Gorka Lasso Cabrera, Ph.D.

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Current Position

10/2019-Present	**Research Assistant Professor** at Kartik Chandran's lab, Albert Einstein School of Medicine, New York City, USA.

Education

01/2003-05/2007	**Ph.D. in Bioinformatics** at the Institute of Life Sciences, University of Wales Swansea, Swansea, UK.
09/1998-09/2002	B.Sc. in Biochemistry, University of Navarra, Pamplona, Spain.

Honours/Awards

2011	**EMBO short-term fellowship** as visiting scientist at Barry Honig's Lab, Columbia University, New York, USA.
2008	Bilbao city hall award "The Eureka Science Cafe", Bilbao, Spain.
2006	Best junior researcher presentations award at workshop "All Wales Bioinformatics Workshop". Cardiff, UK.
2002- 2006	**PhD fellowship**, Basque Government, Spain. ($75,000)

Previous academic appointments

08/2018-09/2019	**Research associate scientist** at Barry Honig's and Anthony Simon's lab, Columbia University, New York City, USA.
08/2013-07/2018	Postdoctoral research scientist at Barry Honig's lab, Columbia University, New York City, USA.
11/2011-12/2011	Visiting scientist at Remo Rohs' Lab, University of Southern California, Los Angeles, USA.
05/2008-07/2013	Postdoctoral research scientist at Mikel Valle's lab, Electron Microscopy, Structural Biology Unit, CICbioGUNE, Derio, Spain.
03/2008-03/2014	Adjunct/honorary research scientist at the School of Medicine, Swansea University, Swansea, UK.
01/2008-04/2008	Postdoctoral research scientist at the bioinformatics unit, CICbioGUNE, Derio, Spain.
12/2007	Visiting scientist at the Intelligent Systems Group, University of the Basque Country, San Sebastian, Spain.

Research Interests

o The integration of genomic, functional and structural information (both experimentally known and computationally inferred) to decipher the molecular basis of pathogen infection.
o Predicting the pathogenic risk of infections caused by pathogens in light of the genetic background of the pathogen and host.

Research Experience

10/2015-03/2019

A structure informed atlas of pan-viral interactions reveals features of human infection.

Barry Honig's lab, Sagi Shapira's lab, Columbia University, New York City, USA.
- o Implemented a computational framework that employs a Bayesian network and structural information to predict pan viral-human protein-protein interactions with an experimental validation rate of ~76%.
- o To date, the largest initiative to model the viral-human interactome. High confidence predictions and interaction models are available through an online webserver.

03/2017-12/2018

Discovery of a new ebolavirus specie and evaluation of its potential risk to infect humans.

Simon Anthony's lab, Columbia University, New York City, USA. USAID's PREDICT international consortium, UC Davis, Davis, USA.
- o Assessed the potential risk of human infection by a new ebolavirus specie, found in bats, by modelling the interaction between the viral GP1 protein and the known human receptor NPC1.

12/2014-10/2016

Novel regulatory mechanisms of p53 by lysine acetylation.

Barry Honig's lab, Wei Gu's lab, Columbia University, New York City, USA.
- o Develop a sequence-based search algorithm to scan the human proteome and identified potential regulators of the tumour suppressor P53, some of which were experimentally validated.

05/2015-06/2016

Structural basis of adhesive binding by desmocolins and desmogleins.

Barry Honig's lab, Larry Shapiro's lab, Columbia University, New York City, USA.
- o Performed electrostatic calculations on X-ray crystal structures of desmocolins and desmogleins, the basic components of desmosomes mediating cell adhesion.
- o Contributed to understanding the binding specificity of these two classes of proteins through electrostatic interactions.

09/2014-12/2015

CryoEM on the Pepino mosaic plant virus.

Barry Honig's lab, Columbia University, New York City, USA; Mikel Valle's lab, CICbioGUNE, Derio, Spain.
- o Molecular dynamics flexible fitting to model the structure of the viral capsid
- o Applied structural similarity search to unravel an evolutionary relationship, not yet discovered, between a (+) ssRNA virus and a (-) ssRNA virus.

05/2008-07/2013

Deciphering the conformational space of pyruvate carboxylase by cryo-EM and molecular modelling.

Mikel Valle's lab, Structural Biology Unit, CICbioGUNE, Derio, Spain.
- o Integrated cryoEM, Bayesian statistics and molecular dynamics to decipher the conformational space at pseudo-atomic resolution of a metabolic enzyme. This work put together two contradictory X-ray structures of the same enzyme.

01/2003-05/2007
Membrane Protein Bioinformatics.
Jonathan Mullin's lab, University of Wales Swansea, Swansea, UK.
- o Applied pattern recognition and machine learning methods to develop algorithms that structurally and functionally characterize polytopic membrane proteins.
- o Developed a web-server to predict membrane re-entrant loops in polytopic membrane proteins.

