

Meeting Report: The Fifth Genomic Standards Consortium (GSC) Workshop

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Abstract

This meeting report summarizes the proceedings of the fifth Genomic Standards Consortium (GSC) workshop held December 12–14, 2007, at the European Bioinformatics Institute (EBI), Cambridge, UK. This fifth workshop served as a milestone event in the evolution of the GSC (launched in September 2005); the key outcome of the workshop was the finalization of a stable version of the MICS specification (v2.0) for publication. This accomplishment enables, and also in some cases necessitates, downstream activities, which are described in the multiauthor, consensus-driven articles in this special issue of OMICS produced as a direct result of the workshop. This report briefly summarizes the workshop and overviews the special issue. In particular, it aims to explain how the various GSC-led projects are working together to help this community achieve its stated mission of further standardizing the descriptions of genomes and metagenomes and implementing improved mechanisms of data exchange and integration to enable more accurate comparative analyses. Further information about the GSC and its range of activities can be found at <http://gensc.org>.

Introduction

THE GENOMIC STANDARDS CONSORTIUM (GSC) is an initiative working toward richer descriptions of our collection of genomes and metagenomes. Established in September 2005, this international community includes representatives from the International Nucleotide Sequence Databases, major genome sequencing centers, bioinformatics centers, and a range of research institutions. The goal of the GSC is to promote mechanisms of standardizing the description of

(meta)genomes and the exchange and integration of (meta)genomic data. The rapid pace of genomic and metagenomic sequencing projects will only increase as the use of ultrahigh-throughput methods becomes common place, and therefore the role of standards becomes even more vital to scientific progress and data sharing.

By the time this special issue goes to press, the first official “product” of GSC consensus-building activities will be published (Field et al., 2008a). The release of a stable version of the “Minimum Information about a Genome Sequence”

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(MIGS) specification is a first milestone accomplishment that will enable the GSC to take further steps toward realizing its goals. The availability of a “stable” version of MIGS now raises issues about implementation and how to progress to a time when we have large amounts of MIGS-compliant data. While the GSC’s Genome Catalog, built with the GenCat software, has already been mentioned in the MIGS publication (Field et al., 2008a), other complementary initiatives are described in the accompanying set of papers in this special issue.

In many ways, the fifth GSC workshop represented an end to the first phase of the development of the GSC. It is now a growing community that has enjoyed five workshops to date, produced two special issues of *OMICs*, and has published its first major output, the MIGS specification (Field et al., 2008a). The workshop officially opened the doors to Phase II of GSC activities. These activities will be focused on implementation of the syntax and semantics that will enable the collection of MIGS/MIMS-compliant information.

Here we review the workshop proceedings, introduce each of the papers in this special issue, and elaborate on how all of these initiatives interrelate and work together to fulfill the GSC mission. These collective papers make a lasting contribution to the future of the GSC by providing published descriptions of key activities and by acting to formulate new working groups that represent a widening of GSC interests beyond the publication of the MIGS checklist (Field et al., 2008a). To make sure this vision is balanced and representative, the authorship of this report includes the editors of the special issue, the organizers of the workshop, the session chairs, and at a minimum the lead authors of each of the contributions to this special issue.

Workshop Proceedings

The fifth workshop was convened by local host **Peter Sterk** at the **European Bioinformatics Center (EBI)** in Cambridge, England, on December 12–14, 2007, with co-organizers **Dawn Field** (NERC Center for Ecology and Hydrology (CEH)), **Tanya Gray** (CEH), **Nikos Kyrpides** (Department of Energy Joint Genome Institute (DOE JGI)), **Frank Oliver Glöckner** (Max Planck Institute for Marine Microbiology (MPI-Bremen)), **George Garrity** (Michigan State University), and **Lynette Hirschman** (MITRE).

