 4503-4513.	0.4	43
14	Structure of the activating IL-1 receptor signaling complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 455-457.	3.6	100
15	Structural Linkage between Ligand Discrimination and Receptor Activation by Type I Interferons. <i>Cell</i> , 2011, 146, 621-632.	13.5	310
16	Structure and Function of ROPs and their GEFs. <i>Signaling and Communication in Plants</i> , 2010, , 49-69.	0.5	3
17	3D structure of a binary ROP-PRONE complex: the final intermediate for a complete set of molecular snapshots of the RopGEF reaction. <i>Biological Chemistry</i> , 2009, 390, 427-435.	1.2	26
18	The Role of the Conserved Switch II Glutamate in Guanine Nucleotide Exchange Factor-Mediated Nucleotide Exchange of GTP-Binding Proteins. <i>Journal of Molecular Biology</i> , 2008, 379, 51-63.	2.0	24

#	ARTICLE	IF	CITATIONS
19	Structural Evidence for a Common Intermediate in Small G Protein-GEF Reactions. <i>Molecular Cell</i> , 2007, 25, 141-149.	4.5	92
20	Purification, crystallization and preliminary X-ray diffraction analysis of the plant Rho protein ROP5. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1070-1072.	0.7	2
21	Purification and crystallization of the catalytic PRONE domain of RopGEF8 and its complex with Rop4 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 607-610.	0.7	6
22	A new family of RhoGEFs activates the Rop molecular switch in plants. <i>Nature</i> , 2005, 436, 1176-1180.	13.7	255