Hugo C. Sámano-Sánchez

Curriculum Vitae

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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. I defended my PhD thesis at the University of Heidelberg, after working with Short Linear Motifs at the host-pathogen interface at EMBL Heidelberg. Currently, I work as a lecturer at the Biomedical Informatics bachelor's programme from the Zhejiang University-University of Edinburgh Institute in China.

Education

10/15 - 12/19   **Ph.D. in Molecular Biology**, European Molecular Biology Laboratory / University of Heidelberg, Heidelberg, Germany.
Magna cum laude.

09/13 - 02/15   **Joint Master Programme in Infectious Diseases, Vaccinology and Drug Discovery**, University of Basel, Switzerland and the National University of Singapore, Singapore.

08/07 - 06/11   **B.Sc. in Genomics Sciences**, National Autonomous University of Mexico, Cuernavaca, Mexico.
With honours.

Specific Training

November 2019   **ELIXIR Instructor Training workshop**, European Molecular Biology Laboratory, Heidelberg, Germany.

January 2019   **EICAT Complementary Scientific Skills Training: Scientific Presentations**, European Molecular Biology Laboratory, Heidelberg, Germany.

Professional Experience

10/21 - current   **Lecturer**, Zhejiang University-University of Edinburgh Institute, Haining, China.

05/20 - 09/21   **Collaborator in the teaching activities of the Biomedical Informatics bachelor's programme**, Zhejiang University-University of Edinburgh Institute, Haining, China.

10/15 - 01/20   **PhD Student / Bridging Postdoctoral Fellow**, European Molecular Biology Laboratory, Heidelgerg, Germany.
- Advisor: Dr. Toby J. Gibson.
- Computational screening for Eukaryotic Short Linear Motifs mimicked by bacterial proteins. Five 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-Barnetche.
- 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 start-up.

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.

- Kumar, K., Michael, S., Alvarado-Valverde, J., Meszaros, B., **Sámano-Sánchez, H.**, Zeke, A., Dobson, L., Lazar, T., Ord, M., Nagpal, A., Farahi, N., Kaser, M., Kraleti, R., Davey, N.E., Pancsa, R., Chemes, L.B., Gibson, T.J., The eukaryotic linear motif resource: 2022 release. *Nucleic Acids Research*, 2022. doi: 10.1093/nar/gkab975

- Mezsaros, B., **Sámano-Sánchez, H.**, Alvarado-Valverde, J., Calyseva, J., Martinez-Perez, E., Alves, R., Shields, D.C., Kumar, M., Rippmann, F., Chemes, L.B., Gibson, T.J. Short linear motif candidates in the cell entry system used by SARS-CoV-2 and their potential therapeutic implications. *Science Signaling*, 2021. doi: 10.1126/scisignal.abd0334

- **Sámano-Sánchez, H.**, Gibson, T.J. Mimicry of Short Linear Motifs by Bacterial Pathogens: A Drugging Opportunity. *Trends in Biochemical Sciences*, 2020. doi: 10.1016/j.tibs.2020.03.003

- Kumar, M., Gouw, M., **Sámano-Sánchez, H.**, Pancsa, R., Glavina, J., Diakogianni, A., Alvarado-Valverde, J., Bukirova, D., Calyseva, J., Palopoli, N., Davey, N.E., Chemes, L.B., Gibson, T.J. ELM - the eukaryotic linear motif resource in 2020. *Nucleic Acids Research*, 2019. doi: 10.1093/nar/gkz1030

- Sampietro, D., **Sámano-Sánchez, H.**, Davey, N.E., Sharan, M., Meszaros, B., 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.**, Kumar, M., Zeke, A., Lang, B., Bely B., Chemes, L.B., Davey, N.E., Deng, Z., Diella, F., Gurth, C.-M., Huber, A.-K., Kleinsorg, S., Schlegel, L.S., Palopoli, N., Roey, K.V., Altenberg, B., Remenyi, A., Dinkel, H., Gibson, J.T. The eukaryotic linear motif resource - 2018 update. *Nucleic Acids Research*. doi: 10.1093/nar/gkx1077

