The MMRF CoMMpass Study℠ in Context

A Look at the Past, Present, and Future of Multiple Myeloma Research
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General Overview

Despite the enormous treatment advances made in the past few years, multiple myeloma (MM), a hematologic malignancy of plasma cells in the bone marrow, remains an incurable disease, and most patients will eventually relapse, with limited options and poor prognosis. The Multiple Myeloma Research Foundation (MMRF) has been working tirelessly to accelerate the pace of MM research. The MMRF is facilitating precision medicine through a comprehensive end-to-end model that begins with generating genomic and clinical data and leads eventually to testing targeted therapies in patients with MM.

This white paper will explain the components of the MMRF’s precision medicine model – The Data Bank, The Learning Network, and The Clinic – with a focus on the cornerstone CoMMpass StudySM, the first large-scale, longitudinal study in MM to attempt to identify genomic drivers of disease at diagnosis and other important time points. Designed to be accessible to a broad audience, this white paper describes key features of the CoMMpass Study and also provides context around its development, including a brief disease background, previous MMRF efforts that helped pave the way for this landmark study, and what the future may hold for patients with MM as well as clinicians.
Multiple Myeloma Research Foundation: Who We Are

The MMRF was established in 1998 as a 501(c)(3) non-profit organization by identical twin sisters Kathy Giusti and Karen Andrews soon after Kathy was diagnosed with multiple myeloma (see www.themmrf.org). The mission of the MMRF is to help accelerate the pace of developing treatments for MM, with the ultimate goal of finding a cure for the disease. The MMRF believes that open, rapid communication of scientific findings is essential for timely innovation. The “standard” practice of keeping data decentralized and private, while perhaps benefiting individual researchers or companies, ultimately serves to slow the pace of research to the detriment of patients with MM in urgent need of new treatment options. Especially in rare and complex cancers such as MM, collaboration and data sharing are essential in order to make meaningful progress.

Multiple Myeloma: Disease Background

Myeloma is a type of hematologic malignancy (blood cancer) in which abnormal plasma cells (white blood cells that produce antibodies) are overproduced in the bone marrow, crowding out normal plasma cells that help fight infection. Myeloma is often found in multiple places in the body and referred to as MM; in rare cases, myeloma is found in one place in the body and referred to as solitary myeloma. The malignant plasma cells produced in MM make monoclonal proteins (M proteins), abnormal antibodies that can collect in blood, urine, and organs, ultimately causing bone damage, kidney failure, and impaired immune system function. A high level of M protein in the blood is considered the hallmark characteristic of MM. Multiple myeloma can begin as a non-cancerous condition called monoclonal gammopathy of unknown significance (MGUS), which can then progress to asymptomatic (smoldering) or active myeloma (Figure 1).¹
MM is a highly heterogeneous disease, with a complex and incompletely understood molecular
pathogenesis. Not only does myeloma differ from one patient to another, with up to 10 different
subtypes identified, but moreover a given individual on average has four slightly different forms of the
disease (clones) that evolve with disease stage and the treatments to which that person is exposed.²

According to the National Cancer Institute’s Surveillance, Epidemiology, and End Results (SEER) Program,
there were an estimated 30,330 new cases of myeloma in the United States in 2016, representing 1.8%
of all new cancer cases.³ Myeloma is estimated to have been responsible for approximately 12,650
deaths in 2016, or 2.1% of all cancer deaths. The median age at myeloma diagnosis is 69 years, and the
disease is more common in men than women and among individuals of African descent.
The treatment of MM has undergone rapid and unprecedented change in the past few years. Chemotherapy, stem cell transplant, and radiation therapy remain standard treatment options; however, a plethora of new treatments has emerged over the past decade. In 2015 alone, four drugs were approved in the relapsed/refractory setting, including the histone deacetylase inhibitor panobinostat (Farydak®), the oral proteasome inhibitor ixazomib (Ninlaro®), and the monoclonal antibodies daratumumab (Darzalex™) and elotuzumab (Empliciti™). The combination of lenalidomide (Revlimid®) plus dexamethasone in the setting of newly diagnosed MM also was approved in 2015. These and other recent drug approvals mean that treatment choices for MM are more complex but also potentially more beneficial.

