

Support for genome analysis and protein folding within the e-infrastructure

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The fields of Protein Structural Biology and Sequence Analysis (Protein/DNA/RNA) are growing communities within the EU research map. Within the European Grid Infrastructure several VRCs (e.g. WeNMR and LSGC) and VOs (e.g. enmr.eu, biomed) have been setup to tackle the computational needs of these fields of science. At the same time the information on how new users can approach and use such applications and tools is disperse and not easy to access for users from the Biological Sciences field who are inexperienced with grids/clouds.

With the objective of bridging the panoply of powerful tools, applications, workflows and knowledge existing within EGI and the end-users, the “Support for genome analysis and protein folding” virtual team project was recently launched within EGI. The project aims at: a) setting up of new training activities and outreach documents based on existing applications and b) the integration of new tools and application in EGI, c) Promote relevant services, tools and applications to potential users from the domain.

These aims will spark the setup of new knowledge networks within the users and EGI therefore potentiating future collaboration in research projects.

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Session Classification: Community building and engagement