

HENG-CHANG CHEN

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Position Postdoctoral Fellow
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I am molecular virologist and data scientist with over seven years of experience; I attempt to understand fundamental mechanisms involved in gene expression by using HIV as my model. To conquer this, I rely on a deep knowledge of human genomics and virology and collaborations with specialists. Using my skills involved in biotechnology and bioinformatics, I am capable of open a new branch of interdisciplinary research lines different from other standard HIV research laboratories.

Education

2008 - 2012	Dr. rer. nat. (Ph.D.)	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

Principle Positions Held

09/2018-Current	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

Language

English | German | French | Spanish | Mandarin

I am fluent in spoken English and German (B1) and French (B1) and Mandarin (native speaker), full professional proficiency in reading and writing. I have a working knowledge of Spanish.

Research and Creative Activities

Research Project

2019-Current **The impact of γ -cytokines on the selection of HIV integration sites, expression and reactivation** (Supervisor: M. Benkirane, Institut de Génétique Humaine, Montpellier, France)
We proof that HIV is prone to strengthen viral RNA expression and reactivation by the same γ -cytokines used for primary CD4⁺ T cells activation upon infection (Chen et al., manuscript under preparation).

2017-Current **The chromatin landscape at the HIV-1 provirus integration site determines viral expression** (Personal Research Collaboration with the lab of Dr. Debyser, KU Leuven, Leuven, Flanders, Belgium)
We proof 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., manuscript under revision; *co-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⁺ T cells and in T cell cultures in vitro (Lucic, B., H.-C. Chen* et al., 2019, *co-first authors).*

2013-2016 **Position effects influence HIV latency reversal** (Supervisor: G. Filion, Centre de Regulació Genòmica, Barcelona, Spain)
We successfully proof that HIV transcription is influenced by the local genomic context: viruses which integrate close to endogenous enhancers display the higher transcriptional level than those integrating far from enhancers (Chen et al., 2017).

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).

Research Experience

09/2018-Current	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
SS 2014	Visiting scientist, ITZ, Ecology & Evolution, TiHo Hannover	Hannover, Germany
SP 2011	Visiting researcher, Institute of Food Research	Norwich, U.K.
2008-2011	Ph.D. fellow, Institute of Biology, Humboldt-Universität zu Berlin	Berlin, Germany
W 2008	Visiting student, Friedrich-Alexander-Universität Erlangen-Nürnberg	Erlangen, Germany

Biotechnology

B-HIVE | Illumina sequencing | Oxford Nanopore sequencing | Hi-C & 4C | CRISPR/Cas9 | ATAC-seq | clinical/ blood samples (primary cells isolation) | BSL3 lab

Computing ability

R: Advanced knowledge
Docker | Python | Linux | awk | SPSS: Working knowledge

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

I have experience in analyzing different types of Big Data, including RNA-seq data, ChIP-seq data, Gene Ontology analysis and Gene Set Enrichment Analysis (GSEA). I set up the analysis pipeline for Oxford Nanopore long-read sequencing data.

Certifications

» **Machine Learning with R Level 1** - issued by IBM (https://www.youracclaim.com/badges/b3728109-db25-49d3-8f4e-1416547fe11a/linked_in)
» **Python for Data Science** - issued by IBM (https://www.youracclaim.com/badges/5004f08c-4077-4d2b-9b6b-212bbfe57518/linked_in_profile)
» **Statistics 101** - issued by IBM (<https://courses.cognitiveclass.ai/certificates/08d0c21d4ac34ad7b2d060032989c821>)

Research Awards and Grants

3/2018 Marie Skłodowska-Curie Actions Proposal Seal of Excellence 786552 - HIV-MAP
2/2017 EMBO Short-term Fellowship ASTF699-2016
2016 Awarded student talk in the 13th Horizons in Molecular Biology Symposium, Göttingen, Germany
2008-2011 Ph.D. fellowship funded by German Research Foundation (DFG)
2004 Student exchange program, Colorado College, Colorado, USA
2003 Bio-prize awarded by the Tzu Chi University, Taiwan (R.O.C.)

Peer Reviewed Publications

Please see the list of peer reviewed publications in the final page.