Teaching Interests

My interdisciplinary education allows me to teach a variety of undergraduate and postgraduate courses in biological sciences. As computational biologist, I would like to provide students with the bioinformatics resources that any life scientist should have. As biochemist and structural biologist, I have a solid background to teach cell biology, biochemistry and macromolecular structure, subjects that align well with my research interests. Also, I am particularly keen to bring students into the microbial world considering that my most recent and future research plan focusses on the pathogen-host interactome. Classes will combine theory and group activities (e.g. assessment of published papers), where multimedia will play an important role. The ultimate goal of the classes will not only be to learn the fundamentals of the subject but to also enlarge the curiosity of the students, improve their communication skills and stimulate their critical thinking.

Teaching Experience

10/2015-12/2015
"Molecular basis of life and disease". Double Discovery Centre. Columbia University, New York, USA
- o Lectures combined theory, multimedia and group activities to encourage critical thinking and group problem solving.

Mentoring Experience

- o Mentored students at the undergraduate, masters and MD-PhD level and research technicians in a variety of tasks: sequence analysis, protein modelling, protein structure analysis (e.g. electrostatics), protein-protein interaction prediction, protein databases and scientific presentations and writing.
- o Provided students with transferable skills such as team work, leadership, organization, problem solving and communication.

Outreach and Engagement

11/2016
Invited speaker at science fair: "The structure of proteins", in collaboration with the Spanish Embassy and the Association of Spanish Scientist in USA. Eastside high school, NJ, USA.

11/2015
Invited speaker at science fair: "From the Big-bang to the origin of life, a walk 13.7 billion years old", in collaboration with the Spanish Embassy and the Association of Spanish Scientist in USA. Eastside high school, NJ, USA.

10/2008-04/2013
Organizer of science communication talks "The Eureka Science Café". Bilbao, Spain.

12/2012

Invited speaker at foreign awareness talks: "The experience of moving abroad from a local perspective". Lauaxeta School. Amorebieta, Spain.

11/2012

Invited speaker at science fair: "Travelling inside a cell. How do proteins work?". University of Navarra, Pamplona, Spain.

10/2010

Invited speaker at science fair: "Exploring the Protein Universe through an Electron Microscope". Bilbao, Spain.

Academic Service

2019	Reviewer for Computational and Structural Biotechnology journal.
2014-Present	Reviewer for Plos One journal.
2011-2016	Associate faculty member of F1000.
2010-2012; 2015	Program committee member, ITBAM conference (2010 Bilbao, Spain; 2011 Toulouse, France; 2012 Vienna, Austria; 2015 Valencia, Spain).
2006-2008	Program committee member of the BioInformatics Research and Development (BIRD) conference. Berlin, Germany.
2004-2006	Research committee member at School of Medicine, Swansea University. Swansea, UK.

Skills

Computational	Operating systems: Linux, OS, Windows
	Programming: Borland Delphi, Perl
Data analysis	Machine Learning
	Pattern recognition
	Clustering
Bioinformatics	Protein sequence analysis
	Protein modelling
	DNA and Protein structure analysis
	Protein-protein interaction prediction
	Molecular dynamics
Experimental	CryoEM microscopy (sample preparation, image acquisition and processing, three-dimensional reconstruction)

Languages

Spanish	Proficient, written and spoken
English	Proficient, written and spoken

Presentations

2019	Invited speaker at seminar: "*Exploiting structure to predict viral-host PPIs and unravel molecular and phenotypic features of viral infection*". Barcelona Supercomputing Center, Barcelona, Spain.
2019	Invited speaker at seminar: "*Exploiting structure to predict viral-host PPIs and unravel molecular and phenotypic features of viral infection*". CICbioGUNE, Derio, Spain.

2011 Invited speaker at seminar: "*P53: Unraveling Protein Structure and Function by Combining Electron Microscopy and Bioinformatics*". University of Southern California, Los Angeles, USA.

2007 Selected abstract for oral presentation at workshop "All Wales Bioinformatics", Swansea, UK.

2006 Selected abstract for oral presentation at workshop "All Wales Bioinformatics". Cardiff, UK.

2006 Selected publication for oral presentation at conference XIV Intelligent Systems on Molecular Biology. Fortaleza, Brazil.

2005 Invited speaker at seminar "*Using Pattern Recognition Approaches to Predict Function of Membrane proteins*". University of the Basque Country, Leioa, Spain.

2005 Invited speaker at seminar "*Using Pattern Recognition Approaches to Predict Function of Membrane proteins*". University of Navarra, Pamplona, Spain.

