

ANNA V. PROTASIO

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Group Leader in Computational Biology,
Department of Pathology, University of Cambridge.

RESEARCH VISION

The non-coding genome of parasitic flatworms. Using a combination of experimental and computational tools, my overarching aim is to expand our understanding of the roles of non-coding genomic elements in parasitic flatworms with a special focus on transposable elements.

EDUCATION

PhD Molecular Biology, 2012

Christ's College, University of Cambridge UK.

Dissertation: Transcriptome characterisation of cercariae and skin-stage schistosomula in the parasitic helminth *Schistosoma mansoni*.

Supervisors: Dr Matthew Berriman (Wellcome Sanger Institute, UK) and Prof. David Dunne (Dept of Pathology, University of Cambridge, UK).

BSc Biochemistry, 2006

Faculty of Sciences, University of the Republic, Montevideo, Uruguay.

Dissertation: Cloning, expression and characterisation of mitochondrial thioredoxin and thioredoxin peroxidase from the parasitic helminth *Echinococcus granulosus*.

Supervisor: Dr Gustavo Salinas (Faculty of Chemistry, Uruguay).

CURRENT APPOINTMENT

Research Group Leader in Computational Biology,

January 2020 – present

Division of Microbiology and Parasitology,

Department of Pathology, University of Cambridge.

PREVIOUS APPOINTMENTS

Research Associate in Bioinformatics,

May 2018 – Nov 2019

Cambridge Institute for Medical Research, University of Cambridge.

Investigated the role of the human silencing complex HUSH in heterochromatin formation (via H₃K₉me³ depositions) of newly inserted endoretroviruses.

Group Leader: Prof. Paul Lehner.

Postdoctoral Research Fellow

May 2016 – April 2018

NCBS-inStem-Cambridge Postdoctoral Fellowship (UK, India)

Using the well-characterised fresh water planarian *Schmidtea mediterranea* (a model organism for the study of stem cell and regenerative biology) to characterise and manipulate the pathways by which non-coding RNAs play their regulatory roles at the organismal level.

Postdoctoral Research Fellow

January 2012 – April 2016

Parasite Genomics Group, Wellcome Sanger Institute, UK

Led the experimental arm of the Parasite Genomics Group at the Wellcome Sanger Institute, running an independent research program studying regulation of gene expression by non-coding RNAs in the parasitic flatworm, *Schistosoma mansoni*. See (Protasio *et al.* 2017). Bioinformatic analyses formed a significant component of this project, including processing of small RNA and poly-A enriched RNA-seq samples, reads mapping, read counting and analysis of differential expression.

INVITED TALKS

- Invited speaker, British Society of Parasitology, Edinburgh, UK** *April 2020*
Session on Flatworm Biology. Postponed.
- Invited lecturer, Biology of Parasitism, Woods Hole, MA, U.S.A.** *July 2020*
Participation as lecturer in the module of Bioinformatics. Postponed to 2021.
- Invited speaker, Schistosomiasis Symposium, Minas Gerais, Brazil** *August 2020*
Postponed.
- Invited speaker, Genome Science 2019, Edinburgh** *September 2019*
Title: "Parasites within parasites: transposable elements in platyhelminthes"

AWARDS

- 2020 Departmental Fellowship, Computational Biology, University of Cambridge.
- 2019 Travel award. Newton Fund Researcher Links Bilateral Workshop, Fudan University, Shanghai.
- 2017 Darwin College Research Affiliation.
- 2015 NCBS-inStem-Cambridge Postdoctoral Fellowship.
- 2012 Japan Society for the Promotion of Science Postdoctoral Fellowship.
- 2012 First prize poster competition, Molecular and Cellular Biology of Helminth Parasites.
- 2010 Travel, tuition and expenses Biology of Parasitism course.
- 2007 Wellcome Trust Sanger Institute 4-year PhD scholarship.
- 2007 Honorary Cambridge Overseas Trust Scholar.
- 2005 First Prize, Sanger Prize Competition (full paid internship).