As for many diseases, there is no one-size-fits-all approach in the treatment of MM. Given the unique characteristics of individual patients, including factors such as genomic profile, age, performance status, and stage of disease, treatment should ideally be tailored to match each patient’s needs. Clinicians and patients face what might be seen as a daunting challenge in determining the correct treatment path, including how to appropriately sequence therapies, and when and how to combine therapies for a maximal clinical risk-to-benefit ratio. The approval of new therapies means that the MM treatment landscape is constantly undergoing refinement.

Despite the substantial progress made in recent years, most patients with MM will eventually relapse on their current therapy and have limited subsequent treatment options and poor prognosis. The relative rarity of MM and the heterogeneity of the disease complicate the ability to design adequately sized clinical trials. New strategies are needed that enable the conduct of adequately sized clinical trials, optimize the utilization of existing clinical data, facilitate the development of targeted therapy, and help inform clinicians and patients about the most appropriate treatment path.
Emerging Focus on Precision Medicine

Challenges such as those faced in MM have led to the emergence of the field of precision medicine. In 2015, President Obama launched the Precision Medicine Initiative, with the goal of accelerating a new era of medicine that delivers the right treatment at the right time to the right person, taking into account an individual’s health history, genes, environment(s), and lifestyles. MMRF Founder Kathy Giusti – in recognition of the MMRF’s longstanding leadership in precision medicine – was appointed to the White House Precision Medicine Working Group, which is made up of key leaders in research, science, technology, epidemiology, investment, policy, and patient advocacy.

The emergence of precision medicine coincides with a strong trend toward patients as active participants, rather than as passive subjects, in the clinical decision-making process. Increasing patients’ knowledge of their unique disease characteristics and disease journey will help to further strengthen the role of precision medicine in the future.

Multiple Myeloma Precision Medicine Model

In 2011, several years prior to the Obama-led initiative, the MMRF launched its own Precision Medicine Model with the CoMMpass Study as its cornerstone. The MMRF has developed an end-to-end system to accelerate precision medicine in cancer with the following three components: The Data Bank, The Learning Network, and The Clinic. These components represent the process by which genomic and other data are generated, made public, analyzed, and – in some cases – utilized in clinical trials.
The Data Bank

The Data Bank represents the data generation, aggregation, and integration component of the MMRF’s Precision Medicine Model. Examples of Data Bank initiatives, which are described below, include the Multiple Myeloma Genomics Initiative (MMGI) and the ongoing CoMMpass Study. Patients serve as an integral part of The Data Bank through the donation of their personal data, including bone marrow and blood sample results, quality of life data, and many other clinical parameters.

Multiple Myeloma Genomics Initiative (MMGI)

In 2005, the MMRF launched the MMGI, a progressive genome-mapping program. The MMGI was formed as a collaboration between the MMRF, an academic partner (Broad Institute of MIT and Harvard), and a non-profit partner (Translational Genomics Research Institute; TGen). Prior to the MMGI, there was limited understanding of the biology of MM and a need for new drug targets. In 2009, the MMGI became the first effort to sequence the MM tumor genome in its entirety, an important first step in the identification of genes and molecular pathways that play a role in the onset and progression of MM (Table 1). The MMGI has since profiled more than 200 myeloma patient samples in a variety of genomic analyses. A free, web-based data portal, called the Multiple Myeloma Genomics Portal (MMGP), was developed in conjunction with the MMGI to serve as a repository of metadata and analysis results. The MMGP represented the first well-developed, centralized repository of MM genomic information. To date, the portal has thousands of registered users, proving the feasibility and utility of such a web-based, open-access site.
Table 1. Genetic Mutations Identified via the MMGI*

<table>
<thead>
<tr>
<th>Mutation</th>
<th>% of patients</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>KRAS and NRAS</strong></td>
<td>40</td>
</tr>
<tr>
<td><strong>BRAF</strong></td>
<td>8</td>
</tr>
<tr>
<td><strong>CDKN2C and CCND1</strong></td>
<td>18</td>
</tr>
<tr>
<td><strong>PI3K/Akt</strong></td>
<td>5</td>
</tr>
<tr>
<td><strong>FGFR3</strong></td>
<td>5</td>
</tr>
<tr>
<td><strong>IGF-1R and ALK</strong></td>
<td>5</td>
</tr>
<tr>
<td><strong>IDH1/2</strong></td>
<td>5</td>
</tr>
<tr>
<td><strong>MyD88</strong></td>
<td>3</td>
</tr>
<tr>
<td><strong>Others</strong></td>
<td>11</td>
</tr>
</tbody>
</table>

*These mutations and their frequencies have been subsequently confirmed in the CoMMpass study.

