

Alejandro Buschiazzo

List of Publications by Year in descending order

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77
papers

3,921
citations

126907

33
h-index

128289

60
g-index

85
all docs

85
docs citations

85
times ranked

4583
citing authors

#	ARTICLE	IF	CITATIONS
1	3D cryo-EM imaging of bacterial flagella: Novel structural and mechanistic insights into cell motility. <i>Journal of Biological Chemistry</i> , 2022, 298, 102105.	3.4	10
2	AID overexpression leads to aggressive murine CLL and nonimmunoglobulin mutations that mirror human neoplasms. <i>Blood</i> , 2021, 138, 246-258.	1.4	10
3	Role of the major determinant of polar flagellation FlhG in the endoflagella-containing spirochete <i>Leptospira</i> . <i>Molecular Microbiology</i> , 2021, 116, 1392-1406.	2.5	3
4	Allostery and protein plasticity: the keystones for bacterial signaling and regulation. <i>Biophysical Reviews</i> , 2021, 13, 943-953.	3.2	5
5	<i>Mycobacterium tuberculosis</i> FasR senses long fatty acyl-CoA through a tunnel and a hydrophobic transmission spine. <i>Nature Communications</i> , 2020, 11, 3703.	12.8	16
6	Causes of abortion in dairy cows in Uruguay. <i>Pesquisa Veterinaria Brasileira</i> , 2020, 40, 325-332.	0.5	21
7	An asymmetric sheath controls flagellar supercoiling and motility in the <i>leptospira</i> spirochete. <i>ELife</i> , 2020, 9, .	6.0	26
8	Protein Dynamics in Phosphoryl-Transfer Signaling Mediated by Two-Component Systems. <i>Methods in Molecular Biology</i> , 2020, 2077, 1-18.	0.9	1
9	Molecular adaptations of NADP-malic enzyme for its function in C4 photosynthesis in grasses. <i>Nature Plants</i> , 2019, 5, 755-765.	9.3	35
10	Two-Component Sensing and Regulation: How Do Histidine Kinases Talk with Response Regulators at the Molecular Level?. <i>Annual Review of Microbiology</i> , 2019, 73, 507-528.	7.3	108
11	Glucose-6-Phosphate Dehydrogenase from the Human Pathogen <i>Trypanosoma cruzi</i> Evolved Unique Structural Features to Support Efficient Product Formation. <i>Journal of Molecular Biology</i> , 2019, 431, 2143-2162.	4.2	9
12	Draft Genome Sequences of 40 Pathogenic <i>Leptospira</i> Strains Isolated from Cattle in Uruguay. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
13	Isolation of pathogenic <i>Leptospira</i> strains from naturally infected cattle in Uruguay reveals high serovar diversity, and uncovers a relevant risk for human leptospirosis. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006694.	3.0	57
14	Conformational plasticity of the response regulator CpxR, a key player in Gammaproteobacteria virulence and drug-resistance. <i>Journal of Structural Biology</i> , 2018, 204, 165-171.	2.8	13
15	The crystal structure of the malic enzyme from <i>Candidatus</i> <i>Phytoplasma</i> reveals the minimal structural determinants for a malic enzyme. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 332-340.	2.3	5
16	Lvr, a Signaling System That Controls Global Gene Regulation and Virulence in Pathogenic <i>Leptospira</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 45.	3.9	19
17	FcpB Is a Surface Filament Protein of the Endoflagellum Required for the Motility of the Spirochete <i>Leptospira</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 130.	3.9	20
18	<i>SIMBAD</i> : a sequence-independent molecular-replacement pipeline. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 595-605.	2.3	25