TEACHING

- Creator and Organiser [Helminth Bioinformatics](#)** *various dates 2019 – 2021*
Wellcome Genome Campus Advanced Courses, UK
Principal applicant, content lead and lead instructor for a 5-day residential course funded by Wellcome Advance Courses in helminths genomics, transcriptomics and bioinformatics. University of Accra, Ghana (September 2019), Thailand (2020) and Uruguay (2021).
- Guest lecturer (Parasitology) Dept of Pathology, University of Cambridge** *2019-2020*
Lectures: "Trematode biology" and "Tapeworm biology".
- Lead Educator and Content Developer for Online Courses** *February 2017 – August 2019*
Wellcome Genome Campus Advanced Courses and FutureLearn, UK.
Worked collaboratively with project managers and led a group of instructors in developing syllabus, contents and presentation of three online courses on **bacterial genomics and bioinformatics** covering: i) [From DNA to protein function](#); ii) [Accessing and analysing bacterial genomes](#); iii) [Comparative genomics](#).
- Course Instructor** *various dates 2008 – 2018*
Wellcome Genome Campus Advanced Courses – Working with Pathogen Genomes.
Work as part of a team of instructors in charge of candidate selection, course planning, course delivery and supervision of students. This is an annual residential course in bioinformatics that takes place in Uruguay and the UK.
- Course Demonstrator** *2015 – 2017*
Parasitology, Part IB Pathology practical classes. University of Cambridge.
Assist students in the interpretation and understanding of practical materials. Course organisers: Dr Shona Wilson/Dr Katerina Artavanis-Tsakonas, Department of Pathology, University of Cambridge.

PUBLICATIONS

A total of 16 peer-reviewed publications, with 4 in preprints, and one book chapter. *h*-index = 11 (source: [Scopus](#)).

Protasio AV*, Rawlinson KA, Miska EA, Berriman M, Rinaldi G. (* Corresponding author). **Evidence for transposable element control by Argonautes in a parasitic flatworm lacking the piRNA pathway.** [bioRxiv](#); <https://doi.org/10.1101/670372>. Under review in the journal MobileDNA.

Protasio AV*, van Dongen S, Collins J, Quintais L, Ribeiro D, *et al.* (* Corresponding author). **MiR-NAs miR-277/4989 regulate transcriptional landscape during juvenile to adult transition in the parasitic helminth *Schistosoma mansoni*** *PLoS Negl Trop Dis.* 2017 May 23;11(5):e0005559 PMID: 23516644.

Protasio AV, Dunne DW, Berriman M. **Comparative study of transcriptome profiles of mechanical and skin-transformed *Schistosoma mansoni* schistosomula.** *PLoS Negl Trop Dis.* 2013 Mar;7(3):e2091. PMID: 23516644.

Protasio AV*, Tsai IJ*, Babbage A, De Silva N, Davidson C, *et al.* (* joint first author). **A systematically improved high quality genome and transcriptome of the human blood fluke *Schistosoma mansoni*.** *PLoS Negl Trop Dis.* 2012 Jan;6(1):e1455. PMID:22253936

Marelli S, Williamson JC, **Protasio AV**, Naamati A, Greenwood JED, Deane JE, Lehner PJ, Matheson NJ. **Antagonism of PP2A is an independent and conserved function of HIV-1 Vif and causes cell cycle arrest.** *eLife* 2020;9:e53036 DOI: 10.7554/eLife.53036. PMID: 32292164.

Douse CH, Tchasovnikarova IA, Timms RT, **Protasio AV**, Seczynska M, Prigozhin DM, Albecka A, Wagstaff J, Williamson JC, Freund SWV, Lehner PJ, Modis Y. **TASOR is a pseudo-PARP that directs HUSH complex assembly and epigenetic transposon control.** [bioRxiv](#); <https://doi.org/10.1101/2020.03.09.974832>.

Wangwiwatsin A, **Protasio AV**, Wilson S, Owusu C, Holroyd NE, Sanders MJ, Keane J, Doenhoff MJ, Rinaldi G, Berriman M. **Transcriptome of the parasitic flatworm *Schistosoma mansoni* during intra-mammalian development.** [bioRxiv](#); doi: <https://doi.org/10.1101/757633>

Crosnier C, **Protasio AV**, Rinaldi G, Wilson S, Berriman M, Wright GJ. **A library of cell-surface and secreted proteins from *Schistosoma mansoni* identifies early serological markers of infection.** [bioRxiv](#); doi: <https://doi.org/10.1101/593616>.

Hernández-Goenaga J, López-Abán J, **Protasio AV**, Vicente Santiago B, Del Olmo E, Vanegas M, Fernández-Soto P, Patarroyo MA, Muro A. **Peptides Derived of Kunitz-Type Serine Protease Inhibitor as Potential Vaccine Against Experimental Schistosomiasis.** *Front Immunol.* 2019 Nov 1;10:2498. doi:10.3389/fimmu.2019.02498. PMID: 31736947.

