

Manuel Irimia obtained his PhD in 2010 at University of Barcelona investigating the origin of vertebrates at a genomic level. After two postdocs at Stanford University and University of Toronto, he joined the Centre for Genomic Regulation (CRG) in June 2014. His lab is interested in understanding the roles that transcriptomic diversification, especially through alternative splicing, plays on vertebrate development and evolution. He has recently been elected EMBO Young Investigator (2018) and obtained an ERC Starting Grant in 2014. He is an ICREA Research Professor from December 2018.

Selected publications

- 1) Marletaz, F., Firbas, P., Maeso, I., Tena, J.J., Bogdanovic, O., Perry, M., Wyatt, C.D.R., [+50 authors], Holland, P.W.H., Escriva, H.†, Gomez-Skarmeta, J.L.†, **Irimia, M.**† (2018). Amphioxus functional genomics and the origins of vertebrate gene regulation. *Nature*, 10.1038/s41586-018-0734-6.
- 2) Grau-Bove, X., Ruiz-Trillo, I.†, **Irimia, M.**† (2018). Origin of exon skipping-rich transcriptomes in animals driven by evolution of gene architecture. *Genome Biol*, 19(1):135.
- 3) Gohr, A.†, **Irimia, M.**† (2018). Matt: Unix tools for alternative splicing analysis. *Bioinformatics*, doi: 10.1093/bioinformatics/bty606.
- 4) Fernandez, J.P., Moreno-Mateos, M.A., Gohr, A., Miao, L., Chan, S.H., **Irimia, M.**†, Giraldez, A.J.† (2018). RES complex is associated with intron definition and required for zebrafish early embryogenesis. *PLoS Genet*, 14(7):e1007473.
- 5) Burguera, D., Marquez, Y., Racioppi, C., Permanyer, J., Torres-Mendez, T., Esposito, R., Albuixech, B., Fanlo, L., D'Agostino, Y., Gohr, A., Navas-Perez, E., Riesgo, A., Cuomo, C., Benvenuto, G., Christiaen, L.A., Martí, E., D'Aniello, S., Spagnuolo, A., Ristatore, F., Arnone, M.I.†, Garcia-Fernández, J.†, **Irimia, M.**† (2017). Evolutionary recruitment of flexible Esrp-dependent splicing programs into diverse embryonic morphogenetic processes. *Nat Commun*, 8:1799.
- 6) Tapial, J., Ha, K.C.H., Sterne-Weiler, T., Gohr, A., Braunschweig, U., Hermoso-Pulido, A., Quesnel-Vallièeres, M., Permanyer, J., Sodaei, R., Marquez, Y., Cozzuto, L., Wang, X., Gómez-Velázquez, M., Rayón, M., Manzanares, M., Ponomarenko, J., Blencowe, B.J.†, **Irimia, M.**† (2017). An Alternative Splicing Atlas Reveals New Regulatory Programs and Genes Simultaneously Expressing Multiple Major Isoforms in Vertebrates. *Genome Res*, 27(10):1759-1768
- 7) Albuixech-Crespo, B., Lopez-Blanch, L., Burguera, D., Maeso, I., Sánchez Arrones, L., Moreno-Bravo, J.A., Somorjai, I., Pascual-Anaya, J., Puellas, E., Bovolenta, P., Garcia-Fernández, J.†, Puellas, L.†, **Irimia, M.**†, Ferran, J.L.† (2017). Molecular regionalization of the developing amphioxus neural tube challenges major partitions of the vertebrate brain. *PLoS Biol*, 15(4):e2001573.
- 8) Parikshak, N.N., Swarup, V., Belgard, T.G., **Irimia, M.**, Ramaswami, G., Hartl, C., Leppa, V., de la Torre-Ubieta, L., Huang, J., Gandal, M., Lowe, J.K., Blencowe, B.J., Horvath, S., Geschwind, D.H. (2016). Genome-wide changes in long noncoding RNA, alternative splicing, and cortical patterning in autism. *Nature*, 540(7633):423-427.
- 9) Solana, J.*†, **Irimia, M.***†, Ayoub, S., Orejuela, M.R., Zywitza, V., Jens, M., Tapial, J., Ray, D., Morris, Q.D., Hughes, T.R., Blencowe, B.J., Rajewsky, N.† (2016). Conserved functional antagonism between CELF and MBNL proteins regulates stem cell-specific alternative splicing and regeneration in planarians. *Elife*, 5:e16797.
- 10) **Irimia, M.**†, Weatheritt, R.J., Ellis, J., Parikshak, N.N., Gonatopoulos-Pournatzis, T., Babor, M., Quesnel-Vallièeres, M., Tapial, J., Raj, B., O'Hanlon, D., Barrios-Rodiles, M., Sternberg, M.J.E., Cordes, S.P., Roth, F.P., Wrana, J.L., Geschwind, D.H., Blencowe, B.B. † (2014). A highly conserved program of neuronal microexons is misregulated in autistic brains. *Cell*, 159:1511-23.

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