

# Hugo Sámano-Sánchez

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## Curriculum Vitae (January 18, 2019)

### Summary

Mostly interested in computational approaches to understand host-pathogen interactions. Trained in Genomic Sciences I soon got into bioinformatics and computational biology. After the university I worked on antibody repertoires to compare immunologic challenges. In 2013 I started a masters at the University of Basel and performed my thesis at the National University of Singapore working with lipidomics data from clinical isolates of malaria patients. Currently, I am on my last year of my PhD working on Short Linear Motifs at the host-pathogen interface.

### Education

- 10/15 - today **Ph.D. in Molecular Biology**, European Molecular Biology Laboratory / University of Heidelberg, Heidelberg, Germany.
- 09/13 - 02/15 **Joint Master Programme in Infectious Diseases, Vaccinology and Drug Discovery**, University of Basel and the National University of Singapore, Switzerland and Singapore.
- 08/07 - 06/11 **B.Sc. in Genomics Sciences**, National Autonomous University of Mexico, Cuernavaca, Mexico.  
With honours.

### Research Experience

- 10/15 - today **PhD Student**, European Molecular Biology Laboratory, Heidelberg, Germany.
- Advisor: Dr. Toby J. Gibson.
  - Computational screening for Eukaryotic Short Linear Motifs being mimicked in bacterial proteins. Two publications.
  - Computational prediction of Linear Motifs at the *Plasmodium*-Host interface.
- 01/14 - 02/15 **Master thesis**, Vivax Malaria Lab, National University of Singapore, Singapore.
- Advisors: Dr. Bruce M. Russell and Prof. Dr. Markus R. Wenk.
  - Data analysis of Mass Spectrometry and Tandem Mass Spectrometry experiments to identify characteristic lipids of *Plasmodium vivax*-infected human reticulocytes. Thesis.
  - Bioinformatics analyses to study receptor-ligand interactions during *Plasmodium vivax* reticulocyte infection. One publication.
- 10/12 - 07/13 **Research Assistant**, National Institute of Public Health, Cuernavaca, Mexico.
- Advisor: Dr. Jesus Martinez-Barnette.
  - Bioinformatics analysis of high-throughput sequencing data from human and murine lymphocyte antigen receptors challenged with inactivated viruses or bacterial pathogens, respectively. Three publications.
- 01/12 - 09/12 **Bioinformatics Consultant**, Winter Genomics (<http://www.wintergenomics.com/>), Cuernavaca, Mexico.
- Advisor: Dr. Enrique Morett.
  - Genome assembly, annotation and structural variation analysis of two *Babesia* species under two growth conditions. Bioinformatics analysis service at the Winter Genomics enterprise (<http://www.wintergenomics.com/>).

- 08/10 – 12/11 **Undergraduate Research Assistant**, Center for Genomic Sciences, National Autonomous University of Mexico, Cuernavaca, Mexico.
- Advisor: Dr. Esperanza Martinez-Romero .
  - Phylogenetic analysis of cospeciation events between scale insects and their symbiotic bacteria. One publication.

## Scientific Publications

\* Contributed equally.

