

Jose M M Caaveiro

List of Publications by Year in descending order

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citations

257450

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79
all docs

79
docs citations

79
times ranked

2883
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. <i>Nature Communications</i> , 2015, 6, 6337.	12.8	185
2	Lipid Phase Coexistence Favors Membrane Insertion of Equinatoxin-II, a Pore-forming Toxin from <i>Actinia equina</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 34209-34216.	3.4	118
3	Structural basis for binding of human IgG1 to its high-affinity human receptor Fc γ RI. <i>Nature Communications</i> , 2015, 6, 6866.	12.8	109
4	Testing Geometrical Discrimination within an Enzyme Active Site: Constrained Hydrogen Bonding in the Ketosteroid Isomerase Oxyanion Hole. <i>Journal of the American Chemical Society</i> , 2008, 130, 13696-13708.	13.7	91
5	Selective and reversible modification of kinase cysteines with chlorofluoroacetamides. <i>Nature Chemical Biology</i> , 2019, 15, 250-258.	8.0	90
6	Affinity Improvement of a Therapeutic Antibody by Structure-Based Computational Design: Generation of Electrostatic Interactions in the Transition State Stabilizes the Antibody-Antigen Complex. <i>PLoS ONE</i> , 2014, 9, e87099.	2.5	78
7	Detection of ligand binding hot spots on protein surfaces via fragment-based methods: application to DJ-1 and glucocerebrosidase. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 491-500.	2.9	77
8	Differential effects of five types of antipathogenic plant peptides on model membranes. <i>FEBS Letters</i> , 1997, 410, 338-342.	2.8	74
9	Differential Interaction of Equinatoxin II with Model Membranes in Response to Lipid Composition. <i>Biophysical Journal</i> , 2001, 80, 1343-1353.	0.5	74
10	Structural analysis of Fc/Fc γ R complexes: a blueprint for antibody design. <i>Immunological Reviews</i> , 2015, 268, 201-221.	6.0	68
11	Glycosylation of IgG-Fc: a molecular perspective. <i>International Immunology</i> , 2017, 29, 311-317.	4.0	57
12	Catalytic activity of MsbA reconstituted in nanodisc particles is modulated by remote interactions with the bilayer. <i>FEBS Letters</i> , 2011, 585, 3533-3537.	2.8	54
13	Assessing the Heterogeneity of the Fc-Glycan of a Therapeutic Antibody Using an engineered Fc γ RIIIa-Immobilized Column. <i>Scientific Reports</i> , 2018, 8, 3955.	3.3	48
14	A pathway for the thermal destabilization of bacteriorhodopsin. <i>FEBS Letters</i> , 1995, 367, 297-300.	2.8	44
15	Molecular Basis of Recognition of Antibacterial Porphyrins by Heme-Transporter IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2011, 50, 7311-7320.	2.5	44
16	Mapping Ultra-weak Protein-Protein Interactions between Heme Transporters of <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 16477-16487.	3.4	43
17	The Atomic Structure of the HIV-1 gp41 Transmembrane Domain and Its Connection to the Immunogenic Membrane-proximal External Region. <i>Journal of Biological Chemistry</i> , 2015, 290, 12999-13015.	3.4	37
18	Quantitative dissection of hydrogen bond-mediated proton transfer in the ketosteroid isomerase active site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2552-61.	7.1	36

