

Matthias Zebisch

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

2,277
citations

471509

17
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

3355
citing authors

#	ARTICLE	IF	CITATIONS
1	Cellular function and molecular structure of ecto-nucleotidases. <i>Purinergic Signalling</i> , 2012, 8, 437-502.	2.2	850
2	Notum deacylates Wnt proteins to suppress signalling activity. <i>Nature</i> , 2015, 519, 187-192.	27.8	348
3	Crystal Structure of the Human Ecto-5'-Nucleotidase (CD73): Insights into the Regulation of Purinergic Signaling. <i>Structure</i> , 2012, 20, 2161-2173.	3.3	164
4	Structural and molecular basis of ZNRF3/RNF43 transmembrane ubiquitin ligase inhibition by the Wnt agonist R-spondin. <i>Nature Communications</i> , 2013, 4, 2787.	12.8	161
5	Notum Is Required for Neural and Head Induction via Wnt Deacylation, Oxidation, and Inactivation. <i>Developmental Cell</i> , 2015, 32, 719-730.	7.0	155
6	Structure and functional properties of Norrin mimic Wnt for signalling with Frizzled4, Lrp5/6, and proteoglycan. <i>ELife</i> , 2015, 4, .	6.0	90
7	Crystallographic Evidence for a Domain Motion in Rat Nucleoside Triphosphate Diphosphohydrolase (NTPDase) 1. <i>Journal of Molecular Biology</i> , 2012, 415, 288-306.	4.2	73
8	Structural insight into signal conversion and inactivation by NTPDase2 in purinergic signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6882-6887.	7.1	71
9	Crystallographic Snapshots along the Reaction Pathway of Nucleoside Triphosphate Diphosphohydrolases. <i>Structure</i> , 2013, 21, 1460-1475.	3.3	44
10	Crystal structure of R-spondin 2 in complex with the ectodomains of its receptors LGR5 and ZNRF3. <i>Journal of Structural Biology</i> , 2015, 191, 149-155.	2.8	43
11	ZNRF3/RNF43 " A direct linkage of extracellular recognition and E3 ligase activity to modulate cell surface signalling. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 118, 112-118.	2.9	40
12	Characterization of Rat NTPDase1, -2, and -3 Ectodomains Refolded from Bacterial Inclusion Bodies. <i>Biochemistry</i> , 2007, 46, 11945-11956.	2.5	34
13	The pro-form of BMP-2 interferes with BMP-2 signalling by competing with BMP-2 for IA receptor binding. <i>FEBS Journal</i> , 2009, 276, 6386-6398.	4.7	34
14	Structure of the Dual-Mode Wnt Regulator Kremen1 and Insight into Ternary Complex Formation with LRP6 and Dickkopf. <i>Structure</i> , 2016, 24, 1599-1605.	3.3	32
15	Structures of <i>Legionella pneumophila</i> NTPDase1 in complex with polyoxometallates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1147-1154.	2.5	25
16	Crystal structure of NTPDase2 in complex with the sulfoanthraquinone inhibitor PSB-071. <i>Journal of Structural Biology</i> , 2014, 185, 336-341.	2.8	25
17	Structural Insight into Activation Mechanism of <i>Toxoplasma gondii</i> Nucleoside Triphosphate Diphosphohydrolases by Disulfide Reduction*. <i>Journal of Biological Chemistry</i> , 2012, 287, 3051-3066.	3.4	21
18	The Biochemical Properties of the Arabidopsis Ecto-Nucleoside Triphosphate Diphosphohydrolase AtAPY1 Contradict a Direct Role in Purinergic Signaling. <i>PLoS ONE</i> , 2015, 10, e0115832.	2.5	14

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19	Contribution of the two domains of <i>E. coli</i> 5'-nucleotidase to substrate specificity and catalysis. FEBS Letters, 2013, 587, 460-466.	2.8	13
20	New crystal forms of NTPDase1 from the bacterium <i>Legionella pneumophila</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 257-262.	0.7	13
21	Crystal structure and substrate binding mode of ectonucleotide phosphodiesterase/pyrophosphatase-3 (NPP3). Scientific Reports, 2018, 8, 10874.	3.3	9
22	Crystallization and preliminary X-ray analysis of the open form of human ecto-5'-nucleotidase (CD73). Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1545-1549.	0.7	6
23	The ATP/ADP Substrate Specificity Switch between <i>Toxoplasma gondii</i> NTPDase1 and NTPDase3 is Caused by an Altered Mode of Binding of the Substrate Base. ChemBioChem, 2013, 14, 2292-2300.	2.6	5
24	Development of a robust crystallization platform for immune receptor TREM2 using a crystallization chaperone strategy. Protein Expression and Purification, 2021, 179, 105796.	1.3	4
25	Crystallization of ectonucleotide phosphodiesterase/pyrophosphatase-3 and orientation of the SMB domains in the full-length ectodomain. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 696-703.	0.8	2