

Damian C Ekiert

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

50
papers

5,689
citations

25
h-index

58
g-index

58
ext. papers

6,580
ext. citations

16.5
avg, IF

5.23
L-index

#	Paper	IF	Citations
50	Role of Ring6 in the function of the E. coli MCE protein LetB.. <i>Journal of Molecular Biology</i> , 2022 , 434, 167463	6.5	0
49	Mechanics of Microsporidian Polar Tube Firing.. <i>Experientia Supplementum (2012)</i> , 2022 , 114, 215-245	2.2	
48	Design of multi-scale protein complexes by hierarchical building block fusion. <i>Nature Communications</i> , 2021 , 12, 2294	17.4	14
47	Targeting allostery in the Dynein motor domain with small molecule inhibitors. <i>Cell Chemical Biology</i> , 2021 , 28, 1460-1473.e15	8.2	1
46	User experience: Using national Cryo EM centers towards studying lipid transport across the bacterial cell envelope. <i>Microscopy and Microanalysis</i> , 2021 , 27, 1422-1422	0.5	
45	Three-dimensional Architecture of the Microsporidian Spore and Rapid Firing Kinetics of the Harpoon-like Invasion Machinery. <i>Microscopy and Microanalysis</i> , 2020 , 26, 2524-2526	0.5	
44	Affinity maturation is required for pathogenic monovalent IgG4 autoantibody development in myasthenia gravis. <i>Journal of Experimental Medicine</i> , 2020 , 217,	16.6	6
43	LetB Structure Reveals a Tunnel for Lipid Transport across the Bacterial Envelope. <i>Cell</i> , 2020 , 181, 653-664.e1933	66.2	133
42	Structure of MlaFB uncovers novel mechanisms of ABC transporter regulation. <i>ELife</i> , 2020 , 9,	8.9	13
41	Structure of bacterial phospholipid transporter MlaFEDB with substrate bound. <i>ELife</i> , 2020 , 9,	8.9	17
40	Structural and functional diversity calls for a new classification of ABC transporters. <i>FEBS Letters</i> , 2020 , 594, 3767-3775	3.8	66
39	3-Dimensional organization and dynamics of the microsporidian polar tube invasion machinery. <i>PLoS Pathogens</i> , 2020 , 16, e1008738	7.6	13
38	3-Dimensional organization and dynamics of the microsporidian polar tube invasion machinery 2020 , 16, e1008738		
37	3-Dimensional organization and dynamics of the microsporidian polar tube invasion machinery 2020 , 16, e1008738		
36	3-Dimensional organization and dynamics of the microsporidian polar tube invasion machinery 2020 , 16, e1008738		
35	Architectures of Lipid Transport Systems for the Bacterial Outer Membrane. <i>Cell</i> , 2017 , 169, 273-285.e176.2	176.2	127
34	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015 , 528, 580-4	50.4	156

