Status & plans

The metaFAIR Task Force is currently active and will continue to be active through 2026. Over the past year, the group has focused on improving metadata standards and FAIR compliance across FAANG submissions, with tangible progress in several key areas:

- Updated metadata rules for **organoid samples**, improving clarity around derivation, culture conditions, and provenance to support more consistent representation across projects.
- Development and publication of **new ChIRP-seq experiment rules**, including:
  - ChIRP-seq input
  - ChIRP-seq hybridisation control
  - ChIRP-seq lncRNA

These additions fill an important gap in metadata coverage for emerging chromatin-associated RNA profiling methods.

The TF is also contributing to a major technical update of the FAANG metadata validation and submission system. This work transitions the system toward a more modular, maintainable, and scalable implementation based on:

- **Python FastAPI**
- **Pydantic models**

This architectural upgrade lays the groundwork for improved validation robustness, clearer error reporting, and future integration with training and onboarding tools.

Given the ongoing work and clear upcoming milestones, the recommendation is **not to sunset the task force**. The TF remains relevant to the broader FAANG and international metadata standards ecosystem and has a defined roadmap for 2026.

Early 2026 activities: Specific goals, deliverables, or events you intend to kick off in Q1–Q2 2026.

Technical deliverables

- Completion and deployment of the updated metadata validation/submission backend using FastAPI and Pydantic
- Iterative refinement of metadata rules based on community feedback and new data types entering FAANG workflows
- Alignment of new rules with external resources (e.g., BioSamples, ENA, International Bioinformatics metadata efforts)

Community training & outreach

- Development of a new set of **short training video modules** covering:
    - FAANG metadata concepts
    - Using the submission/validation tools
    - Troubleshooting common submission issues
- Each module will be concise and focused on a single component, rather than a single long training session, to improve accessibility and user uptake
- Automatically generated accompanying **written guidance** and step-by-step notes derived from video content
- metaFAIR manuscript

These materials will support more efficient onboarding of new submitters and improve metadata quality through clearer guidance.

Web presence: Are your TF webpages on the FAANG site up to date? Note any updates needed.

The FAANG Data Coordination Centre members need to be updated to -

Emily Clark, Alexey Sokolov, Yogmatee Roochun, Raheela Aslam and Milena Mansurove

Coordination with other groups: Many TFs are embedded in international efforts. Please outline practical steps to unify/align efforts and how interested researchers could access/join via the FAANG site.

The metaFAIR Task Force is closely embedded within international metadata and data submission efforts, particularly through alignment with:

- ENA/BioSamples submission requirements
- Existing FAANG metadata rulesets
- Ongoing activities within ERGA, ENSEMBL, and related genomic data initiatives

Practical steps to unify and align efforts in 2026 include:

- Ensuring that new rules and validation logic remain consistent with ENA/BioSamples schema evolution
- Potential collaboration with the High Throughput Phenotyping and Data Storage task force
- Sharing updated Pydantic models and validation logic with related projects to encourage reuse
- Coordinating training materials so they serve both FAANG and partner communities

- Providing clear pathways for interested researchers to participate via the FAANG website, including:
    - Updated contact information
    - Links to mailing lists or Slack/communication channels
    - Opportunities to contribute to rule development or testing

This alignment strengthens interoperability and reduces duplication across international efforts.