

CURRICULUM VITAE

• Personal information

Name: Porrua Fuerte, Odil

Date of birth: 02/05/1981.

Nationality: Spanish

Marital status: Single, two children (born on 30/06/2013 and 16/11/2017)

Address: Institut de Génétique Moléculaire de Montpellier, 1919 route de Mende, 34293 Montpellier.

• Education/Positions

Institution & Location	Degree/position	Dates	Field of study/research topic
Institut de Génétique Moléculaire de Montpellier, France	DR2 CNRS, team co-leader	2022-present	RNA metabolism, genome stability, neurodegenerative diseases
Institut Jacques Monod, Paris, France	CR2-CRCN CNRS	2014-2021	Transcription termination, gene expression
Centre de Génétique Moléculaire, Gif-sur-Yvette, France	Post-doc	2009-2013	Non-coding transcription and RNA quality control in yeast
Université Paris-Saclay, France	HDR	2014	Not applicable
Centro Andaluz de Biología del Desarrollo, Seville, Spain	Ph.D.	2005-2009	Bacterial transcriptional regulation
University Pablo de Olavide, Seville, Spain	Bachelor	1999-2004	Environmental Sciences

• Grants and awards

2024: ANR PRC deterRmind (coordinator, 309 K€ for 3 years)

ANR PRC PrionControl (partner, 195 K€ for 3 years)

La Ligue contre le Cancer (coordinator, 25K€)

2023: ITMO Cancer funding for equipment acquisition (coordinator, 63 K€)

2022: LabUM EpiGenMed (partner, 138 K€ for two years).

2020: FRM funding "Maladie Neurodégénérative" (coordinator, 261 K€ for 3 years)

2019: Prix Maurice Nicloux, awarded by the Société Française de Biochimie et Biologie Moléculaire.

2016: ANR JCJC TerReg (coordinator, 214 K€ for 3.5 years).

• Community commitments

- Member of the administrative council of the Société Française de Biochimie et Biologie Moléculaire (2022-present).

- Member of 3 HDR juries, 3 PhD juries, 2 M2 juries and 1 Maître de Conference recruitment committee.

- Grant reviewing for ANR, the Polish Science Foundation and the Austrian Science Foundation

- Manuscript reviewing for *Nat Struct Mol Biol*, *Nat Commun*, *Nucleic Acids Res*, *Genome Biol*, *EMBO J*, *Cell reports*, *JMB*, *Biochemical Society Transactions*, *Cancer NAR* and *FEBS Letters*.

• Supervision/training

PhD students: Ambre Johan (2025-present), Lisa Vecchio (2024-present), Juanjuan Xie (2018-2021), Nouhou Haidara (2017-2021), Zhong Han (2013-2017) and Agnieszka Tudek (2011-2014).

Post-docs: Marta Giannini (2021-present), Amandine Molliex (2016-2018)

Research assistants/engineers: Thierry Gostan (2022-present), Marie Antoine (2022-2024), Sarah Benlamara (2022-2023), Kehui Wei (2023-2024), Griselda Wentzinger (2020-2022).

Undergraduate students: Ambre Johan (2023), Laia Erta (2022), Jules Mellin (2019) and Dominika Hrossova (2012).

• Invited conferences

2025: FEBS workshop “Conservation and Diversity of Gene Regulatory Mechanisms Across Eukaryotes” (Sant Feliu de Guixols, Spain).

International course on Post-transcriptional regulation (Institut Curie, Orsay).

2024: IBGF external seminar (Salamanca, Spain).

“Transcription and Genome maintenance” J. Monod international conference (Roscoff).

2023: Forum labo 2023 (Paris).

2022: Cancéropôle GSO Workshop “Genome Dynamics and Cancer” (Toulouse).

2021: SFBBM annual congress (Paris).

2020: Otto Warburg Seminar series (Max Planck Institute, virtual)

International course "Non-coding genome" (Institut Curie, Paris).

2019 : Institut Pasteur (Paris).

2018 : Mini-symposium Club Levure et Noyau (Paris).

RNA symposium Jussieu (Paris).

• Selected publications (* indicates corresponding author)

- 1) Hasanova, Z., Klapstova, V., **Porrua, O***, Stefl, R*, and Sebesta, M*. (2023). Human senataxin is a bona fide R-loop resolving enzyme and transcription termination factor. *Nucleic Acids Res* 51(6):2818-2837.
- 2) Xie, J., Aiello, U., Clement, Y., Haidara, N., Girbig, M., Schmitzova, J., Pena, P. Müller, C.W., Libri D.* and **Porrua, O*** (2022). An integrated model for termination of RNA polymerase III transcription. *Science Advances* 8(28):eabm9875. *This study was highlighted by the CNRS.*
- 3) Haidara, N., Giannini, M. and **Porrua, O*** (2022). Modulated termination of non-coding transcription partakes in the regulation of gene expression. *Nucleic Acids Res* 50(3):1430-1448
- 4) Han, Z., Jasnovidova, O., Haidara, N., Tudek, A., Kubicek, K., Libri, D., Stefl, R. and **Porrua, O***. (2020). Termination of non-coding transcription in yeast relies on both an RNA Pol II CTD interaction domain and a CTD-mimicking region in Sen1. *EMBO J* 39(7):e101548. *This work was recommended by the Faculty Opinions.*
- 5) Han, Z., Libri, D. and **Porrua, O*** (2017). Biochemical characterization of the helicase Sen1 provides new insights into the mechanisms of non-coding transcription termination. *Nucleic Acids Res.* 45(3):1355-1370.
- 6) Leonaitė, B.°, Han, Z.°, Basquin, J., Bonneau, F., Libri, D., **Porrua, O*** and Conti, E.* (2017). Sen1 has unique structural features grafted on the architecture of the Upf1-like helicase family. *EMBO J* 36(11):1590-1604.
- 7) **Porrua, O.** and Libri, D*. (2015). Transcription termination and the control of the transcriptome: why, where and how to stop. *Nat Rev Mol Cell Biol* 16(3):190-202. (Review article).
- 8) Tudek, A.°, **Porrua, O.***, Kabzinski, T.°, Lidschreiber, M., Kubicek, K., Fortova, A., Lacroute, F., Vanacova, S., Cramer, P., Stefl, R.* and Libri, D*. (2014) Molecular basis for coupling transcription termination to non-coding RNA degradation. *Mol Cell* 55(3): 467-81.
- 9) **Porrua, O***. and Libri, D*. (2013). A bacterial-like mechanism for transcription termination by the Sen1p helicase in budding yeast. *Nat Struct Mol Biol.* 20(7): 884-91. *This work was recommended twice by the Faculty of 1000.*
- 10) Porrua, O, Hobor, F., Boulay, J., Kubicek, K., D'Aubenton-Carafa, Y., Gudipati, R.K., Stefl, R. and Libri, D*. (2012). *In vivo* SELEX reveals novel sequence and structural determinants of Nrd1-Nab3-Sen1-dependent termination. *EMBO J.* 31(19): 3935-48.

Metrics: h-index of 20; 1967 citations (source: google scholar).