

Michelle A Dunstone

List of Publications by Year in descending order

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47
papers

3,738
citations

159585

30
h-index

223800

46
g-index

51
all docs

51
docs citations

51
times ranked

4592
citing authors

#	ARTICLE	IF	CITATIONS
1	Going full circle: Determining the structures of complement component 9. <i>Methods in Enzymology</i> , 2021, 649, 103-123.	1.0	4
2	Branching out the aerolysin, ETX/MTX-2 and Toxin_10 family of pore forming proteins. <i>Journal of Invertebrate Pathology</i> , 2021, 186, 107570.	3.2	9
3	Ancient but Not Forgotten: New Insights Into MPEG1, a Macrophage Perforin-Like Immune Effector. <i>Frontiers in Immunology</i> , 2020, 11, 581906.	4.8	17
4	Three-Dimensional Chemical Mapping of a Single Protein in the Hydrated State with Atom Probe Tomography. <i>Analytical Chemistry</i> , 2020, 92, 5168-5177.	6.5	15
5	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <i>Nature Communications</i> , 2019, 10, 4288.	12.8	65
6	The first transmembrane region of complement component-9 acts as a brake on its self-assembly. <i>Nature Communications</i> , 2018, 9, 3266.	12.8	56
7	Evaluation of Serum Glycoprotein Biomarker Candidates for Detection of Esophageal Adenocarcinoma and Surveillance of Barrett's Esophagus. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2324-2334.	3.8	25
8	Real-time visualization of perforin nanopore assembly. <i>Nature Nanotechnology</i> , 2017, 12, 467-473.	31.5	88
9	Cryo-electron tomography: an ideal method to study membrane-associated proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160210.	4.0	16
10	The mystery behind membrane insertion: a review of the complement membrane attack complex. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160221.	4.0	132
11	The emerging role of pore forming proteins in cell biology and development. <i>Seminars in Cell and Developmental Biology</i> , 2017, 72, 99-100.	5.0	0
12	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	12.8	112
13	Giant MACPF/CDC pore forming toxins: A class of their own. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 475-486.	2.6	61
14	Stonefish toxin defines an ancient branch of the perforin-like superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15360-15365.	7.1	69
15	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	5.6	114
16	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. <i>PLoS Computational Biology</i> , 2014, 10, e1003791.	3.2	33
17	The Perforin Pore Facilitates the Delivery of Cationic Cargos. <i>Journal of Biological Chemistry</i> , 2014, 289, 9172-9181.	3.4	30
18	The Cellular Redox Environment Alters Antigen Presentation. <i>Journal of Biological Chemistry</i> , 2014, 289, 27979-27991.	3.4	52

