

Pascal F Egea

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Moving Lipids, by the Numbers. Contact (Thousand Oaks (Ventura County, Calif)), 2022, 5, 251525642211030. | 1.3 | 1 |
| 2 | Highlighting membrane protein structure and function: A celebration of the Protein Data Bank. Journal of Biological Chemistry, 2021, 296, 100557. | 3.4 | 42 |
| 3 | Mechanisms of Non-Vesicular Exchange of Lipids at Membrane Contact Sites: Of Shuttles, Tunnels and, Funnels. Frontiers in Cell and Developmental Biology, 2021, 9, 784367. | 3.7 | 17 |
| 4 | Crossing the Vacuolar Rubicon: Structural Insights into Effector Protein Trafficking in Apicomplexan Parasites. Microorganisms, 2020, 8, 865. | 3.6 | 18 |
| 5 | Malaria parasite translocon structure and mechanism of effector export. Acta Crystallographica Section A: Foundations and Advances, 2020, 76, a32-a32. | 0.1 | 0 |
| 6 | Native and Denaturing MS Protein Deconvolution for Biopharma: Monoclonal Antibodies and Antibody-Drug Conjugates to Polydisperse Membrane Proteins and Beyond. Analytical Chemistry, 2019, 91, 9472-9480. | 6.5 | 32 |
| 7 | Structure of the human ClC-1 chloride channel. PLoS Biology, 2019, 17, e3000218. | 5.6 | 66 |
| 8 | Determining the Lipid-Binding Specificity of SMP Domains: An ERMES Subunit as a Case Study. Methods in Molecular Biology, 2019, 1949, 213-235. | 0.9 | 6 |
| 9 | Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry as a Platform for Characterizing Multimeric Membrane Protein Complexes. Journal of the American Society for Mass Spectrometry, 2018, 29, 183-193. | 2.8 | 29 |
| 10 | Rapid LC-MS Method for Accurate Molecular Weight Determination of Membrane and Hydrophobic Proteins. Analytical Chemistry, 2018, 90, 13616-13623. | 6.5 | 12 |
| 11 | Malaria parasite translocon structure and mechanism of effector export. Nature, 2018, 561, 70-75. | 27.8 | 169 |
| 12 | Crystal structure of Mdm12 and combinatorial reconstitution of Mdm12/Mmm1 ERMES complexes for structural studies. Biochemical and Biophysical Research Communications, 2017, 488, 129-135. | 2.1 | 23 |
| 13 | Structure of a putative ClpS N-terminal rule adaptor protein from the malaria pathogen <i>Plasmodium falciparum</i> . Protein Science, 2016, 25, 689-701. | 7.6 | 20 |
| 14 | Structural mapping of the ClpB ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. Protein Science, 2015, 24, 1508-1520. | 7.6 | 20 |
| 15 | Conserved SMP domains of the ERMES complex bind phospholipids and mediate tether assembly. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3179-88. | 7.1 | 174 |
| 16 | The Toxoplasma Dense Granule Proteins GRA17 and GRA23 Mediate the Movement of Small Molecules between the Host and the Parasitophorous Vacuole. Cell Host and Microbe, 2015, 17, 642-652. | 11.0 | 208 |
| 17 | Crystal structure and solution characterization of the thioredoxin-2 from Plasmodium falciparum, a constituent of an essential parasitic protein export complex. Biochemical and Biophysical Research Communications, 2015, 456, 403-409. | 2.1 | 18 |
| 18 | Insights into the Mechanism of Bovine CD38/NAD+Glycohydrolase from the X-Ray Structures of Its Michaelis Complex and Covalently-Trapped Intermediates. PLoS ONE, 2012, 7, e34918. | 2.5 | 21 |

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|----|---|------|-----------|
| 19 | Structural and functional basis for RNA cleavage by Ire1. <i>BMC Biology</i> , 2011, 9, 47. | 3.8 | 61 |
| 20 | Cofactor-mediated conformational control in the bifunctional kinase/RNase Ire1. <i>BMC Biology</i> , 2011, 9, 48. | 3.8 | 51 |
| 21 | 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 |
| 22 | 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 |
| 23 | The unfolded protein response signals through high-order assembly of Ire1. <i>Nature</i> , 2009, 457, 687-693. | 27.8 | 565 |
| 24 | 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 |
| 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 | Targeting proteins to membranes: structure of the signal recognition particle. <i>Current Opinion in Structural Biology</i> , 2005, 15, 213-220. | 5.7 | 206 |
| 28 | 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 |
| 29 | Substrate twinning activates the signal recognition particle and its receptor. <i>Nature</i> , 2004, 427, 215-221. | 27.8 | 270 |
| 30 | Architecture and Selectivity in Aquaporins: 2.5 Å... X-Ray Structure of Aquaporin Z. <i>PLoS Biology</i> , 2003, 1, e72. | 5.6 | 248 |
| 31 | Molecular Recognition of Agonist Ligands by RXRs. <i>Molecular Endocrinology</i> , 2002, 16, 987-997. | 3.7 | 154 |
| 32 | Molecular Recognition of Agonist Ligands by RXRs. <i>Molecular Endocrinology</i> , 2002, 16, 987-997. | 3.7 | 48 |
| 33 | 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 |
| 34 | 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 |
| 35 | Purification and crystallization of the human RXR α ligand-binding domain-9-cisRA complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 434-437. | 2.5 | 8 |
| 36 | Crystal structure of the human RXR α ligand-binding domain bound to its natural ligand: 9-cis retinoic acid. <i>EMBO Journal</i> , 2000, 19, 2592-2601. | 7.8 | 293 |

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|----|---|-----|-----------|
| 37 | Ligand-protein interactions in nuclear receptors of hormones. FEBS Letters, 2000, 476, 62-67. | 2.8 | 87 |