Thomas Ve

List of Publications by Year
in descending order

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47 papers	2,852 citations	304743 22 h-index	214800 47 g-index
52 all docs	52 docs citations	52 times ranked	3391 citing authors

#	Article	IF	Citations
1	Crystal structure of the Toll/interleukinâ€1 receptor (TIR) domain of ILâ€1R10 provides structural insights into TIR domain signalling. FEBS Letters, 2022, 596, 886-897.	2.8	5
2	Structural basis of SARM1 activation, substrate recognition, and inhibition by small molecules. Molecular Cell, 2022, 82, 1643-1659.e10.	9.7	66
3	Structural and biochemical characterization of Acinetobacter baumannii ZnuA. Journal of Inorganic Biochemistry, 2022, 231, 111787.	3.5	3
4	Ucl fimbriae regulation and glycan receptor specificity contribute to gut colonisation by extra-intestinal pathogenic Escherichia coli. PLoS Pathogens, 2022, 18, e1010582.	4.7	6
5	SARM1 is a metabolic sensor activated by an increased NMN/NAD+ ratio to trigger axon degeneration. Neuron, 2021, 109, 1118-1136.e11.	8.1	168
6	MyD88 TIR domain higher-order assembly interactions revealed by microcrystal electron diffraction and serial femtosecond crystallography. Nature Communications, 2021, 12, 2578.	12.8	55
7	Crystal structure determination of the armadillo repeat domain of Drosophila SARM1 using MIRAS phasing. Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 364-373.	0.8	2
8	Nicotinic acid mononucleotide is an allosteric SARM1 inhibitor promoting axonal protection. Experimental Neurology, 2021, 345, 113842.	4.1	24
9	Neurotoxin-mediated potent activation of the axon degeneration regulator SARM1. ELife, 2021, 10, .	6.0	22
10	Regulation of signaling by cooperative assembly formation in mammalian innate immunity signalosomes by molecular mimics. Seminars in Cell and Developmental Biology, 2020, 99, 96-114.	5.0	16
11	NAD ⁺ cleavage activity by animal and plant TIR domains in cell death pathways. Science, 2019, 365, 793-799.	12.6	357
12	Cryo-EM structures of the pore-forming A subunit from the Yersinia entomophaga ABC toxin. Nature Communications, 2019, 10, 1952.	12.8	40
13	The Single Nucleotide Polymorphism Mal-D96N Mice Provide New Insights into Functionality of Mal in TLR Immune Responses. Journal of Immunology, 2019, 202, 2384-2396.	0.8	2
14	Death, TIR, and RHIM: Self-assembling domains involved in innate immunity and cell-death signaling. Journal of Leukocyte Biology, 2019, 105, 363-375.	3.3	43
15	A Sulfonozanamivir Analogue Has Potent Antiâ€influenza Virus Activity. ChemMedChem, 2018, 13, 785-789.	3.2	12
16	Structural Insights into Human Parainfluenza Virus 3 Hemagglutininâ€“Neuraminidase Using Unsaturated 3-N-Substituted Sialic Acids as Probes. ACS Chemical Biology, 2018, 13, 1544-1550.	3.4	10
17	Crystal structure of the Melampsora lini effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. Molecular Plant Pathology, 2018, 19, 1196-1209.	4.2	24
18	Pathological mutations differentially affect the self-assembly and polymerisation of the innate immune system signalling adaptor molecule MyD88. BMC Biology, 2018, 16, 149.	3.8	22