33	Small molecule probes to quantify the functional fraction of a specific protein in a cell with minimal folding equilibrium shifts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4449-54	11.5	27
32	A common solution to group 2 influenza virus neutralization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 445-50	11.5	161
31	Structure of a PE-PPE-EspG complex from Mycobacterium tuberculosis reveals molecular specificity of ESX protein secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 14758-63	11.5	67
30	De novo-designed enzymes as small-molecule-regulated fluorescence imaging tags and fluorescent reporters. <i>Journal of the American Chemical Society</i> , 2014 , 136, 13102-5	16.4	18
29	New approaches to vaccination 2013 , 327-336		0
28	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1243-9	17.6	104
27	Reshaping antibody diversity. <i>Cell</i> , 2013 , 153, 1379-93	56.2	138
26	Structure of a classical broadly neutralizing stem antibody in complex with a pandemic H2 influenza virus hemagglutinin. <i>Journal of Virology</i> , 2013 , 87, 7149-54	6.6	91
25	A virus-like particle that elicits cross-reactive antibodies to the conserved stem of influenza virus hemagglutinin. <i>Journal of Virology</i> , 2012 , 86, 11686-97	6.6	58
24	Broadly neutralizing antibodies against influenza virus and prospects for universal therapies. <i>Current Opinion in Virology</i> , 2012 , 2, 134-41	7.5	116
23	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012 , 489, 526-32	50.4	344
22	Recognition of Sialylated Poly-N-acetylactosamine Chains on N- and O-Linked Glycans by Human and Avian Influenza A Virus Hemagglutinins. <i>Angewandte Chemie</i> , 2012 , 124, 4944-4947	3.6	4
21	Recognition of sialylated poly-N-acetylactosamine chains on N- and O-linked glycans by human and avian influenza A virus hemagglutinins. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4860-3	16.4	76
20	Influenza human monoclonal antibody 1F1 interacts with three major antigenic sites and residues mediating human receptor specificity in H1N1 viruses. <i>PLoS Pathogens</i> , 2012 , 8, e1003067	7.6	69
19	Heterosubtypic antibody recognition of the influenza virus hemagglutinin receptor binding site enhanced by avidity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 17040-5	11.5	119
18	Highly conserved protective epitopes on influenza B viruses. <i>Science</i> , 2012 , 337, 1343-8	33.3	543
17	Recognition of Sialylated Poly-N-acetylactosamine Chains on N- and O-Linked Glycans by Human and Avian Influenza A Virus Hemagglutinins 2012 , 51, 4860		1
16	An insertion mutation that distorts antibody binding site architecture enhances function of a human antibody. <i>MBio</i> , 2011 , 2, e00345-10	7.8	37

15	A highly conserved neutralizing epitope on group 2 influenza A viruses. <i>Science</i> , 2011 , 333, 843-50	33.3	645
14	Computational design of proteins targeting the conserved stem region of influenza hemagglutinin. <i>Science</i> , 2011 , 332, 816-21	33.3	441
13	A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. <i>Science</i> , 2011 , 332, 234-8	33.3	350
12	Structural modeling of the Influenza virus Hemagglutinin protein in complex with a broadly neutralizing antibody. <i>FASEB Journal</i> , 2011 , 25, lb169	0.9	
11	Structural basis of preexisting immunity to the 2009 H1N1 pandemic influenza virus. <i>Science</i> , 2010 , 328, 357-60	33.3	459
10	Vaccination with a synthetic peptide from the influenza virus hemagglutinin provides protection against distinct viral subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18979-84	11.5	239
9	Chapter 12: Attachment and Entry: Receptor Recognition in Viral Pathogenesis. <i>RSC Biomolecular Sciences</i> , 2010 , 220-242		
8	Antibody recognition of a highly conserved influenza virus epitope. <i>Science</i> , 2009 , 324, 246-51	33.3	1031
7	Sequential Cyk-4 binding to ECT2 and FIP3 regulates cleavage furrow ingression and abscission during cytokinesis. <i>EMBO Journal</i> , 2008 , 27, 1791-803	13	74
6	Generation of DNA-free Escherichia coli cells by 2-aminopurine requires mismatch repair and nonmethylated DNA. <i>Journal of Bacteriology</i> , 2006 , 188, 339-42	3.5	7
5	Cytochrome oxidase deficiency protects Escherichia coli from cell death but not from filamentation due to thymine deficiency or DNA polymerase inactivation. <i>Journal of Bacteriology</i> , 2005 , 187, 2827-35	3.5	5
4	Cell death in Escherichia coli dnaE(Ts) mutants incubated at a nonpermissive temperature is prevented by mutation in the cydA gene. <i>Journal of Bacteriology</i> , 2004 , 186, 2147-55	3.5	8
3	Structure of MlaFB uncovers novel mechanisms of ABC transporter regulation		2
2	Structure of bacterial phospholipid transporter MlaFEDB with substrate bound		3
1	Hierarchical design of multi-scale protein complexes by combinatorial assembly of oligomeric helical bundle and repeat protein building blocks		4