

## FULL LIST OF PUBLICATIONS, PATENTS AND CRYSTALLOGRAPHIC STRUCTURES

### **A Buschiazzo - January 2021**

Bibliometric data (Google Scholar):

h-index: 34

i10: 55

Number of citations : 3842

14 papers with  $\geq 100$  citations (4 as 1<sup>st</sup> author; 2 as corresponding author; the most cited as 1<sup>st</sup> author with 255 citations)

### Publications

1. Lara J, Diacovich L, Trajtenberg F, Larrieux N, Malchiodi EL, Fernández MM, Gago G, Gramajo H\*, **Buschiazzo A\*** (2020) *Mycobacterium tuberculosis* FasR senses long fatty acyl-CoA through a tunnel and a hydrophobic transmission spine. *Nat Commun.* **11**:3703 [\*co-corresponding authors]
2. Gibson KH, Trajtenberg F, Wunder EA, Brady MR, San Martin F, Mechaly A, Shang Z, Liu J, Picardeau M, Ko A\*, **Buschiazzo A\***, Sindelar CV\*. (2020) An asymmetric sheath controls flagellar supercoiling and motility in the leptospira spirochete. *eLife.* **11**:9 [\*co-corresponding authors]
3. Macías-Rioseco M, Silveira C, Fraga M, Casaux L, Cabrera A, Francia ME, Robello C, Maya L, Zarantonelli L, Suanes A, Colina R, **Buschiazzo A**, Giannitti F, Riet-Correa F. (2020) Causes of abortion in dairy cows in Uruguay. *Pesqui Vet Bras.* **40**:325-332.
4. Trajtenberg F\*, **Buschiazzo A\*** (2020) Protein Dynamics in Phosphoryl-Transfer Signaling Mediated by Two-Component Systems. *Methods Mol Biol.* **2077**:1-18 [\*co-corresponding authors]
5. **Buschiazzo A\***, Trajtenberg F\*. (2019) Two-Component Sensing and Regulation: How Do Histidine Kinases Talk with Response Regulators at the Molecular Level? *Annu Rev Microbiol.* **73** doi:10.1146/annurev-micro-091018-054627. [\*co-corresponding authors]
6. Alvarez CE, Bovdilova A, Höppner A, Wolff C-C, Saigo M, Trajtenberg F, Zhang T, **Buschiazzo A**, Nagel-Steger L, Drincovich MF, Lercher MJ, Maurino VG. (2019) Molecular adaptations of NADP-malic enzyme for its function in C4 photosynthesis in grasses. *Nat Plants.* **5**:755-765
7. Nieves C, Ferrés I, Díaz-Viraqué F, **Buschiazzo A**, Zarantonelli L, Iraola G. (2019) Draft Genome Sequences of 40 Pathogenic *Leptospira* Strains Isolated from Cattle in Uruguay. *Microbiol Resour Announc.* **8**:e00893-19.
8. Ortiz C, Botti H, **Buschiazzo A\***, Comini MA\*. (2019) Glucose-6-Phosphate Dehydrogenase from the Human Pathogen *Trypanosoma cruzi* Evolved Unique Structural Features to Support Efficient Product Formation. *J Mol Biol.* **431**:2143-2162. [\*co-corresponding authors]
9. Zarantonelli L, Suanes A, Meny P, Buroni F, Nieves C, Salaberry X, Briano C, Ashfield N, Da Silva Silveira C, Dutra F, Easton C, Fraga M, Giannitti F, Hamond C, Macías-Rioseco M, Menéndez C, Mortola A, Picardeau M, Quintero J, Ríos C, Rodríguez V, Romero A, Varela G, Rivero R\*, Schelotto F\*, Riet-Correa F\*, **Buschiazzo A\***; Grupo de Trabajo Interinstitucional de Leptospirosis Consortium. (2018) Isolation of pathogenic *Leptospira* strains from naturally infected cattle in Uruguay reveals high serovar diversity

and uncovers a relevant risk for human leptospirosis. *PLoS Negl Trop Dis*. **12**:e0006694. [\*co-corresponding authors]