The workshop agenda was designed to help the group give updates and reach further consensus on the following key areas of ongoing interest to the GSC, namely the:

- Definition of a set of minimum descriptors for genomes and metagenomes (the MIGS/MIMS checklist)
- Implementation of the checklist to collect, hold, and exchange MIGS/MIMS compliant information [in the Genomic Contextual Data Markup Language (GCDML)]
- Creation of a single unified list of genomes and metagenomes across different databases (made possible through a mapping of identifiers in the Genomic Rosetta Stone project)
- Adoption of a list of terms for completing MIGS/MIMS reports (through the use and development of controlled vocabularies and ontologies)
- Strategic development of the GSC

The above themes also drove the agenda for previous workshops (Field et al., 2008b), but for the first time, this

workshop also included a session organized by **Nikos Kyrpides** on the standardization of genome annotations. This session builds on two previous workshops described by **Tatiana Tatusova** (NCBI) below.

Preworkshop Session: MIGS/MIMS and GCDML Technical Session—Active Work on Final Version of MIGS Checklist for Publication and GCDML

The first session, chaired by **Tanya Gray**, was a technical session that provided developers the chance to meet face to face in a more informal setting. The session’s goal was to formalize technical work on GCDML, and to do so required the completion of a stable version of the MIGS checklist. The discussion of the content and scope of the MIGS/MIMS checklist was led by **George Garrity**. Discussions initiated in this first session continued throughout the workshop and led to several key changes and finalization of MIGS version 2.0, a release stable enough to be ready to implement (Field et al., 2008a).

Once a checklist, defining the scope and content of a specification had been built by the GSC, efforts shifted toward implementation and then collection of compliant reports. Following the last GSC meeting, the redevelopment of the original MIGS XML schema has been led by **Renzo Kottman** (MPI-Bremen), working closely with **Tanya Gray**, and in consultation with a number of groups within the GSC. **Renzo** opened the GCDML session by giving an introduction to the design and current status of GCDML and reviewed feedback collected thus far. A fuller description of GCDML is given in this issue (Kottmann et al., 2008).

Renzo’s introduction was followed by three short talks from early adopters of MIGS/MIMS and GCDML. **Leonid Kagan** and **Sean Murphy** (J. Craig Venter Institute [JCVI]), **Nick Thomson** (Sanger Institute), and **Philip Goldstein** (University of Colorado) covered their efforts toward compliance for metagenomes, genomes, and 16S sequences, respectively. **Jeroen Raes** (European Molecular Biology Laboratory [EMBL]) then suggested that the outlined MIN-IMES (Raes et al., 2007) extension for describing computational aspects of metagenomic data sets should fall into the scope of GCDML. **Inigo San Gil** (Long-Term Ecological Research (LTER) Network Office) finished the session with words of wisdom for the GSC and GCDML from experience gained from the creation of the Ecological Metadata Language (EML) standard. **Inigo’s** participation in this meeting marked the start of a formal collaboration between the GSC and the LTER, which is described more fully in this special issue (San Gil et al., 2008).

Session I: Setting the Stage and Finalizing MIGS

As with all GSC workshops, the first formal session helps to provide context for the rest of the workshop. At workshops I–III this was done with a series of talks on the explosive growth in the number and diversity of genomes and metagenomes. At this, and workshop IV (Field et al., 2008b), the opening session served to give updates on key GSC activities now that this community is beginning to mature. At this workshop updates were invited on related workshops on genome annotation, INSDC activities, and ontology development, and a new community to the GSC, the BarCode of Life initiative.

The session on genome annotation standardization was inspired by two workshops on standardizing genomic annotation cosponsored by the National Center for Biotechnology Information (NCBI) and the American Society for Microbiology (ASM). There is a large overlap in the membership of this group and the GSC and it is hoped that they can work together in a synergistic fashion. **Tatiana Tatusova (National Center for Biotechnology Information [NCBI])**, who organized and hosted both workshops at the NCBI, started the session by describing the motivations and outcomes of the two meetings. In particular, she discussed progress toward standardizing gene nomenclature and the consensus CDS project to harmonizing independent annotations, for example, using illustrations from comparisons of annotations of the *Escherichia coli* genome.

The GSC looks to the INSDC (DDBJ/EMBL/GenBank) for guidance and precedent and **Guy Cochrane (EMBL)** and **Ilene Mizrahi (NCBI)** provided a joint overview and update of relevant INSDC activities. In particular, they confirmed that identifiers from the Genome Project Database are now being shared across the INSDC. This mapping is critical to the ability of the GSC to launch its wider project to map the identifiers across a wide range of databases within the Genomic Rosetta Stone project.

