

# Pascal F Egea

## List of Publications by Year in descending order

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37  
papers

3,370  
citations

304743

22  
h-index

361022

35  
g-index

37  
all docs

37  
docs citations

37  
times ranked

4333  
citing authors

#	ARTICLE	IF	CITATIONS
1	The unfolded protein response signals through high-order assembly of Ire1. <i>Nature</i> , 2009, 457, 687-693.	27.8	565
2	Crystal structure of the human RXRalpha ligand-binding domain bound to its natural ligand: 9-cis retinoic acid. <i>EMBO Journal</i> , 2000, 19, 2592-2601.	7.8	293
3	Substrate twinning activates the signal recognition particle and its receptor. <i>Nature</i> , 2004, 427, 215-221.	27.8	270
4	Architecture and Selectivity in Aquaporins: 2.5 Å... X-Ray Structure of Aquaporin Z. <i>PLoS Biology</i> , 2003, 1, e72.	5.6	248
5	The Toxoplasma Dense Granule Proteins GRA17 and GRA23 Mediate the Movement of Small Molecules between the Host and the Parasitophorous Vacuole. <i>Cell Host and Microbe</i> , 2015, 17, 642-652.	11.0	208
6	Targeting proteins to membranes: structure of the signal recognition particle. <i>Current Opinion in Structural Biology</i> , 2005, 15, 213-220.	5.7	206
7	Conserved SMP domains of the ERMES complex bind phospholipids and mediate tether assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3179-88.	7.1	174
8	Malaria parasite translocon structure and mechanism of effector export. <i>Nature</i> , 2018, 561, 70-75.	27.8	169
9	Lateral opening of a translocon upon entry of protein suggests the mechanism of insertion into membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17182-17187.	7.1	155
10	Molecular Recognition of Agonist Ligands by RXRs. <i>Molecular Endocrinology</i> , 2002, 16, 987-997.	3.7	154
11	Effects of ligand binding on the association properties and conformation in solution of retinoic acid receptors RXR and RAR11 Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 2001, 307, 557-576.	4.2	88
12	Ligand-protein interactions in nuclear receptors of hormones. <i>FEBS Letters</i> , 2000, 476, 62-67.	2.8	87
13	Functional and structural characterization of the insertion region in the ligand binding domain of the vitamin D nuclear receptor. <i>FEBS Journal</i> , 2001, 268, 971-979.	0.2	74
14	Unraveling the interface of signal recognition particle and its receptor by using chemical cross-linking and tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16454-16459.	7.1	72
15	Structure of the human CIC-1 chloride channel. <i>PLoS Biology</i> , 2019, 17, e3000218.	5.6	66
16	Structural and functional basis for RNA cleavage by Ire1. <i>BMC Biology</i> , 2011, 9, 47.	3.8	61
17	Structure of an Fab-Protease Complex Reveals a Highly Specific Non-canonical Mechanism of Inhibition. <i>Journal of Molecular Biology</i> , 2008, 380, 351-360.	4.2	55
18	Cofactor-mediated conformational control in the bifunctional kinase/RNase Ire1. <i>BMC Biology</i> , 2011, 9, 48.	3.8	51

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19	Molecular Recognition of Agonist Ligands by RXRs. <i>Molecular Endocrinology</i> , 2002, 16, 987-997.	3.7	48
20	Highlighting membrane protein structure and function: A celebration of the Protein Data Bank. <i>Journal of Biological Chemistry</i> , 2021, 296, 100557.	3.4	42
21	Native and Denaturing MS Protein Deconvolution for Biopharma: Monoclonal Antibodies and Antibody-Drug Conjugates to Polydisperse Membrane Proteins and Beyond. <i>Analytical Chemistry</i> , 2019, 91, 9472-9480.	6.5	32
22	Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry as a Platform for Characterizing Multimeric Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 183-193.	2.8	29
23	Crystal structure of Mdm12 and combinatorial reconstitution of Mdm12/Mmm1 ERMES complexes for structural studies. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 129-135.	2.1	23
24	Insights into the Mechanism of Bovine CD38/NAD <sup>+</sup> Glycohydrolase from the X-Ray Structures of Its Michaelis Complex and Covalently-Trapped Intermediates. <i>PLoS ONE</i> , 2012, 7, e34918.	2.5	21
25	Structures of SRP54 and SRP19, the Two Proteins that Organize the Ribonucleic Core of the Signal Recognition Particle from <i>Pyrococcus furiosus</i> . <i>PLoS ONE</i> , 2008, 3, e3528.	2.5	21
26	Structures of the Signal Recognition Particle Receptor from the Archaeon <i>Pyrococcus furiosus</i> : Implications for the Targeting Step at the Membrane. <i>PLoS ONE</i> , 2008, 3, e3619.	2.5	21
27	Structural mapping of the C <sub>1</sub> B <sub>1</sub> ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. <i>Protein Science</i> , 2015, 24, 1508-1520.	7.6	20
28	Structure of a putative ClpS N-terminal adaptor protein from the malaria pathogen <i>Plasmodium falciparum</i> . <i>Protein Science</i> , 2016, 25, 689-701.	7.6	20
29	Crystal structure and solution characterization of the thioredoxin-2 from <i>Plasmodium falciparum</i> , a constituent of an essential parasitic protein export complex. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 403-409.	2.1	18
30	Crossing the Vacuolar Rubicon: Structural Insights into Effector Protein Trafficking in Apicomplexan Parasites. <i>Microorganisms</i> , 2020, 8, 865.	3.6	18
31	Peptide Length and Leaving-Group Sterics Influence Potency of Peptide Phosphonate Protease Inhibitors. <i>Chemistry and Biology</i> , 2011, 18, 48-57.	6.0	17
32	Mechanisms of Non-Vesicular Exchange of Lipids at Membrane Contact Sites: Of Shuttles, Tunnels and Funnels. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 784367.	3.7	17
33	Rapid LC-MS Method for Accurate Molecular Weight Determination of Membrane and Hydrophobic Proteins. <i>Analytical Chemistry</i> , 2018, 90, 13616-13623.	6.5	12
34	Purification and crystallization of the human RXR $\alpha$ ligand-binding domain-9-cisRA complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 434-437.	2.5	8
35	Determining the Lipid-Binding Specificity of SMP Domains: An ERMES Subunit as a Case Study. <i>Methods in Molecular Biology</i> , 2019, 1949, 213-235.	0.9	6
36	Moving Lipids, by the Numbers. <i>Contact (Thousand Oaks (Ventura County, Calif))</i> , 2022, 5, 251525642211030.	1.3	1

#	ARTICLE	IF	CITATIONS
37	Malaria parasite translocon structure and mechanism of effector export. Acta Crystallographica Section A: Foundations and Advances, 2020, 76, a32-a32.	0.1	0