10. Mechaly AE, Haouz A, Sassoon N, **Buschiazzo A**, Betton JM, Alzari PM. (2018) Conformational plasticity of the response regulator CpxR, a key player in Gammaproteobacteria virulence and drug-resistance. *J Struct Biol*. **204**:165-171.
11. Simpkin AJ, Simkovic F, Thomas JMH, Savko M, Lebedev A, Uski V, Ballard C, Wojdyr M, Wu R, Sanishvili R, Xu Y, Lisa MN, **Buschiazzo A**, Shepard W, Rigden DJ, Keegan RM. (2018) SIMBAD: a sequence-independent molecular-replacement pipeline. *Acta Crystallogr D Struct Biol*. **74**:595-605.
12. Wunder EA Jr, Slamti L, Suwondo DN, Gibson KH, Shang Z, Sindelar CV, Trajtenberg F, **Buschiazzo A**, Ko AI, Picardeau M. (2018) FcpB Is a Surface Filament Protein of the Endoflagellum Required for the Motility of the Spirochete *Leptospira*. *Front Cell Infect Microbiol*. **8**:130.
13. Alvarez CE, Trajtenberg F, Larrieux N, Saigo M, Golic A, Andreo CS, Hogenhout SA, Mussi MA, Drincovich MF\*, **Buschiazzo A\***. (2018) The crystal structure of the malic enzyme from Candidatus *Phytoplasma* reveals the minimal structural determinants for a malic enzyme. *Acta Crystallogr D Struct Biol*. **74**:332-340. [\*co-corresponding authors]
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15. Imelio JA, Larrieux N, Mechaly AE, Trajtenberg F, **Buschiazzo A**. Snapshots of the Kinase:Regulator Complex DesK:DesR in Different Functional States, by Using Rational Mutagenesis and X-Ray Crystallography. (2017) *Bio Protoc*. **7**:e2510.
16. Mechaly AE, Soto Diaz S, Sassoon N, **Buschiazzo A**, Betton JM, Alzari PM. Structural coupling between autokinase and phosphotransferase reactions in a bacterial histidine kinase. (2017) *Structure*. **25**:939-944.
17. San Martin F, Mechaly AE, Larrieux N, Wunder EA Jr, Ko AI, Picardeau M, Trajtenberg F, **Buschiazzo A**. Crystallization of FcpA from *Leptospira*, a novel flagellar protein that is essential for pathogenesis. (2017) *Acta Crystallogr F Struct Biol Commun*. **73**:123-129.
18. Trajtenberg F, Imelio JA, Machado MR, Larrieux N, Marti MA, Obal G, Mechaly AE, **Buschiazzo A**. Regulation of signaling directionality revealed by 3D snapshots of a kinase:regulator complex in action. (2016) *Elife*. **5**:e21422.
19. Morán-Barrio J, Lisa MN, Larrieux N, Drusin SI, Viale AM, Moreno DM, **Buschiazzo A\***, Vila AJ\*. Crystal structure of the metallo- $\beta$ -lactamase GOB in the periplasmic dizinc form reveals an unusual metal site. (2016) *Antimicrob Agents Chemother*. **60**:6013-6022. [\*co-corresponding authors]
20. Wunder EA Jr, Figueira CP, Benaroudj N, Hu B, Tong BA, Trajtenberg F, Liu J, Reis MG, Charon NW, **Buschiazzo A**, Picardeau M, Ko AI. A novel flagellar sheath protein, FcpA, determines filament coiling, translational motility and virulence for the *Leptospira* spirochete. (2016) *Mol Microbiol*. **101**:457-470.
21. Meyer PA, Socias S, Key J, Ransey E, Tjon EC, **Buschiazzo A**, Lei M, Botka C, Withrow J, Neau D, Rajashankar K, Anderson KS, Baxter RH, Blacklow SC, Boggon TJ, Bonvin AM, Borek D, Brett TJ, Caflisch A, Chang CI, Chazin WJ, Corbett KD, Cosgrove MS, Crosson S, Dhe-Paganon S, Di Cera E, Drennan CL, Eck MJ, Eichman BF, Fan QR, Ferré-