#	Article	IF	Citations
19	Megahertz serial crystallography. Nature Communications, 2018, 9, 4025.	12.8	147
20	Multiple functional self-association interfaces in plant TIR domains. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2046-E2052.	7.1	103
21	Towards the structure of the TIR-domain signalosome. Current Opinion in Structural Biology, 2017, 43, 122-130.	5.7	64
22	The molecular mechanisms of signaling by cooperative assembly formation in innate immunity pathways. Molecular Immunology, 2017, 86, 23-37.	2.2	95
23	Blood Group Antigen Recognition via the Group A Streptococcal M Protein Mediates Host Colonization. MBio, 2017, 8, .	4.1	25
24	Solution structure of the TLR adaptor MAL/TIRAP reveals an intact BB loop and supports MAL Cys91 glutathionylation for signaling. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6480-E6489.	7.1	33
25	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. Nature Structural and Molecular Biology, 2017, 24, 743-751.	8.2	140
26	Protein crystal screening and characterization for serial femtosecond nanocrystallography. Scientific Reports, 2016, 6, 25345.	3.3	22
27	A linker strategy for the production and crystallization of Toll/interleukin-1 receptor/resistance protein domain complexes. Protein Engineering, Design and Selection, 2015, 28, 137-145.	2.1	3
28	Structure and function of Toll/interleukin-1 receptor/resistance protein (TIR) domains. Apoptosis: an International Journal on Programmed Cell Death, 2015, 20, 250-261.	4.9	123
29	Fusion-protein-assisted protein crystallization. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 861-869.	0.8	23
30	Recombinant production of functional full-length and truncated human TRAM/TICAM-2 adaptor protein involved in Toll-like receptor and interferon signaling. Protein Expression and Purification, 2015, 106, 31-40.	1.3	3
31	CorA Is a Copper Repressible Surface-Associated Copper(I)-Binding Protein Produced in Methylomicrobium album BG8. PLoS ONE, 2014, 9, e87750.	2.5	18
32	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. Science, 2014, 344, 299-303.	12.6	300
33	Mechanism of Bacterial Interference with TLR4 Signaling by Brucella Toll/Interleukin-1 Receptor Domain-containing Protein TcpB. Journal of Biological Chemistry, 2014, 289, 654-668.	3.4	73
34	The TLR signaling adaptor TRAM interacts with TRAF6 to mediate activation of the inflammatory response by TLR4. Journal of Leukocyte Biology, 2014, 96, 427-436.	3.3	38
35	Crystallization and X-ray diffraction analysis of the N-terminal domain of the Toll-like receptor signalling adaptor protein TRIF/TICAM-1. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 766-770.	0.7	4
36	The TLR signalling adaptor TRIF/TICAM-1 has an N-terminal helical domain with structural similarity to IFIT proteins. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2420-2430.	2.5	13

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37	Crystallization and preliminary X-ray diffraction analyses of the TIR domains of three TIRâ€“NBâ€“LRR proteins that are involved in disease resistance inArabidopsis thaliana. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1275-1280.	0.7	5
38	Structures of the flax-rust effector AvrM reveal insights into the molecular basis of plant-cell entry and effector-triggered immunity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17594-17599.	7.1	75
39	Cloning, expression, purification, crystallization and preliminary X-ray crystallographic analysis of the TIR domain from theBrucella melitensisTIR-domain-containing protein TcpB. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1167-1170.	0.7	2
40	Intramolecular Interaction Influences Binding of the Flax L5 and L6 Resistance Proteins to their AvrL567 Ligands. PLoS Pathogens, 2012, 8, e1003004.	4.7	93
41	Adaptors in Toll-Like Receptor Signaling and their Potential as Therapeutic Targets. Current Drug Targets, 2012, 13, 1360-1374.	2.1	68
42	The Methylococcus capsulatus (Bath) Secreted Protein, MopE*, Binds Both Reduced and Oxidized Copper. PLoS ONE, 2012, 7, e43146.	2.5	22
43	Structural and Functional Analysis of a Plant Resistance Protein TIR Domain Reveals Interfaces for Self-Association, Signaling, and Autoregulation. Cell Host and Microbe, 2011, 9, 200-211.	11.0	301
44	Crystallization, X-ray diffraction analysis and preliminary structure determination of the TIR domain from the flax resistance protein L6. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 237-240.	0.7	3
45	Crystallization and X-ray diffraction analysis of the C-terminal domain of the flax rust effector protein AvrM. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1603-1607.	0.7	4
46	The AvrM Effector from Flax Rust Has a Structured C-Terminal Domain and Interacts Directly with the M Resistance Protein. Molecular Plant-Microbe Interactions, 2010, 23, 49-57.	2.6	113
47	An Oxidized Tryptophan Facilitates Copper Binding in Methylococcus capsulatus-secreted Protein MopE. Journal of Biological Chemistry, 2008, 283, 13897-13904.	3.4	45