Norman Morrison (NERC Environmental Bioinformatics Center, University of Manchester) and **Neil Sarkar [The Encyclopedia of Life (EoL)]** set the stage for the controlled vocabularies and ontologies session by describing the Environment Ontology project (EnvO) (<http://www.environmentontology.org>). This newly launched project includes, as a founding member, the GSC community, and is producing an Environment Ontology for describing the environmental context of biological samples and an open source Gazetteer of place names (Gaz). Combined, these artefacts will greatly improve the community's ability to annotate, and in the future, mine information about the exact origins of samples, including genomes, metagenomes, or 16S sequences.

The GSC has a strong track record of engaging and learning from a wide range of communities and projects that are also facing and solving the challenges of metadata collection integration and exploitation. The last talk of the session was by **Sujeewan Ratnasingham (University of Guelph)** who introduced the Barcode of Life Project (a group also engaged in EnvO), an international project to collect specific DNA sequences (barcodes) for all nonmicrobial species.

Session II: Extending GCDML from Curated Metadata to Derived Calculations: (Gene Calling and Genomic Annotation)

Nikos Kyrpides opened day 2 chairing a session designed to bring together representatives from all the major sequencing centers for a discussion on how to cope with the challenges that the annotations of the current genome collection derived from so many different computational pipelines. His introduction set the stage and the talks from each of the speakers on the current practice and perspectives within the major sequencing centers underscored the common ground shared as well as the heterogeneity of approaches among the centers. The centers were represented by **Nikos Kyrpides (JGI)**, **Nick Thomson (Sanger Institute)**, **Chinnappa Kodira (Broad Institute)**, **Ramana Madupu**

(JCVI), **Eric Pelletier (Genoscope)**, and **Owen White (University of Maryland)**.

Although the main goal of this session was to initiate discussions for standardized gene calling for microbial genome projects across the large sequencing centers, **Owen White** suggested that given the magnitude of the problem and its long historical persistence, rather than trying to directly overcome it, we could start beginning to "manage it" by enabling users of the data to understand clearly how the data were generated. Accordingly, he proposed the wide use of Standard Operating Procedures (SOPs). This suggestion was well received among the centers and the wider GSC in the subsequent discussions. This has led to a call for a centralized SOP repository elaborated in an article in this special issue led by **Sam Angulioi (University of Maryland)** and **Owen White** that includes all of the contributors to this session (Angulioi et al., 2008).

Session III: Toward Controlled Vocabularies and Ontologies for Describing Genomes and Metagenomes: A Focus on EnvO

Lynette Hirschman chaired a session exploring how the community achieves MIGS/MIMS compliance using controlled vocabularies and ontologies. In particular, the session focused on the capture of information about the environment from which a sample was obtained, due to the recent rapid growth of the EnvO project (<http://environmentontology.org>) and the significant overlapping membership in the GSC and EnvO. **Lynn Schriml (University of Maryland)** spoke first on the GEMINA database and its contribution to, and uptake of, the EnvO project (both EnvO and Gaz). **Nikos Kyrpides** outlined the shift from free text to controlled vocabularies and ontologies that he envisions for his Genomes Online Database (GOLD). **Lynette Hirschman** then gave an overview of her work on text mining of GenBank and GOLD entries. The focus was on our ability to extract habitat information from free text in database fields and publications, to aid future collection of MIGS/MIMS compliant information from legacy genomes. An extended discussion followed and **Lynette** leads a paper on the development of "Habitat-Lite," a light-weight list of general habitat terms in this special issue (Hirschman et al., 2008).

Session IV: Toward a Single, Global List of Genomes and Metagenomes: A Genomic Rosetta Stone

This session was chaired by **Peter Sterk (EBI)** included two short talks, and was followed by an extended and productive discussion session. The Genomic Rosetta Stone (GRS) project was established at the last workshop (Field et al., 2008b) and now involves more than 10 databases coming together in a federation to build a mapping of genomic and metagenomic identifiers using the INSDC GPIDs as the primary identifier. The development of a pilot Resolver system has been led by **Tanya Gray**, as it is necessary to have a single list of genomes and metagenomes to import information into the Genome Catalog (<http://gensc.org/>).