- Sampietro, D., **Sámano-Sánchez, H.**, ..., Gibson, T.J., Kumar, M. Conserved SQ and QS motifs in bacterial effectors suggest pathogen interplay with the ATM kinase family during infection. *bioRxiv*, 2018. doi: 10.1101/364117
- Gouw, M., Michael, S., **Sámano-Sánchez, H.**, ..., Gibson, J.T. The eukaryotic linear motif resource - 2018 update. *Nucleic Acids Research*. doi: 10.1093/nar/gkx1077
- Kosaisavee, V., ..., **Sámano-Sánchez, H.**, ..., Rénia, L., Russell, B. Strict tropism for CD71+/CD234+ human reticulocytes limits the zoonotic potential of *Plasmodium cynomolgi*. *Blood*, 2017. doi: 10.1182/blood-2017-02-764787
- Gouw, M., **Sámano-Sánchez, H.**, ..., Dinkel, H. Exploring Short Linear Motifs Using the ELM Database and Tools. *Current Protocols in Bioinformatics*, 2017. doi: 10.1002/cpbi.26
- Godoy-Lozano, E.E., ..., **Sámano-Sánchez, H.**, ..., Martínez-Barnette, J. Lower IgG somatic hypermutation rates during acute dengue virus infection is compatible with a germinal center-independent B cell response. *Genome Medicine*, 2016. doi: 10.1186/s13073-016-0276-1
- Cortina-Ceballos, B., ..., **Sámano-Sánchez, H.**, ..., Martínez-Barnette, J. Longitudinal analysis of the peripheral B cell repertoire reveals unique effects of immunization with a new Influenza virus strain. *Genome Medicine*, 2015. doi: 10.1186/s13073-015-0239-y
- Cortina-Ceballos, B.\*, Godoy-Lozano, E.E.\*, **Sámano-Sánchez, H.\***, ..., Martínez-Barnette, J. Reconstructing and mining the B cell repertoire with ImmuneDiversity. *mAbs*, 2015. doi: 10.1080/19420862.2015.1026502
- Rosenblueth, M., Sayavedra, L., **Sámano-Sánchez, H.**, Roth, A., Martínez-Romero, E. Evolutionary Relationships of Flavobacteria and Enterobacterial Endosymbionts with their Scale Insect Hosts (Hemiptera: Coccoidea). *Journal of Evolutionary Biology*, 2011. doi: 10.1111/j.1420-9101.2012.02611.x

## Awards and Scholarships

- Travel Fellow Award from the National Institute of Allergy and Infectious Diseases to attend the 5th International Conference of Research on *Plasmodium vivax* Malaria.
- Travel Fellow Award from the *Fundação de Amparo à Pesquisa do Estado de São Paulo* to participate in the Science of Eradication: Malaria course in Sao Paulo, Brazil.
- Scholarship from the Swiss Tropical and Public Health Institute to study the Joint master program on Infectious Diseases, Vaccinology and Drug Discovery.

## Talks and Posters

### Invited talks

- Institutional seminar at the Biotechnology Research Institute (IIB), National University of San Martin (UNSAM), Buenos Aires, Argentina, 2017.

### Selected talks

- VIII Argentinian Bioinformatics and Computational Biology Congress, Posadas, Argentina, 2017.
- 5th International Conference of Research on *Plasmodium vivax* Malaria, Bali, Indonesia, 2015.

### Poster presentations

- EMBO Workshop on Molecular advances and parasite strategies in host infection, Les Embiez Island, France, 2018.
- EMBO Conference on Hijacking host signalling and epigenetic mimicry during infections, Paris, France, 2017.
- 2nd Interdisciplinary signaling workshop, Visegrad, Hungary, 2017.
- The modularity of signaling proteins and networks, Seefeld, Austria, 2016.

## Teaching

### Organizer

- Bioinformatics Tools for Protein Structure, Disorder and Interaction Analysis, National University of San Martin, Buenos Aires, Argentina, 2017.

### Mentor and lecturer

- Protein bioinformatics part of EMBL Predoc Course, Heidelberg, Germany, 2018.
- Basic Teaching Module part of EMBL Predoc Course: Phylogenetics, Tools for 3D molecule interactive visualization and R datasets. Heidelberg, Germany, 2016.

### Teaching assistant

- Linear Algebra. National Autonomous University of Mexico. Cuernavaca, Mexico, 2012.
- Seminars on Genomic Applications. National Autonomous University of Mexico. Cuernavaca, Mexico, 2011.
- Discrete Mathematics. National Autonomous University of Mexico. Cuernavaca, Mexico, 2010 and 2011.

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## Skills and Interests

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| Programming languages | R/Bioconductor, Bash, basics of Python, Perl and C                     |
| Languages             | Spanish (native), English (advanced), French (basic)                   |
| Research interests    | Host-Pathogen interactions. Genomic approaches in infectious diseases. |
| Other interests       | Traveling, cooking, photography  |

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## References

- Dr. Toby, J. Gibson (toby.gibson@embl.de). Team Leader at the European Molecular Biology Laboratory, Heidelberg, Germany.
- Dr. Bruce M. Russell (b.russell@otago.ac.nz). Associate Professor at University of Otago, Otago, New Zealand.
- Dr. Jesús Martínez-Barnetche ((jmbarnet@insp.mx). Director and Principal Investigator at the Center for Research on Infectious Diseases (CISEI) of the National Institute of Public Health, Cuernavaca, Mexico.