ALK = anaplastic lymphoma kinase; BRAF = B-Raf proto-oncogene, serine/threonine kinase; CCND1 = cyclin D1; CDKN2C = cyclin-dependent kinase 4 inhibitor C; FGFR3 = fibroblast growth factor receptor 3; IDH1/2 = isocitrate dehydrogenase 1/2; IGF-1R = insulin-like growth factor-1 receptor; KRAS = V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog; MyD88 = myeloid differentiation primary response gene 88; NRAS = neuroblastoma RAS viral oncogene homolog; PI3K/Akt = phosphatidylinositol-4,5-bisphosphate 3-kinase/protein kinase B.

One of the success stories of the MMGI and the associated MMGP concerns the **BRAF** gene mutation, which has moved through The Data Bank and The Learning Network and soon will be studied in The Clinic component of the MMRF Precision Medicine Model. Reported in 2011, the identification of the **BRAF** mutation via genome-mapping represented a possible actionable target for **BRAF** mutation-positive MM patients. This finding was subsequently confirmed in the CoMMpass study. Further pre-clinical work identified other alterations in the same pathway that suggested that a combined therapeutic approach, one that includes additional drug targets aside from **BRAF**, might be optimal in some MM patients with **BRAF** mutations. A clinical trial is currently being designed to test the **BRAF** inhibitor, vemurafenib, in the **BRAF** mutation-positive MM indication.
The work by the MMGI has helped to increase the understanding of the genomic profile of MM and the heterogeneity of the disease. However, the genomic information generated by this initiative is limited by the fact that it provides only “snapshots” at single time points of the disease in various patients. During the course of the MMGI, clinicians and researchers came to understand that what was needed to further the understanding of the biology behind disease progression was a longitudinal study that followed patients through their entire journey with the disease. A prospectively designed longitudinal study such as this would enable a more detailed understanding of the changes that occur through the course of MM and the clonal heterogeneity of the disease.
The MMRF CoMMpass Study℠

Leveraging their experience and findings from the MMGI, the MMRF helped to launch the CoMMpass Study ([Relating] Clinical Outcomes in Multiple Myeloma to Personal Assessment of Genetic Profiles) in 2011. CoMMpass is the first large-scale, longitudinal study in MM focused on disease progression and response to treatment based on patients’ genomic or molecular profiles (Clinicaltrials.gov identification number: NCT01454297).

Study Design and Implementation

CoMMpass is a prospective, longitudinal, observational study in newly diagnosed symptomatic patients with MM. Now closed to enrollment, patients were included who were 18 years or older and who were candidates for an immunomodulatory drug (e.g., lenalidomide [Revlimid®], pomalidomide [Pomalyst®], or thalidomide [Thalomid®]) and/or a proteasome inhibitor (e.g., bortezomib [Velcade®] or carfilzomib [Kyprolis®]) as part of their initial treatment regimen. In addition to therapy with an immunomodulatory drug and/or proteasome inhibitor, patients received a corticosteroid such as dexamethasone (dex) and, in some cases, a chemotherapy agent such as cyclophosphamide. Initial therapy could be administered in doublet combinations such as Revlimid®-dex or Velcade®-dex; or triplet combinations such as Revlimid®-Velcade®-dex or Velcade®-cyclophosphamide-dex.

In 2015, CoMMpass reached its target enrollment of 1,000 MM patients, a remarkable achievement in a relatively rare disease and a testament to the commitment of patients to help advance the field of MM. CoMMpass involves an active assessment schedule, including bone marrow samples at baseline, at response to treatment, and at relapse. Each patient is followed for up to eight years. Preplanned interim analyses occur every six months.

Executing properly on such an ambitious initiative needs multiple players. CoMMpass is a multi-site, multi-national study involving non-profit, industry, and academic partners. Approximately 90
community and academic cancer centers from across North America and Europe are participating in the study. Providing financial and scientific support, industry partners include Takeda Pharmaceuticals Co. Ltd (formerly Millennium Pharmaceuticals, Inc.); Amgen, Inc. (formerly Onyx Pharmaceuticals, Inc.); Janssen Pharmaceuticals, Inc.; and Bristol-Myers Squibb Co. Other collaborators include TGen, GNS Healthcare, Spectrum Health Hospitals, the Department of Veterans Affairs, the US Oncology Network, and the Van Andel Research Institute. After an initial period of prioritized access, participating institutions have agreed to give up intellectual property and patent rights on the data to the public domain. Creating an intellectual property-free zone has allowed these various constituents to collaborate maximally on data analysis and sharing initiatives, unhindered by the usual concerns around protecting one’s work – essentially breaking down the data silos that impede research today and accelerating the pace of research in order to bring new treatments to patients as quickly as possible.