These two talks highlighted different aspects of the project: that of how to manage linking the identifiers (**Peter Dawyndt, University of Ghent**) and that of creating a client to consume the future mapping from the Resolver (**James Cole, Michigan State University**). First, **Peter** discussed the

completion of a mapping of the StrainInfo.net database, which integrates microbial culture collections, and the SILVA database of ribosomal sequences (<http://www.arb-silva.de/>) and the GOLD database of genomes and metagenomes (Liolios et al., 2008). **James** then described how the Ribosomal Database Project (RDP, <http://rdp.cme.msu.edu/>), a member of the GRS project from the start, has built a beta client tool that retrieves identifiers from the Resolver for display on the RDP Web site.

Peter Sterk then led a discussion of how to pull the entire project together and carry it forward. **Dawn Field** drew a diagram of the component parts and pointed out that, although we had a federation of databases, a pilot Resolver, and a first client tool, the group needed to develop a way to collect, hold, and organize the mapping in an up-to-date state. **Tatiana Tatusova** made a crucial suggestion that the NCBI LinkOut infrastructure could accommodate this requirement on behalf of the community. It would require all participating databases to register and keep their mapping up to date but the process for doing this was well documented by the LinkOut group. This idea was well received in the GSC as an option because the use of existing, stable, and well-maintained infrastructure is strongly preferred over the creation of new resources. Finally, **Peter Dawyndt** pointed out that GCDML should be the “glue” by which all the metadata from heterogeneous resources could be integrated; a single, integrated source of metadata describing genomes and metagenomes is the future vision of the GSC’s Genome Catalogue. The Genomic Rosetta Stone project roadmap is described in more detail in this special issue (Brabant et al., 2008).

Session V: GSC Roadmap

Day 3, as is traditional for GSC workshops, was run as a day for building strategy, wrapping up, and agreeing on a roadmap to the next workshop and beyond. **Dawn Field** started the day with a review of progress thus far at the workshop. Importantly, she also highlighted that there had been a correspondence from the Gordon and Betty Moore Foundation (GBMF). **Leonid Kagan (JCVI)**, representing the CAMERA project, read out the e-mail announcement that in brief stated that the CAMERA project’s Advisory Board strongly encouraged CAMERA to adopt GCDML at the soonest possible date based on its involvement in the project thus far. Furthermore, the GBMF stated that it strongly intends to act quickly to invoke compliance to MIGS/MIMS for the substantial number of genomic and metagenomic projects it funds as a condition of the Foundation’s award process. This very positive news was warmly welcomed and the GSC thanked the members of the CAMERA project and the GBMF, for their substantial contributions to GSC activities through active collaboration and as early adopters of MIGS/MIMS and GCDML (Kottmann et al., 2008).

The workshop then split into two groups of participants and **George Garrity** and **Frank Oliver Glöckner** led parallel sessions on strategic development and technical development of GCDML, respectively. The groups came together in the afternoon to report on their progress and deliberate the MIGS checklist one last time before publication. Several key items were added under “Investigation” in these final discussions, largely influenced by discussions at the work-

shop. Namely, these were explicit submission to the Trace Archive, INSDC, and links to relevant SOPs and other electronic identifiers.

This last group session was also useful in mapping out the special issue of *OMICS*. A list of potential contributions was drawn up and discussed and it was agreed that there was enough interest from authors that **Dawn Field**, **George Garrity**, and **Susanna Sansone (EBI)** could take forward the issue as guest editors. The content of the special issue is described as a whole below. Although it appeared too soon to be able to write a fully formulated “How to” document on achieving MIGS/MIMS compliance it seemed to be an excellent idea, and **Bob Vaughan** and **Guy Cochrane (EBI-EMBL)** offered to lead the development of such material for the future. Such a document would be aimed at providing biologists with an overview of the principles and practicalities of MIGS/MIMS compliance, including use of the GSC’s Genome Catalog.

The Special Issue of OMICS: The Starting Point for New Activities

Since the fifth workshop, the GSC has been actively engaged in developing this special issue focused on implementation of the syntax and semantics required to capture richer sets of information about genomes and metagenomes. Writing of these papers has proceeded through e-mails and teleconferences, and has included an extended community consultation phase in which draft papers were made available on the GSC Web site. The Editors have also worked wherever possible to help build linkages between the papers and groups of authors. This has resulted in a set of multi-author, consensus-driven contributions that are interlinked and form a key part of the short and long-term agenda of the GSC.

