

David A Jacques

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,490
citations

394286

19
h-index

345118

36
g-index

44
all docs

44
docs citations

44
times ranked

3516
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into HIV uncoating from single-particle imaging techniques. <i>Biophysical Reviews</i> , 2022, 14, 23-32.	1.5	11
2	Target-induced clustering activates Trim-Away of pathogens and proteins. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 278-289.	3.6	44
3	A lysine ring in HIV capsid pores coordinates IP6 to drive mature capsid assembly. <i>PLoS Pathogens</i> , 2021, 17, e1009164.	2.1	32
4	Rapid HIV-1 Capsid Interaction Screening Using Fluorescence Fluctuation Spectroscopy. <i>Analytical Chemistry</i> , 2021, 93, 3786-3793.	3.2	4
5	SARS-CoV-2 proteases PLpro and 3CLpro cleave IRF3 and critical modulators of inflammatory pathways (NLRP12 and TAB1): implications for disease presentation across species. <i>Emerging Microbes and Infections</i> , 2021, 10, 178-195.	3.0	178
6	Self-Assembly of Fluorescent HIV Capsid Spheres for Detection of Capsid Binders. <i>Langmuir</i> , 2020, 36, 3624-3632.	1.6	11
7	MxB sensitivity of HIV-1 is determined by a highly variable and dynamic capsid surface. <i>ELife</i> , 2020, 9, .	2.8	14
8	Fluorescence Biosensor for Real-Time Interaction Dynamics of Host Proteins with HIV-1 Capsid Tubes. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 34586-34594.	4.0	18
9	The Human Immunodeficiency Virus Capsid Is More Than Just a Genome Package. <i>Annual Review of Virology</i> , 2018, 5, 209-225.	3.0	15
10	Kinetics of HIV-1 capsid uncoating revealed by single-molecule analysis. <i>ELife</i> , 2018, 7, .	2.8	91
11	IP6 is an HIV pocket factor that prevents capsid collapse and promotes DNA synthesis. <i>ELife</i> , 2018, 7, .	2.8	131
12	Interactions between LHX3- and ISL1-family LIM-homeodomain transcription factors are conserved in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017, 7, 4579.	1.6	5
13	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 710-728.	1.1	205
14	HIV-1 uses dynamic capsid pores to import nucleotides and fuel encapsidated DNA synthesis. <i>Nature</i> , 2016, 536, 349-353.	13.7	190
15	<sc>GATA</sc>1 directly mediates interactions with closely spaced pseudopalindromic but not distantly spaced double <sc>GATA</sc> sites on <sc>DNA</sc>. <i>Protein Science</i> , 2015, 24, 1649-1659.	3.1	10
16	Exploring the structure of biological macromolecules in solution using Quokka, the small angle neutron scattering instrument, at ANSTO. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2015, 798, 44-51.	0.7	4
17	The structure of haemoglobin bound to the haemoglobin receptor IsdH from <i>Staphylococcus aureus</i> shows disruption of the native α -globin haem pocket. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1295-1306.	2.5	19
18	Host Cofactors and Pharmacologic Ligands Share an Essential Interface in HIV-1 Capsid That Is Lost upon Disassembly. <i>PLoS Pathogens</i> , 2014, 10, e1004459.	2.1	238

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19	Structure of the Hemoglobin-IsoD Complex Reveals the Molecular Basis of Iron Capture by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6728-6738.	1.6	58
20	The structure of α -haemoglobin in complex with a haemoglobin-binding domain from <i>Staphylococcus aureus</i> reveals the elusive α -haemoglobin dimerization interface. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1032-1037.	0.4	6
21	Intracellular immunity: finding the enemy within—how cells recognize and respond to intracellular pathogens. <i>Journal of Leukocyte Biology</i> , 2014, 96, 233-244.	1.5	34
22	HIV-1 evades innate immune recognition through specific cofactor recruitment. <i>Nature</i> , 2013, 503, 402-405.	13.7	396
23	New Insights into DNA Recognition by Zinc Fingers Revealed by Structural Analysis of the Oncoprotein ZNF217. <i>Journal of Biological Chemistry</i> , 2013, 288, 10616-10627.	1.6	36
24	A Structural Basis for the Regulation of the LIM-Homeodomain Protein Islet 1 (Isl1) by Intra- and Intermolecular Interactions. <i>Journal of Biological Chemistry</i> , 2013, 288, 21924-21935.	1.6	21
25	Reliable structural interpretation of small-angle scattering data from bio-molecules in solution - the importance of quality control and a standard reporting framework. <i>BMC Structural Biology</i> , 2012, 12, 9.	2.3	17
26	Crystallization and diffraction of an Isl1-Ldb1 complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1398-1401.	0.7	1
27	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 620-626.	2.5	125
28	A Novel Structure of an Antikinase and its Inhibitor. <i>Journal of Molecular Biology</i> , 2011, 405, 214-226.	2.0	21
29	The structure of TTHA0988 from <i>Thermus thermophilus</i> , a Kipl—KipA homologue incorrectly annotated as an allophanate hydrolase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 105-111.	2.5	7
30	Structural Basis for Hemoglobin Capture by <i>Staphylococcus aureus</i> Cell-surface Protein, IsoD. <i>Journal of Biological Chemistry</i> , 2011, 286, 38439-38447.	1.6	50
31	¹ H, ¹³ C and ¹⁵ N backbone and side chain resonance assignments of the N-terminal domain of the histidine kinase inhibitor Kipl from <i>Bacillus subtilis</i> . <i>Biomolecular NMR Assignments</i> , 2010, 4, 167-169.	0.4	1
32	Small-angle scattering for structural biology—Expanding the frontier while avoiding the pitfalls. <i>Protein Science</i> , 2010, 19, 642-657.	3.1	341
33	Structure of the sporulation histidine kinase inhibitor Sda from <i>Bacillus subtilis</i> and insights into its solution state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 574-581.	2.5	11
34	Histidine Kinase Regulation by a Cyclophilin-like Inhibitor. <i>Journal of Molecular Biology</i> , 2008, 384, 422-435.	2.0	29
35	The Structure of the KinA-Sda Complex Suggests an Allosteric Mechanism of Histidine Kinase Inhibition. <i>Journal of Molecular Biology</i> , 2007, 368, 407-420.	2.0	77
36	Encapsulation and controlled release of biomolecules from silica microparticles. <i>Journal of Materials Chemistry</i> , 2006, 16, 4494.	6.7	25