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19	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. <i>Scientific Reports</i> , 2019, 9, 15481.	3.3	36
20	Structural basis for broad neutralization of HIV-1 through the molecular recognition of 10E8 helical epitope at the membrane interface. <i>Scientific Reports</i> , 2016, 6, 38177.	3.3	34
21	Hydrogen Bond Coupling in the Ketosteroid Isomerase Active Site. <i>Biochemistry</i> , 2009, 48, 6932-6939.	2.5	31
22	A Pore-Forming Toxin Requires a Specific Residue for Its Activity in Membranes with Particular Physicochemical Properties. <i>Journal of Biological Chemistry</i> , 2015, 290, 10850-10861.	3.4	31
23	Discovery and Optimization of Inhibitors of the Parkinson's Disease Associated Protein DJ-1. <i>ACS Chemical Biology</i> , 2018, 13, 2783-2793.	3.4	27
24	Differential Effect of Membrane Composition on the Pore-Forming Ability of Four Different Sea Anemone Actinoporins. <i>Biochemistry</i> , 2016, 55, 6630-6641.	2.5	26
25	Dynamic elements govern the catalytic activity of CapE, a capsular polysaccharide synthesizing enzyme from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2013, 587, 3824-3830.	2.8	24
26	Interaction of wheat Î±-thionin with large unilamellar vesicles. <i>Protein Science</i> , 1998, 7, 2567-2577.	7.6	23
27	Binding of Hydrophobic Hydroxamic Acids Enhances Peroxidase's Stereoselectivity in Nonaqueous Sulfoxidations. <i>Journal of the American Chemical Society</i> , 2002, 124, 782-787.	13.7	23
28	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016, 291, 19210-19219.	3.4	23
29	Discovery and characterization of natural tropolones as inhibitors of the antibacterial target CapF from <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2015, 5, 15337.	3.3	22
30	Structural and Thermodynamic Basis of Epitope Binding by Neutralizing and Nonneutralizing Forms of the Anti-HIV-1 Antibody 4E10. <i>Journal of Virology</i> , 2015, 89, 11975-11989.	3.4	22
31	Selective binding of antimicrobial porphyrins to the heme receptor IsdHNEAT3 of <i>Staphylococcus aureus</i> . <i>Protein Science</i> , 2013, 22, 942-953.	7.6	20
32	Functional characterization of Val60, a key residue involved in the membrane oligomerization of fragaceatoxin C, an actinoporin from <i>Actinia fragacea</i> . <i>FEBS Letters</i> , 2015, 589, 1840-1846.	2.8	20
33	Adhesive Dimerization of Human P-Cadherin Catalyzed by a Chaperone-like Mechanism. <i>Structure</i> , 2016, 24, 1523-1536.	3.3	20
34	Contributions of Interfacial Residues of Human Interleukin15 to the Specificity and Affinity for Its Private Î±-Receptor. <i>Journal of Molecular Biology</i> , 2009, 389, 880-894.	4.2	19
35	Heme Binding Mechanism of Structurally Similar Iron-Regulated Surface Determinant Near Transporter Domains of <i>Staphylococcus aureus</i> Exhibiting Different Affinities for Heme. <i>Biochemistry</i> , 2013, 52, 8866-8877.	2.5	19
36	Thermodynamic and Structural Characterization of the Specific Binding of Zn(II) to Human Protein DJ-1. <i>Biochemistry</i> , 2014, 53, 2218-2220.	2.5	19

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37	Incorporation of Rapid Thermodynamic Data in Fragment-Based Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 2155-2159.	6.4	18
38	Disruption of cell adhesion by an antibody targeting the cell-adhesive intermediate (X-dimer) of human P-cadherin. <i>Scientific Reports</i> , 2017, 7, 39518.	3.3	18
39	Molecular basis for governing the morphology of type-I collagen fibrils by Osteomodulin. <i>Communications Biology</i> , 2018, 1, 33.	4.4	18
40	Identification and Characterization of the X-Dimer of Human P-Cadherin: Implications for Homophilic Cell Adhesion. <i>Biochemistry</i> , 2014, 53, 1742-1752.	2.5	17
41	Crystal structure of the capsular polysaccharide synthesizing protein CapE of <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2013, 33, .	2.4	16
42	Bidirectional Transformation of a Metamorphic Protein between the Water-Soluble and Transmembrane Native States. <i>Biochemistry</i> , 2015, 54, 6863-6866.	2.5	15
43	Functional Contacts between MPER and the Anti-HIV-1 Broadly Neutralizing Antibody 4E10 Extend into the Core of the Membrane. <i>Journal of Molecular Biology</i> , 2017, 429, 1213-1226.	4.2	14
44	The Isolation of New Pore-Forming Toxins from the Sea Anemone <i>Actinia fragacea</i> Provides Insights into the Mechanisms of Actinoporin Evolution. <i>Toxins</i> , 2019, 11, 401.	3.4	14
45	Tyrosine Sulfation Restricts the Conformational Ensemble of a Flexible Peptide, Strengthening the Binding Affinity for an Antibody. <i>Biochemistry</i> , 2018, 57, 4177-4185.	2.5	13
46	Non-core Region Modulates Interleukin-11 Signaling Activity. <i>Journal of Biological Chemistry</i> , 2011, 286, 8085-8093.	3.4	12
47	Crystal structure of the enzyme CapF of <i>Staphylococcus aureus</i> reveals a unique architecture composed of two functional domains. <i>Biochemical Journal</i> , 2012, 443, 671-680.	3.7	12
48	Intramolecular H-bonds govern the recognition of a flexible peptide by an antibody. <i>Journal of Biochemistry</i> , 2018, 164, 65-76.	1.7	12
49	Unexpectedly enhanced stereoselectivity of peroxidase-catalyzed sulfoxidation in branched alcohols. <i>Biotechnology and Bioengineering</i> , 2002, 79, 105-111.	3.3	11
50	Affinity for the Interface Underpins Potency of Antibodies Operating In Membrane Environments. <i>Cell Reports</i> , 2020, 32, 108037.	6.4	10
51	Solubilization of membrane proteins with novel N-acylamino acid detergents. <i>Molecular BioSystems</i> , 2010, 6, 677.	2.9	9
52	Structural and thermodynamic characterization of the self-adhesive properties of human P-cadherin. <i>Molecular BioSystems</i> , 2012, 8, 2050.	2.9	9
53	Peripheral Membrane Interactions Boost the Engagement by an Anti-HIV-1 Broadly Neutralizing Antibody. <i>Journal of Biological Chemistry</i> , 2017, 292, 5571-5583.	3.4	9
54	Haemolytic actinoporins interact with carbohydrates using their lipid-binding module. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160216.	4.0	9