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19	Crystallization of FcpA from <i>Leptospira</i> , a novel flagellar protein that is essential for pathogenesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 123-129.	0.8	13
20	Structural Coupling between Autokinase and Phosphotransferase Reactions in a Bacterial Histidine Kinase. <i>Structure</i> , 2017, 25, 939-944.e3.	3.3	33
21	Snapshots of the Signaling Complex DesK:DesR in Different Functional States Using Rational Mutagenesis and X-ray Crystallography. <i>Bio-protocol</i> , 2017, 7, e2510.	0.4	5
22	Regulation of signaling directionality revealed by 3D snapshots of a kinase:regulator complex in action. <i>ELife</i> , 2016, 5, .	6.0	54
23	What Makes a Bacterial Species Pathogenic?: Comparative Genomic Analysis of the Genus <i>Leptospira</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004403.	3.0	253
24	A novel flagellar sheath protein, FcpA, determines filament coiling, translational motility and virulence for the <i>Leptospira</i> spirochete. <i>Molecular Microbiology</i> , 2016, 101, 457-470.	2.5	93
25	Crystal Structure of the Metallo- β -Lactamase GOB in the Periplasmic Divalent Zinc Form Reveals an Unusual Metal Site. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6013-6022.	3.2	32
26	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	12.8	113
27	Structural Basis of Pullulanase Membrane Binding and Secretion Revealed by X-Ray Crystallography, Molecular Dynamics and Biochemical Analysis. <i>Structure</i> , 2016, 24, 92-104.	3.3	26
28	A coiled coil switch mediates cold sensing by the thermosensory protein <i>DesK</i> . <i>Molecular Microbiology</i> , 2015, 98, 258-271.	2.5	50
29	Consecutive interactions with HSP90 and eEF1A underlie a functional maturation and storage pathway of AID in the cytoplasm. <i>Journal of Experimental Medicine</i> , 2015, 212, 581-596.	8.5	35
30	Conformational plasticity of a native retroviral capsid revealed by x-ray crystallography. <i>Science</i> , 2015, 349, 95-98.	12.6	32
31	Consecutive interactions with HSP90 and eEF1A underlie a functional maturation and storage pathway of AID in the cytoplasm. <i>Journal of Cell Biology</i> , 2015, 209, 2091-2104.	5.2	0
32	Allosteric Activation of Bacterial Response Regulators: the Role of the Cognate Histidine Kinase Beyond Phosphorylation. <i>MBio</i> , 2014, 5, e02105.	4.1	50
33	Structural insights into bacterial resistance to cerulenin. <i>FEBS Journal</i> , 2014, 281, 2324-2338.	4.7	35
34	Structural and Molecular Basis of the Peroxynitrite-mediated Nitration and Inactivation of <i>Trypanosoma cruzi</i> Iron-Superoxide Dismutases (Fe-SODs) A and B. <i>Journal of Biological Chemistry</i> , 2014, 289, 12760-12778.	3.4	51
35	<i>HemR</i> is an <i>OmpR</i> -like response regulator from <i>Leptospira</i> , which simultaneously effects transcriptional activation and repression of key haem metabolism genes. <i>Molecular Microbiology</i> , 2014, 94, 340-352.	2.5	23
36	Structure of a human IgA1 Fab fragment at 1.55 Å resolution: potential effect of the constant domains on antigen-affinity modulation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 388-397.	2.5	29

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37	Structural Basis for Feed-Forward Transcriptional Regulation of Membrane Lipid Homeostasis in <i>Staphylococcus aureus</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003108.	4.7	37
38	<i>Trypanosoma cruzi</i> trans-Sialidase in Complex with a Neutralizing Antibody: Structure/Function Studies towards the Rational Design of Inhibitors. <i>PLoS Pathogens</i> , 2012, 8, e1002474.	4.7	36
39	The Crystal Structure of the MAP Kinase LmaMPK10 from <i>Leishmania Major</i> Reveals Parasite-Specific Features and Regulatory Mechanisms. <i>Structure</i> , 2012, 20, 1649-1660.	3.3	19
40	Swapping FAD Binding Motifs between Plastidic and Bacterial Ferredoxin-NADP(H) Reductases. <i>Biochemistry</i> , 2011, 50, 2111-2122.	2.5	15
41	Expression, crystallization and preliminary X-ray crystallographic analysis of glucose-6-phosphate dehydrogenase from the human pathogen <i>Trypanosoma cruzi</i> in complex with substrate. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1457-1461.	0.7	8
42	Crystal structure of an enzymatically inactive trans-sialidase-like lectin from <i>Trypanosoma cruzi</i> : The carbohydrate binding mechanism involves residual sialidase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1154-1161.	2.3	19
43	Phylogenetic analysis of bovine leukemia viruses isolated in South America reveals diversification in seven distinct genotypes. <i>Archives of Virology</i> , 2010, 155, 481-489.	2.1	54
44	Crystal structure of <i>Mycobacterium tuberculosis</i> LppA, a lipoprotein confined to pathogenic mycobacteria. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 769-772.	2.6	2
45	Structural and Enzymatic Insights into the ATP Binding and Autophosphorylation Mechanism of a Sensor Histidine Kinase. <i>Journal of Biological Chemistry</i> , 2010, 285, 24892-24903.	3.4	46
46	Evidence of Adaptability in Metal Coordination Geometry and Active-Site Loop Conformation among B1 Metallo- β -lactamases. <i>Biochemistry</i> , 2010, 49, 7930-7938.	2.5	33
47	Structural plasticity and catalysis regulation of a thermosensor histidine kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16185-16190.	7.1	155
48	Structure of <i>Mycobacterium tuberculosis</i> Rv2714, a representative of a duplicated gene family in Actinobacteria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 972-977.	0.7	6
49	Active nuclear import and cytoplasmic retention of activation-induced deaminase. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 517-527.	8.2	124
50	Discovery of novel inhibitors of <i>Trypanosoma cruzi</i> trans-sialidase from in silico screening. <i>Biorganic and Medicinal Chemistry Letters</i> , 2009, 19, 589-596.	2.2	68
51	A New Generation of Specific <i>Trypanosoma cruzi</i> trans-Sialidase Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 2700-2703.	13.8	77
52	Structural insights into sialic acid enzymology. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 565-572.	6.1	70
53	Kinetic and Mechanistic Analysis of <i>Trypanosoma cruzi</i> Trans-Sialidase Reveals a Classical Ping-Pong Mechanism with Acid/Base Catalysis. <i>Biochemistry</i> , 2008, 47, 3507-3512.	2.5	55
54	Molecular Recognition and Interfacial Catalysis by the Essential Phosphatidylinositol Mannosyltransferase PimA from <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 20705-20714.	3.4	121

