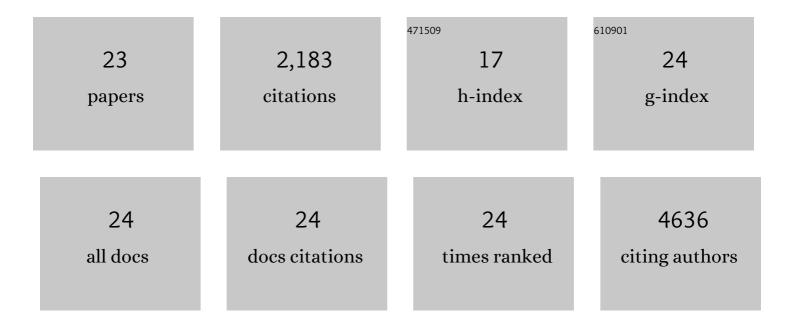
## Sergio G Bartual

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The citron homology domain as a scaffold for Rho1 signaling. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
2	A missense mutation in the catalytic domain of <i>O</i> â€GlcNAc transferase links perturbations in protein <i>O</i> â€GlcNAcylation to Xâ€linked intellectual disability. FEBS Letters, 2020, 594, 717-727.	2.8	40
3	Genetic recoding to dissect the roles of site-specific protein O-GlcNAcylation. Nature Structural and Molecular Biology, 2019, 26, 1071-1077.	8.2	50
4	Mechanisms of redundancy and specificity of the Aspergillus fumigatus Crh transglycosylases. Nature Communications, 2019, 10, 1669.	12.8	18
5	Structural insights into the binding and catalytic mechanisms of the <i>Listeria monocytogenes</i> bacteriophage glycosyl hydrolase PlyP40. Molecular Microbiology, 2018, 108, 128-142.	2.5	12
6	Three-dimensional structures of Lipoproteins from Streptococcus pneumoniae and Staphylococcus aureus. International Journal of Medical Microbiology, 2018, 308, 692-704.	3.6	11
7	Tetrahydroisoquinoline-7-carboxamide Derivatives as New Selective Discoidin Domain Receptor 1 (DDR1) Inhibitors. ACS Medicinal Chemistry Letters, 2017, 8, 327-332.	2.8	31
8	Structure-Based Design of Tetrahydroisoquinoline-7-carboxamides as Selective Discoidin Domain Receptor 1 (DDR1) Inhibitors. Journal of Medicinal Chemistry, 2016, 59, 5911-5916.	6.4	51
9	Structural basis of PcsB-mediated cell separation in Streptococcus pneumoniae. Nature Communications, 2014, 5, 3842.	12.8	82
10	Structural Basis for Selective Recognition of Endogenous and Microbial Polysaccharides by Macrophage Receptor SIGN-R1. Structure, 2014, 22, 1595-1606.	3.3	31
11	Structure and Cell Wall Cleavage by Modular Lytic Transglycosylase MltC of <i>Escherichia coli</i> . ACS Chemical Biology, 2014, 9, 2058-2066.	3.4	41
12	Crystal structures of CbpF complexed with atropine and ipratropium reveal clues for the design of novel antimicrobials against Streptococcus pneumoniae. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 129-135.	2.4	10
13	Molecular architecture of <i>Streptococcus pneumoniae</i> surface thioredoxinâ€fold lipoproteins crucial for extracellular oxidative stress resistance and maintenance of virulence. EMBO Molecular Medicine, 2013, 5, 1852-1870.	6.9	99
14	Pneumococcal surface proteins: when the whole is greater than the sum of its parts. Molecular Oral Microbiology, 2012, 27, 221-245.	2.7	92
15	Crystallization and preliminary X-ray diffraction analysis of phosphoglycerate kinase fromStreptococcus pneumoniae. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1285-1289.	0.7	8
16	Target highlights in CASP9: Experimental target structures for the critical assessment of techniques for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2011, 79, 6-20.	2.6	19
17	Structure of the bacteriophage T4 long tail fiber receptor-binding tip. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20287-20292.	7.1	159
18	Two-chaperone assisted soluble expression and purification of the bacteriophage T4 long tail fibre protein gp37. Protein Expression and Purification, 2010, 70, 116-121.	1.3	43

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#	Article	IF	CITATIONS
19	Molecular epidemiology of clinical Acinetobacter baumannii and Acinetobacter genomic species 13TU isolates using a multilocus sequencing typing scheme. Clinical Microbiology and Infection, 2008, 14, 708-715.	6.0	60
20	Comparison of prokaryotic diversity at offshore oceanic locations reveals a different microbiota in the Mediterranean Sea. FEMS Microbiology Ecology, 2006, 56, 389-405.	2.7	580
21	Diversity of halophilic archaea in the crystallizers of an Adriatic solar saltern. FEMS Microbiology Ecology, 2005, 54, 491-498.	2.7	67
22	Genetic analysis of housekeeping genes reveals a deep-sea ecotype of Alteromonas macleodii in the Mediterranean Sea. Environmental Microbiology, 2005, 7, 649-659.	3.8	70
23	Development of a Multilocus Sequence Typing Scheme for Characterization of Clinical Isolates of Acinetobacter baumannii. Journal of Clinical Microbiology, 2005, 43, 4382-4390.	3.9	595