What We Have Learned So Far From CoMMpass

Due to regular interim analyses, important findings have begun to emerge from CoMMpass. Baseline characteristics of the CoMMpass population (Figure 2)\(^5\) show broad representation and are consistent with characteristics of MM patients in the general population. Based on the seventh interim analysis (IA7), the average age was 64 years and the majority of participants were males of non-Hispanic/non-Latino descent. Approximately 18% of CoMMpass patients self-reported as African American, an important feature, given the higher incidence of persons of African descent in the MM population compared to the general population.\(^3\) Genomic alterations that were first observed by MMGI have been confirmed by CoMMpass (Table 1).
At the annual meeting of the American Society of Hematology (ASH) in 2015, seven CoMMpass-related abstracts were presented, based on the IA7 data on a range of topics such as initiating trunk mutations and distinct molecular subtypes, symptom burden in older patients with MM, and associations between performance status and health-related quality of life (Table 2). In an abstract by Manojlovic et al., African Americans were reported to be no more statistically likely to have a high-risk mutation burden than persons of European descent.
Table 2. CoMMpass-Related Abstracts Presented at ASH Meeting 2015

<table>
<thead>
<tr>
<th>Authors</th>
<th>Institution</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fiala, et al.⁷</td>
<td>Washington University School of Medicine</td>
<td>The Association Between Performance Status and Health-Related Quality of Life</td>
</tr>
<tr>
<td>Fiala, et al.⁸</td>
<td>Washington University School of Medicine</td>
<td>The Association of International Staging System (ISS) Stage with Disease and Symptom Burden in Patients with Newly Diagnosed Multiple Myeloma</td>
</tr>
<tr>
<td>Gruber, et al.⁹</td>
<td>GNS Healthcare (A)</td>
<td>Investigation of Mechanisms of Response in Multiple Myeloma Via Bayesian Causal Inference: An Early Analysis of the CoMMpass Study Data</td>
</tr>
<tr>
<td>Keats, et al.¹⁰</td>
<td>Translational Genomics Research Institute (TGEN) (A)</td>
<td>Identification of Initiating Trunk Mutations and Distinct Molecular Subtypes: An Interim Analysis of the MMRF CoMMpass Study</td>
</tr>
<tr>
<td>Keller, et al.¹¹</td>
<td>Washington University School of Medicine</td>
<td>Presenting Characteristics and Symptom Burden of Newly Diagnosed Older Multiple Myeloma Patients in the CoMMpass Study</td>
</tr>
<tr>
<td>Lagana, et al.¹²</td>
<td>Icahn School of Medicine at Mount Sinai</td>
<td>Towards a Network-Based Molecular Taxonomy of Newly Diagnosed Multiple Myeloma</td>
</tr>
<tr>
<td>Manojlovic, et al.⁶</td>
<td>TGEN (A)</td>
<td>In-Depth Molecular Profiling of Multiple Myeloma in African Americans</td>
</tr>
</tbody>
</table>

(A) = MMRF collaborator; ASH = American Society of Hematology.

Other preliminary findings from IA7 demonstrate improved progression-free survival with triplet therapy versus doublet therapy (Figure 3).⁹,¹⁰,¹³ Research also indicates improved progression-free survival with triplet therapy followed by stem cell transplant compared to triplet therapy alone (Figure 4).⁹,¹³ Given the preliminary nature of these findings, further work must be done to confirm the results and share them with the research community. Eventually, these data will help contribute to a clearer treatment pathway for each MM patient based on the characteristics of his or her disease.
Figure 3. Progression-Free Survival (First PD) by First-Line Therapy Classification (in >3% of Patients)

Bortezomib-based triplet therapy is predominantly bortezomib-lenalidomide-dexamethasone. Bortezomib-based doublet therapy included bortezomib plus dexamethasone. IMID/carfilzomib-based triplet therapy included the immunomodulatory drug (IMID) lenalidomide plus carfilzomib plus dexamethasone. IMID-based doublet therapy included lenalidomide plus dexamethasone. PD = progressive disease.
Figure 4. Progression-Free Survival With or Without Transplant

See footnotes in previous figure for bortezomib- or carfilzomib-based triplet combinations.