- Kosaisavee, V., Suwanarusk, R., Chua, A.C.Y., Kyle, D.E., Malleret, B., Zhang, R., Imwong, M., Imerbsin, R., Ubalee, R., **Sámano-Sánchez, H.**, Yeung, B.K.S., Ong, J.J.Y., Lombardini, E., Nosten, F., Tan, K.S.W., Bifani, P., Snounou, G., 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.**, Roey, K.V., Diella, F., Gibson, T.J., 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., Tellez-Sosa, J., Sanchez-Gonzalez, G., **Sámano-Sánchez, H.**, Aguilar-Salgado, A., Salinas-Rodriguez, A., Cortina-Ceballos, B., Vivanco-Cid, H., Hernandez-Flores, K., Pfaff, J.M., Kahle, K.M., Doranz, B.J., Gomez-Barreto, R.E., Valdovinos-Torres, H., Lopez-Martinez, I., Rodriguez, M.H., Martínez-Barnetche, 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., Godoy-Lozano, E.E., Tellez-Sosa, M., Ovilla-Munoz, M., **Sámano-Sánchez, H.**, Aguilar-Salgado, A., Gomez-Barreto, R.E., Valdovinos-Torres, H., Lopez-Martinez, I., Aparicio-Antonio, R., Rodriguez, M.H., Martínez-Barnetche, 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.***, Aguilar-Salgado, A., Velasco-Herrera, M.D.C., Vargas-Chavez, C., Velazquez-Ramirez, D., Romero, G., Moreno, J., Tellez-Sosa, J., Martínez-Barnetche, 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 *Fundação de Amparo à Pesquisa do Estado de São Paulo* to participate in the Science of Eradication: Malaria course in Sao Paulo, Brazil (2015).
- Travel Fellow Award from the National Institute of Allergy and Infectious Diseases to attend the 5th International Conference of Research on *Plasmodium vivax* Malaria (2015).
- Scholarship from the Swiss Tropical and Public Health Institute to study the Joint master program on Infectious Diseases, Vaccinology and Drug Discovery (2013-2015).

Talks and Posters

Invited talks

- Talk to the Parasitology Unit of the Center for Infectious Diseases, Heidelberg University Hospital, Heidelberg, Germany, 2019.
- Institutional seminar at the Biotechnology Research Institute (IIB), National University of San Martin (UNSAM), Buenos Aires, Argentina, 2017.

Selected talks

- Cold Spring Harbor Asia Conference: Bacterial Infection and Host Defense, Suzhou, China, 2019.
- VIII Argentinian Bioinformatics and Computational Biology Congress, Posadas, Argentina, 2017.
- 5th International Conference of Research on *Plasmodium vivax* Malaria, Bali, Indonesia, 2015.

Poster presentations

- BioMalPar XV: Biology and Pathology of the Malaria Parasite, Heidelberg, Germany, 2019.
- 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

Mentor

- Master thesis supervisor of Davide Sampietro, Erasmus student from Universitá deli Studi di Milano - Bicocca, 2018.

Organizer

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

Lecturer

- IBI1, IBMS1, ICMB1, ADS2, GP2, MI2, BMI3, CBSB3 and IBMS3 courses of the Biomedical Informatics and Biomedical Sciences Programmes, Zhejiang University-University of Edinburgh Institute, China, 2020-2022.
- Biomedical Disorders 1 course of the Integrative Biomedical Sciences PhD programme, Zhejiang University-University of Edinburgh Institute, China, 2021-2022.
- 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.

Skills and Interests

Programming languages	R/Bioconductor, Bash. Basics of: Python, Perl and C.
Software	ggplot2, Git, SLURM, Singularity, PyMOL, UCSF Chimera, Modeller, MEGA, IGV, XCMS, Bowtie2, minimap2, samtools, Alfred, LaTeX
Languages	Spanish (native), English (advanced), French (basic), Chinese (entry level)
Research interests	Host-Pathogen interactions. Genomic approaches in infectious diseases.
Other interests	Traveling, cooking, photography

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.