

# 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 **Faculty**, Zhejiang University-University of Edinburgh Institute, Haining, China.
- 05/20 - 09/21 **Lecturer**, *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, Heidelberg, 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.

## Appointments

- 05/22 - current **PhD Supervisor**, *College of Medicine and Veterinary Medicine*, University of Edinburgh, Scotland.
- 10/21 - current **Lecturer**, *Biomedical Sciences and Biomedical Informatics bachelor programmes*, Zhejiang University-University of Edinburgh Institute, Haining, China.
- 09/21 - current **Honorary Lecturer**, *College of Medicine and Veterinary Medicine*, University of Edinburgh, Scotland.

## Scientific Publications

\* Contributed equally.

- **Sámamo-Sánchez, H.**, Gibson, T.J., Chemes, L.B., Using Linear Motif Database Resources to Identify SH2 Domain Binders. *Methods Mol Biol*, 2023. doi: 10.1007/978-1-0716-3393-9\_9
- Kumar, K., Michael, S., Alvarado-Valverde, J., Meszaros, B., **Sámamo-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., **Sámamo-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
- **Sámamo-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., **Sámamo-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., **Sámamo-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., **Sámamo-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

- Second prize at the Teaching Competition for young faculty of Zhejiang University-University of Edinburgh Institute (2022).
- 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 for the BioLinkX seminar series, Zhejiang University Student Bioinformatics Association, Hangzhou, China, 2023.
- 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.

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## Teaching

### Mentor

- PhD assistant supervisor of Jiayuan Chen, University of Edinburgh Biomedical Sciences programme, 2022-current
- PhD co-supervisor of Xiaomeng Li, dual degree ZJU-UoE Integrative Biomedical Sciences programme, 2021-current
- PhD co-supervisor of Shengjie Jin, University of Edinburgh Biomedical Sciences programme, 2021-current
- PhD assistant supervisor of Chenyu Wang, University of Edinburgh Biomedical Sciences programme, 2021-current
- Master thesis supervisor of Davide Sampietro, Erasmus student from Università deli Studi di Milano - Bicocca, 2018.

### Course Organizer

- Biomedical Informatics 3 (BMI3), Biomedical Informatics Programme, Zhejiang University-University of Edinburgh Institute, China, 2023. This is a core course on algorithm design.
- Integrative Biomedical Sciences 3 (IBMS3), Biomedical Informatics and Biomedical Sciences Programmes, Zhejiang University-University of Edinburgh Institute, China, 2022. This is a core course on career development and experimental design.
- Bioinformatics Tools for Protein Structure, Disorder and Interaction Analysis, National University of San Martin, Buenos Aires, Argentina, 2017.

### Lecturer

- Advanced Mathematics 1 (AM1), Introduction to Biomedical Informatics 1 (IBI1), Applied Data Sciences 2 (ADS2), Genomics and Proteomics 2 (GP2), Infection 3 (IN3), Computational Biology and Systems Biology 3 (CBSB3) and Integrative Biomedical Sciences 4 (IBM4) courses of the Biomedical Informatics and Biomedical Sciences Programmes, Zhejiang University-University of Edinburgh Institute, China, 2020-2023.
- Biomedical Disorders 1 and 2 courses of the Integrative Biomedical Sciences PhD programme, Zhejiang University-University of Edinburgh Institute, China, 2021-2023.
- Biomedical Frontiers course of the Artificial Intelligence and Digital Health MSc. programme, Zhejiang University, China, 2023.
- 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

Programming languages	R/Bioconductor, Bash. Basics of: Python, Perl and C.
Software	GROMACS, 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. Genomics 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.