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19	Stepwise visualization of membrane pore formation by suliyisin, a bacterial cholesterol-dependent cytolysin. <i>ELife</i> , 2014, 3, e04247.	6.0	145
20	Torquing about pores. <i>Nature Chemical Biology</i> , 2013, 9, 605-606.	8.0	1
21	Predicting giant transmembrane β -barrel architecture. <i>Bioinformatics</i> , 2012, 28, 1299-1302.	4.1	25
22	Perforin evolved from a gene duplication of MPEG1, followed by a complex pattern of gene gain and loss within Euteleostomi. <i>BMC Evolutionary Biology</i> , 2012, 12, 59.	3.2	43
23	Packing a punch: the mechanism of pore formation by cholesterol dependent cytolysins and membrane attack complex/perforin-like proteins. <i>Current Opinion in Structural Biology</i> , 2012, 22, 342-349.	5.7	95
24	Screening of 71 <i>P. multocida</i> Proteins for Protective Efficacy in a Fowl Cholera Infection Model and Characterization of the Protective Antigen PlpE. <i>PLoS ONE</i> , 2012, 7, e39973.	2.5	32
25	The structural basis for membrane binding and pore formation by lymphocyte perforin. <i>Nature</i> , 2010, 468, 447-451.	27.8	364
26	Perforin: structure, function, and role in human immunopathology. <i>Immunological Reviews</i> , 2010, 235, 35-54.	6.0	171
27	The structure and function of mammalian membrane-attack complex/perforin-like proteins. <i>Tissue Antigens</i> , 2010, 76, 341-351.	1.0	63
28	Constraints within major histocompatibility complex class I restricted peptides: Presentation and consequences for T-cell recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5534-5539.	7.1	58
29	The Type III Effectors NleE and NleB from Enteropathogenic <i>E. coli</i> and OspZ from <i>Shigella</i> Block Nuclear Translocation of NF- κ B p65. <i>PLoS Pathogens</i> , 2010, 6, e1000898.	4.7	201
30	The Molecular Basis for Perforin Oligomerization and Transmembrane Pore Assembly. <i>Immunity</i> , 2009, 30, 684-695.	14.3	123
31	Antigen Ligation Triggers a Conformational Change within the Constant Domain of the β 220 T Cell Receptor. <i>Immunity</i> , 2009, 30, 777-788.	14.3	111
32	Temperature sensitivity of human perforin mutants unmasks subtotal loss of cytotoxicity, delayed FHL, and a predisposition to cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9809-9814.	7.1	114
33	The MACPF/CDC family of pore-forming toxins. <i>Cellular Microbiology</i> , 2008, 10, 1765-1774.	2.1	250
34	Structural and Biological Basis of CTL Escape in Coronavirus-Infected Mice. <i>Journal of Immunology</i> , 2008, 180, 3926-3937.	0.8	23
35	Enzymatic Properties of an Ecto-nucleoside Triphosphate Diphosphohydrolase from <i>Legionella pneumophila</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 12909-12918.	3.4	54
36	Prevention of Cytotoxic T Cell Escape Using a Heteroclitic Subdominant Viral T Cell Determinant. <i>PLoS Pathogens</i> , 2008, 4, e1000186.	4.7	14

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37	Characterization of TolC Efflux Pump Proteins from <i>Pasteurella multocida</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 4166-4171.	3.2	11
38	Epitope-specific TCR \hat{I}^2 repertoire diversity imparts no functional advantage on the CD8 ⁺ T cell response to cognate viral peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2034-2039.	7.1	50
39	A Common Fold Mediates Vertebrate Defense and Bacterial Attack. <i>Science</i> , 2007, 317, 1548-1551.	12.6	261
40	Specificity on a knife-edge: the \hat{I}^2 T cell receptor. <i>Current Opinion in Structural Biology</i> , 2006, 16, 787-795.	5.7	44
41	Lack of prominent peptide-major histocompatibility complex features limits repertoire diversity in virus-specific CD8 ⁺ T cell populations. <i>Nature Immunology</i> , 2005, 6, 382-389.	14.5	142
42	T Cell Determinants Incorporating \hat{I}^2 -Amino Acid Residues Are Protease Resistant and Remain Immunogenic In Vivo. <i>Journal of Immunology</i> , 2005, 175, 3810-3818.	0.8	56
43	Crystal structure of HLA-G: A nonclassical MHC class I molecule expressed at the fetal-maternal interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3360-3365.	7.1	139
44	Crystal structure of the human T cell receptor CD3 \hat{A} heterodimer complexed to the therapeutic mAb OKT3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7675-7680.	7.1	148
45	Functional and Structural Characteristics of NY-ESO-1-related HLA A2-restricted Epitopes and the Design of a Novel Immunogenic Analogue. <i>Journal of Biological Chemistry</i> , 2004, 279, 23438-23446.	3.4	61
46	The Structure of H-2Kb and Kb $\hat{m}8$ Complexed to a Herpes Simplex Virus Determinant: Evidence for a Conformational Switch That Governs T Cell Repertoire Selection and Viral Resistance. <i>Journal of Immunology</i> , 2004, 173, 402-409.	0.8	31
47	The production and purification of the human T-cell receptors, the CD3 \hat{A} \hat{I}^3 and CD3 \hat{A} \hat{I}^1 heterodimers: complex formation and crystallization with OKT3, a therapeutic monoclonal antibody. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1425-1428.	2.5	4