

Thomas S Walter

List of Publications by Year in descending order

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49
papers

6,137
citations

147801

31
h-index

214800

47
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52
all docs

52
docs citations

52
times ranked

10771
citing authors

#	ARTICLE	IF	CITATIONS
1	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021, 184, 2183-2200.e22.	28.9	331
2	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021, 184, 2348-2361.e6.	28.9	936
3	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021, 184, 2201-2211.e7.	28.9	442
4	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021, 184, 2939-2954.e9.	28.9	519
5	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021, 184, 4220-4236.e13.	28.9	630
6	Bacteriophage PRD1 as a nanoscaffold for drug loading. <i>Nanoscale</i> , 2021, 13, 19875-19883.	5.6	3
7	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. <i>Communications Biology</i> , 2020, 3, 9.	4.4	16
8	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. <i>Nature Communications</i> , 2019, 10, 1456.	12.8	17
9	The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. <i>Nature Communications</i> , 2019, 10, 846.	12.8	37
10	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25057-25067.	7.1	53
11	Pathogen-derived HLA-E bound epitopes reveal broad primary anchor pocket tolerability and conformationally malleable peptide binding. <i>Nature Communications</i> , 2018, 9, 3137.	12.8	57
12	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 770-775.	7.1	42
13	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017, 8, 14.	12.8	117
14	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017, 14, 805-810.	19.0	106
15	The crystal structure of human dopamine β -hydroxylase at 2.9 Å... resolution. <i>Science Advances</i> , 2016, 2, e1500980.	10.3	80
16	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016, 1, 16150.	18.3	36
17	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. <i>Scientific Reports</i> , 2015, 5, 14150.	3.3	14
18	The Human Otubain2-Ubiquitin Structure Provides Insights into the Cleavage Specificity of Poly-Ubiquitin-Linkages. <i>PLoS ONE</i> , 2015, 10, e0115344.	2.5	31

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19	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 282-288.	8.2	88
20	Plate Tectonics of Virus Shell Assembly and Reorganization in Phage ϕ 8, a Distant Relative of Mammalian Reoviruses. <i>Structure</i> , 2013, 21, 1384-1395.	3.3	45
21	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013, 4, 1929.	12.8	148
22	A plate-based high-throughput assay for virus stability and vaccine formulation. <i>Journal of Virological Methods</i> , 2012, 185, 166-170.	2.1	94
23	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 424-429.	8.2	347
24	<i>In situ</i> macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 592-600.	2.5	113
25	Structural and Functional Insights of RANKL-RANK Interaction and Signaling. <i>Journal of Immunology</i> , 2010, 184, 6910-6919.	0.8	103
26	Crystal structure of equine rhinitis A virus in complex with its sialic acid receptor. <i>Journal of General Virology</i> , 2010, 91, 1971-1977.	2.9	13
27	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. <i>Journal of Virology</i> , 2009, 83, 12895-12906.	3.4	115
28	Equine Rhinitis A Virus and Its Low pH Empty Particle: Clues Towards an Aphthovirus Entry Mechanism?. <i>PLoS Pathogens</i> , 2009, 5, e1000620.	4.7	64
29	The structure of NMB1585, a MarR-family regulator from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 204-209.	0.7	9
30	Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 597-600.	0.7	3
31	Crystal structure of a 3-oxoacyl-(acylcarrier protein) reductase (BA3989) from <i>Bacillus anthracis</i> at 2.4 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 562-567.	2.6	22
32	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 14-18.	0.7	31
33	Structures of an alanine racemase from <i>Bacillus anthracis</i> (BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (Ala-P). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 327-333.	0.7	16
34	The Crystal Structure and Mutational Binding Analysis of the Extracellular Domain of the Platelet-activating Receptor CLEC-2. <i>Journal of Biological Chemistry</i> , 2007, 282, 3165-3172.	3.4	64
35	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. <i>Journal of General Virology</i> , 2007, 88, 2228-2236.	2.9	52
36	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Å resolution. <i>Protein Science</i> , 2007, 16, 2294-2300.	7.6	30

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37	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
38	Application of high-throughput technologies to a structural proteomics-type analysis of Bacillus anthracis. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1267-1275.	2.5	24
39	Lysine Methylation as a Routine Rescue Strategy for Protein Crystallization. Structure, 2006, 14, 1617-1622.	3.3	483
40	Benefits of Automated Crystallization Plate Tracking, Imaging, and Analysis. Structure, 2005, 13, 175-182.	3.3	42
41	Sample preparation and mass-spectrometric characterization of crystal-derived protein samples. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 643-645.	2.5	5
42	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
43	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
44	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
45	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. Structure, 2004, 12, 341-353.	3.3	5
46	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
47	A procedure for setting up high-throughput nanolitre crystallization experiments. II. Crystallization results. Journal of Applied Crystallography, 2003, 36, 315-318.	4.5	43
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