Cover Image Publications

2015	Natural Product Reports	Vol. 32, No. 1, January
2013	Molecular Cell	Vol. 52, Issue 5, 12 December

Publications and Press

Scientific Image | Imatge científica - HIV Infection | Infecció per VIH
El-lipse, NÚM. 66, 2013
(Parc Recerca Biomèdica Barcelona monthly newspaper)

Image Credits

iCLIP: Genomic views of protein-RNA interactions	EMBO Practical Course
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Acknowledgements

Martinez, J.P., F. Sasse, M. Brönstrup, J. Diez and A. Meyerhans. 2015. Antiviral drug discovery: broad-spectrum drugs from nature. *Nat. Prod. Rep.* DOI: [10.1039/C4NP00085D](https://doi.org/10.1039/C4NP00085D)

Professional Organizations and Activities

Memberships and Affiliations

2013-2018 Verband Biologie, Biowissenschaften & Biomedizin in Deutschland (VBIO e.V.)
2013-2018 Vereinigung für Allgemeine und Angewandte Mikrobiologie (VAAM)
2015-2016 IAS (International AIDS Society)
2014-2015 SciArt Center (<http://www.sciartcenter.org>)
2010-2013 Gesellschaft für Biochemie und Molekularbiologie (GBM)

Service to Professional Organizations

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

Competitively Invited Talks and Oral Presentations

Invited Talks

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.)
6th 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
1/2017 Chromatin and HIV latency (Hosted by DEFOSSEZ, P.-A.)
CNRS UMR7216, Université Paris 7 Paris, France
2016 HIV expression and genome architecture
Curs "Les noves 'Bio' Il", Centre for Genomic Regulation (CRG) Barcelona, Spain
2015 Open the Chamber of Secrets of HIV-1 Latency
L'Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS) Barcelona, Spain

Oral Presentations

06/2017 Faculty-selected talks: The invisible world of HIV latency in the human genome
8th CRG Postdoctoral Symposium Barcelona, Spain
2016 Visualisation of HIV latency by the new technology Barcoded HIV Ensembles
13th Horizons in Molecular Biology Symposium Göttingen, Germany
2015 Visualisation of HIV-1 latency on chromatin landscapes
6th CRG Postdoctoral Symposium Barcelona, Spain
2014 Lighting talk: Visualisation of HIV-1 latency
The 2nd EMBO Conference Visualizing Biological Data (VIZBI) Heidelberg, Germany
2010 A novel orphan *phoPQ*-independent regulator influences *Salmonella* intracellular survival and antimicrobial peptides resistance
National Symposium on Zoonoses Research Berlin, Germany

Teaching and Mentoring

Mentoring

SP 2017 Gerlinde VANSANT (FWO grant), CRG Barcelona, Spain
SS 2014 Oguzhan BEGIK (Erasmus programme), CRG Barcelona, Spain
SP 2012 Fundació Catalunya E²C³-Centre Recerca practical course, CRG Barcelona, Spain
SP 2010 Molecular microbiological manipulation/master student, Free University Berlin, Germany
SP 2009 Molecular microbiological manipulation/bachelor student, Free University Berlin, Germany

Workshop

SP 2015 Art, Science and Data Visualisation, CRG PhD retreat Castellar de n'Hug, Spain

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

Peer Reviewed Publications

2020

» 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. Vlahovicek, G. Filion and M. Lusic. 2019. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. *Nat. Communications*. doi: [10.1038/s41467-019-12046-3](https://doi.org/10.1038/s41467-019-12046-3) (*Co-first authors) (Q1; IF: 11.878; citation: 3)

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; citation: 10)

» **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) (*Corresponding authorship) (Q1; citation: 3)

» 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. Vlahovicek, G. Filion and M. Lusic. 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: <https://doi.org/10.1101/287896>. (*Co-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; citation: 56)

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; citation: 12)

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.2008.05.001](https://doi.org/10.1016/j.micinf.2008.05.001). (Q2; IF: 2.669; citation: 32)

Conference publications

» 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.

Manuscript under revision

» Vansant*, G., **H.-C. Chen***, E. Zorita, Trejbalová, K., Miklík, D., G. Filion, and Z. Debyser. 2020. The chromatin landscape at the HIV-1 provirus integration site determines viral expression. *Nucleic Acids Research*. (*Co-first authors)