

EDITORIAL



Five years on – *FEBS Open Bio* celebrates its launch anniversary

Mary Purton

FEBS Open Bio Editorial Office, Cambridge, UK

As 2016 draws to a close, *FEBS Open Bio* celebrates the 5th anniversary of its launch in late 2011. *FEBS Open Bio* was the first journal owned by FEBS (The Federation of European Biochemical Societies) to be completely open access and its launch was a new departure for the federation, which also owns three successful subscription journals. Five years on, and *FEBS Open Bio* is flourishing. Now accepted for indexing in Web of Science and with an Impact Factor of 2.101 for 2015, it has recently accepted its 500th paper.

A year ago, *FEBS Open Bio* joined *The FEBS Journal* and *FEBS Letters* to form FEBS Press, with these three journals published in partnership with Wiley. In January 2017, *Molecular Oncology* will join FEBS Press. At the same time, *Molecular Oncology* converts to open access, becoming the second fully open access journal published by FEBS Press.

FEBS was keen to ensure that the *FEBS Open Bio* employed the same robust editorial standards as its other journals, so that the research it publishes is reliable and reproducible [1]. An editorial board of active scientists was recruited to handle peer review. The journal belongs to the Committee on Publication Ethics (COPE) and all submissions are screened for plagiarism. Articles accepted for publication are copyedited and authors receive proofs for checking. The journal is listed in the Directory of Open Access Journals (DOAJ) and all published articles are deposited in PubMedCentral (PMC) and indexed widely. Authors using the Think. Check. Submit. tool to check out *FEBS Open Bio* can be assured that they are submitting to a trusted journal.

The review process for *FEBS Open Bio* focuses on the technical soundness of manuscripts, leaving the assessment of their impact and biological significance to the scientific community. This approach, also followed by other 'megajournals', such as *PLOS One*, allows authors to publish confirmatory and even negative results that might be turned down by journals more focused on impact.

FEBS Open Bio is keen to support Open Data initiatives such as CODATA [2] and the OECD 'Brussels Declaration' [3]. There is no limit on the number of figures and tables within an article, with supplementary files for data that can't easily be displayed within the standard article format. Authors must deposit all 'structured' data sets (e.g. gene sequences, protein structures, microarray data) in the appropriate public databases and include the accession number in their paper. In addition, to assist authors who want to share the raw data underlying the figures and tables in their paper, data files submitted alongside the paper will now be uploaded free of charge to the figshare repository with cross-referencing of article/data DOIs for 'joined-up' access.

To celebrate the journal's 5th anniversary, we have put together four Virtual Issues, showcasing content across four subject areas, which contain articles from the past 5 years of publication. Some of these have been highly cited; others have only been published in the last 12 months but have been highly downloaded.

The Virtual Issue on Cancer biology contains our most cited paper, by Takahashi et al. [4] Published in 2014, this paper provides mechanistic insights into acquired chemoresistance in hepatocellular carcinoma. in particular the role of noncoding RNAs in extracellular vesicles. Another more recent paper reports on a 'drug repositioning' screen for potential therapeutics for drug-resistant breast cancer [5]. The Plant biology Virtual Issue contains three of the four papers published in 2011, all of which have accrued six or more citations to date [6-8]. Also, in this issue is our second most highly cited paper by Jensen et al., [9] which reports a proteomics approach to find gene targets of the ATAF1 transcription factor in Arabidopsis thaliana. Another Virtual Issue features articles on Microbiology, ranging from a bacteriocidin that is active against both Gram-positive and -negative bacteria [10] to the role of the Mycobacterium tuberculosis PE25/PPE41 protein complex in inducing necrosis in macrophages [11]. The final Virtual Issue gathers together papers on Computational & systems biology, from a report on a meta-database for gene set analysis [12] to transcriptome analyses building network models for specific types of cancer [13,14] and for brain metabolism [15].

Some of our most cited articles have been widely shared – which is encouraged under our CC BY license – with up to 23 versions of one article indexed by Google Scholar. There are no restrictions on reposting the final version of articles.