What We Expect to Learn From CoMMpass

As the CoMMpass data continue to mature, it is the MMRF’s intent that the findings will help to answer some of the questions most important to patients, including: Is my genomic profile predictive? How is my disease doing? Should I be on three drugs? Should I have a transplant? If and when I relapse, what should I be thinking about? Similarly for clinicians, CoMMpass will hopefully begin to answer questions such as: How and when should I combine therapies? How should I sequence therapy? Which clinical and genomic variables predict treatment response? What is the role of maintenance therapy when the patient is experiencing a complete response to therapy?

CoMMpass may also eventually help us to understand the role of minimal residual disease (MRD), or low-level disease occurring during a period of remission. Efforts are currently under way to improve the ability to detect and quantify MRD in order to more accurately assess response to treatment, thereby
enabling more appropriate and timely treatment decisions. Researchers are comparing the effectiveness of measuring MRD using flow cytometry versus next-generation sequencing, as well as evaluating the potential for measuring circulating myeloma tumor cells in the blood versus needing a bone marrow biopsy.

The Learning Network

The Learning Network encompasses initiatives designed to share data and facilitate collaboration and discovery, such as the Gateway web portals and the Myeloma Disease Model described below. Translational research initiatives, also a part of The Learning Network, help bring potential therapies from “bench to bedside” by testing theoretical discoveries generated in The Data Bank stage in a laboratory setting prior to testing in humans.

Researcher and CoMMunity Gateway Web Portals

The Researcher Gateway was launched in 2013 as an open-access research portal serving as a data repository for CoMMpass and other genomic and/or clinical studies. Building on the MMRF’s experience with the MMGP, the Researcher Gateway is designed to have a user-friendly interface that enables clinicians and researchers to view data sets and enter queries. The web portal houses genomic, clinical, and outcomes data in one easily accessible location. Patient data are de-identified to protect patient privacy and allow researchers to extract only the specific information in which they are interested.
The CoMMunity Gateway enables CoMMpass Study participants and other MM patients to connect with each other, based on their subtype and specific disease characteristics (see https://community.themmrf.org/). The web portal also allows MM patients to be matched with ongoing clinical trials according to their unique profile and treatment needs.

Myeloma Disease Model

One notable collaboration for the MMRF is with GNS Healthcare, a leading precision medicine company that applies causal machine learning technology to match health interventions to individual patients.

Using data generated by CoMMpass, the MMRF/GNS Healthcare partnership, also termed the Myeloma Disease Model, is identifying potential drivers of clinical outcomes and their associated molecular pathways. Interim results have recently been presented.9

Translational Network

The MMRF recently established and supports a transformative MMRF Translational Network of Excellence, which is focused on the most promising research on novel preclinical models for new targets and drug validation, immune biology, immune therapeutics, and MRD in myeloma and myeloma-related diseases. This groundbreaking initiative has been made possible due to decade-long efforts by the MMRF to generate assets and create a highly integrated clinical consortium necessary for such a task.

In a highly collaborative manner, the 4 to 6 leading academic centers involved in the Translational Network of Excellence will use and share their cutting edge technologies, platforms, and tools to accomplish the ambitious goal of rapidly advancing scientific findings to the clinic. Due to the MMRF’s commitment to transparency, data generated through this effort will be made freely available through the MMRF scientific portals, and cell lines/models and other tools could be obtained through additional resources within the network. The hope is that the MMRF Translational Network of Excellence will be the catalyst needed to spark essential and remarkable progress for myeloma patients and could serve as a model for other cancers.
The Clinic

The Clinic represents the clinical trial component of the model in which investigational therapies, generated from discoveries made in The Data Bank and The Learning Network, are tested in patients with MM for their safety, efficacy, and feasibility as real-world treatment options.

