

**HENG-CHANG CHEN**Update 7<sup>th</sup> of February, 2024**Current Position** Junior Research Group Leader

Quantitative Virology Research Group  
Population Diagnostics Center  
Łukasiewicz Research Network - PORT  
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[Official](#) and [Personal](#) websites

ORCID



GitHub



Personal website



I am a *molecular virologist* and *data scientist* with over eight years of experience and my studies are bound to *molecular barcodes*, which are molecular tags, enabling the achievement of research with resolution of *single viruses*. Together with *in silico modeling* and *AI-based approaches*, my laboratory investigates the mechanistic interplay between viruses (i.e. *HIV-1* and *SARS-CoV-2*) and the *host genome*, with the emphasis on (1) the investigation of latent *HIV-1* reservoirs and stochastic *HIV-1* transcription and (2) the identification of functional annotations of *SARS-CoV-2* mutational signatures responsible for cross-species transmission.

**1. Education**

2008 - 2012	<b>Dr. rer. nat. (Ph.D.)</b>	Institute of Biology, Humboldt-Universität zu Berlin	Berlin, Germany
2004 - 2006	M.Sc.	College of Medicine, National Taiwan University	Taipei, Taiwan
2000 - 2004	B.Sc.	College of Life Science, Tzu Chi University	Hualien, Taiwan

**2. Positions**

11/2022-present	Junior Research Group Leader	Łukasiewicz-PORT	Wrocław, Poland
09/2018-09/2022	Postdoctoral scientist	Institut de Génétique Humaine (IGH)	Montpellier, France
2014-08/2018	Postdoctoral scientist	Centre de Regulació Genòmica (CRG)	Barcelona, Spain
2011-2013	Lab Manager	Centre de Regulació Genòmica (CRG)	Barcelona, Spain

**3. Language**

English | German (**B1**) | French (**B1**) | Spanish | Mandarin (**native speaker**)

**4. Research Experience**

11/2022-present	Junior Research Group Leader, Łukasiewicz-PORT	Wrocław, Poland
09/2018-09/2022	Postdoctoral scientist, Institut de Génétique Humaine (IGH)	Montpellier, France
2014-7/2018	Postdoctoral fellow, Centre de Regulació Genòmica (CRG)	Barcelona, Spain
1/2017-2/2017	Visiting scientist, CNRS UMR7216, Université Paris 7	Paris, France
2008-2011	Ph.D. fellow, Institute of Biology, Humboldt-Universität zu Berlin	Berlin, Germany

**5. Computing expertise**

**R** | Shiny: Advanced knowledge  
HTML5 | CSS3 | **awk** | **Linux** | **vim** | Latex | **Markdown** | Syntax | **Python**: Working knowledge

GitHub: <https://github.com/HCAngelC>

**6. Research Awards and Grants**

2023-2027	<b>National Science Centre Poland (NCN) SONATA BIS 12</b> - ID: 563746 (3,724,878 PLN)
3/2018	<b>Marie Skłodowska-Curie Actions Proposal Seal of Excellence</b> 786552 - HIV-MAP
2/2017	<b>EMBO Short-term Fellowship</b> ASTF699-2016
2016	Awarded student talk at the 13 <sup>th</sup> Horizons in Molecular Biology Symposium, Göttingen, Germany
2008-2011	Ph.D. fellowship funded by the German Research Foundation (DFG)
2004	Student exchange program, Colorado College, Colorado, USA (refused)
2003	Bio-prize awarded by the Tzu Chi University, Taiwan (R.O.C.)

**7. Publications****7.1. Peer-reviewed publications**

A completed list of peer-reviewed publications is recorded in the end of the curriculum vitae.

**7.2. Monographs and press**

» **Chen, H.-C.** 2013. Scientific Image - HIV Infection, *El-lipse*, NÚM. 66.

I regularly post blog articles for public science. Please see my personal website: <http://chenhcinaki.wix.com/silence> for details.

### 7.3. Cover page & image credit

- » **Image credit** “MRN: un maillon dans la chaîne de protection du génome”, Institut des sciences biologiques (INSB) CNRS web site sketch, May, 2021
- » **Cover image** Natural Product Reports (ISSN: 0265-0568), Vol. 32, No. 1, January, 2015
- » **Cover image** Molecular Cell (ISSN: 1097-2765), Vol. 52, Issue 5, 12 December, 2013
- » **Image credit** “iCLIP: Genomic views of protein-RNA interactions”, EMBO Practical Course, 2013

### 8. Membership and service

- 2023-present **Topic Editor, Frontiers in Virology Fundamental Virology**  
*Research topic: Unintegrated- and integrated forms of HIV DNAs in the host genomic space*
- 2023-present **MDPI Journals (Epigenomes, Vaccines, Viruses) Volunteer Reviewers (Approval)**

### 9. Peer-reviewed activities

*A completed list of peer-reviewed activities is recorded in the end of the curriculum vitae.*

### 10. Competitively Invited Talks

- 2/2024 Using quantitative and genomic approaches to study HIV latency (Hosted by STANISZEWSKA, M.)  
CEZAMAT, Warsaw University of Technology Warsaw, Poland
- 3/2022 Molecular barcodes and HIV: from HIV integration sites to its pathogenesis (Hosted by STOPKA, T.)  
BIOCEV Vestec, Czech Republic
- 6/2018 Fluctuations in HIV expression and the host genome (Hosted by DEBYSER, Z. & Francqui Foundation)  
Workshop on “Nuclear architecture and retroviral integration” Leuven, Flanders, Belgium
- 9/2017 HIV expression, PEV and 3D genome (Hosted by PARISSI, V. & EMILIANI, S.)  
6<sup>th</sup> International Conference on Retroviral Integration Bordeaux, France
- 3/2017 HIV latency, chromatin and genome architecture (Hosted by LEE, C.-K.)  
College of Medicine, National Taiwan University Taipei, Taiwan
- 2/2017 HIV latency and genome evolution in reservoirs  
METU Evolutionary Biology Conference, Middle East Technical University Ankara, Turkey

### 11. Professional Organizations and Activities

- 2016 Organization committee of the CRG postdoctoral Retreat Barcelona, Spain
- 2014 Organization committee of the V CRG postdoctoral Symposium Barcelona, Spain

### 12. Teaching and Mentoring

*A completed list of peer-reviewed publications is recorded in the following page.*

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***A complete list of Teaching and Mentoring***

**Mentoring (Alumni)**

06/2023-08/2023 *Jędrzej Mazur* (intern), Łukasiewicz-PORT

Wrocław, Poland

*Current position: Ph.D. student, Center for Structural Systems Biology, Leibniz Institute of Virology, Germany.*

SP 2017	<i>Gerlinde VANSANT</i> (FWO grant), CRG	Barcelona, Spain
SS 2014	<i>Oguzhan BEGIK</i> (Erasmus programme), CRG	Barcelona, Spain
SP 2012	Fundació Catalunya E <sup>2</sup> C <sup>3</sup> -Centre Recerca practical course, CRG	Barcelona, Spain
SP 2010	3 <sup>rd</sup> -year master student, Free University	Berlin, Germany
SP 2009	2 <sup>nd</sup> -year bachelor student, Free University	Berlin, Germany

**Workshop**

SP 2015 Art, Science and Data Visualization, CRG PhD retreat

Castellar de n'Hug, Spain

*I illustrate the principle of **scientific data visualization** from the point of view of fine art.*

**Informal Teaching and talks**

2016	CRG summer school	Barcelona, Spain
2013	Lab Workshop assistant, CRG Teaching Day	Barcelona, Spain
2012	Lab introducer, CRG Open Day	Barcelona, Spain

*Description of research accomplishments***2023 - 2027**

» **Role of HIV antisense transcripts in the establishment of latency: genome-wide map antisense RNAs to understand how they regulate HIV transcription**

(Principal Investigator: **H.C. Chen**, Łukasiewicz Research Network - PORT, Wrocław, Poland)

Project is funded by National Science Centre Poland (NCN) SONATA BIS 12 (ID: 563746; Reg. No: DEC-2022/46/E/NZ6/00022; 3,724,878 PLN)

**2020 - 2022**

» **Understanding the intrinsic mechanism of elite controller patients to restrict HIV infection**

(Supervisor: **M. Benkirane**, Institut de Génétique Humaine, Montpellier, France)

We attempt to understand why the intrinsic property of elite controller CD4<sup>+</sup> T cells does not favor the selection of HIV integration sites, transcription, and reactivation. Furthermore, we conducted an A.I. approach to massively analyze RNA-seq data to seek possible molecular determinants responsible for elite control.

—Chen et al., manuscript under preparation—

**2019 - 2022**

» **Genetically defective HIV proviruses are prone to be present in host genomic repeat regions**

(Supervisor: **M. Benkirane**, Institut de Génétique Humaine, Montpellier, France)

We developed a new technology LAMP-seq to associate the nearly full-length HIV genomic sequences with host genomic sequences surrounding integration sites. We show that the genetic integrity of the proviruses present in host genomic repeat regions is less intact than those outside the host genomic repeat regions.

—Chen et al., manuscript under preparation—

» **The impact of immunity stimuli on the selection of HIV integration sites and reactivation**

(Supervisor: **M. Benkirane**, Institut de Génétique Humaine, Montpellier, France)

We prove that HIV displays different transcriptional profiles in primary CD4<sup>+</sup> T cells activated by different immunity stimuli. HIV proviruses are prone to integrate and be reactivated by the same stimuli used for primary CD4<sup>+</sup> T cell activation upon infection.

—Chen et al., manuscript under preparation—

**2017-2020**

» **The chromatin landscape at the HIV-1 provirus integration site determines viral expression**

(Personal Research Collaboration with the lab of **Z. Debyser**, KU Leuven, Leuven, Flanders, Belgium)

We prove that LEDGins, which are small molecule inhibitors of HIV integrase-LEDGF/p75 interaction enable to retarget HIV out of gene-dense and actively transcribed regions and consequently reduce viral RNA expression and increase the proportion of silent provirus (*Vansant\*, G., H.-C. Chen\* et al., 2020; \*Shared first authors*).

**2015-2018**

» **The selection of HIV integration sites in the 3D genome**

(Supervisor: **G. Filion**, Centre de Regulació Genòmica, Barcelona, Spain)

We show the bias of HIV integration in the 3D genomic architecture: viruses tend to integrate in spatial proximity of super-enhancers in primary CD4<sup>+</sup> T cells and in T cell cultures in vitro (*Lucic\*, B., H.-C. Chen\* et al., 2019, \*Shared first authors*).

**2013-2016**

» **Position effects influence HIV latency reversal**

(Supervisor: **G. Filion**, Centre de Regulació Genòmica, Barcelona, Spain)

We successfully proved that HIV transcription is influenced by the local genomic context: viruses that integrate close to endogenous enhancers display a higher transcriptional level than those integrating far from enhancers (*Chen et al., 2017 & Chen et al., 2018*).

**2008-2011**

» **Identification and characterization of a novel *Salmonella* gene product STM0029**

(Supervisor: **L.H. Wieler & K. Tedin**, Humboldt-Universität zu Berlin, Berlin, Germany)

We reveal the importance of a novel *Salmonella* gene product STM0029 which contributes to the resistance to host antimicrobial peptide killing (*DOI: 10.18452/16658*).

**2004-2006**

» **Characterization of a putative function of the two-component system ScnRK in *Streptococcus mutans***

(Supervisor: **J.S. Chia**, National Taiwan University, Taipei, Taiwan)

We identify the function of *S. mutans* two-component system ScnRK involved in the resistance of hydrogen peroxide and murine macrophage killing (*Chen et al., 2008*).

## A completed list of Publications

## I. Peer-Reviewed Research Publications

2023

- » Thenin-Houssier, S., S. Machida, C. Jahan, J. Bonnet-Madin, S. Abbou, **H.-C. Chen**, R. Tesfaye, O. Cuvier, and M. Benkirane. 2023. POLE3 is a transcriptional repressor of unintegrated linear HIV-1 DNA required for efficient virus integration and escape from innate immune sensing. *Sci. Adv.* DOI:[10.1126/sciadv.adh3642](https://doi.org/10.1126/sciadv.adh3642)
- » Więcek, K., and **Chen, H.-C.\*** 2023. Understanding latent HIV-1 reservoirs through host genomics approaches. *iScience* DOI:[10.1016/j.isci.2023.108342](https://doi.org/10.1016/j.isci.2023.108342) (Q1; IF: 6.107) (\*Co-first and senior author and correspondence)
- » **Chen, H.-C.\*** 2023. A systematic review of the barcoding strategy that contributes to COVID-19 diagnostics at a population level. *Front. Mol. Biosci.* DOI:[10.3389/fmolb.2023.1141534](https://doi.org/10.3389/fmolb.2023.1141534) (Q1; IF: 5.2) (\*Correspondence)
- » **Chen, H.-C.\*** 2023. The Dynamic Linkage between Provirus Integration Sites and the Host Functional Genome Property Alongside HIV-1 Infections Associated with Antiretroviral Therapy. *Vaccines* DOI:[10.3390/vaccines11020402](https://doi.org/10.3390/vaccines11020402) (Q1; IF: 7.8) (\*Correspondence)

2022

- » **Chen, H.-C.** 2022. The dynamic linkage between intact provirus integration sites and the host functional genome property alongside HIV-1 infections associated with antiretroviral therapy. *BioRxiv* DOI:[10.1101/2022.12.02.518849](https://doi.org/10.1101/2022.12.02.518849)
- » **Chen, H.-C.** 2022. Use molecular barcodes to study emerging infectious diseases. *AUTHOREA* DOI:[10.22541/au.165285401.15076943/v1](https://doi.org/10.22541/au.165285401.15076943/v1)
- » **Chen, H.-C.** 2022. Position matters - a discussion of HIV gene expression (中文主題名稱：原來擺對位置很重要——淺談人類免疫缺陷病毒的基因表現). *Science Education Monthly* (科學教育月刊) ISSN 1021-3708, 454, P25-32, DOI: [10.6216/SEM](https://doi.org/10.6216/SEM)

2021

- » Lucic, B.\*, **H.-C. Chen\***, M. Kuzman\*, E. Zorita\*, J. Wegner, V. Minneker, W. Wang, R. Fronza, M. Schmidt, and R. Stadhouders, V. Roukos, K. Vlahovick, G. Filion and M. Lucic. 2021. Author Correction: Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. *Nat. Commun.* DOI:[10.1038/s41467-021-26471-w](https://doi.org/10.1038/s41467-021-26471-w)

2020

- » Vansant\*, G., **H.-C. Chen\***, E. Zorita, Trejbalová, K., Miklik, D., G. Filion, and Z. Debyser. 2020. The chromatin landscape at the HIV-1 provirus integration site determines viral expression. *Nucleic Acids Res.* DOI:[10.1093/nar/gkaa536](https://doi.org/10.1093/nar/gkaa536) (\*Shared first authors) (Q1; IF: 11.147)
- » Machida, S., D. Depierre, **H.-C. Chen**, S. Houssier, G. Petitjean, C. Doyen, M. Takaku, O. Cuvier and M. Benkirane. 2020. Exploring histone loading on HIV DNA reveals a dynamic nucleosome positioning between unintegrated and integrated viral genome. *PNAS* DOI:[10.1073/pnas.1913754117](https://doi.org/10.1073/pnas.1913754117) (Q1; IF: 9.58)

2019

- » Lucic, B.\*, **H.-C. Chen\***, M. Kuzman\*, E. Zorita\*, J. Wegner, V. Minneker, W. Wang, R. Fronza, M. Schmidt, and R. Stadhouders, V. Roukos, K. Vlahovick, G. Filion and M. Lucic. 2019. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. *Nat. Commun.* DOI:[10.1038/s41467-019-12046-3](https://doi.org/10.1038/s41467-019-12046-3) (\*Shared first authors) (Q1; IF: 11.878)

2018

- » Abner, E., M. Stoszko, L. Zeng, **H.-C. Chen**, A. Izquierdo-Bouldstridge, T. Konuma, E. Zorita, E. Fanunza, Q. Zhang, T. Mahmoudi, M.-M. Zhou, G. Filion, and A. Jordan. 2018. A new quinoline BRD4 inhibitor targets a distinct latent HIV-1 reservoir for re-activation from other 'shock' drugs. *J Virol.* DOI:[10.1128/JVI.02056-17](https://doi.org/10.1128/JVI.02056-17) (Q1; IF: 4.324)
- » **Chen, H.-C.\***, E. Zorita, and G. Filion\*. 2018. Using Barcoded HIV Ensembles (B-HIVE) for single provirus transcriptomics. *Curr Protoc Mol Biol.* DOI:[10.1002/cpmb.56](https://doi.org/10.1002/cpmb.56) (\*Correspondence) (Q1)
- » Lucic, B.\*, **H.-C. Chen\***, M. Kuzman\*, E. Zorita\*, J. Wegner, V. Minneker, V. Roukos, W. Wang, R. Fronza, M. Schmidt, M. Benkirane, R. Stadhouders, K. Vlahovick, G. Filion and M. Lucic. 2018. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. 2018. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. *BioRxiv* DOI:[10.1101/287896](https://doi.org/10.1101/287896) (\*Shared first authors)

2017

- » **Chen, H.-C.**, J.P. Martinez, E. Zorita, A. Meyerhans, and G. Filion. 2017. Position effects influence HIV latency reversal. *Nat Struct Mol Biol.* DOI:[10.1038/nsmb.3328](https://doi.org/10.1038/nsmb.3328) (Q1; IF: 12.109)

2015

- » Corrales, M., P. Cusco, D.R. Usmanova, **H.-C. Chen**, N.S. Bogatyreva, G.J. Filion, and D.N. Ivankov. 2015. Machine learning: how much does it tell about protein folding rates? *PLoS One* DOI:[10.1371/journal.pone.0143166](https://doi.org/10.1371/journal.pone.0143166) (Q1; IF: 2.776)

2008

- » Chen, P.M., **H.-C. Chen**, C.T. Ho, C.J. Jung, H.T. Lien, J.Y. Chen, and J.S. Chia. 2008. The two-component system ScnRK of *Streptococcus mutans* affects hydrogen peroxide resistance and murine macrophage killing. *Microbes and Infection* DOI: [10.1016/j.micinf.2007.12.006](https://doi.org/10.1016/j.micinf.2007.12.006) (Q2; IF: 2.669; citation: 32)

## II. Peer-Reviewed Monographs

2020

- » **Chen, H.-C.** 2020. *Translated title:* Position matters: discussions about position effect variegation and HIV gene expression (article written in Chinese). *Science Monthly* (ISSN: 0250-331X). *article accepted*  
Due to the issue of intellectual property, I refused to publish this article in the journal Science Monthly.

## III. Press

**2013**

» **Chen, H.-C.** 2013. Scientific Image - HIV Infection, [\*El-lipse\*](#), NÙM. 66.

**IV. Conference publications**

**2019**

» Vansant, G., **H.-C. Chen**, E. Zorita, G. Filion, and Z. Debyser. 2019. HIV integration site selection affects transcription. **CSHL retroviruses**. Cold Spring Harbor, New York.

**V. Cover Images & Image Credits**

» “MRN: un maillon dans la chaîne de protection du génome”, Institut des sciences biologiques (INSB) CNRS web site sketch, May, 2021

» Natural Product Reports (ISSN: 0265-0568), Vol. 32, No. 1, January, 2015

» Molecular Cell (ISSN: 1097-2765), Vol. 52, Issue 5, 12 December, 2013

» iCLIP: Genomic views of protein-RNA interactions, EMBO Practical Course, 2013

*Peer-reviewed activities*

12/2023	MDPI viruses
10/2023	MDPI Journal of Clinical Medicine
09/2023	MDPI pathogens
08/2023	MDPI mathematics
07/2023	MDPI viruses
06/2023	MDPI International Journal of Molecular Sciences
06/2023	MDPI epigenomes
05/2023	PLOS Neglected Tropical Diseases
04/2023	STAR Protocols: Cell Press (Field: Bioinformatics)
11/2022	PLOS Computational Biology
09/2022	STAR Protocols: Cell Press (Field: Molecular Biology & Bioinformatics)
06/2022	STAR Protocols: Cell Press (Field: Molecular Biology & Bioinformatics)
03/2022	STAR Protocols: Cell Press (Field: Bioinformatics: python)
02/2022	STAR Protocols: Cell Press (Field: Bioinformatics: curl)
02/2022	STAR Protocols: Cell Press (Field: Bioinformatics: C++)
08/2021	STAR Protocols: Cell Press (Field: Bioinformatics: Perl)
03/2021	STAR Protocols: Cell Press (Field: Molecular Biology)