Publications

1. **Lasso G**, Mayer SV, Winkelman ER, Chu T, Elliot O, Patino-Galindo JA, Park k, Rabadan R, Honig B, Shapira SD. (2019) A structure informed atlas of human-virus interactions. **Cell** Sep 5; 178(6):1526-1541.

2. Goldstein T, Anthony SJ, Gbakima A, Bird BH, Bangura J, Tremeau-Bravard A, Belaganahalli MN, Wells HL, Dhanota JK, Liang E, Grodus M, Jangra RK, DeJesus VA, **Lasso G**, Smith BR, Jambai A, Kamara BO, Kamara S, Bangura W, Monagin C, Shapira S, Johnson CK, Saylors K, Rubin EM, Chandran K, Lipkin WI, Mazet JAK. (2018) The discovery of Bombali virus adds further support for bats as hosts of ebolaviruses. **Nat Microbiol** 3, 1084-1089.

3. Larrea D, de Paz HD, Matilla I, Guzman-Herrador DL, **Lasso G**, de la Cruz F, Cabezon E, Llosa M. (2017) Substrate translocation involves specific lysine residues of the central channel of the conjugative coupling protein TrwB. **Mol Genet Genomics** Oct;292(5)1037-1049.

4. Stockman VB, Ghamsari L, **Lasso G**, Honig B, Shapira SD, Wang HH. (2016) A High-Throughput Strategy for Dissecting Mammalian Genetic Interactions. **PLoS One** Dec 9;11(12):e0167617.

5. Wang D, Kon N, **Lasso G**, Jiang L, Leng W, Zhu WG, Qin J, Honig B, Gu W. (2016) Acetylation-regulated interaction between p53 and SET reveals a widespread regulatory mode. **Nature** Oct 6;538(7623):118-122.

6. Harrison OJ, Brash J, **Lasso G**, Katsamba PS, Ahlsen G, Honig B, Shapiro L. (2016) Structural basis of adhesive binding by desmocollins and desmogleins. **Proc. Natl. Acad. Sci. U S A** Jun 28;113(26):7160-5.

7. Agirrezabala X, Méndez-López E, **Lasso G**, Sánchez-Pina MA, Aranda M, Valle M. (2015) The near-atomic cryoEM structure of flexible filamentous plant virus shows homology of its coat protein with nucleoproteins of animal viruses. **ELife** Dec 16;4:e11795.

8. Petrey D, Chen TS, Deng L, Garzon JI, Hwang H, **Lasso G**, Lee H, Silkov A, Honig B. (2015) Template-based prediction of protein function. **Curr Opin Struct Biol** Feb 9;32C:33-38.

9. **Lasso G**, Yu LP, Gil D, Lázaro M, Tong L, Valle M (2014). Functional conformations for pyruvate carboxylase during catalysis explored by cryoelectron microscopy. **Structure** Jun 10;22(6):911-22.

10. Julián P, Milon P, Agirrezabala X, **Lasso G**, Gil D, Rodnina MV, Valle M (2011). The cryo-EM structure of a complete 30S translation initiation complex from Escherichia coli. **PLoS Biol** 9(7): e1001095.

11. Melero R, Rajagopalan S, Lázaro M, Joerger AC, Brandt T, Veprintsev DB, **Lasso G**, Gil D, Scheres SH, Carazo JM, Fersht AR, Valle M (2011). Electron microscopy studies on the

quaternary structure of p53 reveal different binding modes for p53 tetramers in complex with DNA. **Proc. Natl. Acad. Sci. U S A** 108(2):557-62.

12. **Lasso G**, Yu LP, Gil D, Xiang S, Tong L, Valle M (2010). Cryo-EM analysis reveals new insights into the mechanism of action of pyruvate carboxylase. **Structure** 18(10):1300-10.

13. **Lasso G**, Matthiesen R (2010). Computational methods for analysis of two-dimensional gels. **Methods Mol Biol** 593:231-62 (book chapter).

14. Yu LP, Xiang S, **Lasso G**, Gil D, Valle M, Tong L (2009). A symmetrical tetramer for S. aureus pyruvate carbosylase in complex with coenzyme A. **Structure** 10;17(6):823-32.

15. Hackenberg M, **Lasso G**, Matthiesen R (2009). ContDist: a tool for the analysis of quantitative gene and promoter properties. **BMC Bioinformatics** 10:7.

16. **Lasso G**, Antoniw JF, Mullins JGL (2006). A combinatorial pattern discovery approach for the prediction of membrane dipping (re-entrant) loops. **Bioinformatics** 22 (14), e290-e297.

References

- ❖ Professor Barry Honig
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- ❖ Dr. Anthony Simon
  - Affiliation: Assistant Professor, Epidemiology, Center for Infection and Immunity, Columbia University.
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