Multiple Myeloma Research Consortium

The design and implementation of these clinical trials would be performed in part by the Multiple Myeloma Research Consortium (MMRC), which was created by the MMRF in 2004 to accelerate the launch and completion of Phase 1 and 2 studies of novel agents and combinations. The MMRC – comprised of 22 centers in the US and Canada – employs a unique collaborative model, bringing together academic research centers and industry partners in order that new treatments can be brought to patients as quickly as possible. Over 70 MMRC-facilitated trials have been launched to date to test molecularly targeted therapies, immune therapies, and other novel therapies (Figure 5). Precision medicine is not just about molecularly targeted treatments; immune and novel agents will likely be needed in combination for many/all patients, and it is important to have a robust portfolio so that there are trials for every patient/subtype. Given this broad and extensive experience, the MMRC is ideally positioned to serve in the Precision Medicine Model as the umbrella organization to rapidly test ideas and hypotheses in targeted populations as they emerge from The Data Bank and The Learning Network.
Figure 5. MMRC Trial Pipeline

**Molecularly Targeted Therapies**
- BRAF
- IGF-1R/ALK
- CDK
- IDH1/2
- FGFR3

**Antibodies & Immunotherapies**
- Elotuzumab
- Anti-CD38 Abs
- Adoptive, CAR T cell
- PD-1, PDL-1 Abs
- Vaccines

**Novel Agents/Classes/Mechanisms**
- HDAC
- BTK
- CRM1
- KSP
- HSP90

ALK = anaplastic lymphoma kinase; BTK = Bruton’s tyrosine kinase; CAR = chimeric antigen receptor; CDK = cyclin-dependent kinase; CRM1 = chromosomal maintenance 1; FGFR3 = fibroblast growth factor receptor 3; HDAC = histone deacetylase inhibitors; HSP90 = heat shock protein 90; IDH1/2 = isocitrate dehydrogenase 1/2; IGF-1 = insulin-like growth factor-1; KSP = kinesin spindle protein; PD-1 = programmed death receptor 1; PDL-1 = programmed death ligand 1.
**Next Steps for the CoMMpass Study and for MM Research**

The ongoing CoMMpass Study, representing the cornerstone of the MMRF’s Precision Medicine Model, has already provided valuable insights into topics such as the diverse baseline characteristics of newly diagnosed MM patients, the effectiveness of triplet versus doublet therapy, and the importance of stem cell transplantation. As the data continue to mature, patients and clinicians will be better able to answer key questions in the clinical decision-making process, such as how and when to combine therapy and to sequence therapy. In addition, the genomic and clinical data generated from CoMMpass will enhance the understanding of underlying disease mechanisms and how they change over time, help to identify new drug targets, and allow exploration of the interplay of targeted therapy and immune therapy, among other factors. CoMMpass provides a road map for the future of MM treatment. The ultimate goal is for all patients with MM to have genomic and immune profiling in order for them to get the best possible treatment for their particular disease.

The MMRF’s Precision Medicine Model enables a comprehensive end-to-end approach that starts with data generation and integration in The Data Bank, collaboration and discovery in The Learning Network, and accelerated clinical trials in The Clinic. The Precision Medicine Model, with an emphasis on open-access data sharing and analysis and multi-stakeholder involvement, provides an invaluable template that could be applied to other disease states, particularly rare or heterogeneous diseases where data and patients are scarce.

Through the collaborative and integrated approach of the Precision Medicine Model, the MMRF represents a new and exciting era in medicine, one that focuses on improving the lives of patients as quickly and efficiently as possible.
Glossary/Acronym List

Antibody = a large, Y-shaped protein used by the immune system to identify and neutralize pathogens

CoMMpass Study = Clinical Outcomes in Multiple Myeloma to Personal Assessment of Genetic Profiles study; a large-scale, longitudinal study initiated in 2011 to understand molecular drivers of MM at diagnosis and at other key time points

CoMMunity Gateway = web portal for CoMMpass patients and other patients with MM to share their journey and be matched with clinical trials

IA7 = the seventh interim analysis of the CoMMpass Study

M proteins = abnormal antibodies that can collect in blood, urine, and organs, ultimately causing bone damage, kidney failure, and impaired immune system function

MM = multiple myeloma; a type of blood cancer, or hematologic malignancy, in which abnormal plasma cells are overproduced in the bone marrow

MMGI = Multiple Myeloma Genomics Institute

MMGP = Multiple Myeloma Genomics Portal

MMRC = Multiple Myeloma Research Consortium

MMRF = Multiple Myeloma Research Foundation

MRD = Minimal residual disease

Plasma cell = a type of white blood cell that produce antibodies

Researcher Gateway = an open-access research portal serving as a data repository for CoMMpass and other MM-related studies

SEER = Surveillance, Epidemiology, and End Results (a US National Cancer Institute program)

White blood cells = cells of the immune system involved in fighting infection
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13. Giusti K. The MMRF Precision Medicine Model. Available at: