Thomas S Walter

List of Publications by Year
in descending order

49 papers	6,137 citations	147801 31 h-index	214800 47 g-index
52 all docs	52 docs citations	52 times ranked	10771 citing authors

#	Article	IF	Citations
1	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. Cell, 2021, 184, 2348-2361.e6.	28.9	936
2	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. Cell, 2021, 184, 4220-4236.e13.	28.9	630
3	Antibody evasion by the P.1 strain of SARS-CoV-2. Cell, 2021, 184, 2939-2954.e9.	28.9	519
4	Lysine Methylation as a Routine Rescue Strategy for Protein Crystallization. Structure, 2006, 14, 1617-1622.	3.3	483
5	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. Cell, 2021, 184, 2201-2211.e7.	28.9	442
6	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. Nature Structural and Molecular Biology, 2012, 19, 424-429.	8.2	347
7	The antigenic anatomy of SARS-CoV-2 receptor binding domain. Cell, 2021, 184, 2183-2200.e22.	28.9	331
8	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 651-657.	2.5	234
9	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1426-1431.	2.5	228
10	Picornavirus uncoating intermediate captured in atomic detail. Nature Communications, 2013, 4, 1929.	12.8	148
11	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. Nature Communications, 2017, 8, 14.	12.8	117
12	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. Journal of Virology, 2009, 83, 12895-12906.	3.4	115
13	In situ macromolecular crystallography using microbeams. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 592-600.	2.5	113
14	High-speed fixed-target serial virus crystallography. Nature Methods, 2017, 14, 805-810.	19.0	106
15	Structural and Functional Insights of RANKLâ€“RANK Interaction and Signaling. Journal of Immunology, 2010, 184, 6910-6919.	0.8	103
16	A plate-based high-throughput assay for virus stability and vaccine formulation. Journal of Virological Methods, 2012, 185, 166-170.	2.1	94
17	A procedure for setting up high-throughput nanolitre crystallization experiments. I. Protocol design and validation. Journal of Applied Crystallography, 2003, 36, 308-314.	4.5	91
18	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. Nature Structural and Molecular Biology, 2014, 21, 282-288.	8.2	88

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19	The crystal structure of human dopamine Î²-hydroxylase at 2.9 Ã... resolution. Science Advances, 2016, 2, e1500980.	10.3	80
20	High-resolution structure of the catalytic region of MICAL (molecule interacting with CasL), a multidomain flavoenzyme-signaling molecule. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16836-16841.	7.1	75
21	The Crystal Structure and Mutational Binding Analysis of the Extracellular Domain of the Platelet-activating Receptor CLEC-2. Journal of Biological Chemistry, 2007, 282, 3165-3172.	3.4	64
22	Equine Rhinitis A Virus and Its Low pH Empty Particle: Clues Towards an Aphthovirus Entry Mechanism?. PLoS Pathogens, 2009, 5, e1000620.	4.7	64
23	Pathogen-derived HLA-E bound epitopes reveal broad primary anchor pocket tolerability and conformationally malleable peptide binding. Nature Communications, 2018, 9, 3137.	12.8	57
24	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25057-25067.	7.1	53
25	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. Journal of General Virology, 2007, 88, 2228-2236.	2.9	52
26	SPINE high-throughput crystallization, crystal imaging and recognition techniques: current state, performance analysis, new technologies and future aspects. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1137-1149.	2.5	51
27	Plate Tectonics of Virus Shell Assembly and Reorganization in Phage Î¦8, a Distant Relative of Mammalian Reoviruses. Structure, 2013, 21, 1384-1395.	3.3	45
28	A procedure for setting up high-throughput nanolitre crystallization experiments. II. Crystallization results. Journal of Applied Crystallography, 2003, 36, 315-318.	4.5	43
29	Benefits of Automated Crystallization Plate Tracking, Imaging, and Analysis. Structure, 2005, 13, 175-182.	3.3	42
30	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 770-775.	7.1	42
31	The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. Nature Communications, 2019, 10, 846.	12.8	37
32	Structure of human Aichi virus and implications for receptor binding. Nature Microbiology, 2016, 1, 16150.	13.3	36
33	Semi-automated microseeding of nanolitre crystallization experiments. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 14-18.	0.7	31
34	The Human Otubain2-Ubiquitin Structure Provides Insights into the Cleavage Specificity of Poly-Ubiquitin-Linkages. PLoS ONE, 2015, 10, e0115344.	2.5	31
35	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Ã... resolution. Protein Science, 2007, 16, 2294-2300.	7.6	30
36	Application of high-throughput technologies to a structural proteomics-type analysis ofBacillus anthracis. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1267-1275.	2.5	24

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37	Crystal structure of a 3â€oxoacylâ€(acylcarrier protein) reductase (BA3989) from Bacillus anthracis at 2.4â€Å... resolution. Proteins: Structure, Function and Bioinformatics, 2008, 70, 562-567.	2.6	22
38	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. Nature Communications, 2019, 10, 1456.	12.8	17
39	Structures of an alanine racemase fromBacillus anthracis(BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (<scp>L</scp>-Ala-P). Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 327-333.	0.7	16
40	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. Communications Biology, 2020, 3, 9.	4.4	16
41	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. Scientific Reports, 2015, 5, 14150.	3.3	14
42	Crystal structure of equine rhinitis A virus in complex with its sialic acid receptor. Journal of General Virology, 2010, 91, 1971-1977.	2.9	13
43	The structure of NMB1585, a MarR-family regulator fromNeisseria meningitidis. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 204-209.	0.7	9
44	Sample preparation and mass-spectrometric characterization of crystal-derived protein samples. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 643-645.	2.5	5
45	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. Structure, 2004, 12, 341-353.	3.3	5
46	Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 597-600.	0.7	3
47	Bacteriophage PRD1 as a nanoscaffold for drug loading. Nanoscale, 2021, 13, 19875-19883.	5.6	3
48	Reduced Neutralization of SARS-CoV-2 B.1.1.7 Variant from Naturally Acquired and Vaccine Induced Antibody Immunity. SSRN Electronic Journal, 0, , .	0.4	2
49	Sample Preparation and Data Collection for High-Speed Fixed-Target Serial Femtosecond Crystallography. Protocol Exchange, 0, , .	0.3	1