

# Declan A Doyle

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9381913/publications.pdf>

Version: 2024-02-01

32  
papers

3,626  
citations

304743

22  
h-index

434195

31  
g-index

35  
all docs

35  
docs citations

35  
times ranked

4157  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein over-expression in Escherichia coli triggers adaptation analogous to antimicrobial resistance. <i>Microbial Cell Factories</i> , 2021, 20, 13.	4.0	10
2	BioStruct-Africa: empowering Africa-based scientists through structural biology knowledge transfer and mentoring – recent advances and future perspectives. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1843-1850.	2.4	3
3	The N-acyltransferase Lnt: Structure-function insights from recent simultaneous studies. <i>International Journal of Biological Macromolecules</i> , 2018, 117, 870-877.	7.5	7
4	Efflux drug transporters at the forefront of antimicrobial resistance. <i>European Biophysics Journal</i> , 2017, 46, 647-653.	2.2	67
5	Small-Molecule Inhibitors of AF6 PDZ-Mediated Protein-Protein Interactions. <i>ChemMedChem</i> , 2014, 9, 1458-1462.	3.2	7
6	Heterologous expression and purification of an active human $\text{TRPV3}$ ion channel. <i>FEBS Journal</i> , 2013, 280, 6010-6021.	4.7	6
7	Dual-Mode Phospholipid Regulation of Human Inward Rectifying Potassium Channels. <i>Biophysical Journal</i> , 2011, 100, 620-628.	0.5	69
8	High-performance liquid chromatography separation and intact mass analysis of detergent-solubilized integral membrane proteins. <i>Analytical Biochemistry</i> , 2011, 410, 272-280.	2.4	24
9	Unusual binding interactions in PDZ domain crystal structures help explain binding mechanisms. <i>Protein Science</i> , 2010, 19, 731-741.	7.6	34
10	Direct and Specific Activation of Human Inward Rectifier K <sup>+</sup> Channels by Membrane Phosphatidylinositol 4,5-Bisphosphate. <i>Journal of Biological Chemistry</i> , 2010, 285, 37129-37132.	3.4	71
11	Expression and purification of recombinant human inward rectifier K <sup>+</sup> (KCNJ) channels in <i>Saccharomyces cerevisiae</i> . <i>Protein Expression and Purification</i> , 2010, 71, 115-121.	1.3	21
12	Expression and Purification of Recombinant Human Inward Rectifier K <sup>+</sup> (KCNJ) Channel. <i>Biophysical Journal</i> , 2010, 98, 701a.	0.5	0
13	Regulator of G-Protein Signaling 14 (RGS14) Is a Selective H-Ras Effector. <i>PLoS ONE</i> , 2009, 4, e4884.	2.5	40
14	RhoB can adopt a Mg <sup>2+</sup> free conformation prior to GEF binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 498-505.	2.6	7
15	Structural diversity in the RGS domain and its interaction with heterotrimeric G protein $\alpha$ -subunits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6457-6462.	7.1	174
16	Structure of PICK1 and other PDZ domains obtained with the help of self-binding C-terminal extensions. <i>Protein Science</i> , 2007, 16, 683-694.	7.6	57
17	The scientific impact of the Structural Genomics Consortium: a protein family and ligand-centered approach to medically-relevant human proteins. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 107-119.	1.2	66
18	Structural Characterization and pH-Induced Conformational Transition of Full-Length KcsA. <i>Biophysical Journal</i> , 2006, 90, 1752-1766.	0.5	34

#	ARTICLE	IF	CITATIONS
19	Role of Aromatic Localization in the Gating Process of a Potassium Channel. <i>Biophysical Journal</i> , 2006, 90, L01-L03.	0.5	35
20	Crystal structure of the CorA Mg <sup>2+</sup> transporter. <i>Nature</i> , 2006, 440, 833-837.	27.8	233
21	Structural basis for protein-protein interactions in the 14-3-3 protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17237-17242.	7.1	340
22	Two Different Conformational States of the KirBac3.1 Potassium Channel Revealed by Electron Crystallography. <i>Structure</i> , 2005, 13, 1463-1472.	3.3	100
23	Transmembrane helix prediction: a comparative evaluation and analysis. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 295-308.	2.1	117
24	Modeling of an Ion Channel in Its Open Conformation. <i>Biophysical Journal</i> , 2005, 89, L01-L03.	0.5	35
25	Molecular insights into ion channel function (Review). <i>Molecular Membrane Biology</i> , 2004, 21, 221-225.	2.0	21
26	Structural themes in ion channels. <i>European Biophysics Journal</i> , 2004, 33, 175-9.	2.2	28
27	Structural changes during ion channel gating. <i>Trends in Neurosciences</i> , 2004, 27, 298-302.	8.6	73
28	Crystal Structure of the Potassium Channel KirBac1.1 in the Closed State. <i>Science</i> , 2003, 300, 1922-1926.	12.6	763
29	Shifting the Equilibrium Mixture of Gramicidin Double Helices Toward a Single Conformation with Multivalent Cationic Salts. <i>Biophysical Journal</i> , 1998, 75, 635-640.	0.5	22
30	Crystal structure of the Gramicidin/Potassium thiocyanate complex. <i>Journal of Molecular Biology</i> , 1997, 266, 963-977.	4.2	54
31	Crystal Structures of a Complexed and Peptide-Free Membrane Protein's Binding Domain: Molecular Basis of Peptide Recognition by PDZ. <i>Cell</i> , 1996, 85, 1067-1076.	28.9	1,097
32	Caesium-binding sites in the gramicidin pore. <i>Biochemical Society Transactions</i> , 1994, 22, 1043-1045.	3.4	11