- D'Amaré AR, Fromme JC, Garcia KC, Gaudet R, Gong P, Harrison SC, Heldwein EE, Jia Z, Keenan RJ, Kruse AC, Kvensakul M, McLellan JS, Modis Y, Nam Y, Otwinowski Z, Pai EF, Pereira PJ, Petosa C, Raman CS, Rapoport TA, Roll-Mecak A, Rosen MK, Rudenko G, Schlessinger J, Schwartz TU, Shamoo Y, Sondermann H, Tao YJ, Tolia NH, Tsodikov OV, Westover KD, Wu H, Foster I, Fraser JS, Maia FR, Gonen T, Kirchhausen T, Diederichs K, Crosas M, Sliz P. Data publication with the structural biology data grid supports live analysis. (2016) *Nat Commun.* **7**:10882.
22. Fouts DE, Matthias MA, Adhikarla H, Adler B, Amorim-Santos L, Berg DE, Bulach D, **Buschiazzo A**, Chang YF, Galloway RL, Haake DA, Haft DH, Hartskeerl R, Ko AI, Levett PN, Matsunaga J, Mechaly AE, Monk JM, Nascimento AL, Nelson KE, Palsson B, Peacock SJ, Picardeau M, Ricaldi JN, Thaipandungpanit J, Wunder EA Jr, Yang XF, Zhang JJ, Vinetz JM. What makes a bacterial species pathogenic? : comparative genomic analysis of the genus *Leptospira*. (2016) *PLoS Negl Trop Dis.* **10**:e0004403.
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  25. Obal G, Trajtenberg F, Carrión F, Tomé L, Larrieux N, Zhang X, Pritsch O\*, **Buschiazzo A\***. Conformational plasticity of a native retroviral capsid revealed by x-ray crystallography. (2015) *Science.* **349**:95-98. [\*co-corresponding authors]
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- constant domains on antigen-affinity modulation. (2013) *Acta Crystallogr. Sect. D Biol. Crystallogr.* **69**:388-397.
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52. Shepard W, Haouz A, Grana M, **Buschiazzo A**, Betton JM, Cole ST, Alzari PM. The crystal structure of Rv0813c from *Mycobacterium tuberculosis* reveals a new family of fatty acid-binding protein-like proteins in bacteria. (2007) *J. Bacteriol.* **189**:1899-1904.
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### **Patents**

1. "Crystallographic structure of TcPRACA and uses therefor"

Minoprio, P., Alzari, P.M., **Buschiazzo, A.**, Degrave, W., Gregoire, C. and Chamond, N.  
Institut Pasteur (Paris, France)

European Patent Office, BRPI0410975, 2006-07-04.

United States Patent Application, A1, Document N° 20050250195, Nov 10 2005.

### **Deposited experimental 3D structures in the Protein Data Bank (PDB)**

One hundred (100) structures solved, with access codes:

1MR5, 1MS0, 1MS1, 1MS3, 1MS4, 1MS5, 1MS8, 1MS9, 1MZ5, 1MZ6, 1N1S, 1N1T, 1N1V, 1N1Y, 1RZU, 1RZV, 1S0I, 1S0J, 1W61, 1W62, 2A75, 2AGS, 2AH2, 2CKD, 2F3X, 2F41, 2FHR, 2FWV, 2GEJ, 2GEK, 2UYO, 2UYQ, 2V7S, 2WAM, 2XNC, 2XNJ, 2YOC, 3B69, 3EHF, 3EHG, 3EHH, 3EHJ, 3GIE, 3GIF, 3GIG, 3I0V, 3I11, 3I13, 3I14, 3I15, 3M8O, 3OPZ, 3PG1, 3PJQ, 3QNX, 3QNY, 3QNZ, 3QO0, 3QO1, 3UIB, 4A0X, 4A0Y, 4A0Z, 4A12, 4DVH, 4EMX, 4LE0, 4LE1, 4LE2, 4LDZ, 4LS5, 4LS6, 4LS7, 4LS8, 4PH0, 4PH1, 4PH2, 4PH3, 4Q7E, 5CEE, 5IUJ, 5IUK, 5IUL, 5IUM, 5IUN, 5K0W, 6BY0, 6C7N, 6D23, 6D24, 6NQW, 6NQX, 6NQY, 6NQZ, 6OC8, 6O6P, 6O6O, 6O6N, 6PWB, 6XQK (except for the last one, which is on hold until publication, the rest are publicly available)