



Laboratory of RNA Biology and Functional Genomics led by Prof. Andrzej Dziembowski has several open positions (start April 2018; Funding guaranteed for 20 months, application deadline: 20th March 2018).

We are passionate about science and our projects are focused on post-transcriptional gene expression regulatory mechanisms (<http://adz.ibb.waw.pl>). We perform collaborative, integrative science and combine functional studies with transcriptomic and proteomic analysis in order to gain deep insight into analyzed processes [Ukleja, M., et al. (2016). *Nature communications* **7**, 10433; Wrobel, L., et al. (2015). *Nature* **524**, 485-488; Szczepinska, T., et al. (2015). *Genome research* **25**, 1622-1633; Lubas, M., et al. (2013). *The EMBO j* **32**, 1855-1868; Mroczek, S., et al. (2012). *Genes & development* **26**, 1911-1925; Pena, A., et al. (2012). *EMBO J* **31**, 1605-1616; Tomecki, R., et al. (2010); Lubas, M., et al. (2011). *Molecular cell* **43**, 624-637; *EMBO J* **29**, 2342-235; Lebreton, A., et al. (2008). *Nature* **456**, 993-996]

The laboratory is well equipped and has very supportive technical staff. We work in the Institute of Biochemistry and Biophysics of the Polish Academy of Sciences (ibb.waw.pl) - one of the top ranked Polish research institutes which is a part of the Ochota Campus, a large biomedical research center in Poland.

Open positions are funded by **Foundation for Polish Science TEAM program** (<http://www.fnp.org.pl/en/oferta/team-2-2/>) co-financed with support of the Smart Growth Operational Programme (PO IR).

The project entitled "Functional interactions of proteins involved in post-transcriptional regulatory mechanism in humans" focuses on identification of novel factors involved in RNA metabolism and description of novel functional interactions between the existing ones. It is based on genome wide siRNA screenings, a methodology which was recently implemented in the laboratory.

To explore factors and relationships in human RNA catabolism we conduct multiple synthetic lethal screens involving human exonucleases and siRNA library which covers almost all human genes. The screening is a starting point for more detailed molecular analysis specific for particular identified functional interactions. It is divided into two parts:

- **Molecular analysis of functional interactors of the DIS3 protein**
- **Identification and analysis of functional interactors of DIS3L, DIS3L2, RRP6, XRN1 and XRN2**

Open positions starting from April 2018:

1 X Post-doctoral fellow - we are looking for candidate with experience in bioinformatics analysis of transcriptomic data, especially TAIL-seq approach) -

Salary 7200 PLN/months + quarterly bonus (~6000 PLN/month net in yearly settlement)

Please e-mail CV, summary and relevance of your current research (500 word max), why you are interested in the position (200 word max) and names of up to three references to: **team.project.ad@gmail.com**. Application deadline - **20th March 2018**

Selected candidates only will be contacted with invitation for a final interview. Please include in your CV a statement:

"I hereby give consent for my personal data included in the job offer to be processed for the purposes of recruitment procedure under the Data Protection Act 1997 (Dz. U. no. 133, item 883), consolidated text: *Journal of Laws* 2016, item 922 as amended".