Erik Bongcam-Rudloff participated in the Belgrade BioInformatics Conference 2016, 20-24 June, Belgrade (RS), and gave a presentation entitled, "Next Generation Biotechnologies, the bad & the good: a look into the future". The conference was a great success with many attendees, and high-level presentations and discussions.

The full programme and further information can be found on the conference website.

Terri Attwood & Domenica D’Elia attended the first conference of the COST Action CHARME (CA15110), The CHARME of standardisation in life sciences, 21-22 June, Warsaw (PL). Terri presented GOBLET’s CHARME, an overview of GOBLET’s scope and aims, and integration plans and activities with the CHARME’s Working Group 5. Domenica talked about objectives and basic actions of CHARME’s Working Group 4, with a presentation on Development of a strategic dissemination plan to support a successful European standardisation strategy. Management Committee & parallel WG meetings were held on 21 June. The Conference had more than 70 participants, including MC members and representatives of large European standardisation initiatives, projects and consortia.

Pedro Fernandes & Domenica D’Elia participated in BITS 2016, the 13th Annual Meeting of the Bioinformatics Italian Society, 15-17 June, Salerno (IT). In a satellite event organised by the ELIXIR-IT Training Programme, Pedro gave a talk on "Effective academic teaching: learning principles & didactic strategies that will transform your way of delivering bioinformatics courses". Domenica presented a poster on the CHARME COST Action.

Applications are invited for a postdoctoral position in Computational & Functional Genomics at IMGT, the International ImMunoGeneTics information system, Montpellier (FR).
Computational reproducibility poses new challenges for scientific replication. Part of the problem is that research papers don’t effectively support reproducibility of computational analyses. Companion websites that make data and software shareable may be useful, but are not enough. Frameworks for creating descriptive and interactive publications by linking them with associated objects (e.g., software source code, data-sets and annotations, data pipelines and workflows) are needed.

A prerequisite of modern life-science R&D is high-quality research data. By enabling the reuse of research assets, research becomes considerably more efficient and economical. This can only be achieved reliably and efficiently if these are generated according to standards and Standard-Operating Procedures (SOPs). Thus, standards are important drivers in the life-sciences, because they guarantee that data become accessible, shareable and comparable along the value chain.

To discuss these challenges, the EU COST Action, CHARME (Harmonising standardisation strategies to increase efficiency & competitiveness of European life-science research), EMBnet (The Global Bioinformatics Network) and NETTAB (International Workshop Series on Network Tools & Applications for Biology) are organising a workshop on Reproducibility, standards & SOP in Bioinformatics, to be held in Rome (IT), 25-26 October 2016.