Three of these papers are workshop reports describing the fourth (Field et al., 2008b) and fifth GSC workshops and the first ISA-TAB workshop (Sansone et al., 2008). Three represent the official collaborative launches of core GSC-led projects under active development, GCDML (Kottmann et al., 2008), GRS (Brabant et al., 2008), Habitat-Lite (Hirschman et al., 2008). Two represent calls for a new GSC-led project (a central repository for Standard Operating Procedures) (Anguoli et al., 2008) and an eJournal, in particular to contain highly structured “Genome Notes” (Garrity et al; 2008). One final paper defines new linkages with another community, the NSF’s LTERs (San Gil et al., 2008).

All of these papers are meant to serve not as an end point, but as a starting point for the outlined projects. To facilitate this, a dedicated GSC Wiki page describing the special issue has been launch that contains a “work space” for each project. Each page holds Supplementary Information from the published papers and is designed to offer a portal for capturing feedback from the GSC and the wider community.

Conclusions

In summary, there were several key outcomes of this workshop, including the finalization of a publishable version of MIGS (Field et al., 2008a), a significantly increased number of contributors to the GSC wiki and a vastly improved online content, and further linkages within the wider community. It also marked the first promise of adoption by a

major funder, the GBMF, and further confirmed community buy-in to GSC principles and ongoing activities.

Following the workshop, the GSC has made plans to hold the next GSC meeting in combination with CAMERA's "Metagenomics 2008" conference to be held in San Diego in November 2008. The GSC has also engaged with the Microarray Gene Expression Data (MGED) Society on the standardization of high-throughput sequencing experiments and the development of the "Minimum Information about a Nucleotide high-throughput sequencing experiment (MIN-SEQE)." Most importantly, with the publication of this special issue of *OMICS*, the GSC has produced a more detailed Roadmap for the future (<http://gensc.org>).

It is always essential that all of the GSC current and future projects be viewed as a "whole." Therefore, the material in this special issue has been used to update the **GSC Executive Summary** (Field et al., 2008b) that has been maintained since the fourth workshop (GSC Entry in Wikipedia: http://en.wikipedia.org/wiki/Genomic_Standards_Consortium).

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Authors Disclosure Statement

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References

Angiuoli, S., Cochrane, G., Field, D., Garrity, G.M., Gussman, A., Kodira, C.D., et al. (2008). Towards an online repository

of standard operating procedures (SOPs) for (meta)genomic annotation. *OMICS* (this issue).

Brabant, B.V., Gray T., Verslyppe, B., Kyrpides, N., Dietrich, K., Glöckner, F.G., et al. (2008). Laying the foundation for a genomic Rosetta stone (GRS): creating information hubs through the use of consensus identifiers. *OMICS* (this issue).

Field, D., Garrity, G.M., Gray, T., Morrison, N., Selengut, J.D., Sterk, P., et al. (2008a). The "Minimum Information about a Genome Sequence" (MIGS) specification. *Nat Biotechnol.* 26, 541–547.

Field, D., Glockner, F.O., Garrity, G.M., Gray, T., Sterk, P., Cochrane, G., et al. (2008b). Meeting report: the 4th Genomic Standards Consortium (GSC) workshop. *OMICS* (this issue).

Garrity, G.M., Field, D., Kyrpides, N., Hirschman, L., Sansone, S.-A., Anguilo, S., et al. (2008). Toward a standards-compliant genomic and metagenomic publication record. *OMICS* (this issue).

Hirschman, L., Clark, C., Bretonnel, C., Mardis, S., Luciano, J., Cole, J., et al. (2008). Habitat-Lite: a GSC case study based on free text terms for environmental metadata. *OMICS* (this issue).

Kottmann, R., Gray, T., Murphy, S., Kagan, L., Kravitz, S., Lombardot, T., et al. (2008). A standard MIGS/MIMS compliant XML Schema: towards the development of the Genomic Contextual Data Markup Language (GCDML). *OMICS* (this issue).

