

Wim P Burmeister

List of Publications by Year in descending order

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33
papers

1,396
citations

331670

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395702

33
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docs citations

33
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	The crystal structures of <i>Sinapis alba</i> myrosinase and a covalent glycosylâ€ enzyme intermediate provide insights into the substrate recognition and active-site machinery of an S-glycosidase. <i>Structure</i> , 1997, 5, 663-676.	3.3	280
2	Crystal Structure of Species D Adenovirus Fiber Knobs and Their Sialic Acid Binding Sites. <i>Journal of Virology</i> , 2004, 78, 7727-7736.	3.4	156
3	Crystal structure of a monocotyledon (maize ZMGl1) Î ² -glucosidase and a model of its complex with p-nitrophenyl Î ² -d-thioglucoside. <i>Biochemical Journal</i> , 2001, 354, 37-46.	3.7	107
4	Crystal structure of a monocotyledon (maize ZMGl1) Î ² -glucosidase and a model of its complex with p-nitrophenyl Î ² -d-thioglucoside. <i>Biochemical Journal</i> , 2001, 354, 37.	3.7	76
5	EBV Lytic-Phase Protein BGLF5 Contributes to TLR9 Downregulation during Productive Infection. <i>Journal of Immunology</i> , 2011, 186, 1694-1702.	0.8	76
6	Structure of the Fiber Head of Ad3, a Non-CAR-Binding Serotype of Adenovirus. <i>Virology</i> , 2001, 285, 302-312.	2.4	62
7	Crystal structure at 1.1Å... resolution of an insect myrosinase from <i>Brevicoryne brassicae</i> shows its close relationship to Î ² -glucosidases. <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 1311-1320.	2.7	58
8	The Monomeric dUTPase from Epstein-Barr Virus Mimics Trimeric dUTPases. <i>Structure</i> , 2005, 13, 1299-1310.	3.3	49
9	A Bridge Crosses the Active-Site Canyon of the Epsteinâ€ Barr Virus Nuclease with DNase and RNase Activities. <i>Journal of Molecular Biology</i> , 2009, 391, 717-728.	4.2	46
10	Structure of RavA MoxR AAA+ protein reveals the design principles of a molecular cage modulating the inducible lysine decarboxylase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22499-22504.	7.1	45
11	Structure of the Epstein-Barr Virus Oncogene BARF1. <i>Journal of Molecular Biology</i> , 2006, 359, 667-678.	4.2	43
12	The Crystal Structure of the Epsteinâ€ Barr Virus Protease Shows Rearrangement of the Processed C Terminus. <i>Journal of Molecular Biology</i> , 2002, 324, 89-103.	4.2	39
13	Allosteric competitive inactivation of hematopoietic CSF-1 signaling by the viral decoy receptor BARF1. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 938-947.	8.2	39
14	Low-Resolution Structure of Vaccinia Virus DNA Replication Machinery. <i>Journal of Virology</i> , 2013, 87, 1679-1689.	3.4	37
15	The vaccinia virus DNA polymerase structure provides insights into the mode of processivity factor binding. <i>Nature Communications</i> , 2017, 8, 1455.	12.8	31
16	The â€ Bridgeâ€ in the Epstein-Barr Virus Alkaline Exonuclease Protein BGLF5 Contributes to Shutoff Activity during Productive Infection. <i>Journal of Virology</i> , 2012, 86, 9175-9187.	3.4	28
17	The Flexible Motif V of Epstein-Barr Virus Deoxyuridine 5â€ ² -Triphosphate Pyrophosphatase Is Essential for Catalysis. <i>Journal of Biological Chemistry</i> , 2009, 284, 25280-25289.	3.4	27
18	Crystal Structure of the Vaccinia Virus DNA Polymerase Holoenzyme Subunit D4 in Complex with the A20 N-Terminal Domain. <i>PLoS Pathogens</i> , 2014, 10, e1003978.	4.7	27

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19	The glucosinolateâ€“myrosinase system. New insights into enzymeâ€“substrate interactions by use of simplified inhibitors. <i>Organic and Biomolecular Chemistry</i> , 2005, 3, 1872.	2.8	25
20	Crystal Structure of the Vaccinia Virus Uracil-DNA Glycosylase in Complex with DNA. <i>Journal of Biological Chemistry</i> , 2015, 290, 17923-17934.	3.4	24
21	CryoEM structure of adenovirus type 3 fibre with desmoglein 2 shows an unusual mode of receptor engagement. <i>Nature Communications</i> , 2019, 10, 1181.	12.8	24
22	Domain Organization of Vaccinia Virus Helicase-Primase D5. <i>Journal of Virology</i> , 2016, 90, 4604-4613.	3.4	22
23	Identification of new interacting partners of the shuttling protein ubinuclein (Ubn-1). <i>Experimental Cell Research</i> , 2012, 318, 509-520.	2.6	17
24	Solution Structure of the C-terminal Domain of A20, the Missing Brick for the Characterization of the Interface between Vaccinia Virus DNA Polymerase and its Processivity Factor. <i>Journal of Molecular Biology</i> , 2021, 433, 167009.	4.2	14
25	Structure Determination of Feline Calicivirus Virus-Like Particles in the Context of a Pseudo-Octahedral Arrangement. <i>PLoS ONE</i> , 2015, 10, e0119289.	2.5	11
26	Interaction of Ubinuclein-1, a nuclear and adhesion junction protein, with the 14-3-3 epsilon protein in epithelial cells: Implication of the PKA pathway. <i>European Journal of Cell Biology</i> , 2013, 92, 105-111.	3.6	10
27	Structural analysis of point mutations at the <i>Vaccinia virus</i> A20/D4 interface. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 687-691.	0.8	7
28	Kinetics, inhibition and oligomerization of Epstein-Barr virus protease. <i>FEBS Letters</i> , 2006, 580, 6570-6578.	2.8	5
29	Production and characterisation of Epsteinâ€“Barr virus helicaseâ€“primase complex and its accessory protein BBLF2/3. <i>Virus Genes</i> , 2015, 51, 171-181.	1.6	4
30	Inhibition of Epsteinâ€“Barr virus replication by small interfering RNA targeting the Epsteinâ€“Barr virus protease gene. <i>Antiviral Therapy</i> , 2009, 14, 655-662.	1.0	3
31	A micromolar O-sulfated thiohydroximate inhibitor bound to plant myrosinase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 152-155.	0.7	2
32	Intermediate-resolution crystal structure of the human adenovirus B serotype 3 fibre knob in complex with the EC2-EC3 fragment of desmogleinâˆ2. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 750-757.	0.8	1
33	Structure des enzymes de rÃ©plication du virus Epstein-Barr. <i>Virologie</i> , 2012, 16, 185-198.	0.1	1