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55	The Crystal Structure of Rv0813c from <i>Mycobacterium tuberculosis</i> Reveals a New Family of Fatty Acid-Binding Protein-Like Proteins in Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 1899-1904.	2.2	14
56	Benzoic acid and pyridine derivatives as inhibitors of <i>Trypanosoma cruzi</i> trans-sialidase. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 2106-2119.	3.0	41
57	The crystal structure of <i>M. leprae</i> ML2640c defines a large family of putative S-adenosylmethionine-dependent methyltransferases in mycobacteria. <i>Protein Science</i> , 2007, 16, 1896-1904.	7.6	14
58	Structural and Kinetic Analysis of Two Covalent Sialosyl-Enzyme Intermediates on <i>Trypanosoma rangeli</i> Sialidase. <i>Journal of Biological Chemistry</i> , 2006, 281, 4149-4155.	3.4	75
59	Crystal structure, catalytic mechanism, and mitogenic properties of <i>Trypanosoma cruzi</i> proline racemase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1705-1710.	7.1	92
60	Structural basis of lipid biosynthesis regulation in Gram-positive bacteria. <i>EMBO Journal</i> , 2006, 25, 4074-4083.	7.8	104
61	Continuous fluorimetric assay for high-throughput screening of inhibitors of trans-sialidase from <i>Trypanosoma cruzi</i> . <i>Analytical Biochemistry</i> , 2006, 357, 302-304.	2.4	19
62	Crystallization and preliminary crystallographic analysis of PimA, an essential mannosyltransferase from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 518-520.	0.7	12
63	Crystal structure of glycogen synthase: homologous enzymes catalyze glycogen synthesis and degradation. <i>EMBO Journal</i> , 2004, 23, 3196-3205.	7.8	155
64	Structural Insights into the Catalytic Mechanism of <i>Trypanosoma cruzi</i> trans-Sialidase. <i>Structure</i> , 2004, 12, 775-784.	3.3	197
65	Preliminary crystallographic studies of glycogen synthase from <i>Agrobacterium tumefaciens</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 526-528.	2.5	5
66	<i>Trypanosoma cruzi</i> Trans-sialidase Operates through a Covalent Sialyl-Enzyme Intermediate: Tyrosine Is the Catalytic Nucleophile. <i>Journal of the American Chemical Society</i> , 2003, 125, 7532-7533.	13.7	188
67	The High Resolution Structures of Free and Inhibitor-bound <i>Trypanosoma rangeli</i> Sialidase and its Comparison with <i>T. cruzi</i> Trans-sialidase. <i>Journal of Molecular Biology</i> , 2003, 325, 773-784.	4.2	67
68	The Crystal Structure and Mode of Action of Trans-Sialidase, a Key Enzyme in <i>Trypanosoma cruzi</i> Pathogenesis. <i>Molecular Cell</i> , 2002, 10, 757-768.	9.7	214
69	The trans-sialidase from the african trypanosome <i>Trypanosoma brucei</i> . <i>FEBS Journal</i> , 2002, 269, 2941-2950.	0.2	54
70	Probing molecular function of trypanosomal sialidases: single point mutations can change substrate specificity and increase hydrolytic activity. <i>Glycobiology</i> , 2001, 11, 305-311.	2.5	51
71	Structural basis of sialyltransferase activity in trypanosomal sialidases. <i>EMBO Journal</i> , 2000, 19, 16-24.	7.8	124
72	The tyrosine aminotransferase from <i>Trypanosoma rangeli</i> : sequence and genomic characterization. <i>FEMS Microbiology Letters</i> , 2000, 189, 253-257.	1.8	0

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73	Trypanosoma rangeli sialidase: cloning, expression and similarity to T.cruzi trans-sialidase. Glycobiology, 1997, 7, 1167-1173.	2.5	44
74	Medium scale production and purification to homogeneity of a recombinant trans-sialidase from Trypanosoma cruzi. Cellular and Molecular Biology, 1996, 42, 703-10.	0.9	26
75	Sequence of a Trypanosoma rangeli gene closely related to Trypanosoma cruzi trans-sialidase. Molecular and Biochemical Parasitology, 1993, 62, 115-116.	1.1	23
76	Identification of the gene(s) coding for the trans-sialidase of Trypanosoma cruzi.. EMBO Journal, 1992, 11, 1705-1710.	7.8	101
77	Sequence of the gene for a Trypanosoma cruzi protein antigenic during the chronic phase of human Chagas disease. Molecular and Biochemical Parasitology, 1992, 54, 125-128.	1.1	24