Lioliou, K., Mavromatis, K., Tavernarakis, N., and Kyrpides, N. (2008). The Genomes On Line Database (GOLD) in 2007: status of genomic and metagenomic projects and their associated metadata. *Nucleic Acids Res* 36(Database issue) D475–D479.

Raes, J., Foerstner, K.U., and Bork, P. (2007). Get the most out of your metagenome: computational analysis of environmental sequence data. *Curr Opin Microbiol* 10, 490–498.

San Gil, I., Sheldon, W., Schmidt, T., Servilla, M., Aguilar, R., Greis, C., et al. (2008). Defining linkages between the GSC and NSF's LTER program: how does the Ecological Metadata Language relate to GCDML and other outcomes. *OMICS* (this issue).

Sansone, S.-A., Rocca-Serra, P., Brandizi, M., Brazma, A., Field, D., Fostel, J., et al. (2008). The first RSBI (ISA-TAB) workshop: "can a simple format work for complex studies?" *OMICS* (this issue).

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1. Nikos Kyrpides, Dawn Field, Peter Sterk, Renzo Kottmann, Frank Oliver Glöckner, Lynette Hirschman, George M. Garrity, Guy Cochrane, John Wooley. 2010. Meeting Report from the Genomic Standards Consortium (GSC) Workshop 8. *Standards in Genomic Sciences* 3:1, 93-96. [[CrossRef](#)]
2. Lynette Hirschman, Peter Sterk, Dawn Field, John Wooley, Guy Cochrane, Jack Gilbert, Eugene Kolker, Nikos Kyrpides, Folker Meyer, Ilene Mizrahi, Yasukazu Nakamura, Susanna-Assunta Sansone, Lynn Schriml, Tatiana Tatusova, Owen White, Pelin Yilmaz. 2010. Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Workshop at the Pacific Symposium on Biocomputing 2010. *Standards in Genomic Sciences* 2:3, 357-360. [[CrossRef](#)]
3. Christina Holmes, Fiona McDonald, Mavis Jones, Vural Ozdemir, Janice E. Graham. 2010. Standardization and Omics Science: Technical and Social Dimensions Are Inseparable and Demand Symmetrical Study. *OMICS: A Journal of Integrative Biology* 14:3, 327-332. [[Abstract](#)] [[Full Text HTML](#)] [[Full Text PDF](#)] [[Full Text PDF with Links](#)]
4. Dawn Field, Susanna Sansone, Edward F. DeLong, Peter Sterk, Iddo Friedberg, Renzo Kottmann, Lynette Hirschman, George Garrity, Guy Cochrane, John Wooley, Folker Meyer, Sarah Hunter, Owen White. 2010. Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010. *Standards in Genomic Sciences* 3:3, 232-234. [[CrossRef](#)]
5. Elizabeth Glass, Folker Meyer, Jack A Gilbert, Dawn Field, Sarah Hunter, Renzo Kottmann, Nikos Kyrpides, Susanna Sansone, Lynn Schriml, Peter Sterk, Owen White, John Wooley. 2010. Meeting Report from the Genomic Standards Consortium (GSC) Workshop 10. *Standards in Genomic Sciences* 3:3, 225-231. [[CrossRef](#)]
6. Dawn Field, Iddo Friedberg, Peter Sterk, Renzo Kottmann, Frank Oliver Glöckner, Lynette Hirschman, George M. Garrity, Guy Cochrane, John Wooley, Jack Gilbert. 2009. Meeting Report: Metagenomics, Metadata and Meta-analysis; (M3) Special Interest Group at ISMB 2009. *Standards in Genomic Sciences* 1:3, 278-282. [[CrossRef](#)]
7. John C. Wooley, Dawn Field, Frank-Oliver Glöckner. 2009. Extending Standards for Genomics and Metagenomics Data: A Research Coordination Network for the Genomic Standards Consortium (RCN4GSC). *Standards in Genomic Sciences* 1:1, 85-90. [[CrossRef](#)]
8. Dawn Field, Peter Sterk, Nikos Kyrpides, Renzo Kottmann, Frank Oliver Glöckner, Lynette Hirschman, George M. Garrity, John Wooley, Paul Gilna. 2009. Meeting Report from the Genomic Standards Consortium (GSC) Workshops 6 and 7. *Standards in Genomic Sciences* 1:1, 68-71. [[CrossRef](#)]