We would like to thank our editors and reviewers, who maintain the scientific standards of the journal, and assist authors in improving their papers. We also thank those authors who took a risk in publishing with a new journal, entrusting us with their work. We look forward to receiving many more submissions in the coming years.

References

- 1 Bohannon J (2013) Who is afraid of peer view? *Science* **342**, 60–65.
- 2 International Council for Science: Committee on Data for Science and Technology CODATA http:// www.codata.org/ (accessed 7 November 2016).
- 3 OECD Principles and Guidelines for Access to Research Data from Public Funding (2007) http:// www.oecd.org/science/sci-tech/oecdprinciplesandguid elinesforaccesstoresearchdatafrompublicfunding.htm (accessed 7 November 2016).
- 4 Takahashi K, Yan IK, Kogure T, Haga H and Patel T (2014) Extracellular vesicle-mediated transfer of long noncoding RNA ROR modulates chemosensitivity in human hepatocellular cancer. *FEBS Open Bio* **4**, 458–467.
- 5 Yusuke O, Nishiya N, Shito T, Yamamoto R, Yamamoto Y, Oyama C and Uehara Y (2015) Small molecules inhibiting the nuclear localization of YAP/ TAZ for chemotherapeutics and chemosensitizers against breast cancers. *FEBS Open Bio* **5**, 542–549.
- 6 Pietrowska-Borek M, Nuc K, Zielezińska M and Guranowski A (2011) Diadenosine polyphosphates (Ap₃A and Ap₄A) behave as alarmones triggering the synthesis of enzymes of the phenylpropanoid pathway in *Arabidopsis thaliana*. *FEBS Open Bio* **1**, 1–6.
- 7 Giró M, Ceccoli RD, Poli HO, Carrillo N and Lodeyro AF (2011) An *in vivo* system involving co-expression of cyanobacterial flavodoxin and ferredoxin–NADP⁺ reductase confers increased tolerance to oxidative stress in plants. *FEBS Open Bio* 1, 7–13.

- 8 Mamedov T and Yusibov V (2011) Green algae *Chlamydomonas reinhardtii* possess endogenous sialylated N-glycans. *FEBS Open Bio* 1, 15–22.
- 9 Jensen MK, Lindemose S, de Masi F, Reimer JJ, Nielsen M, Perera V, Workman CT, Turck F, Grant MR, Mundy J et al. (2013) ATAF1 transcription factor directly regulates abscisic acid biosynthetic gene NCED3 in Arabidopsis thaliana. FEBS Open Bio 3, 321–327.
- 10 Acuña L, Picariello G, Sesma F, Morero RD and Bellomio A (2012) A new hybrid bacteriocin, Ent35– MccV, displays antimicrobial activity against pathogenic Gram-positive and Gram-negative bacteria. *FEBS Open Bio* 2, 12–19.
- 11 Tundup S, Mohareer K and Hasnain SE (2014) Mycobacterium tuberculosis PE25/PPE41 protein complex induces necrosis in macrophages: role in virulence and disease reactivation? FEBS Open Bio 4, 822–828.
- 12 Araki H, Knapp C, Tsai P and Print C (2012) GeneSetDB: a comprehensive meta-database, statistical and visualisation framework for gene set analysis. *FEBS Open Bio* 2, 76–82.
- 13 Szeto CY-Y, Lin CH, Siu Choi SC, Yip TTC, Ngan RK-C, Tsao GS-W and Lung ML (2014) Integrated mRNA and microRNA transcriptome sequencing characterizes sequence variants and mRNA-microRNA regulatory network in nasopharyngeal carcinoma model systems. *FEBS Open Bio* 4, 128–140.
- 14 Barresi V, Trovato-Salinaro A, Spampinato G, Musso N, Castorina S, Rizzarelli E and Condorelli DC (2016) Transcriptome analysis of copper homeostasis genes reveals coordinated upregulation of SLC31A1, SCO1, and COX11 in colorectal cancer. *FEBS Open Bio* 6, 794–806.
- 15 Sertbaş M, Ülgen K and Çakır T (2014) Systematic analysis of transcription-level effects of neurodegenerative diseases on human brain metabolism by a newly reconstructed brain-specific metabolic network. *FEBS Open Bio* **4**, 542–553.