Suttiprapa S, Rinaldi G, Tsai IJ, Mann VH, Dubrovsky L, Yan HB, Holroyd N, Huckvale T, Durrant C, **Protasio AV**, Pushkarsky T, Iordanskiy S, Berriman M, Bukrinsky MI, Brindley PJ. **HIV-1 Integrates Widely throughout the Genome of the Human Blood Fluke *Schistosoma mansoni*.** *PLoS Pathog.* 2016 Oct 20;12(10):e1005931. doi: 10.1371/journal.ppat.1005931. PMID: 27764257.

Lamolle G, **Protasio AV**, Iriarte A, Jara E, Simon D, Musto, H. **An isochore-like structure in the genome of the flatworm *Schistosoma mansoni*.** *Genome Biol Evol.* 2016 Aug 16;8(8):2312-8. doi: 10.1093/gbe/evw170. PMID:27435793.

Winter AD, Gillan V, Maitland K, Emes RD, Roberts B, McCormack G, Weir W, **Protasio AV**, Holroyd N, Berriman M, Britton C, Devaney E. **A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites.** *BMC Genomics.* 2015 Apr 22;16:331. doi:10.1186/s12864-015-1536-y. PMID: 25896062.

Horn M, Fajtová P, Rojo Arreola L, Ulrychová L, Bartošová-Sojková P, Franta Z, **Protasio AV**, Opavský D, Vondrášek J, McKerrow JH, Mareš M, Caffrey CR, Dvořák J **Trypsin- and Chymotrypsin-like serine proteases in *Schistosoma mansoni* – ‘the undiscovered country’.** *PLoS Negl Trop Dis.* 2014 Mar 27;8(3):e2766. PMID: 24676141.

Zerlotini A, Aguiar E, Yu F, Xu H, Li Y, Young N, Gasser R, **Protasio AV**, Berriman M, Roos D, Kissinger J, Oliveira G. **SchistoDB: an updated genome resource for the three key schistosomes of humans.** *Nucleic Acids Res.* 2013 Jan;41(Database issue). PMID: 23161692.

Fitzsimmons CM, Jones FM, Pinot de Moira A, **Protasio AV**, Khalife J, Dickinson HA, Tukahebwa EM, Dunne DW. **Progressive cross-reactivity in IgE responses: an explanation for the slow development of human immunity to schistosomiasis?** *Infect Immun.* 2012 Dec;80(12):4264-70. PMID: 23006852.

Parikh PP, Zheng J, Logan-Klumper F, Stoeckert CJ Jr, Louis C, Topalis P, **Protasio AV**, Sheth AP, Carrington M, Berriman M, Sahoo SS. **The Ontology for Parasite Lifecycle (OPL): towards a consistent vocabulary of lifecycle stages in parasitic organisms.** *J Biomed Semantics.* 2012 May 23;3(1):5. PMID: 22621763.

Laing R, Hunt M, **Protasio AV**, Saunders G, Mungall K, et al. **Annotation of two large contiguous regions from the *Haemonchus contortus* genome using RNA-seq and comparative analysis with *Caenorhabditis elegans*** *PLoS One* 6(8): e23216. PMID: 21858033.

Otero L, Bonilla M, **Protasio AV**, Fernández C, Gladyshev VN, Salinas G. **Thioredoxin and glutathione systems differ in parasitic and free-living platyhelminths.** *BMC Genomics.* 2010 Apr 13;11:237. PMID: 20385027.

Berriman M, Haas BJ, LoVerde PT, Wilson RA, Dillon GP, ... **Protasio AV** ... *et al.* **The genome of the blood fluke *Schistosoma mansoni*.** *Nature.* 2009 Jul 16;460(7253):352-8. PMID: 19606141.

Fitzpatrick JM, **Protasio AV**, McArdle AJ, Williams GA, Johnston DA, Hoffmann KF. **Use of genomic DNA as an indirect reference for identifying gender-associated transcripts in morphologically identical, but chromosomally distinct, *Schistosoma mansoni* cercariae.** *PLoS Negl Trop Dis.* 2008;2(10):e323. PMID: 18941520.

Book Chapter, Cantacessi C and **Protasio AV**. (2018) “Fundamentals of Bioinformatics, Principles and Techniques of Biochemistry and Molecular Biology”. Cambridge University Press, 8th edition. **ISBN: 9781316614761.**

REFERENCES

Professor Paul J. Lehner

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