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55	Asymmetric sulfoxidations mediated by γ -chymotrypsin. <i>Biotechnology and Bioengineering</i> , 2002, 78, 104-109.	3.3	8
56	Computer-guided library generation applied to the optimization of single-domain antibodies. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 423-431.	2.1	8
57	New pharmacological effect of fulvestrant to prevent oxaliplatin-induced neurodegeneration and mechanical allodynia in rats. <i>International Journal of Cancer</i> , 2019, 145, 2107-2113.	5.1	8
58	Electrokinetic charge of the anesthetic-induced bR480 and bR380 spectral forms of bacteriorhodopsin. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1995, 1236, 331-337.	2.6	7
59	Structural basis for antigen recognition by methylated lysine-specific antibodies. <i>Journal of Biological Chemistry</i> , 2021, 296, 100176.	3.4	6
60	High-level expression of human CH2 domain from the Fc region in <i>Pichia pastoris</i> and preparation of anti-CH2 antibodies. <i>Journal of Biochemistry</i> , 2021, 170, 289-297.	1.7	5
61	Mechanism of dimerization and structural features of human LI-cadherin. <i>Journal of Biological Chemistry</i> , 2021, 297, 101054.	3.4	4
62	Structure and role of the linker domain of the iron surface-determinant protein IsdH in heme transportation in <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 101995.	3.4	4
63	In-Cell Enzymology To Probe His-Heme Ligation in Heme Oxygenase Catalysis. <i>Biochemistry</i> , 2016, 55, 4836-4849.	2.5	3
64	Abolition of aggregation of CH2 domain of human IgG1 when combining glycosylation and protein stabilization. <i>Biochemical and Biophysical Research Communications</i> , 2021, 558, 114-119.	2.1	3
65	Unfolding is the driving force for mitochondrial import and degradation of the Parkinson's disease-related protein DJ-1. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	3
66	Reply to "The Broadly Neutralizing, Anti-HIV Antibody 4E10: an Open and Shut Case?" <i>Journal of Virology</i> , 2016, 90, 3276-3277.	3.4	2
67	Epitope-dependent thermodynamic signature of single-domain antibodies against hen egg lysozyme. <i>Journal of Biochemistry</i> , 2021, 170, 623-629.	1.7	2
68	Molecular basis for the activation of actinoporins by lipids. <i>Methods in Enzymology</i> , 2021, 649, 277-306.	1.0	2
69	Antibody recognition of complement Factor H reveals a flexible loop involved in Atypical Hemolytic Uremic Syndrome pathogenesis. <i>Journal of Biological Chemistry</i> , 2022, , 101962.	3.4	2
70	Focal accumulation of aromaticity at the CDRH3 loop mitigates 4E10 polyreactivity without altering its HIV neutralization profile. <i>IScience</i> , 2021, 24, 102987.	4.1	1
71	Intramolecular H-Bonds Govern the Recognition of a Flexible Peptide by an Antibody. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
72	Ca ²⁺ -induced structural changes and intramolecular interactions in N-terminal region of diacylglycerol kinase alpha. <i>Protein Science</i> , 2022, 31, .	7.6	1

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73	Heme-Transfer Mechanism of Structurally Similar Isd NEAT Domains of Staphylococcus Aureus Exhibiting Different Affinities for Heme. Biophysical Journal, 2014, 106, 660a.	0.5	0
74	Lipid-Protein Partnering during Pore Formation of Fragaceatoxin C. Biophysical Journal, 2016, 110, 28a.	0.5	0